

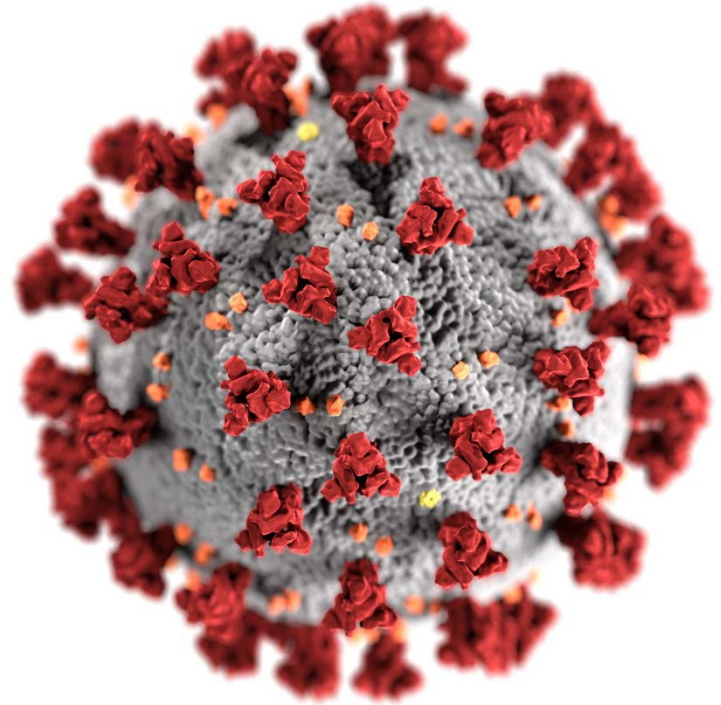
# Detecting and prioritizing SARS-CoV-2 variants

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

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(CDPHE)



[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
- 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

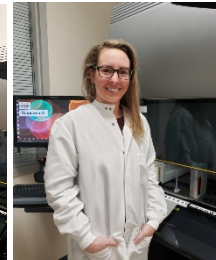
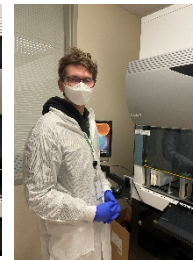


# CDPHE sequencing capacity

- Funded PulseNet Regional Lab  
[www.cdc.gov/pulsenet/index.html](http://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

