Interpreting, Reporting and Communication of WGS Data

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Enterics Unit Supervisor
March 7, 2019
General Foodborne Surveillance Philosophy

Lab
Identify clusters

Epi
Investigate clusters
Genomic Characterization

- Taxonomic ID and serotyping/serogrouping
  - Kraken, SeqSero, Serotype Finder, srst2
- Virulence factor and Plasmid detection
  - ARIBA
- Antibiotic resistance gene detection
  - ARIBA

Subtyping and phylogenetic comparisons

- hqSNP analysis
  - CDC LyveSet (locally or from CDC)
  - NYSDOH-Wadsworth *Salmonella* Enteritidis and Typhimurium pipeline
- wgMLST analysis
  - PulseNet Listeria Pilot lab
  - MentaLiST
- MLST analysis
  - stringMLST
How the results will be formatted and communicated

What kinds of data can/will analysis provide

What/why samples will be sequenced

How long will analysis take

How the results will be interpreted

Communication Methods

Project initiation

• In-person meetings to discuss:

   - How is the data communicated?
What is a cluster for WGS?

- PFGE-any 2 isolate match within 60 days
- WGS cluster-needs to be determined
• SE-5 OBs, ≤3 SNPs within OB

• STM-12 outbreaks analyzed, ≤ 2 SNPs within OB, 1 exception (complicated outbreak)

• Campylobacter

• Exception is emerging Salmonella I 4,5, [12]:i:- associated with porcine exposure clone shows less diversity

• General rule (using LyveSet and NY pipeline) is 0-5 SNPs within 60 days
  • Once a cluster/outbreak is identified, can consider expending SNP differences and time
<table>
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<tr>
<th>Defined Outbreak Samples</th>
<th>0-2 SNPs</th>
<th>0-2 SNPs</th>
<th>0-1 SNPs</th>
<th>0 SNPs</th>
<th>1SNP</th>
<th>0-3 SNPs</th>
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<td>Outbreak 7- Spring 2014</td>
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</table>

Retrospective Typhimurium Outbreaks

- Analyzed 12 outbreaks
- 11 OBs differed by ≤1 SNP
- Outbreak 12, n=3, 2 isolates 0 SNPs apart, 1 16 SNPs different
  - Melon outbreak
  - Likely increased diversity due to environment/longer outbreak
# Campy-White Lily restaurant – Salad, 2002

<table>
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<th>Date</th>
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Non-WGS Outbreak #1: Chicken at a Restaurant

July 17, 2018

- Two *Campylobacter jejuni* cases interviewed through routine surveillance

- Both reported eating a chicken liver pâté dish from a restaurant in Minneapolis with meal dates of June 23 and June 30

- 3\textsuperscript{rd} case interviewed on July 20 and reported eating a liver pâté dish at the restaurant on July 3

- Minneapolis Health Department (MHD) notified and investigation initiated
Introducing the Food & Wine Dish of Year 2018: The Paris-Brest at Grand Cafe in Minneapolis
EH Investigation

• No temperatures taken during food prep
• Cooked liver measured at 145° F
• Restaurant advised not to sell the dish until approved to do so by MHD
EH Investigation

• Chefs instructed to take final cooking temperatures and ensure minimum cook temperature of 165° F

• Restaurant required to send action plan to MHD showing correction in recipe

• Foodborne illness consumer warning printed on restaurant’s online menu
WGS Analysis

• Isolates from the two cases sequenced and were not closely related to each other (11,706 SNPs apart)
Cluster 2017001: 2 new isolates are 1-5 SNPs from others in the cluster. Now 8 isolates total. (Marijke, SE11B6)
E2017005289
E2017004460

Cluster 2017008: 2 new isolates are 1-5 SNPs from others in the cluster. Now 4 isolates total. (SE11B116)
I2017005940-1
E2017003821

Cluster 2017010: 1 new isolate is 0 SNPs from others in the cluster. Now 3 isolates total. (SE11B6)
E2017006068

NEW Cluster 2017013: 2 isolates are 0 SNPs from each other.
E20170003849 (SE235B78)
E20170005056 (SE181B93)

NEW Cluster 2017014: 2 isolates are 0 SNPs from each other. (SE9B161)
E2017004452
E2017004814

NEW Cluster 2017015: 2 isolates are 0 SNPs from each other. (SE11B6)
I2017005906-1
E2017006005
• Increase knowledge on cgMLST

What are allele codes

What is cgMLST

How does Bionumerics work

What do previous outbreaks look like using cgMLST

How does cgMLST compare to SNP
In-person meetings to discuss:

- How the results will be formatted and communicated
- How long will analysis take
- What/why samples will be sequenced
- What kinds of data can/will analysis provide
- How the results will be interpreted
## SNP/cgMLST Comparison

<table>
<thead>
<tr>
<th>Organism</th>
<th>N</th>
<th>SNP Range</th>
<th>Allele Range</th>
<th>Allele Code</th>
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<td>0-2</td>
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<td>S. Enteritidis</td>
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<td>?</td>
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<tr>
<td>S. Typhimurium</td>
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<td>0-3</td>
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<td>S. Heidelberg</td>
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<td>0-2</td>
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<td>E. Coli 0157</td>
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<td>Campy jejuni</td>
<td>5</td>
<td>0-2</td>
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Anticipated Communication Outcomes with Epi

- Lab/epi team meeting-show epi BN 7.6
- Illustrate WGS data and clusters, discuss timing
- Determine what to communicate-allele code, MLST type, AST, cluster info, etc
- Determine best communication methods
  - Stat-PFGE inbox email/phone call
  - LIMS (new LIMS in 2019)
  - Spreadsheets
- Try for a while, meet, adjust/perfect-reduce friction
• It needs to improve
• Maintain high quality
How to Improve TAT

• Lab meetings to discuss:
  • How do we speed up getting an isolate
  • How long will analysis take
  • How can we do the sequencing faster
  • How can we do the analysis faster
  • How do we measure our TAT
Isolation Timeline *Salmonella*

- **0 to 1 d**: Stool sample collected
- **1 d**: Results CIDT
- **2 d**: Specimen Received at PHL*
- **6 d**: Identification of isolated pathogen
- **12 d**: WGS Completed
External Partners

Lab

Identify clusters

Investigate clusters

Epi

FDA

USDA

CDC

3/18/2019