



# How Whole Genome Sequencing is Changing the Food Safety Landscape: The CDC Perspective

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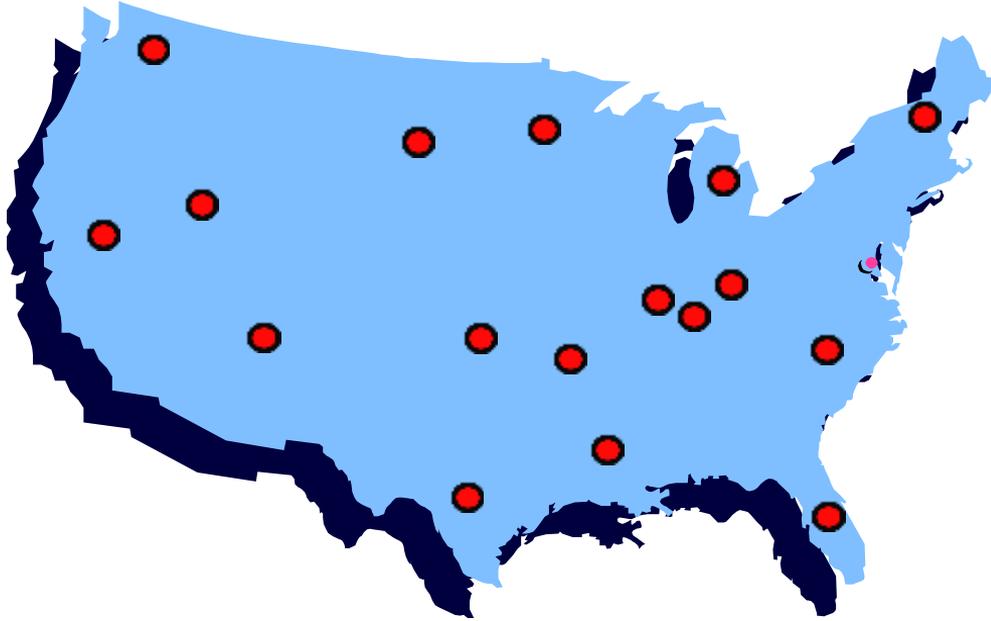
Outbreak Response and Prevention Branch

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2019 Food Safety Summit

Rosemont, IL

# Foodborne Diseases in the United States: A Changing Landscape



Disseminated Foodborne Outbreak Linked to a Commercially  
Distributed Product

# Detecting Disseminated Outbreaks with PulseNet

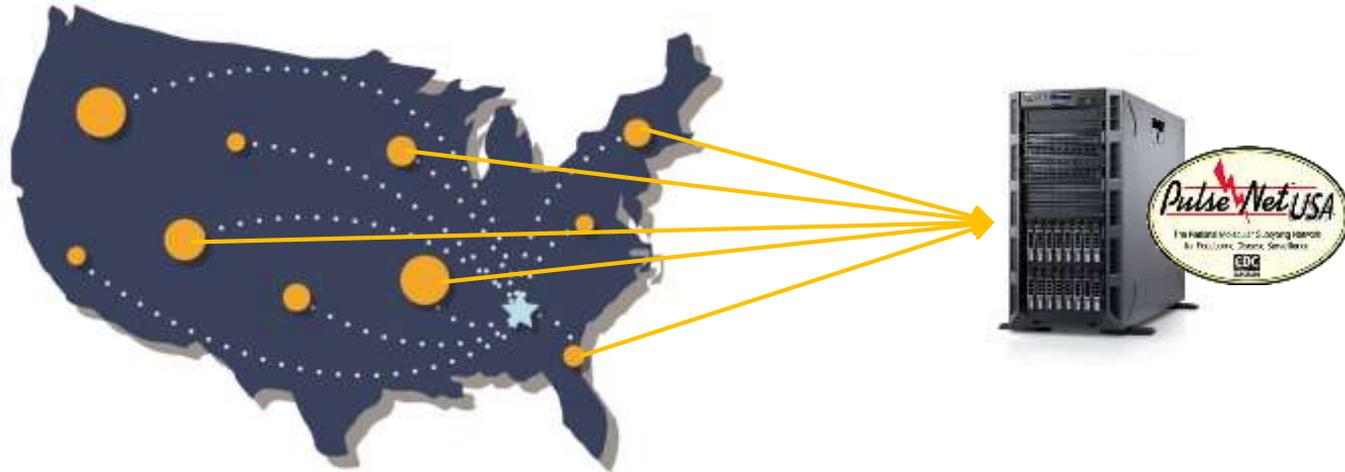
- Subtyping enteric bacteria is essential to identifying highly disseminated outbreaks
- PulseNet laboratory network established in 1996
  - Over 80 participating laboratories in the US
  - 60,000+ isolates subtyped annually
- Hospital and clinic labs send bacteria collected from ill people to state public health laboratories for “DNA fingerprinting”

