

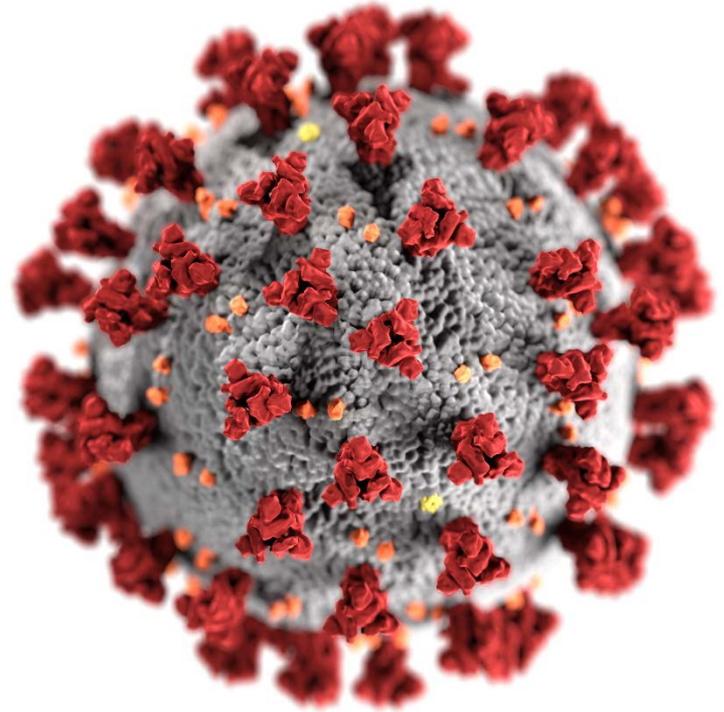
Detecting and prioritizing SARS-CoV-2 variants

COVID-19 Genomic Epidemiology Toolkit: Module 2.6: Detecting & prioritizing variants

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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
- 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
- 2.5 Confirming reinfection
- 2.6 Detecting & prioritizing variants**
- 2.7 Wastewater-based variant tracking

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 data repositories
- 3.6 Sequencing strategies

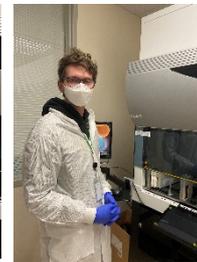


CDPHE sequencing capacity

- Funded PulseNet Regional Lab
www.cdc.gov/pulsenet/index.html
- State support for COVID-19 specific positions and additional instrumentation
- CDC/State funded cloud computing resources for genome sequence analyses

