WGS Transition Overview

Matthew Wise, MPH, PhD
Outbreak Response and Prevention Branch
Division of Foodborne, Waterborne, and Environmental Diseases

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Where are we today?

- Lots of isolates already being sequenced
- WGS routinely being used in multistate outbreaks and many single state outbreaks
- Some WGS data available in SEDRIC
  - Trees for multistate investigations
  - *Listeria* allele codes
- States migrating to new Bionumerics
Many Logistical Challenges Ahead

- Changes to existing workflows will be needed
  - Lab/epi communication
  - Prioritization of interviews / follow up
  - Detecting clusters/outbreaks

- Some data we have relied upon may be available later (e.g., serotype)

- Uncertainty about resources (more outbreaks, cost of WGS)

- Concern about turnaround time to get WGS results

- Coordination of CDC and state follow up on NCBI “matches”
Many Scientific Challenges Too

- What are the right relatedness thresholds for outbreak detection?
- Outbreak case definitions are more fluid
- Does our traditional outbreak definition still apply?
- How do we investigate and better understand “strains of concern”?
- All PulseNet subtyping data will be publicly available
  - Industry and academia will be looking at our data too and raising new questions
What Are We Doing to Prepare?

- OutbreakNet weekly Friday calls
  - Prioritization of WGS and interviewing (Beth/Mackenzie)
  - Local cluster detection and triage of clusters (Lisha/Madhu)

- DFWED cluster detection work group
  - New methods to detect clusters using WGS
  - Anomaly detection methods combining epi and geographic information with WGS
  - Source prediction models

- OAMD and CSTE training courses
Looking Forward

- “Known knowns” (things we know that we know)
  - Workflow and processes will have to adapt
  - WGS will give us more specificity to make connections between isolates

- “Known unknowns” (things that we know we don't know)
  - How will the number of outbreaks change?
  - How will costs and resource constraints affect investigations?

- “Unknown unknowns” (things we don't know we don't know)
  
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