**Bacteria with the same “DNA fingerprint” are *more likely* to come from a common source than bacteria with different fingerprints**

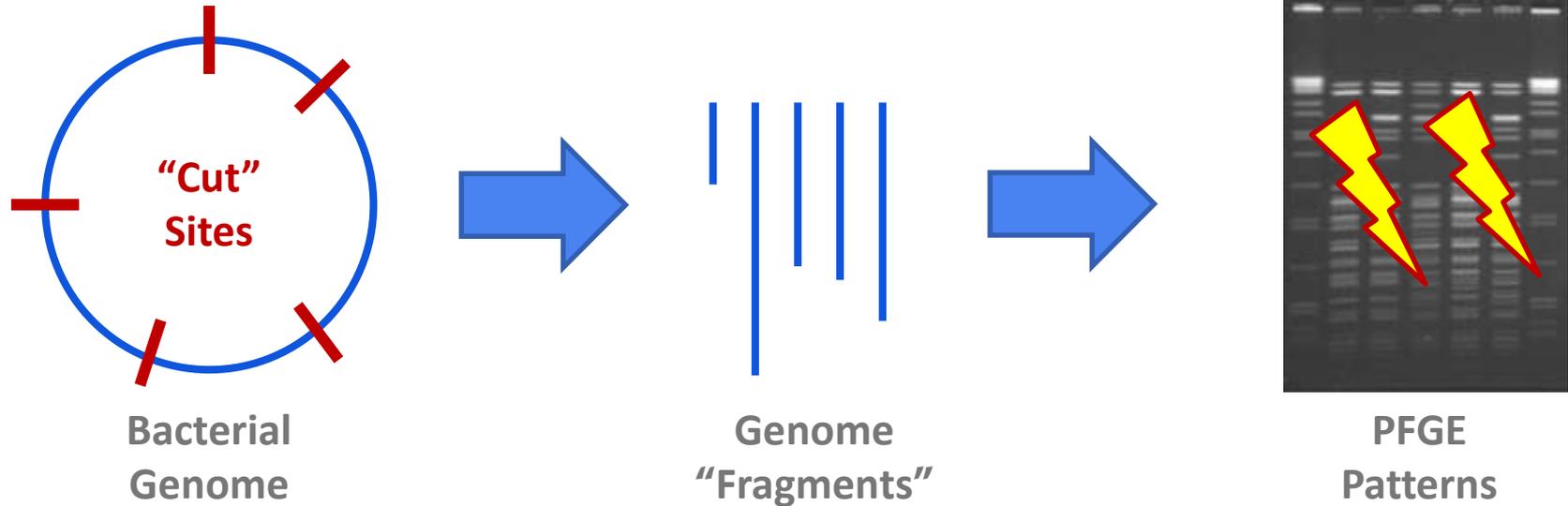
**The more specific the fingerprint, *the higher* the likelihood the bacteria come from a common source**

# Detecting Outbreaks with PulseNet

- DNA Fingerprints transmitted to PulseNet and monitored for temporal clusters
- PulseNet notifies epidemiologists and we decide which clusters to investigate



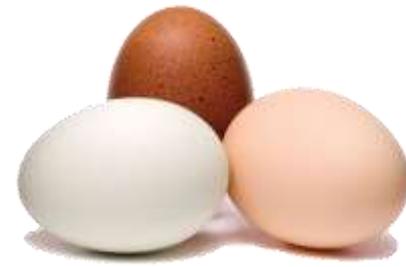
# Conceptual Framework for PFGE Subtyping



