Identifying transmission in a healthcare cluster

COVID-19 Genomic Epidemiology Toolkit: Module 2.2

Nicholas Lehnertz, MD MPH MHS
Physician and Epidemiologist
Minnesota Department of Health
Toolkit map

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1.1 What is genomic epidemiology?
1.2 The SARS-CoV-2 genome
1.3 How to read phylogenetic trees

Part 2: Case Studies
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2.2 Healthcare cluster transmission
2.3 Community Transmission

Part 3: Implementation
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3.2 Getting started with MicrobeTrace
3.3 Linking epidemiologic data
COVID-19 outbreaks at two skilled nursing facilities

- 2 skilled nursing facilities in the same metropolitan area contacted the Minnesota Department of Health (MDH) after identifying confirmed COVID-19 cases in residents and health care personnel (HCP)
  - Facility A
  - Facility B
- During April – June 2020, facility-wide, serial testing was implemented at both facilities to:
  - Identify residents with SARS-CoV-2 infection
  - Inform mitigation efforts
Facility A

- On April 14, census included 78 residents and 156 HCP
- Serial testing of residents and staff was performed from April 30 – June 11

- Serial testing of residents’ specimens (N = 77)*
  - 66% (N = 51) of those tested had positive test results
  - 27% (N = 14 ) were hospitalized
  - 24% (N = 12 ) died

- Serial testing of HCP’s specimens (N = 156):
  - 69% (N = 108) were tested, of those 35% (N = 38) were positive

* One resident had refused testing

Taylor et al. (2020), "Genome Sequencing Inform Infection Risk at Two Skilled Nursing Facilities with COVID-19 Outbreaks – Minnesota, April- June 2020". http://dx.doi.org/10.15585/mmwr.mm6937a3
Facility A

Residents
(N=77)

HCP
(N=108)
Facility B

- On April 29, census included 183 residents and 324 HCP
- Serial testing of residents and staff was performed from May 7 – June 11

Serial testing of residents’ specimens (N = 182)*:
- 63% (N = 114) of those tested had positive test results
- 17% (N = 19) were hospitalized
- 35% (N = 40) died

Serial testing of HCP’s specimens (N = 324):
- 72% (N = 233) tested, of those 33% (N = 76) had positive test results

* One resident had refused testing

Taylor et al. (2020), “Genome Sequencing Inform Infection Risk at Two Skilled Nursing Facilities with COVID-19 Outbreaks – Minnesota, April- June 2020”. http://dx.doi.org/10.15585/mmwr.mm6937a3
Facility B

Residents
(N = 182)

HCP
(N = 233)
Facility challenges during COVID-19

- Limited staffing
- Sourcing nursing staff from outside agencies
- PPE shortages
- Poor infection prevention and control
- Limited space for appropriate cohorting
- Reluctance of staff to be routinely tested
- Difficulty with isolating and masking among residents in memory care
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Ample opportunities for multiple introductions of SARS-CoV-2 into facilities
Hypothesis investigated by genomic sequencing

- **Hypothesis 1**
  - Outbreak cases in Facilities A and B are both a result of a single introduction and ongoing transmission
  - Expected sequencing result: SARS-CoV-2 genomes from all outbreak cases form a single cluster, comprised of identical or closely related sequences

- **Hypothesis 2**
  - Outbreak cases within Facilities A and B are a result of multiple introductions
  - Expected sequencing result: SARS-CoV-2 genomes from all outbreak cases form multiple distinct clusters, each comprised of identical or closely related sequences
Cases whose samples were sequenced

- **Facility A**
  - 18 (35%) residents’ specimens were sequenced
  - 6 (18%) HCP’s specimens were sequenced
- **Facility B**
  - 75 (66%) residents’ specimens were sequenced
  - 5 (7%) HCP’s specimens were sequenced
Phylogenetic tree of SARS-CoV-2 case genomes

Facility A

Trees drawn with Nextstrain
Phylogenetic tree of SARS-CoV-2 case genomes

Facility A

Trees drawn with Nextstrain
Phylogenetic tree of SARS-CoV-2 case genomes
Recommendations for Facilities

- Continued vigilance with infection prevention and control
  - WGS results suggest it only takes one introduction for an outbreak to occur
- Screening of residents and staff
- Universal testing of all residents and staff
Limitations

- Most sequenced samples were from residents, very few samples from healthcare personnel (HCP)
  - Unsampled HCP could have represented separate introductions or missing cases in a transmission chain
- Limited participation by some HCP
- Not all samples able to be sequenced
- It's possible that two cases with highly related genomes could represent two separate introduction events into a community
Learn more

- Other modules in Part 2: Case Studies
  - SARS-CoV-2 sequencing in Arizona – Module 2.1
  - Community Transmission – Module 2.3

- COVID-19 Genomic Epidemiology Toolkit
  - Find further reading
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