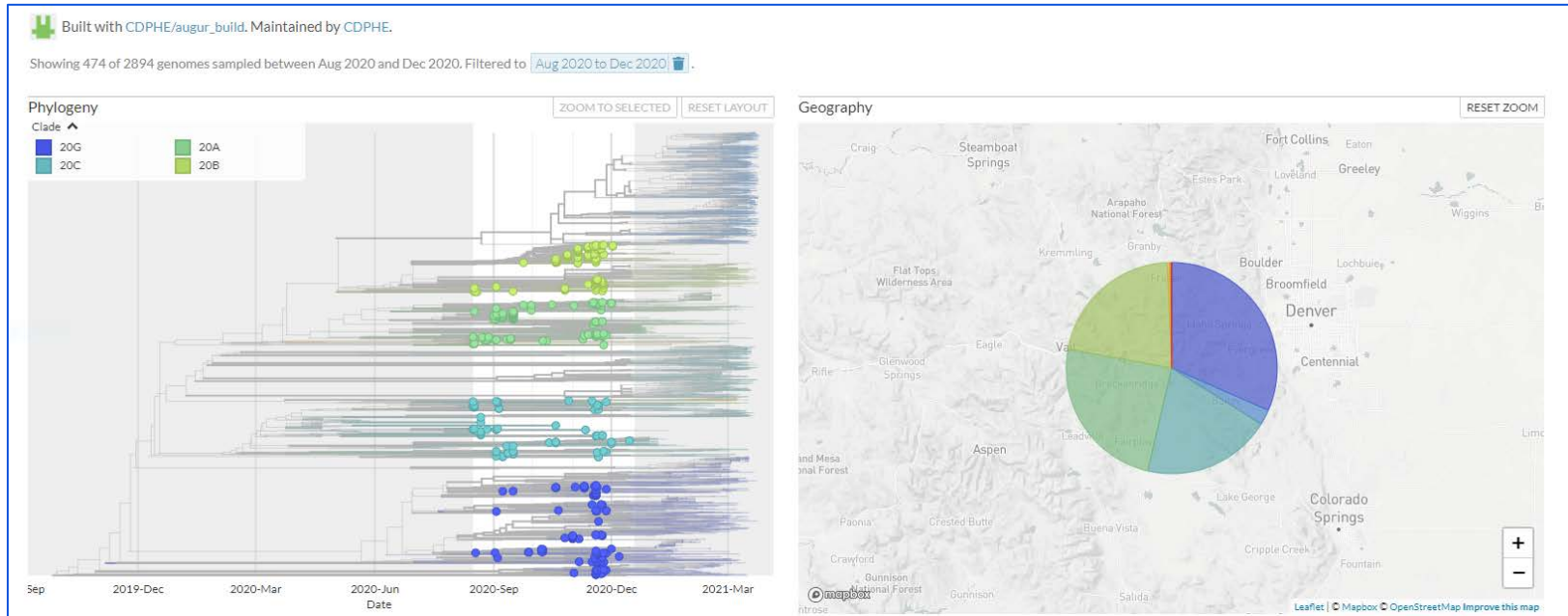


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# CDPHE sequencing priorities: August – December 2020

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



[https://nextstrain.org/groups/spheres/ncov/colorado?c=clade\\_membership&dmax=2020-12-31&dmin=2020-08-01&f\\_division=Colorado&p=full](https://nextstrain.org/groups/spheres/ncov/colorado?c=clade_membership&dmax=2020-12-31&dmin=2020-08-01&f_division=Colorado&p=full)


# 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

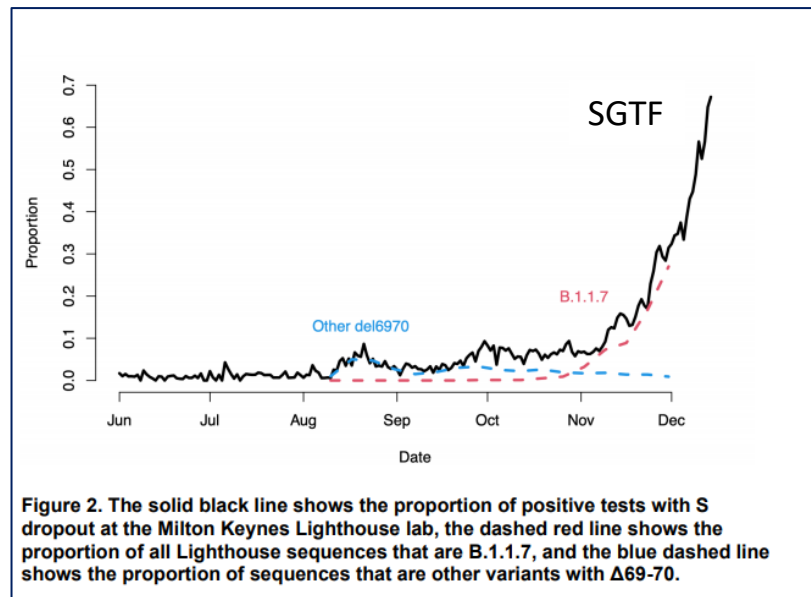
- First described in December 2020
- Classified as Variant of Concern (VOC)
- Deletion within spike (S) gene
- Produces a characteristic S Gene Target Failure (SGTF) on the ThermoFisher TaqPath RT-PCR assay.
- Module 1.4 – Emerging variants of SARS-CoV-2

