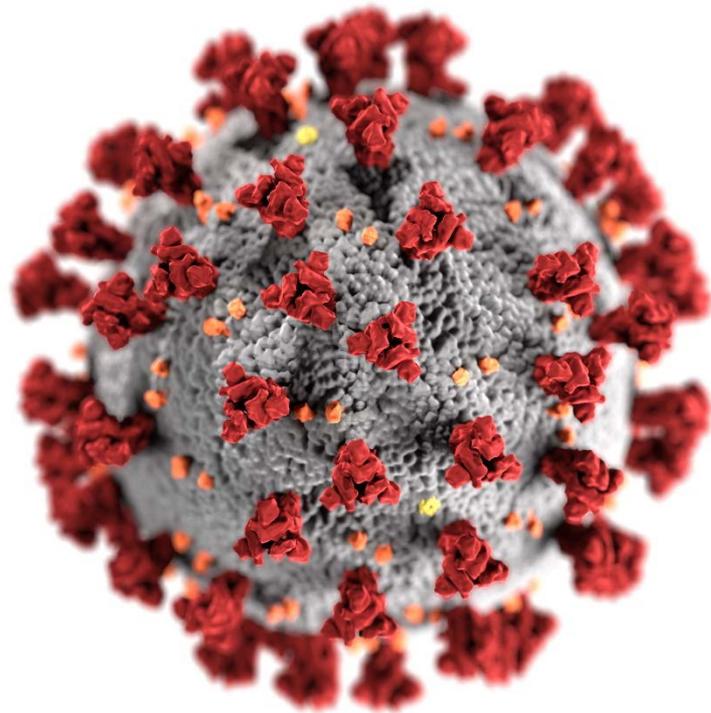


Investigating Workplace-Community Transmission in an Outbreak

COVID Genomic Epidemiology Toolkit: Module 2.3

Nicholas Lehnertz, MD MPH MHS
Physician and Epidemiologist
Minnesota Department of 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**

Part 3: Implementation

- 3.1 Getting started with Nextstrain
- 3.2 Getting started with Microbetrace
- 3.3 Phylogenetics with USHER

COVID-19 in Meat Processing Plants

- Meat and poultry processing is essential to the U.S. food infrastructure, employing approximately 500,000 workers
- Many states have reported COVID-19 cases among workers in meat processing plants*
- Challenges to preventing COVID-19 in these workers:
 - Workplace: maintaining physical distance, screening and isolation of ill workers
 - Community: language barriers, crowded living conditions
- Distinguishing workplace from community transmission can help focus prevention efforts in this population

* [MMWR: COVID-19 Among Workers in Meat and Poultry Processing Facilities — 19 States, April, 2020](#)



Outbreak in a Meat Processing Plant, Minnesota

- From March 15 to July 1, **446** cases identified reported working at Processing Plant A
- 9 cases identified in March – April 2020
 - 4 (1%) cases tested positive in March
 - 5 (1%) cases tested positive in April
 - Initial cases in mid-March were administration and office workers
- 437 cases identified in May – June 2020
 - 211 (47%) cases identified in May
 - 226 (51%) additional cases identified in June



Characteristics of Processing Plant A

- Physical environment consisted of multiple buildings
- Travel between these buildings was strictly controlled to reduce likelihood of spreading possible contaminants
 - Movement restricted between buildings involved in raw processing and those handling the finished product
- Cases involved employees who worked in administration and on the food line
- Many of the employees reported sharing transportation and residence with other employees



Hypotheses for genomic sequencing

■ Hypothesis 1

- Transmission among cases primarily occurred at the processing plant
- Expected sequencing result: SARS-CoV-2 genomes from most cases in the plant would be *closely related, supporting a single introduction*

■ Hypothesis 2

- Cases were exposed to SARS-CoV-2 in the community, outside the processing plant
- Expected sequencing result: SARS-CoV-2 genomes from most cases in the plant are *distantly related, supporting multiple introductions*