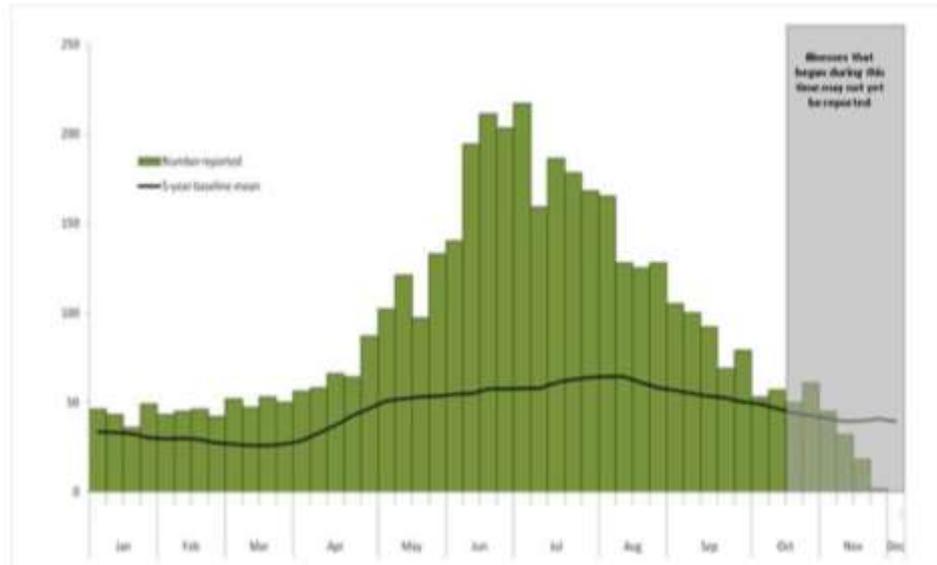
*Banding patterns provide an efficient, but indirect, look into whether two bacteria are genetically related*

*Other lab workflows needed for serotype, resistance, and virulence*

# 2010 Outbreak of *Salmonella* Enteritidis Infections Linked to Shell Eggs

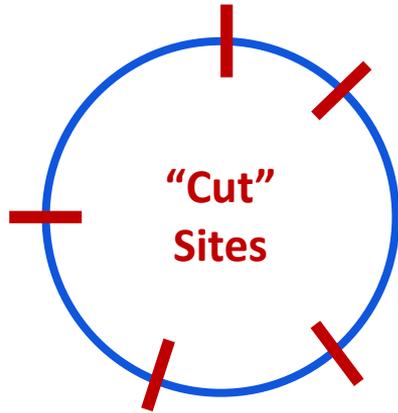


Number of *Salmonella* Enteritidis cases matching PFGE pattern JEGX01.0004 reported to PulseNet, United States, 2010\*

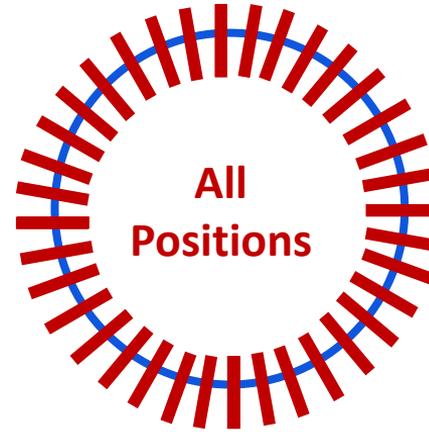


- Most common PFGE pattern in the PulseNet database
- 3,578 illnesses reported during the outbreak period
- 1,639 presumed to be unrelated “background” cases
- Complicated investigation into the source