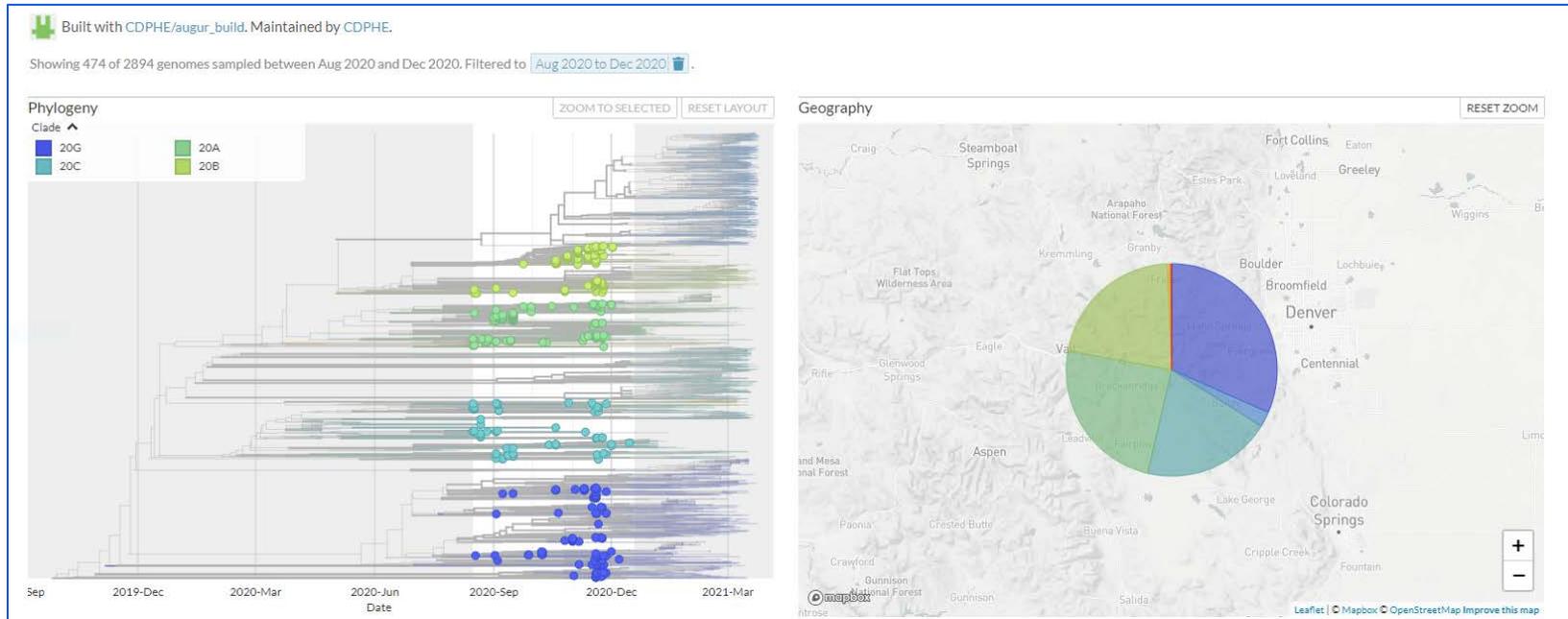


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CDPHE sequencing priorities: August – December 2020

- First run completed in August 2020
- > 450 sequences supporting more than 100 individual investigations



CDPHE sequencing priorities: August – December 2020

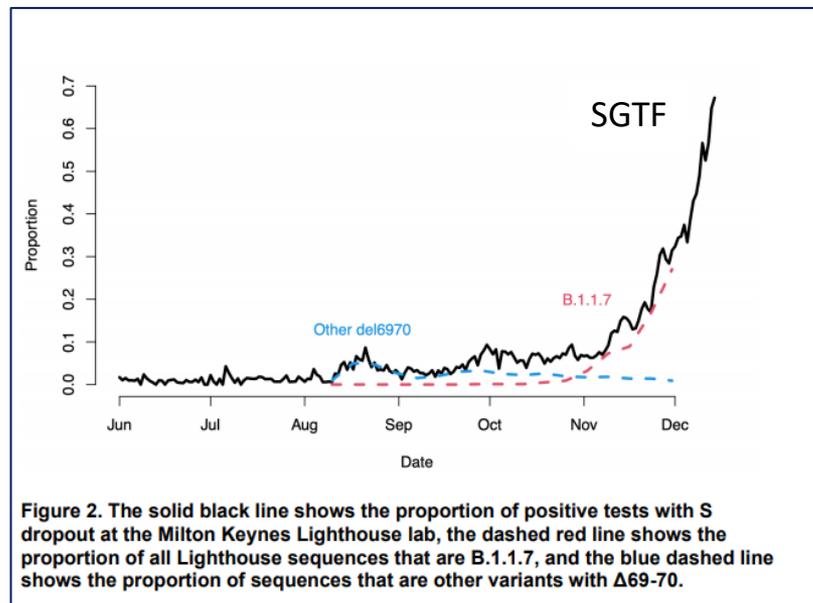
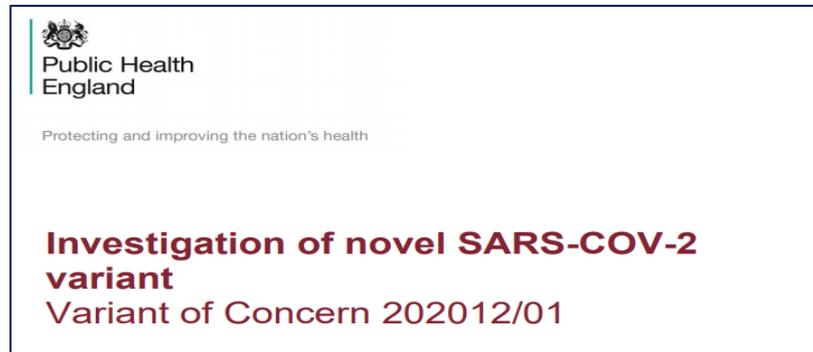
- Initial focus on congregate living facilities for:
 1. Outbreak investigation
 - Was virus introduced into a facility by one transmission event or many?
 2. Confirming reinfection
 - Was a particular resident reinfected, or was the viral shedding from a previous infection?

