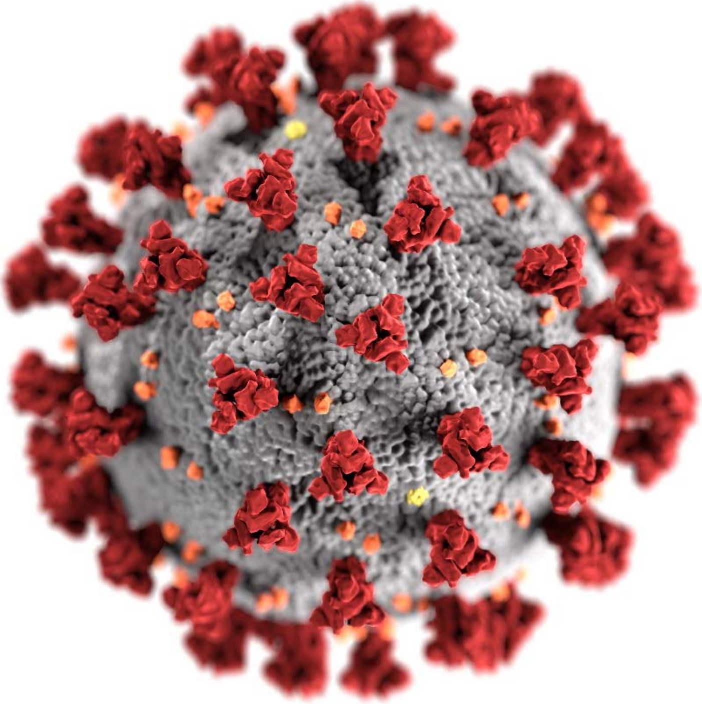
Superspreading event in a pre-symptomatic population

COVID-19 Genomic Epidemiology Toolkit: Module 2.4



Glen R. Gallagher, PhD
Division Director, Molecular Diagnostics and Virology
Massachusetts Department of Public Health

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
- 1.4 Emerging variants of SARS-CoV-2

Part 2: Case Studies

- 2.1 SARS-CoV-2 sequencing in Arizona
- 2.2 Healthcare cluster transmission
- 2.3 Workplace-community transmission
- **2.4 Superspreading event**

Part 3: Implementation

- 3.1 Getting started with Nextstrain
- 3.2 Getting started with MicrobeTrace
- 3.3 Linking epidemiologic data

Skilled nursing facility (SNF) in Boston, MA

- 142-bed skilled nursing facility in Massachusetts
  - Short-term care, long-term care, and memory units
- Mean resident age was 83 years (IQR: 61 – 98)
- Minority (28%) of residents were male
- Selected to establish a dedicated COVID-19 rehabilitation center
  - Universal SARS-CoV-2 screening conducted in April 2020 prior to relocation of all residents

Goldberg *et al.* (2020) CID, PMID: 32667967

Intensive infection-prevention measures at SNF

- Strict visitation policy
- Daily symptom and temperature checks for residents and staff
- Masking
  - Universal masking for staff
  - Mandatory masking for residents leaving their room
- Increased attention to hand hygiene
- Facility admissions heavily restricted

Goldberg *et al.* (2020) CID, PMID: 32667967

Universal testing revealed a superspreading event

- Universal SARS-CoV-2 screening among reportedly asymptomatic residents and staff
- Overall, 61% (118/194) of persons tested positive by PCR
  - **85%** (82/97) of residents
  - **37%** (36/97) of staff
- Two weeks after initial testing, 31% (30/97) died; of those, 80% (24) tested positive

