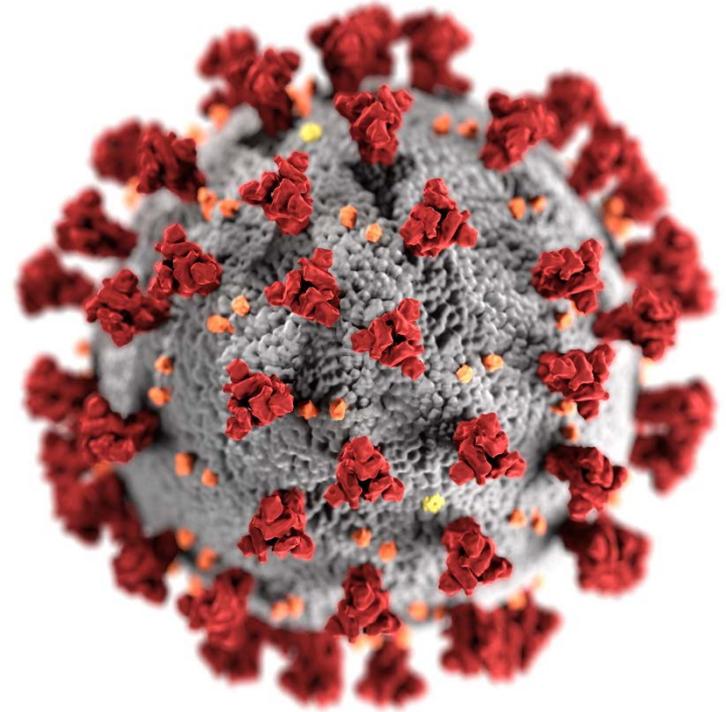


# Identifying transmission in a healthcare cluster

## COVID-19 Genomic Epidemiology Toolkit: Module 2.2

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Minnesota Department of Health



[cdc.gov/coronavirus](https://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