[https://assets.publishing.service.gov.uk/government/uploads/system/uploads/attachment\\_data/file/959426/Variant\\_of\\_Concern\\_VOC\\_202012\\_01\\_Technical\\_Briefing\\_5.pdf](https://assets.publishing.service.gov.uk/government/uploads/system/uploads/attachment_data/file/959426/Variant_of_Concern_VOC_202012_01_Technical_Briefing_5.pdf)

  
Public Health  
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Protecting and improving the nation's health

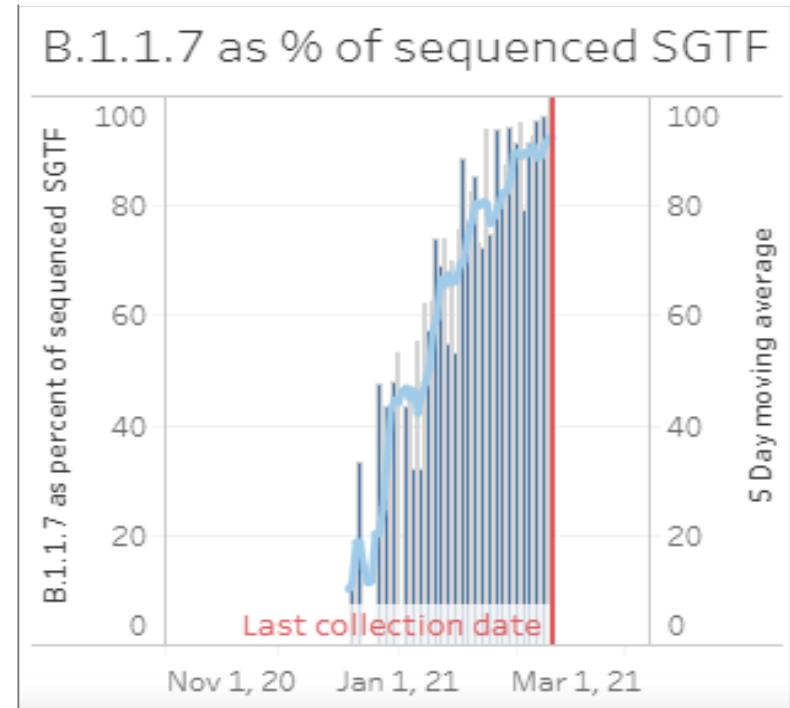
**Investigation of novel SARS-COV-2 variant**  
Variant of Concern 202012/01



# 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

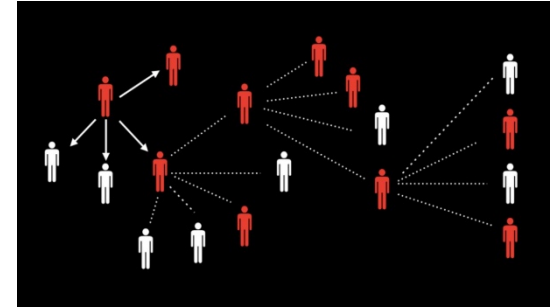
B.1.1.7 as % of sequenced SGTF US Data, Illumina-Helix



# Variant detection and response prioritization

Variant emergence increased statewide engagement for a broad surveillance program

