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
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 Community transmission
2.4 Superspreading event

Part 3: Implementation
3.1 Getting started with Nextstrain
3.2 Getting started with MicrobeTrace
3.3 Phylogenetics with UShER
3.4 Walking through Nextstrain trees
3.5 Public genome repositories
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 screening testing conducted in April 2020 before all residents relocated
Intensive infection-prevention measures at SNF

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

Presymptomatic Transmission of Severe Acute Respiratory Syndrome Coronavirus 2 Among Residents and Staff at a Skilled Nursing Facility: Results of Real-time Polymeras Chain Reaction and Serologic Testing, 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 RT-PCR
  - 85% (82/97) of residents
  - 37% (36/97) of staff

- Two weeks after initial testing, 31% (30/97) died; of those, 80% (24) had tested positive
Presymptomatic Transmission of Severe Acute Respiratory Syndrome Coronavirus 2 Among Residents and Staff at a Skilled Nursing Facility: Results of Real-time Polymerase Chain Reaction and Serologic Testing, Goldberg et al. (2020) CID, PMID: 32667967
Whole-genome sequencing (WGS) to investigate SARS-CoV-2 spread

- Genomes sequenced for **70% (83)** of 118 total cases
Sequencing revealed rapid spread

- 90% (75/83) genomes comprised a single cluster
- Very little genetic variation, even for a single introduction

59 identical sequences

Sequencing revealed rapid spread

- Looking at the same tree but with date of specimen collection as the x-axis
- March 20: estimated date of common ancestor for this cluster
- Supports spread of SARS-CoV-2 among asymptomatic persons

Not all introductions lead to rapid transmission

- Additional, small clusters also detected
  - Indicated multiple introductions with varied outcome
- Superspreading can dramatically influence 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
    - 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-aways

- Intensive infection-prevention measures are essential but can be insufficient

- Screening of reportedly asymptomatic 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 might have had unidentified symptoms
Acknowledgements

- Broad Institute
  - Jacob Lemieux, MD, PhD
Learn more

- Other modules in Part 2: Case Studies
  - Healthcare cluster transmission – Module 2.2
  - Investigating Workplace-Community Transmission – Module 2.3
- COVID-19 Genomic Epidemiology Toolkit
  - Find further reading
  - Complete a feedback survey
  - 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)

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.