Goldberg *et al.* (2020) CID, PMID: 32667967

Timeline of specimen collection for PCR

April 1

Residents

97 NP swabs

- 54% (52) SARS-CoV-2 positive

April 5

Residents*

45 NP swabs

- 69% (31) SARS-CoV-2 positive

*negative on April 1

April 6

Residents

0 NP swabs

Staff

97 NP swabs

- 37% (36) SARS-CoV-2 positive

NP: Nasopharyngeal

Goldberg *et al.* (2020) CID, PMID: 32667967

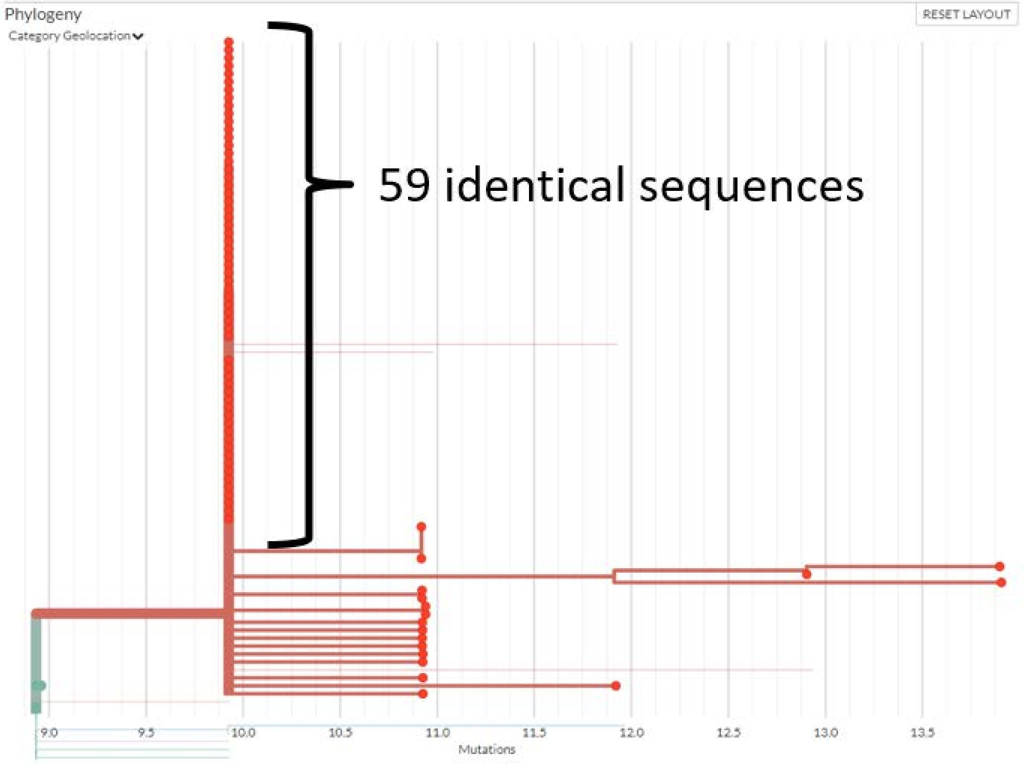
WGS to investigate SARS-CoV-2 spread

- Of 118 total cases, **70% (83)** had genomes sequenced

Sequencing revealed rapid spread

- 90% (75/83) genomes comprised a single cluster

- Very little genetic variation, even for single introduction



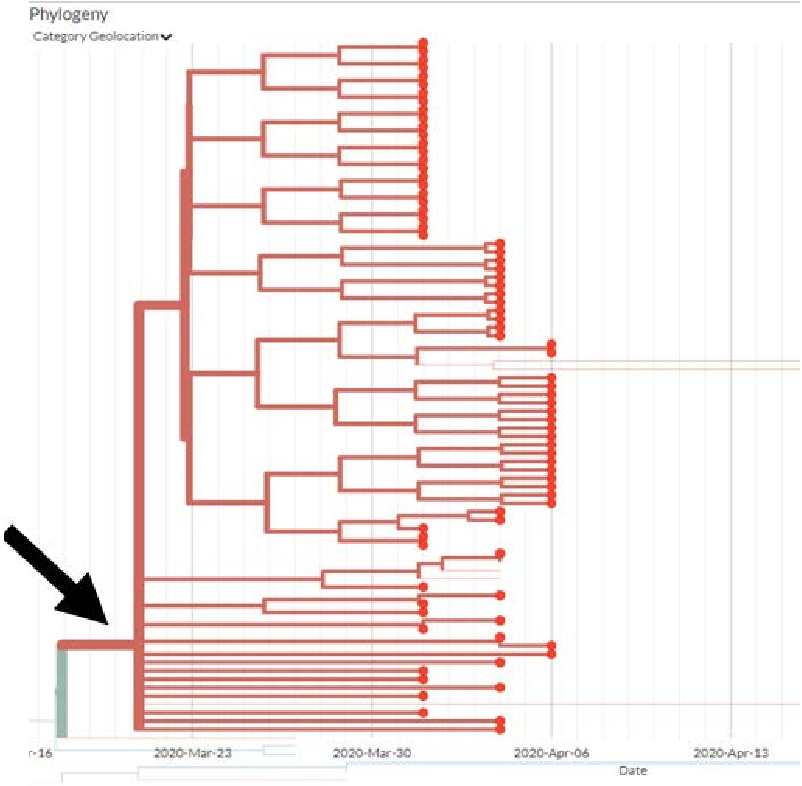
59 identical sequences

https://auspice.broadinstitute.org/sars-cov-2/boston/gisaid-0929?d=tree&f_SNF_A_EXPOSURE=YES&m=div&p=full