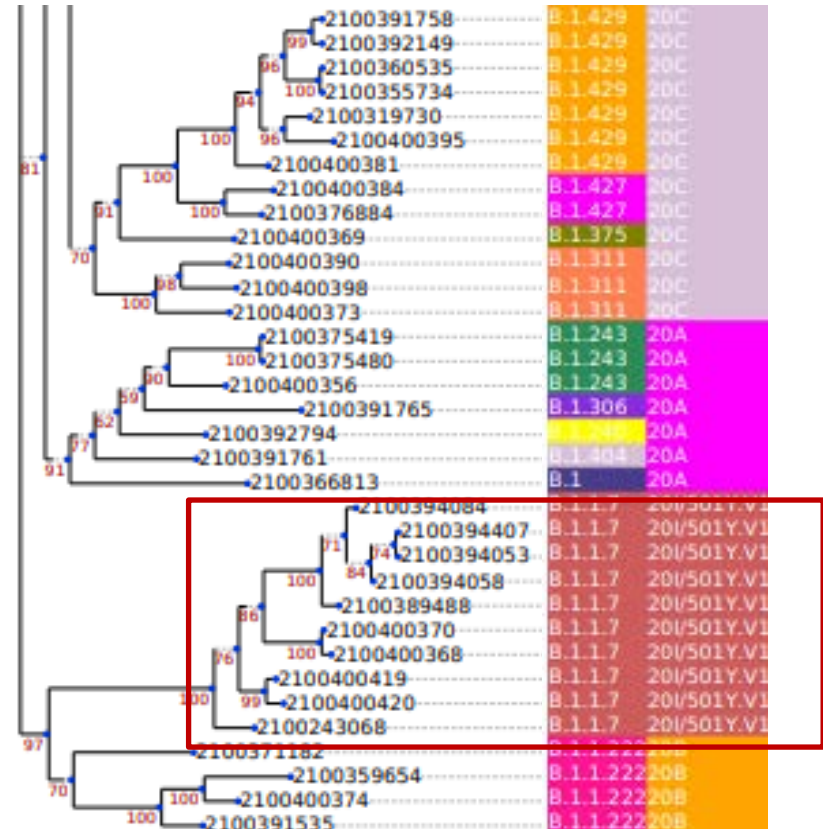
- Case investigation and contract tracing (CI/CT):
  - Daily meetings
  - Communicate sequence data as needed
- Epidemiology feedback:
  - Helps with contact tracing
  - Consistently detects secondary positive cases
  - Limited by turnaround time