- This information informed cohorting and contact tracing in subsequent outbreaks at similar facilities.

Emergence of VOC B.1.1.7

- First described in December 2020
- Classified as Variant of Concern (VOC)
- Deletion within spike (S) gene
- Produces a characteristic S Gene Target Failure (SGTF) on the ThermoFisher TaqPath RT-PCR assay.
- Module 1.4 – Emerging variants of SARS-CoV-2

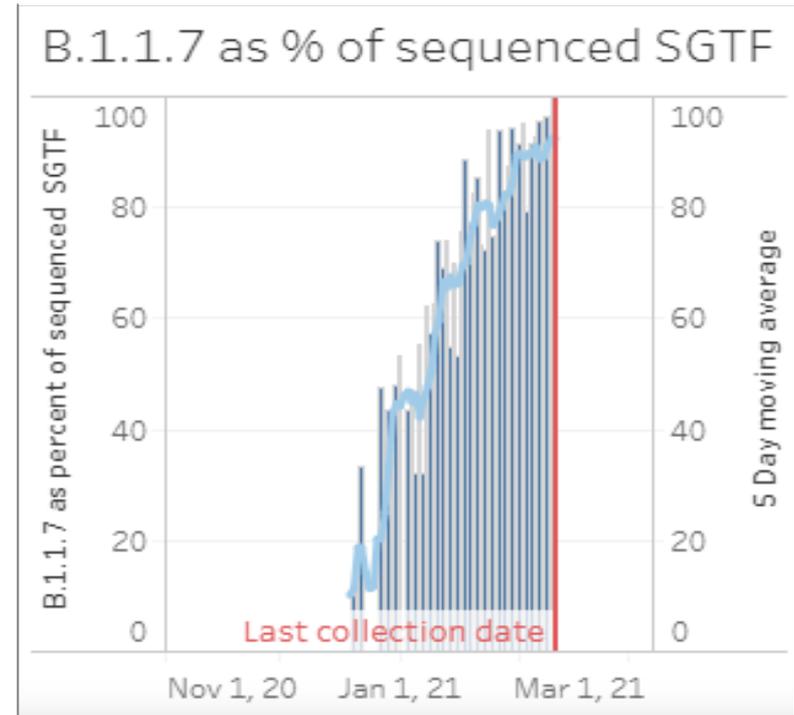
https://assets.publishing.service.gov.uk/government/uploads/system/uploads/attachment_data/file/959426/Variant_of_Concern_VOC_202012_01_Technical_Briefing_5.pdf



CDPHE sequencing priorities: Dec 2020 – present

- Pivot priority to SGTF
 - SGTF specimens identified at clinical and commercial labs routed to CDPHE
 - First U.S. case of B.1.1.7 detected in Colorado, Dec 2020
 - Unlike other locations, 100% of SGTF specimens sequenced in CO from Dec 2020 - Jan 2021 were B.1.1.7

