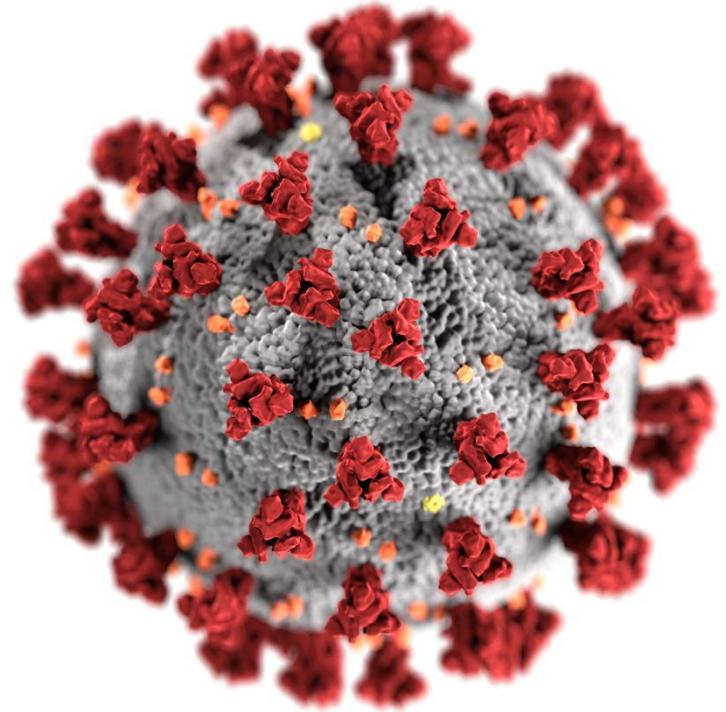


Identifying transmission in a healthcare cluster

COVID-19 Genomic Epidemiology Toolkit: Module 2.2

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cdc.gov/coronavirus

Toolkit map

Part 1: Introduction

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

Part 2: Case Studies

- 2.1 SARS-CoV-2 sequencing in Arizona
- 2.2 Healthcare cluster transmission**
- 2.3 Community Transmission

Part 3: Implementation

- 3.1 Getting started with Nextstrain
- 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