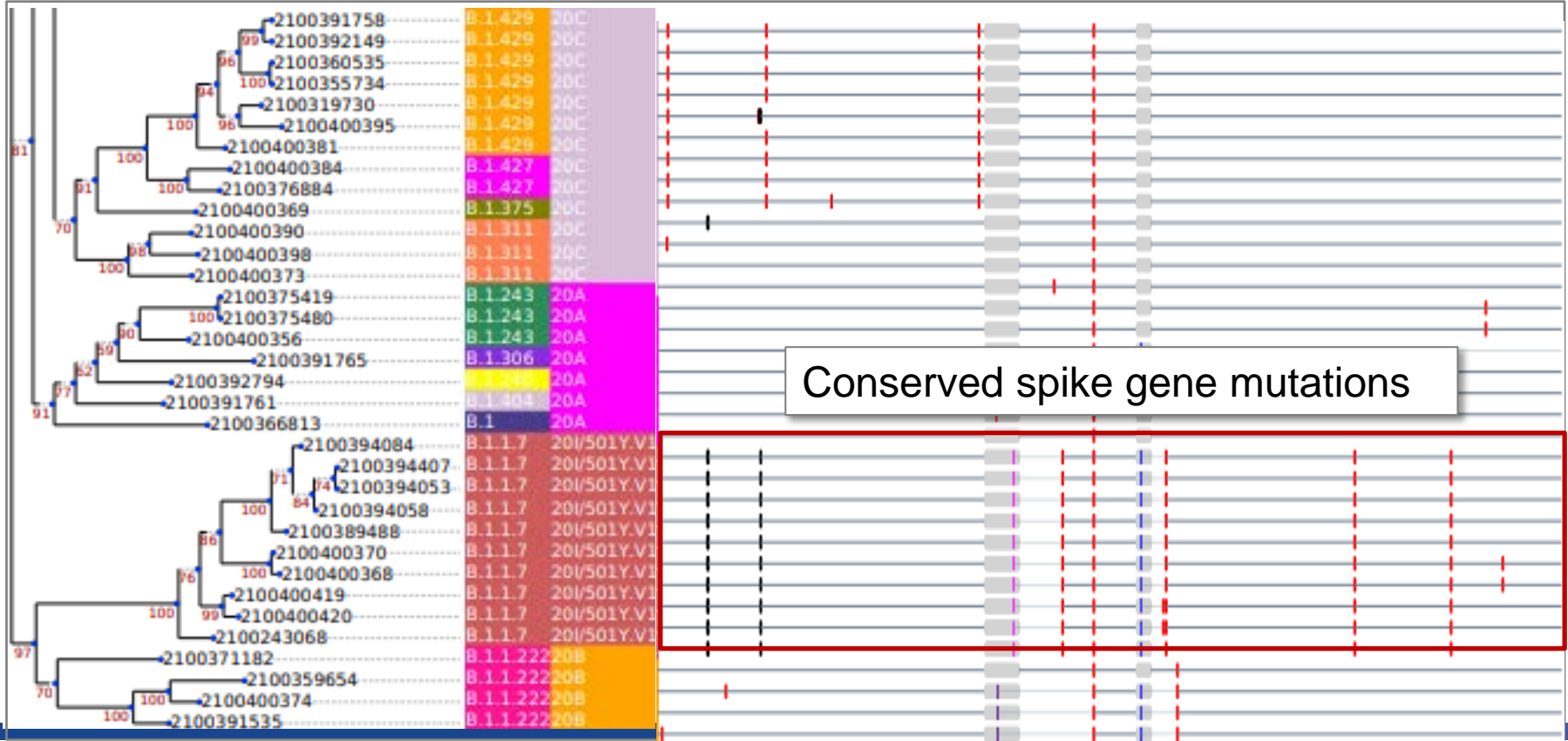


# Example B.1.1.7 cluster investigation

- 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