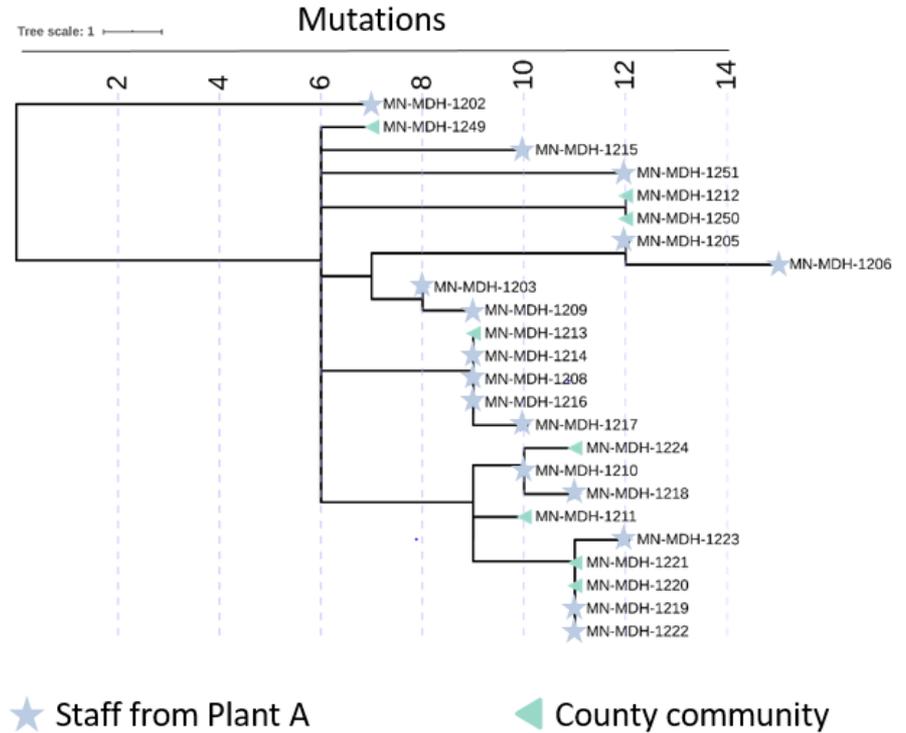


Cases whose samples were successfully sequenced

- **Processing Plant A**
 - 16/446 (4%) cases
 - Low number of sequences due to many samples being discarded after testing per outside lab protocol
- **County community**
 - 8 resident cases
 - 6 of the 8 residents living in the community with no known contact with plant members

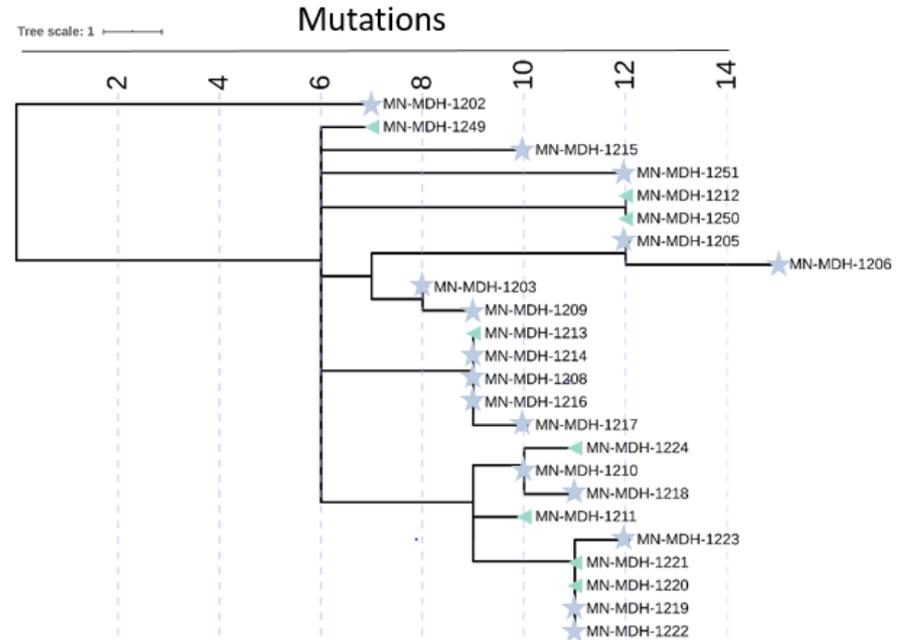
Sequencing revealed multiple introductions

- SARS-CoV-2 genomes sequenced from Plant A workers were only distantly related
- These findings do not support a single introduction to the plant, followed by on-site transmission
- Data also support limited transmission occurring at the plant



Sequencing revealed multiple introductions

- 6 of 8 sampled community cases had no known contact with plant members
- Genomes from 5 of these community cases clustered with genomes from employees
- These findings support multiple introductions to the plant of community-acquired infections



★ Staff from Plant A

▲ County community

Take-aways from genomic epidemiology

- When epidemiologic findings point to potential transmission at a site, genomic data can help provide clarity
- Interventions at the community level are critical (e.g., provision of more independent housing and transportation, provision of masks, culturally appropriate messaging and peer support)
- With evidence suggesting that there were repeated introductions at the plant from the community, these findings reinforce the need for continued mitigation strategies at the plant, including symptom screening, enforcement of distancing and masking, and other mitigation strategies



Limitations

- Representativeness
 - Only 4% of cases in the processing plant were sequenced, thus the collection is not representative of the outbreak



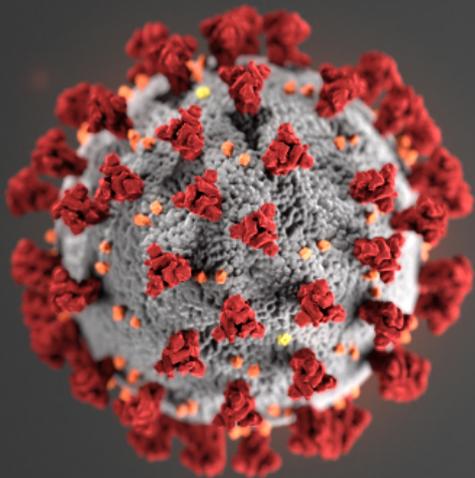
Learn more

- Other modules in Part 2: Case Studies
 - SARS-CoV-2 sequencing in Arizona – Module 2.1
 - Healthcare cluster transmission – Module 2.2
- COVID-19 Genomic Epidemiology Toolkit
 - Find further reading
 - Subscribe to receive updates on new modules as they are released
go.usa.gov/xAbMw

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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.