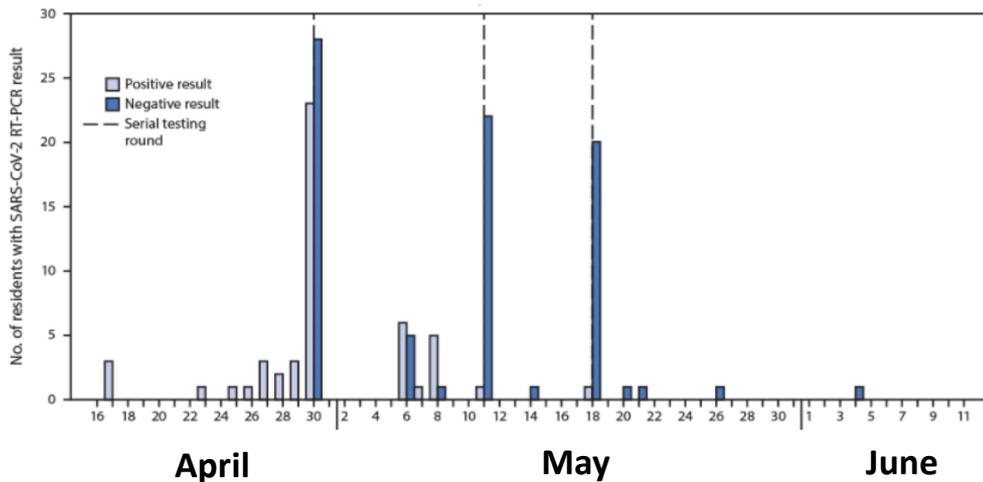
Facility A

- 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

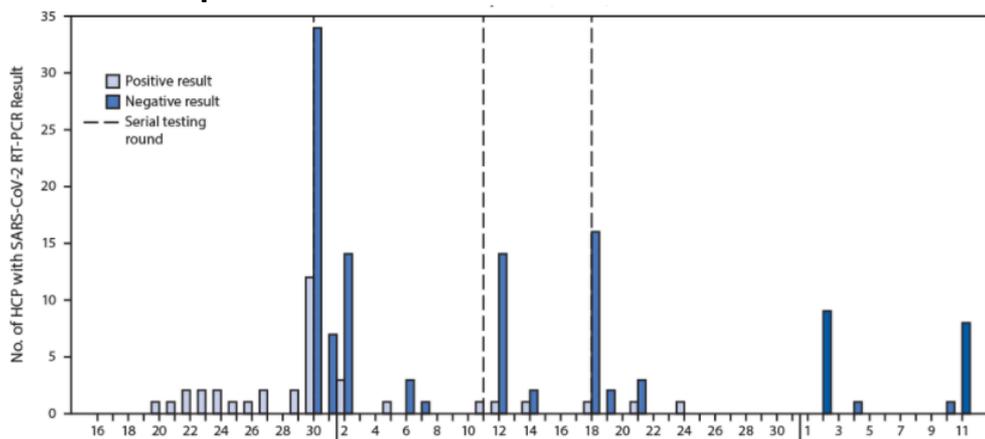
* One resident had refused testing

Facility A

Residents
(N=77)



HCP
(N=108)



Facility B

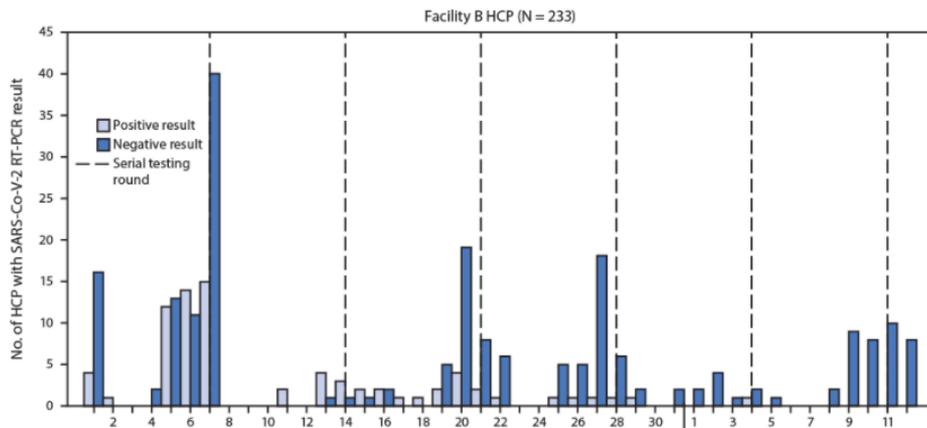
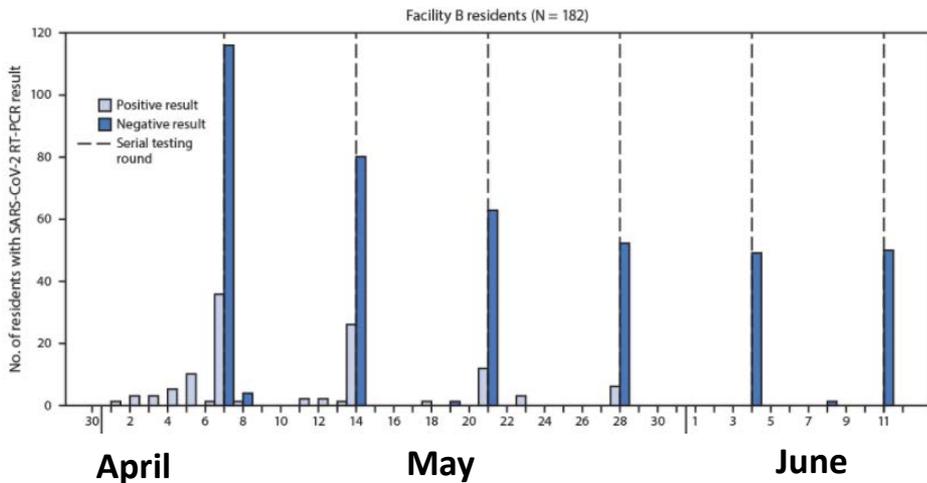
- On April 29, census included 183 residents and 324 HCP
- Serial testing of residents and staff was performed from May 7 – June 11
- Serial testing of residents' specimens (N = 182)*:
 - 63% (N = 114) of those tested had positive test results
 - 17% (N = 19) were hospitalized
 - 35% (N = 40) died
- 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

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 area 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**