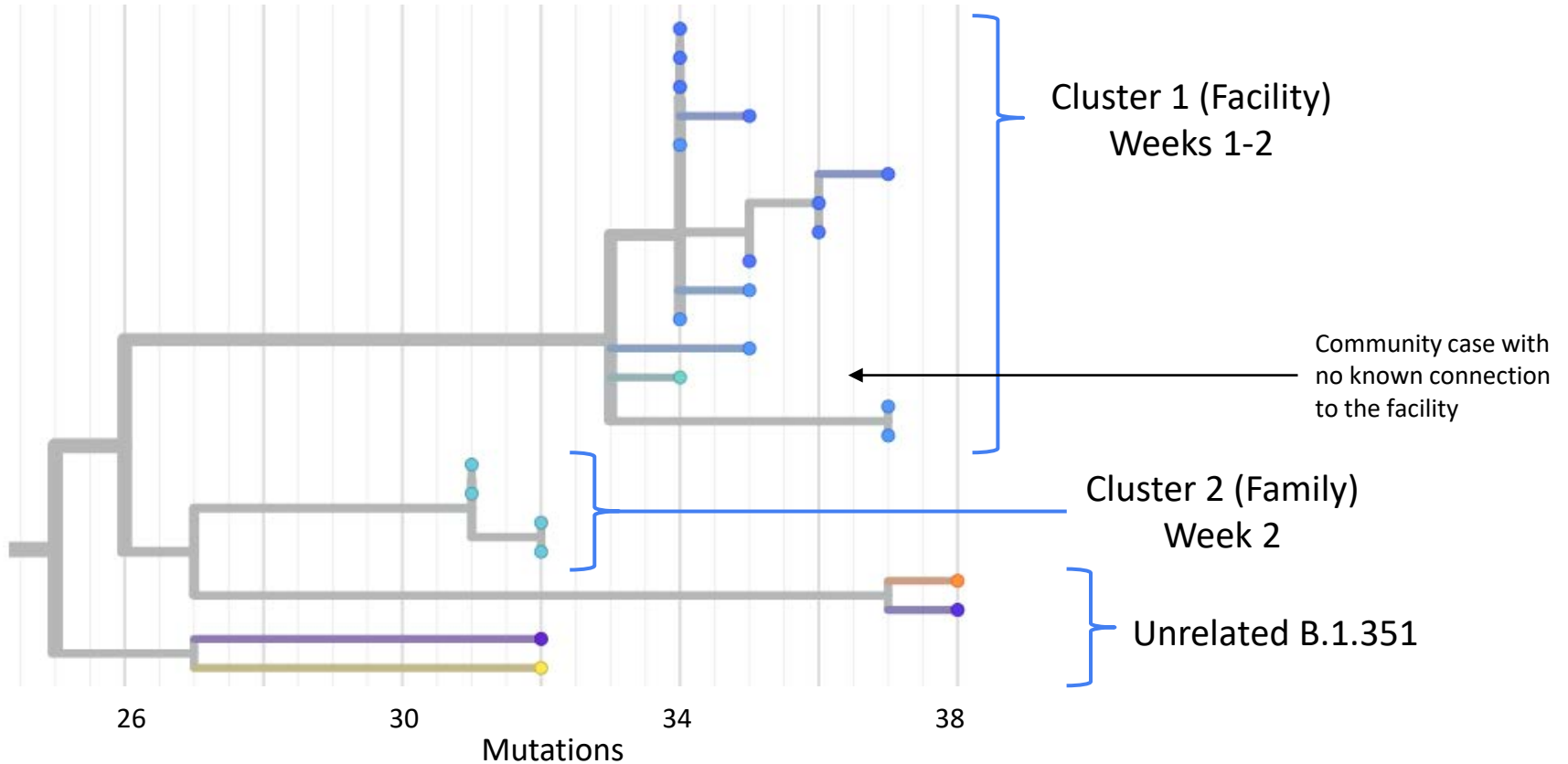
# Detecting other variants with sentinel surveillance