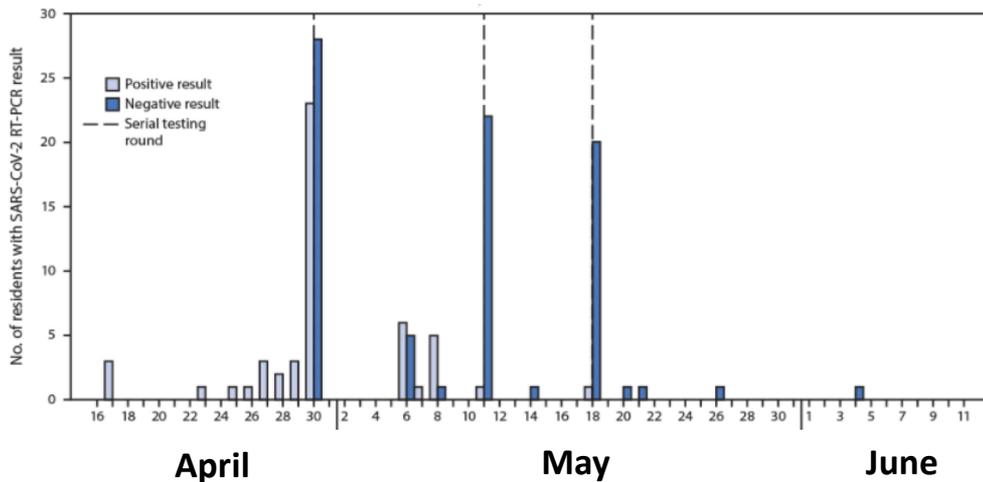
# Facility A

- 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

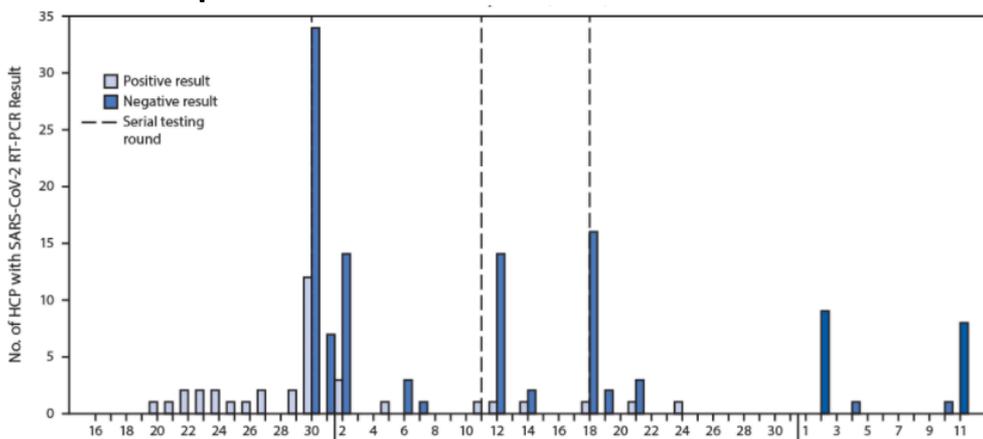
\* One resident had refused testing

# Facility A

Residents  
(N=77)



HCP  
(N=108)



# Facility B

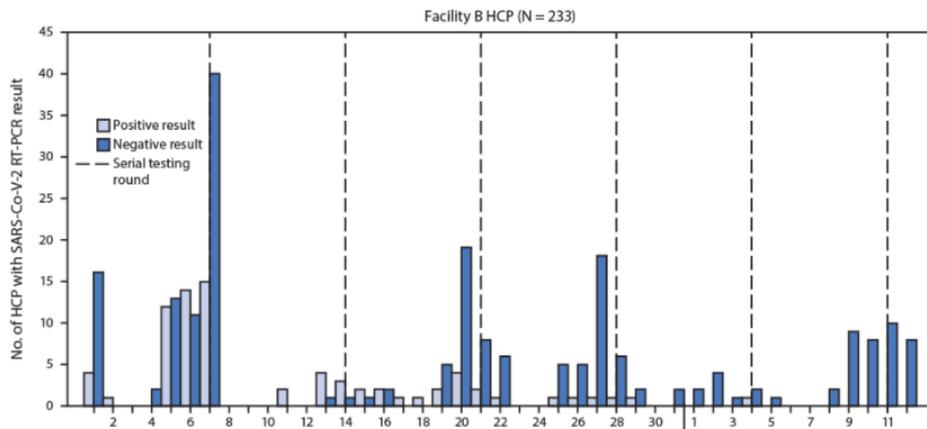
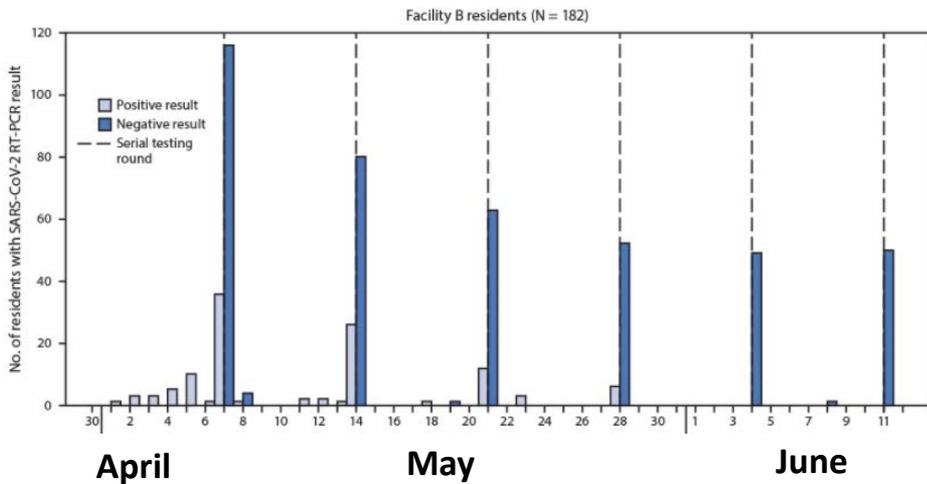
- On April 29, census included 183 residents and 324 HCP
- Serial testing of residents and staff was performed from May 7 – June 11
- Serial testing of residents' specimens (N = 182)\*:
  - 63% (N = 114) of those tested had positive test results
  - 17% (N = 19) were hospitalized
  - 35% (N = 40) died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