# WGS Provides a Higher Resolution View of the Bacterial Genome



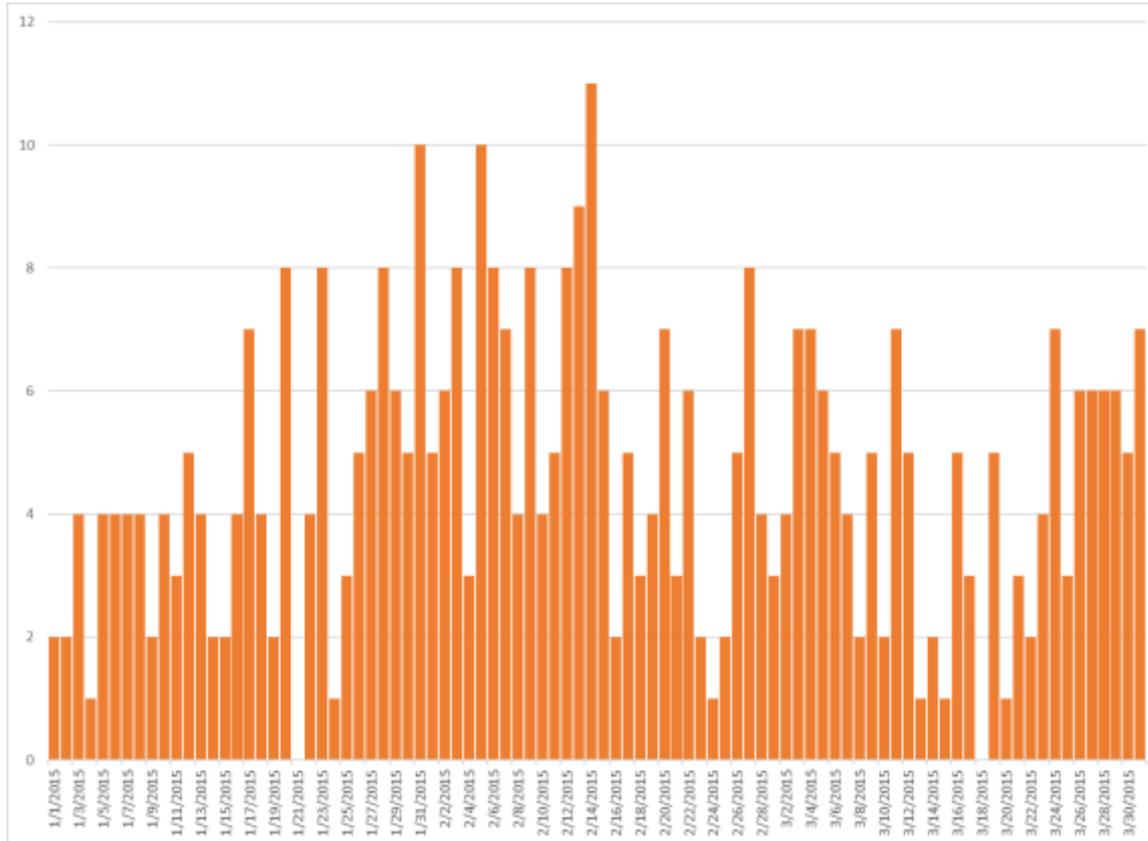
PFGE gives us indirect information about the bacterial genome



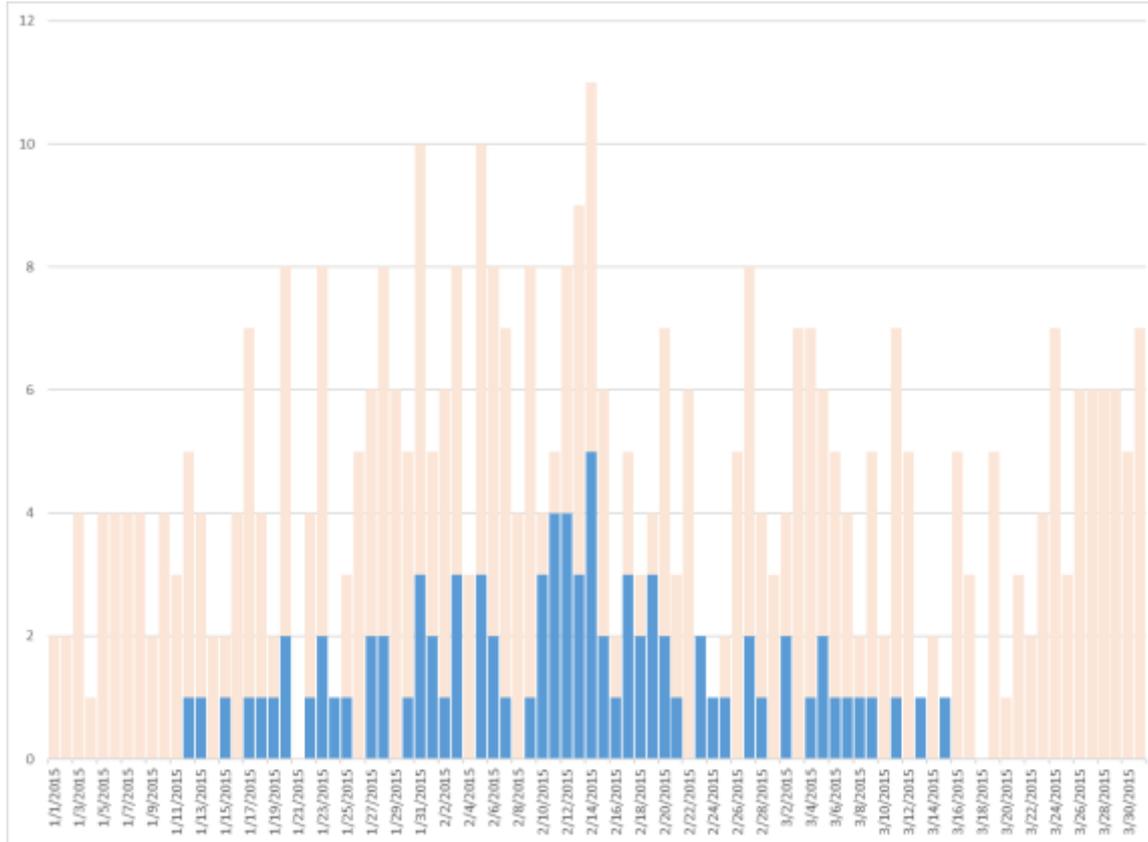
WGS has the ability to give us information at nearly every position in the genome