- 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

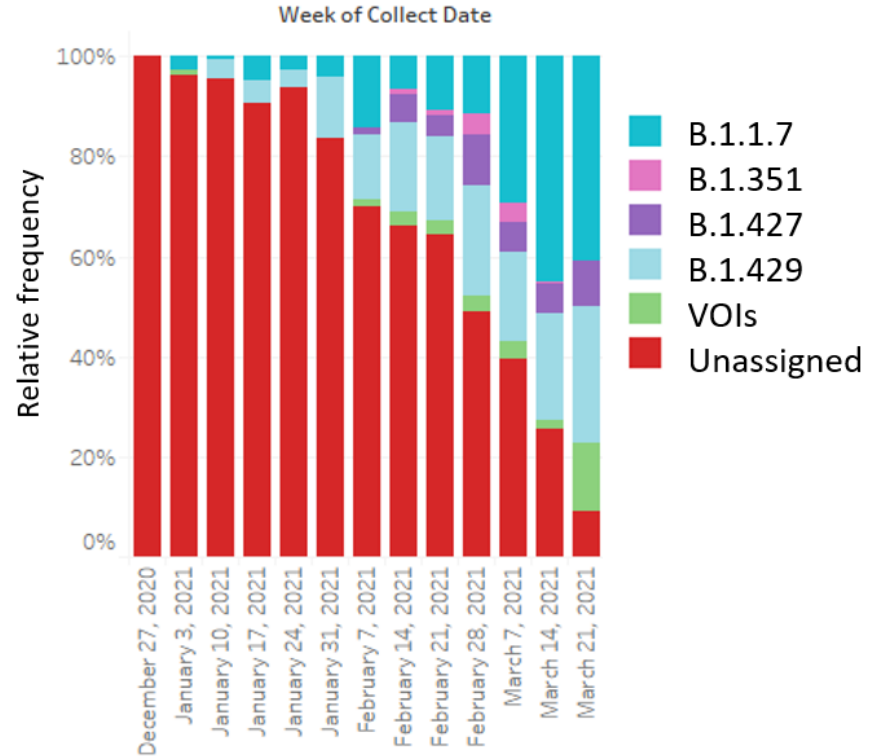


# Tracking proportions of VOC/VOI

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

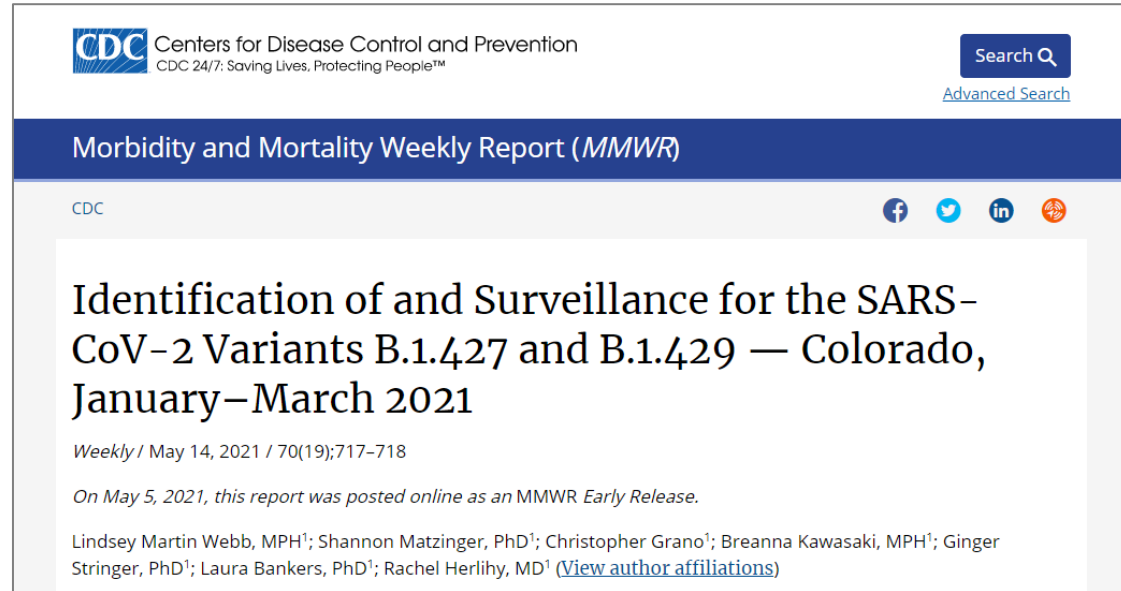
CDC COVID Data Tracker:

<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. A dark blue header bar contains the text "Morbidity and Mortality Weekly Report (MMWR)". Below this is a row of social media icons for Facebook, Twitter, LinkedIn, and YouTube. The main content area features the article title "Identification of and Surveillance for the SARS-CoV-2 Variants B.1.427 and B.1.429 — Colorado, January–March 2021" in a large, bold, black font. Below the title is the text "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." At the bottom, the authors are listed: "Lindsey Martin Webb, MPH<sup>1</sup>; Shannon Matzinger, PhD<sup>1</sup>; Christopher Grano<sup>1</sup>; Breanna Kawasaki, MPH<sup>1</sup>; Ginger Stringer, PhD<sup>1</sup>; Laura Bankers, PhD<sup>1</sup>; Rachel Herlihy, MD<sup>1</sup> ([View author affiliations](#))".

# Summary

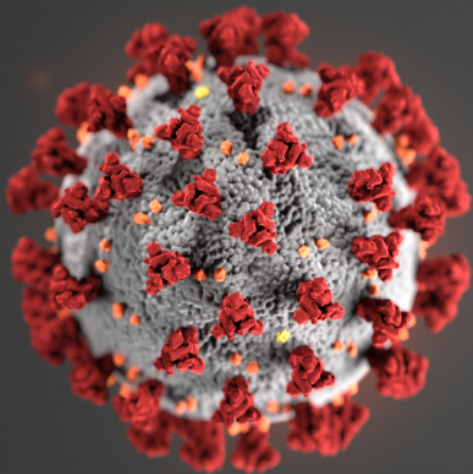
- Sequencing efforts support both national and statewide characterization of SARS-CoV2 transmission and COVID-19 severity.
- Sequencing adds valuable information for case investigation, contact tracing, and outbreak response
  - Most VOC cases identified by sequencing have led to detection and quarantine 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](https://go.usa.gov/xAbMw)





For more information, contact CDC  
1-800-CDC-INFO (232-4636)  
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.