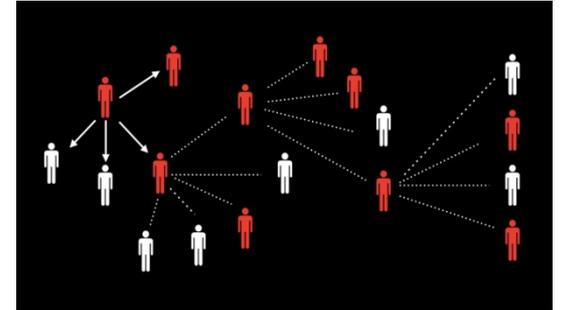
B.1.1.7 as % of sequenced SGTF US Data, Illumina-Helix



Variant detection and response prioritization

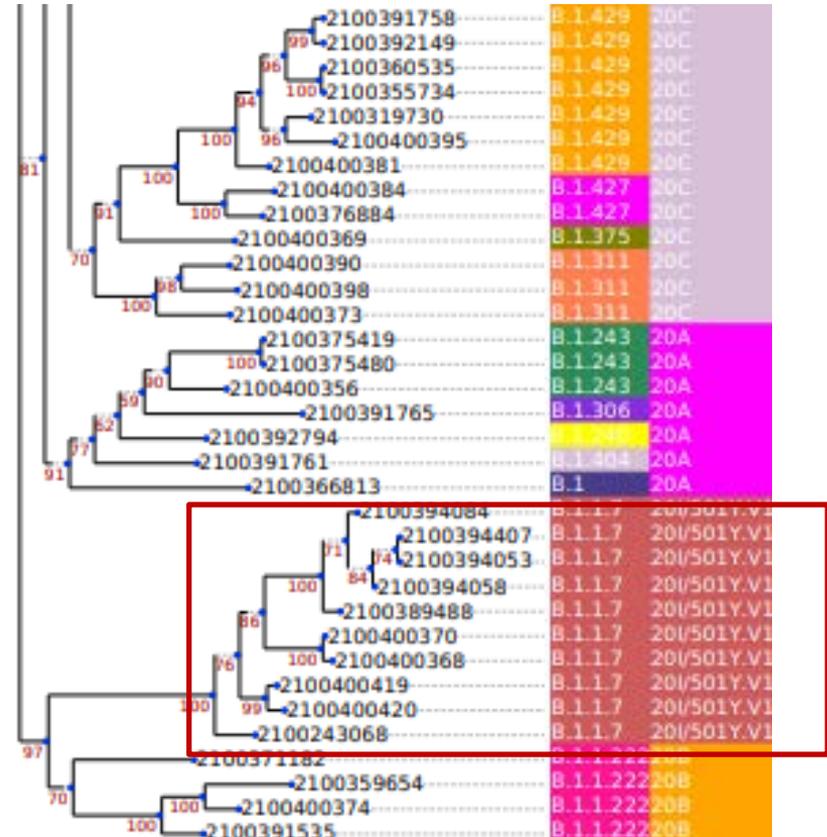
Variant emergence increased statewide engagement for a broad surveillance program

- Case investigation and contract tracing (CI/CT):
 - Daily meetings
 - Communicate sequence data as needed
- Epidemiology feedback:
 - Helps with contact tracing
 - Consistently detects secondary positive cases
 - Limited by turnaround time