*Serotype, virulence, and resistance information can be directly identified from the sequence data*

# Hypothetical Contaminated Product Outbreak with “Background” Illnesses: PFGE View

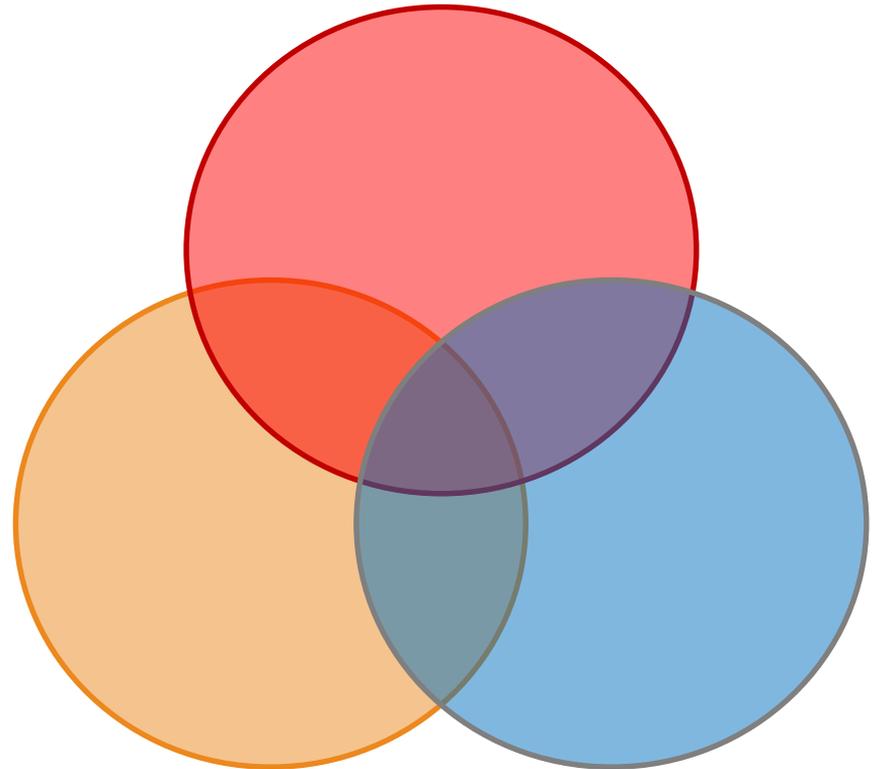


# Hypothetical Contaminated Product Outbreak with “Background” Illnesses: WGS View



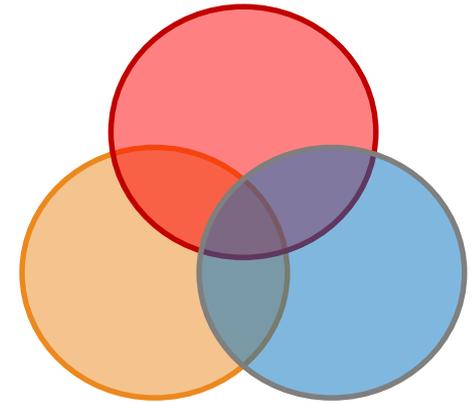
# Testing Hypotheses: How Do We Determine a Food is the Cause of an Outbreak ?