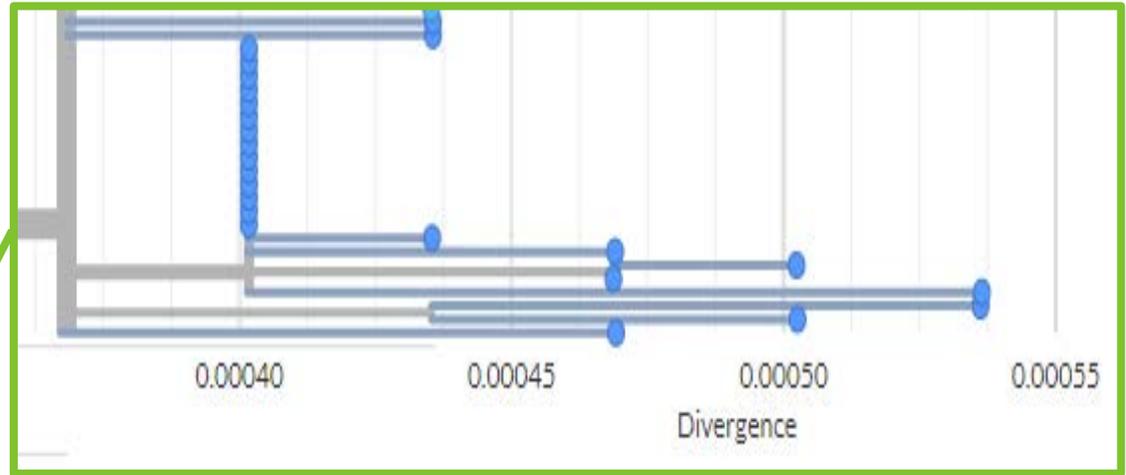
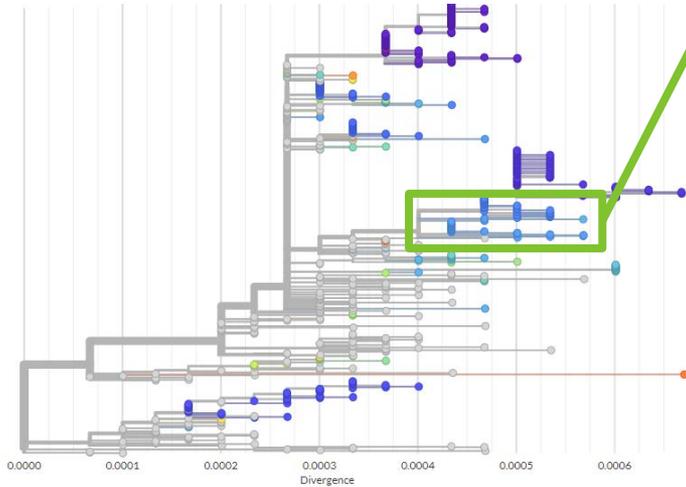
- 18 (35%) residents' specimens were sequenced
- 6 (18%) HCP's specimens were sequenced

- **Facility B**

- 75 (66%) residents' specimens were sequenced
- 5 (7%) HCP's specimens were sequenced

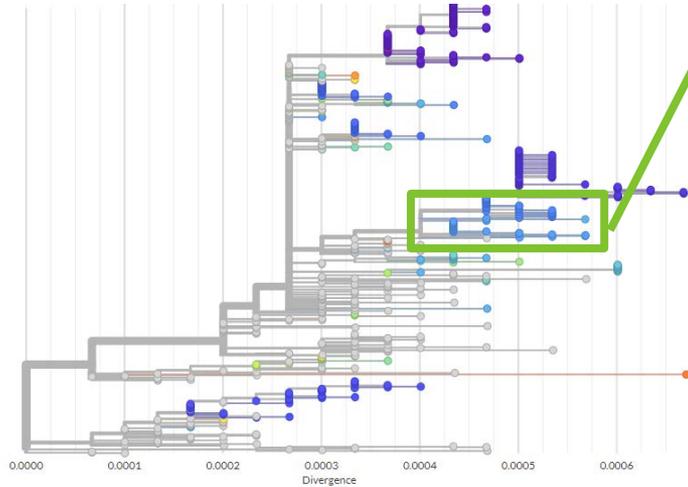
Phylogenetic tree of SARS-CoV-2 case genomes