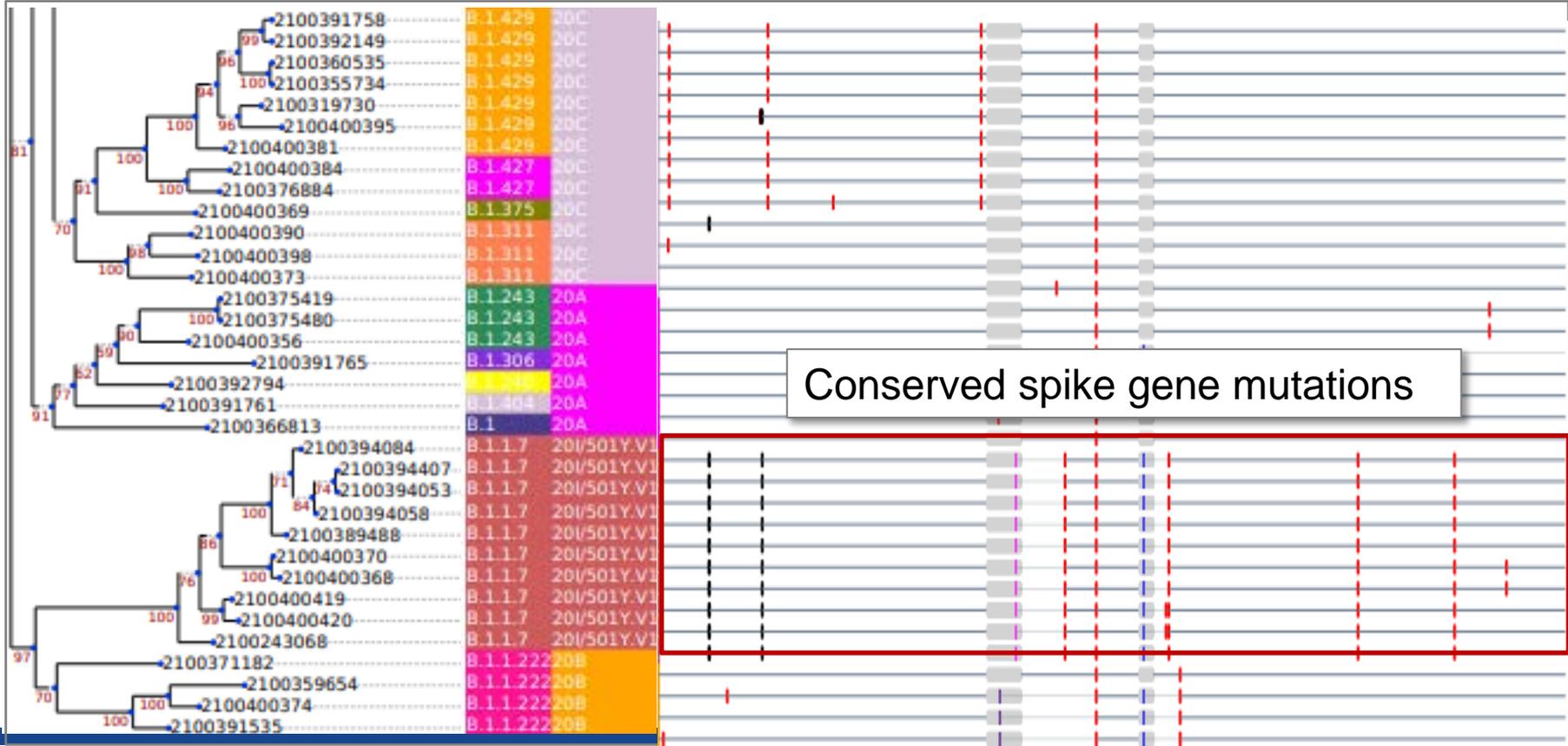


Example B.1.1.7 cluster investigation

- Individual specimen with SGTF identified at a commercial laboratory
- Index specimen unavailable for sequencing
- But CI/CT identified 10 additional B.1.1.7 cases among family and coworkers