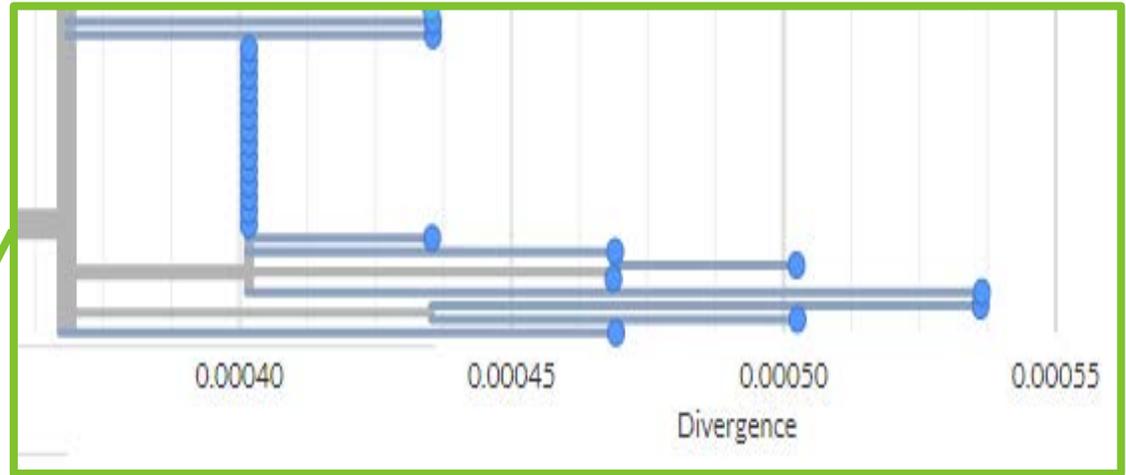
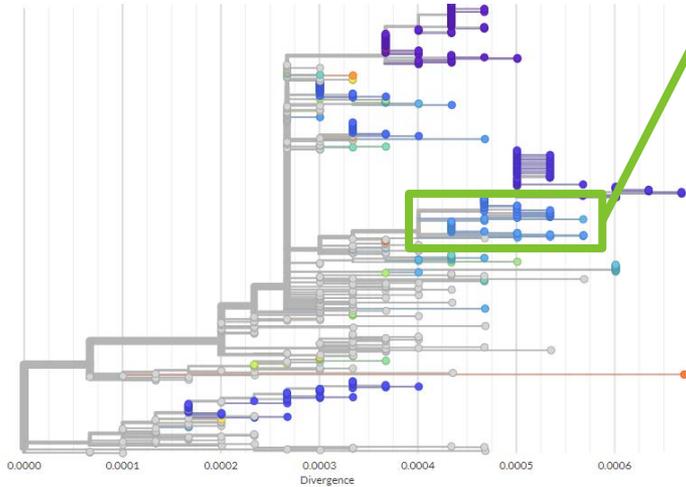
- 18 (35%) residents' specimens were sequenced
- 6 (18%) HCP's specimens were sequenced

- **Facility B**

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

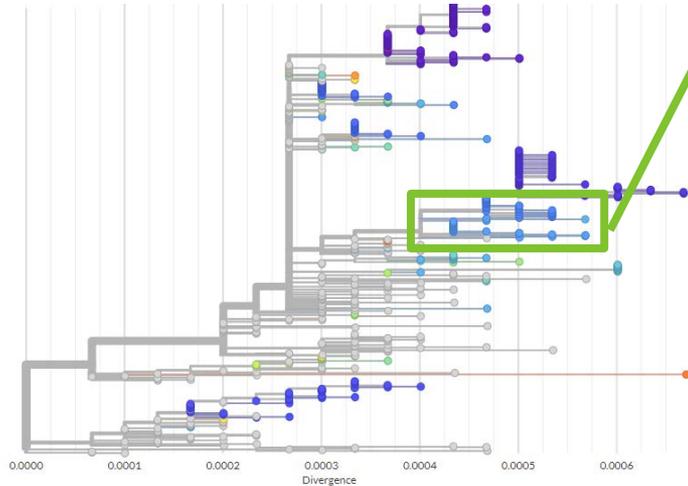
# Phylogenetic tree of SARS-CoV-2 case genomes