Sequencing revealed rapid spread

- Date of common ancestor for this cluster estimated to March 20

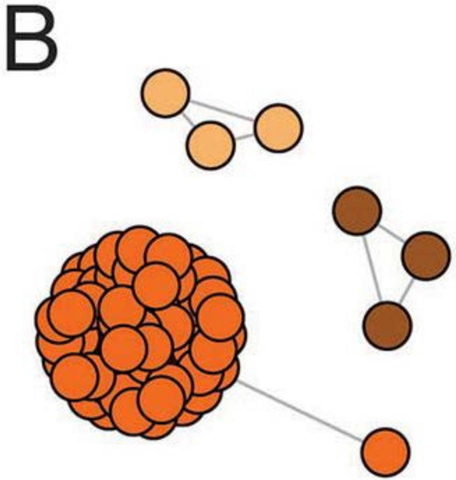
- Supports spread of SARS-CoV-2 among asymptomatic persons



https://auspice.broadinstitute.org/sars-cov-2/boston/gisaid-0929?d=tree&f_SNF_A_EXPOSURE=YES&m=div&p=full

Not all introductions lead to rapid transmission

- Additional, small clusters also detected
  - Indicate multiple introductions with varied outcome
- Superspreading dramatically influences transmission dynamics
- All 3 putative introductions occurred despite infection control practices at the facility



Adapted from Lemieux *et al.* (2020) Science, PMID: 33303686

Summary

- Genetic diversity in the main cluster was strikingly low, even for recent transmission from a single introduction
- This event might reflect:
  - Low diversity within the index patient, or
  - Superspreading event where transmission to secondary cases occurred through unusually close or prolonged contact, or the initial case having a very high viral load at the time
- Led to very little onward transmission, with little large-scale effect because it occurred in a relatively isolated population.

Take-away

- Intensive infection-prevention measures are essential but may be insufficient
- Screening of reportedly asymptompatic persons can identify early transmission and prevent further spread
- Genomic sequencing of this superspreading event revealed extremely low genetic diversity

Limitations

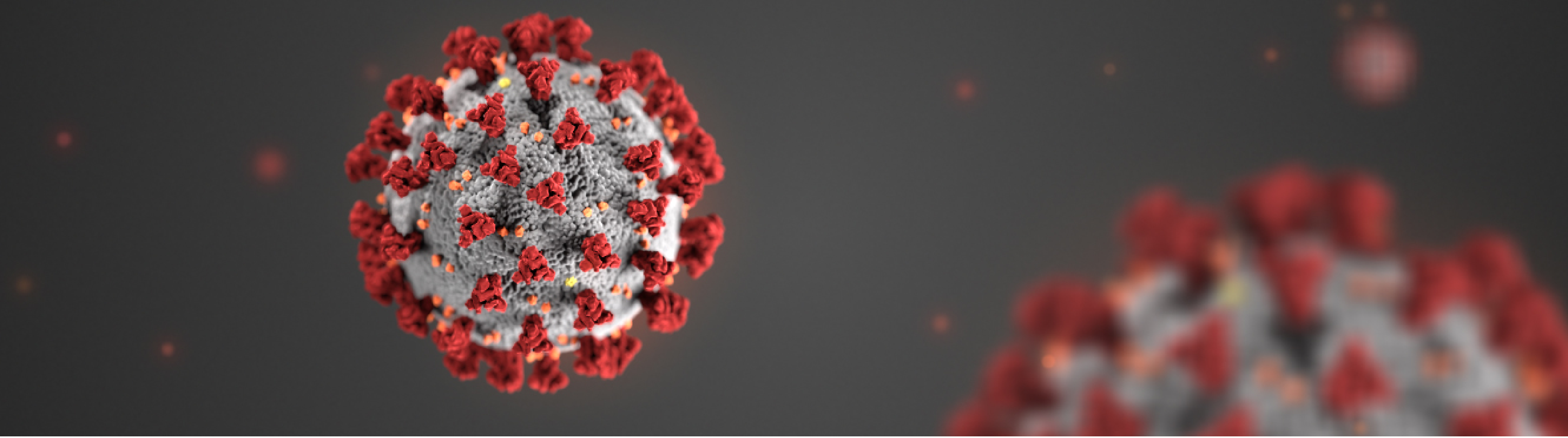
- Some staff and/or residents may have had unidentified symptoms

Acknowledgements

- Broad Institute
  - Jacob Lemieux

Learn more

- Other modules in Part 2: Case Studies
  - Healthcare cluster transmission – Module 2.2
  - Investigating Workplace-Community Transmission in an Outbreak – 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

FOR WEBSITE

- Further Reading:
  - Lemieux et al. 2020. Science. https://science.sciencemag.org/content/early/2020/12/09/science.abe3261
  - Goldberg et al. 2020. CID. https://doi.org/10.1093/cid/ciaa991

- Resources:
  - Nextstrain build: https://auspice.broadinstitute.org/sars-cov-2/boston/gisaid-0929?f_SNF_A_EXPOSURE=YES