Example B.1.1.7 cluster investigation



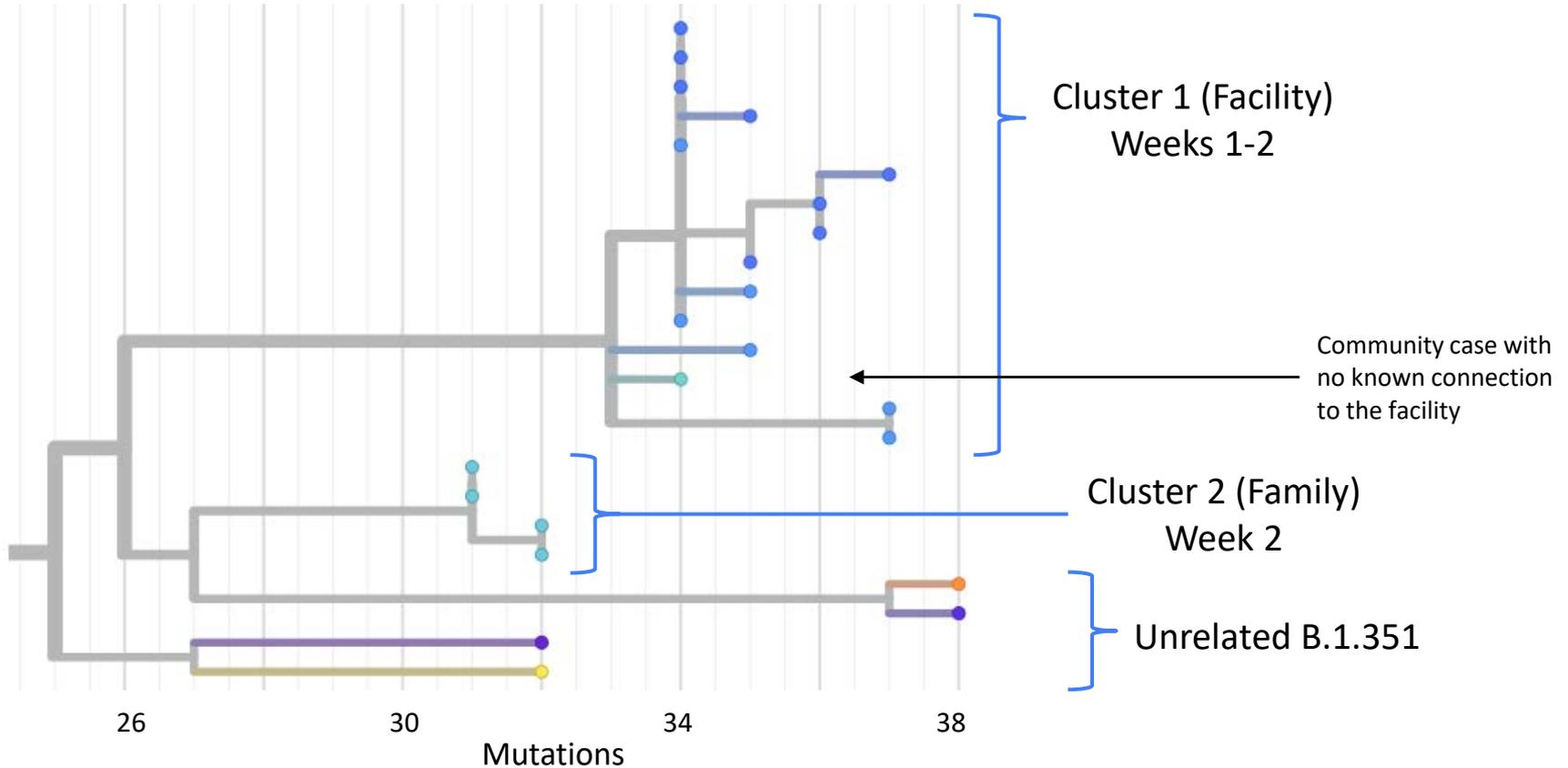
Detecting other variants with sentinel surveillance

- Surveillance by convenience sampling
 - **Random sampling:** 30 positive specimens per week from each clinical laboratory within statewide sentinel surveillance network
 - **CDPHE-tested:** all positive specimens identified at the state lab
- Better surveillance sampling → sequencing increased > 5-fold:
 - December 2020: 180 specimens / week
 - April 2021: 1,000 – 1,200 specimens / week

Detecting other variants with sentinel surveillance

- Surveillance sequencing led to the detection of the first B.1.351 in Colorado
 - Multiple positives were identified as B.1.351 from the same county and connected to a congregate living facility (March 1, 2021)
 - Case investigation and contact tracing at the facility identified additional cases of B.1.351
 - The following week (March 8, 2021), multiple specimens from another county were identified among members of a single family