- Three types of evidence used:
  - **Epidemiologic**: association between illness and exposure
  - **Traceback**: suspected food item converges on a common source of contamination
  - **Microbiologic**: pathogen found in the food, farm or facility



# WGS Strengthens the Lines of Evidence Used to Link Outbreaks to a Food Source

- **Epidemiologic evidence**
  - Excludes unrelated illnesses from the analysis
  - Groups together seemingly unrelated illnesses, increasing power
- **Tracing suspect foods to a common source of contamination**
  - Helps ensure that traceback is performed on those exposures most likely to be linked to the exposure of interest
- **Testing foods and the growing/production environment for pathogens**
  - Increases the confidence that bacteria from people and foods are connected in some way



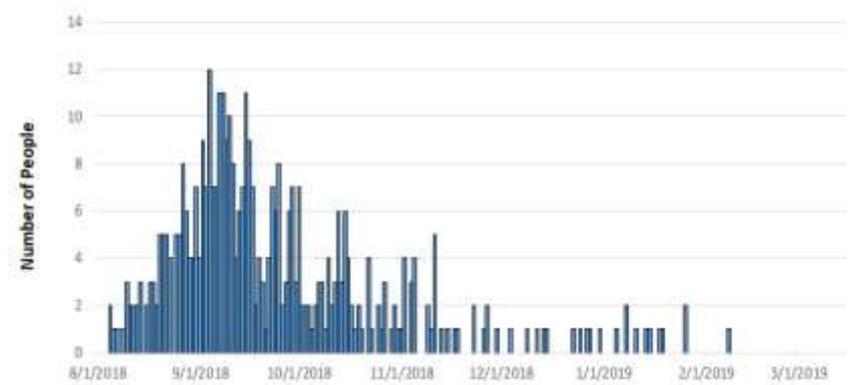
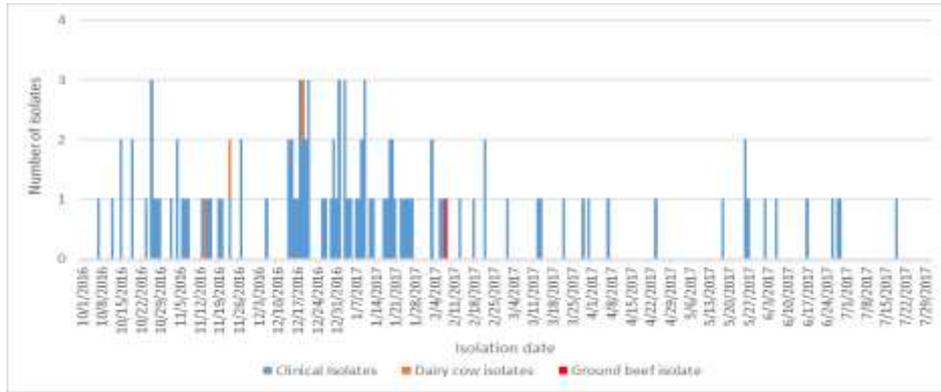
# WGS Impact Extends Beyond Just Improving Outbreak Investigations

- Spread of antimicrobial resistance genes/plasmids across multiple strains of bacteria
- Persistent sources of food contamination that result in consistent numbers of illnesses without a rapid rise in cases
- Repeated outbreaks that link back to pathogen reservoirs in animals or the environment
- Better understanding the burden of illness attributable to certain food categories by combining genomic data with other data sources





# “Strains of Concern” Investigations Becoming More Common and Are Important



- **2016-2017 *Salmonella* Newport outbreak linked to ground beef**
  - Illnesses over a 10-month period
  - Outbreak strain found in 4 dairy cattle from a single state and ground beef collected from an ill person’s home
  - Traceback of ground beef did not converge on a single slaughter facility
- **Strain returned in 2018, causing a large outbreak of over 400 illnesses and resulting in recall of over 10 million pounds of ground beef**

# Outbreak of Listeriosis Linked to Deli-Sliced Meats and Cheeses

- 8 hospitalizations from 2016-2019, including one death
- CDC investigated in 2017 but did not find a common source

The CDC's announcement Wednesday also comes as **Consumer Reports is analyzing the results of our own testing of counter-sliced deli meat.** One of our samples of turkey, purchased from a deli in New York City, contained a strain of listeria similar to the one involved in this current outbreak

Then **Consumer Reports sent its findings to the CDC late in 2018,** as well as to the New York City's Department of Health and Mental Hygiene, because the bacteria poses serious risks—especially to pregnant women, older people, and other vulnerable groups.