## Facility A



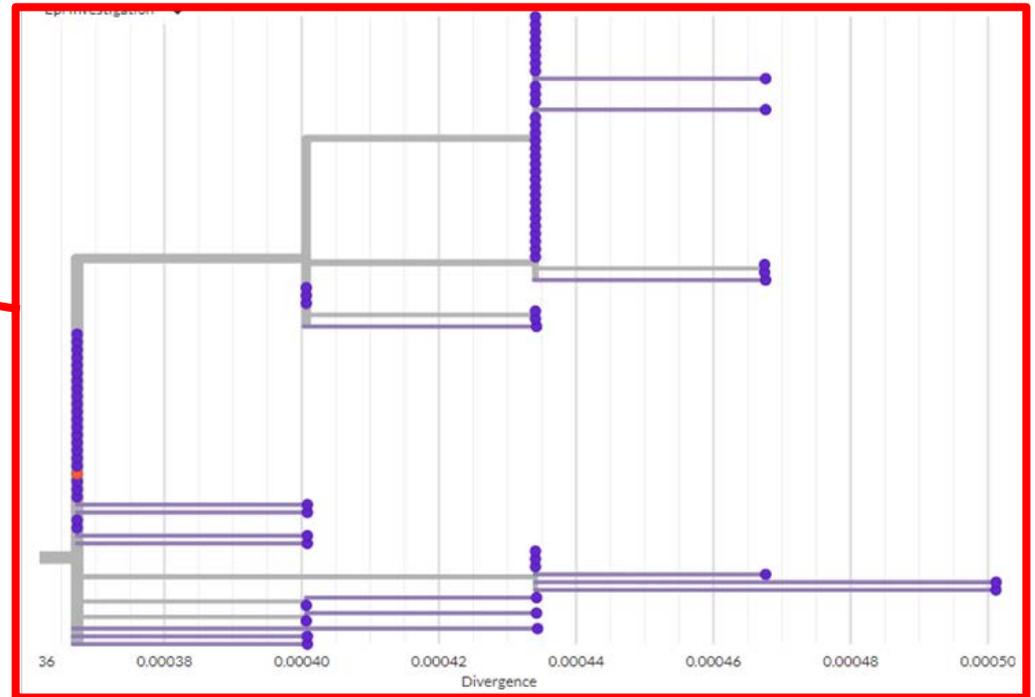
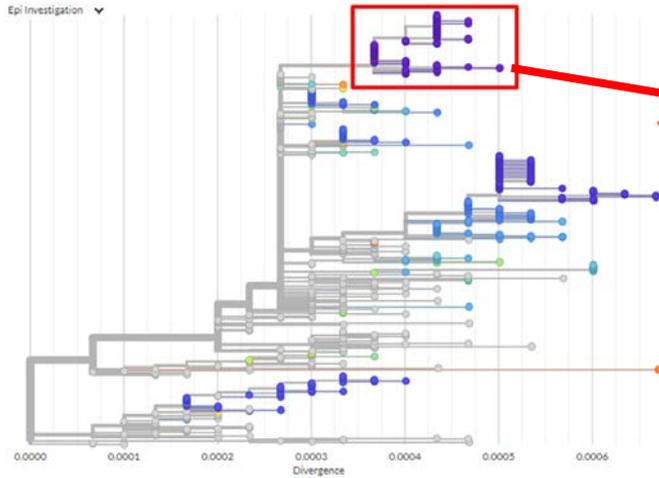
# Phylogenetic tree of SARS-CoV-2 case genomes

## Facility A



# Phylogenetic tree of SARS-CoV-2 case genomes

## Facility B



# Recommendations for Facilities

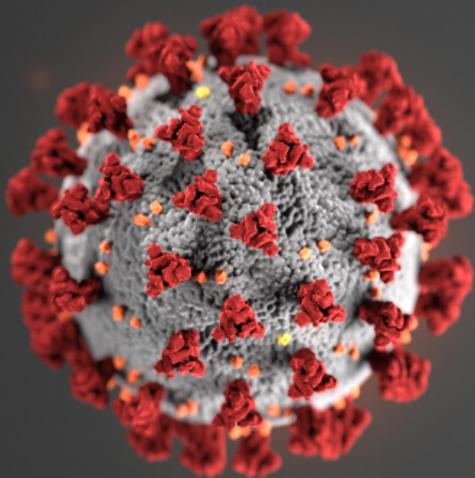
- Continued vigilance with infection prevention and control
  - WGS results suggest it only takes one introduction for an outbreak to occur
- Screening of residents and staff
- Universal testing of all residents and staff

# 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](https://go.usa.gov/xAbMw)



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TTY: 1-888-232-6348 [www.cdc.gov](http://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.