Two B.1.351 clusters identified in March 2021

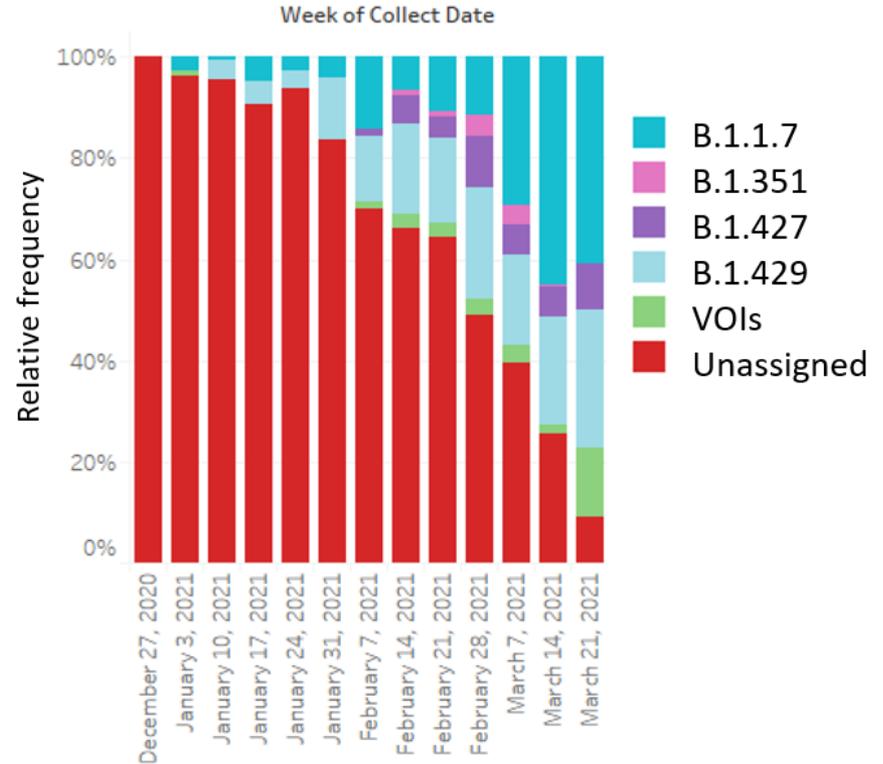


Tracking proportions of VOC/VOI

- CO continues to track VOC/VOI (Variant of Interest) proportions
- Excludes all:
 - Known SGTF submissions
 - Known VOC/VOI investigations
 - Special studies with CDC

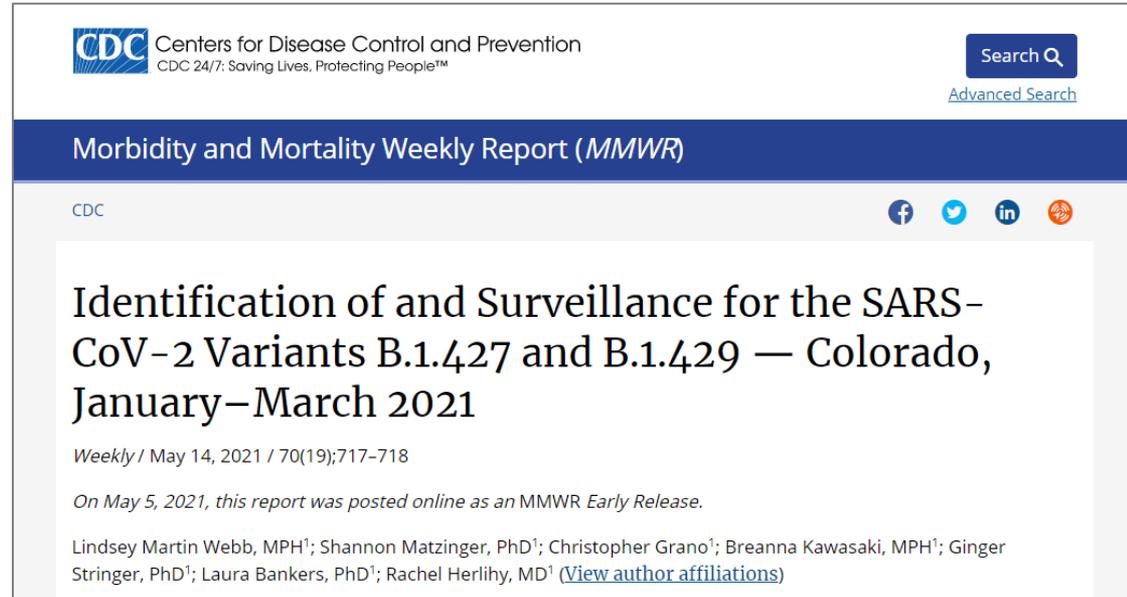
CDC COVID Data Tracker:

<https://covid.cdc.gov/covid-data-tracker/#variant-proportions>



Sequencing supports understanding virus transmission and COVID-19 severity

- VOC B.1.427/B.1.429
MMWR
- Vaccine breakthrough
- Reinfection
- Wastewater surveillance
 - See Module 2.7



The screenshot shows the CDC website interface for a Morbidity and Mortality Weekly Report (MMWR) article. At the top left is the CDC logo with the text "Centers for Disease Control and Prevention" and "CDC 24/7: Saving Lives. Protecting People™". To the right is a search bar with a magnifying glass icon and the text "Search Q", with a link for "Advanced Search" below it. The main header is a dark blue bar with the text "Morbidity and Mortality Weekly Report (MMWR)". Below this is a light blue bar with the CDC logo on the left and social media icons for Facebook, Twitter, LinkedIn, and YouTube on the right. The article title is "Identification of and Surveillance for the SARS-CoV-2 Variants B.1.427 and B.1.429 — Colorado, January–March 2021". Below the title is the publication information: "Weekly / May 14, 2021 / 70(19);717–718". A note states: "On May 5, 2021, this report was posted online as an MMWR Early Release." The authors are listed as: "Lindsey Martin Webb, MPH¹; Shannon Matzinger, PhD¹; Christopher Grano¹; Breanna Kawasaki, MPH¹; Ginger Stringer, PhD¹; Laura Bankers, PhD¹; Rachel Herlihy, MD¹ ([View author affiliations](#))".

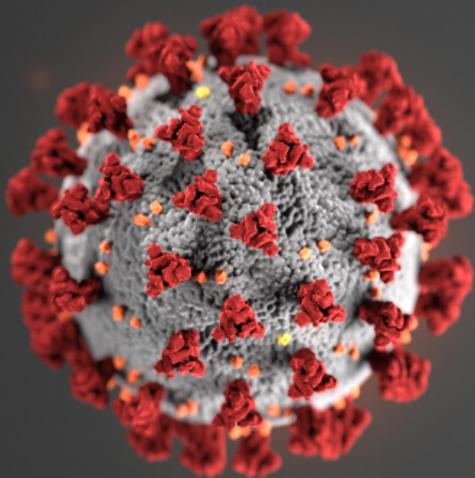
Summary

- Sequencing efforts support both national and statewide characterization of SARS-CoV2 transmission and COVID-19 severity.
- Sequencing adds valuable information for case investigation, contact tracing, and outbreak response
 - Most VOC cases identified by sequencing have led to detection and quarantine of secondary positives.
- Contribution of SGTF investigation to overall surveillance in CO
 - Layered approach to balance investigation of all SGTFs
 - Continue to monitor whether targeted surveillance impacts overall surveillance
- Detecting emerging variants
 - Unbiased, statewide surveillance is necessary to monitor and detect emerging VOCs not associated with SGTFs.

Learn more

- Other modules
 - Emerging variants of SARS-CoV-2 – Module 1.4
 - Distinguishing workplace from 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.