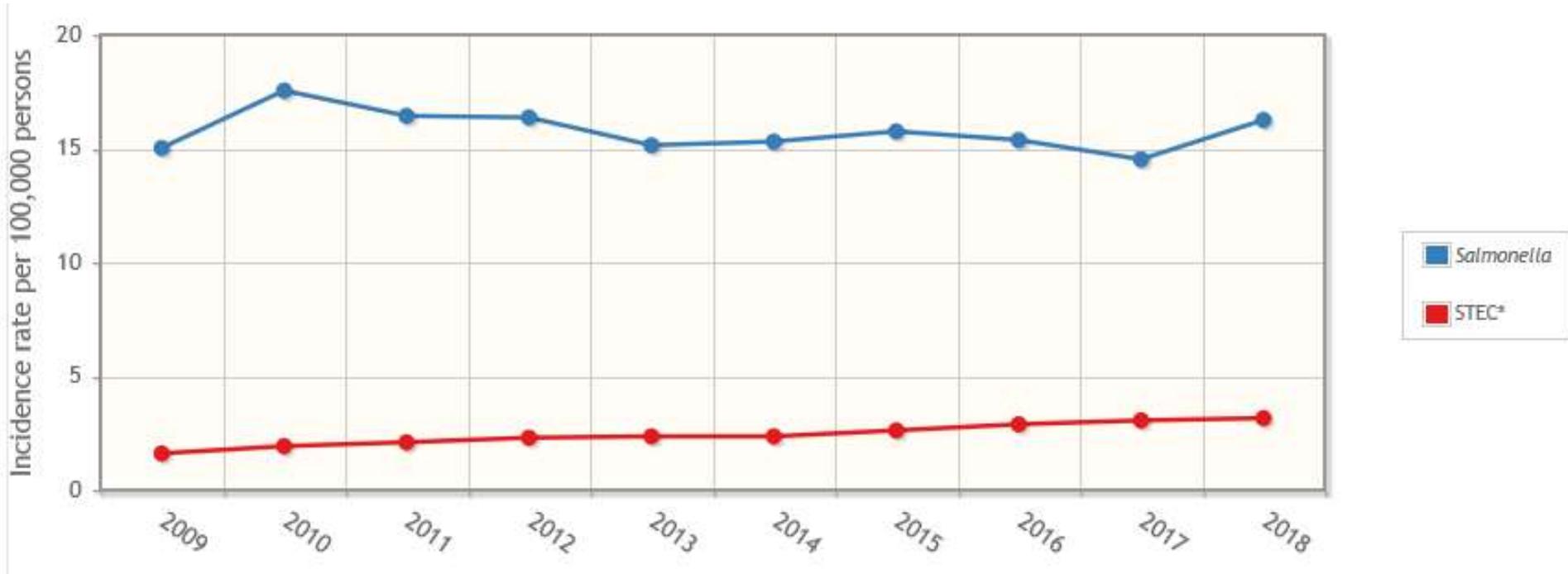
The **CDC found that the listeria in CR's deli meat sample was closely related genetically to the listeria that previously made people sick,** according to Brittany Behm, spokesperson for the agency. Two additional illnesses were reported since the sample was collected, she added.



# Full Implementation of WGS in PulseNet

- **PulseNet is rapidly transitioning from PFGE to WGS**
  - Already switched for *Listeria* and *Campylobacter*
  - Transition is happening during May 2019 for *Salmonella* and STEC
- **This will require fundamental shifts in:**
  - How outbreaks are defined and detected
  - The current processes for interagency, interdisciplinary, and private-public-academic collaboration
- **Despite the advantages of WGS, it does not solve all problems**
  - Multi-vehicle outbreaks with complex contamination routes

# No Improvements in Incidence of *Salmonella* and STEC Infections Since 2009



# Recognized Outbreaks Are Currently a Small Fraction of All Foodborne Illnesses

- Only about 12% of all *Salmonella*, STEC, and *Listeria* illnesses reported to PulseNet are associated with a potential outbreak
- The vast majority of illnesses do not have a known or suspected cause (the “baseline”)
- WGS will allow us to move beyond just acute outbreaks to find where the major sources of illness are