Facility A



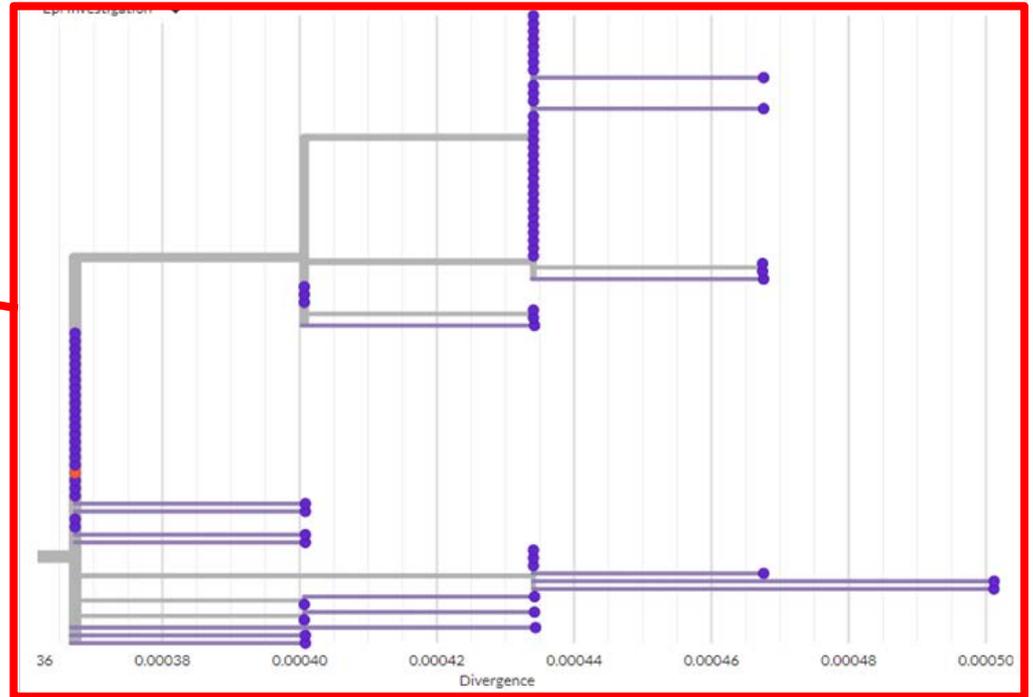
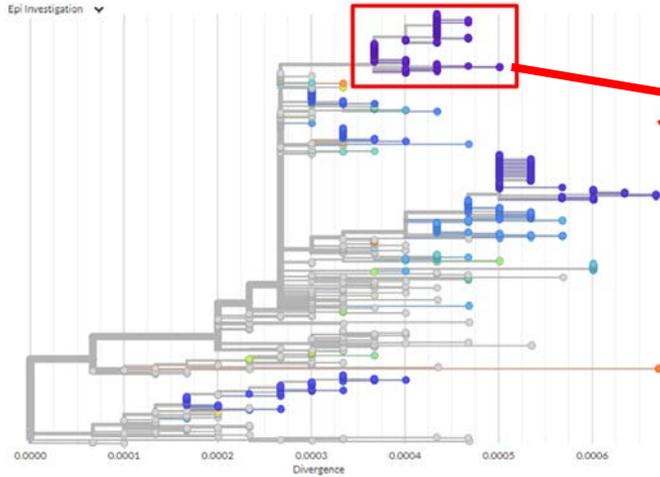
Phylogenetic tree of SARS-CoV-2 case genomes

Facility A



Phylogenetic tree of SARS-CoV-2 case genomes

Facility B



Recommendations for Facilities

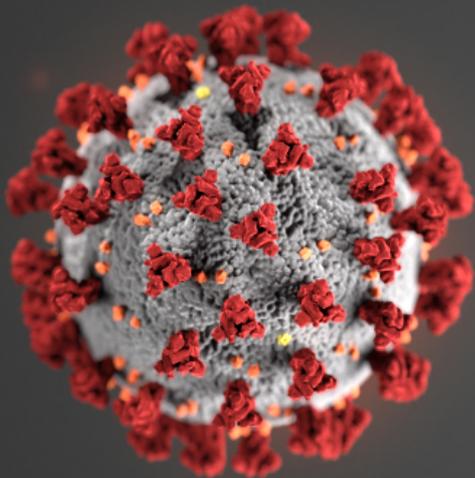
- Continued vigilance with infection prevention and control
 - WGS results suggest it only takes one introduction for an outbreak to occur
- Screening of residents and staff
- Universal testing of all residents and staff

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
 - Subscribe to receive updates on new modules as they are released
go.usa.gov/xAbMw



For more information, contact CDC
1-800-CDC-INFO (232-4636)
TTY: 1-888-232-6348 www.cdc.gov

The findings and conclusions in this report are those of the authors and do not necessarily represent the official position of the Centers for Disease Control and Prevention.

