Boots on the ground: State Public Health Laboratory’s Perspective on Virus Pathogen Surveillance

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Viral Sub-Species Workshop, April 2024
MN-PHL is part of state government system (not necessary the case nationwide)

- Governor
  - Commissioner of Health
    - Health Protection Bureau
    - Health Improvement Bureau
    - Health Systems Bureau
    - Health Operations Bureau
      - Environmental Health
        - Infection control and Epi
          - PHL
What does a public health laboratory do (or not do)?

“Provide information for decision making”

Clinical Labs
- Diagnostic testing
- Medical management
- Focus is on individual health
- Report relevant data to public health

Public Health Labs
- Diagnostic testing, characterization
- Surveillance and response
- Focus is on population health
- Communicate public health needs to clinical labs
Infectious Disease Genomic Sequencing Program at MN-PHL

Organisms Sequenced in 2023

- Streptococcus pneumoniae: 19.4%
- Salmonella: 16.9%
- Escherichia: 14.8%
- Clostridium difficile: 12.4%
- Campylobacter: 10.6%
- Streptococcus pyogens: 9.8%
- Candid auris: 7.6%
- ...: 6.2%

Organisms Sequenced in 2024

- Streptococcus pneumoniae: 24.7%
- Salmonella: 13.6%
- Escherichia: 17.2%
- Clostridium difficile: 11.7%
- Campylobacter: ...%
- Streptococcus pyogens: ...%
- Candid auris: ...%
- ...: 6.2%

~7,000 SARS-COV-2
~800-1,000 Flu
~800 RSV
State Public Health System, including the Laboratories, are at Various Stage of Pathogen Genomic Surveillance

https://www.cdc.gov/amd/investments/maps.html
COVID Pandemic Response is the First Time State and Local Public Health Laboratories Go Full Steam with Viral Genomic Surveillance

**SPHERES:** SARS-CoV-2 Sequencing for Public Health Emergency Response, Epidemiology, and Surveillance

**MN-SOS:** Minnesota molecular surveillance of SARS-CoV-2. Participants including Mayo and Univ. of Minnesota and all the other specimen sharing testing sites.
SARS-CoV-2 genomic mutation (VOCs & VOIs) surveillance at population level

Nation’s Second Omicron variant case identified (First Domestically transmitted Omicron variant associate with acquisition at a convention)

Minnesota’s First Gamma variant case identified

Nation’s First Alpha variant case identified

https://www.health.state.mn.us/diseases/coronavirus/stats/case.html
COVID Outbreak Detection utilizing Genomic Epidemiology at Whole Genome Level


A riverside outdoor concert in Minnesota, summer 2020

Genomically related outbreaks in two congregate settings linked by individuals from one household who were employees at each facility.
• Early pandemic response phase: “Too many cooks in the kitchen”. Public communication was challenging after “variants” concept emerged.

• Ongoing limitation of Laboratory Information Management System (LIMS) handling WGS data

• The SPHERE provided the first-ever direct communication platform among state/local public health laboratories, federal agencies and academic researchers.
Nomenclature for RSV typing

- Viral subtypes A and B
- G-protein based genotyping
- Whole genome-based lineage typing

Nextstrain RSV genomes visualized with GBKViz
Goya et al., 2020
LeadGene Biomedical
Sequencing and bioinformatics methods

- Tiled, overlapping amplicon approach (n = 50 x ~350bp)
- Sequenced on ONT GridION platform (similar to SCV2)
- QC and genome assembly using nf-core/viralrecon (modified)
- Phylogenies constructed using Nextstrain pipeline (Augur)
- Cross-reference to RSV-NET hospitalization data

Phylogenies visualized and annotated using ITOL software
WGS of RSV from 2023-2024 respiratory season

• Through March:
  • RSV-A: 214 sequences
  • RSV-B: 201

• Diversity of RSV-A lineages

• RSV-B dominated by B.D.E.1, but…

Phylogenies visualized and annotated using ITOL software
Even WGS lineage types are not specific enough

TreeTime MRCA: 2009-MAR-21

TreeTime MRCA: 2005-JUN-06

Phylogenies visualized and annotated using Nextstrain software
General thoughts from end-user perspective

• You see one public health laboratory; you see ONE public health laboratory (Easy usage of viral sub-species classification tools, data submission tools, bioinformatic tools)

• Current limitation of Public Health Laboratory Information Management System (LIMS) and Epidemiology database handling genomic epidemiology information (i.e. phylogeny) requires reasonable viral pathogen nomenclature system(s) for different purposes (i.e. outbreak investigation, public communication etc.)

• During public health emergency, state/local public health community need faster consensus of lineage designation, followed with sustainable updates and timely communication
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Thank You!

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