Centers for Disease Control and Prevention
CDC 24/7: Saving Lives, Protecting People™

COVID Data Tracker

United States
At a Glance

Cases Total
33,530,880
Last 30 Days

Deaths Total
603,018
Last 30 Days

67.1% of Adults with At Least
One Vaccination

Community Transmission Moderate

Variant Proportions

CDC's national genomic surveillance program identifies new and emerging SARS-CoV-2 variants to determine implications for COVID-19 diagnostics, treatments, and vaccines authorized for use in the United States. Monitoring the spread of emerging variants in the United States relies on widespread, rapid sequencing. To accelerate sequencing in the United States, CDC contracted with commercial diagnostic laboratories along with partnering with the Association of Public Health Laboratories (APHL). CDC's collaborative approach with these organizations implemented the National SARS-CoV-2 Strain Surveillance (NS3) program to provide a comprehensive and population-based US surveillance system.

Based on these data, sequences with similar genetic changes associated with important epidemiological and biological events are grouped into lineages. A viral lineage is a group of viruses defined by a founding variant and its descendants. The proportion of lineages circulating in the United Stated are tracked and characterized to determine if they are considered variants of high consequence (VOHC), variants of concern (VOC), or variants of interest (VOI). These data, along with data from many other sources, are used to inform national and state public health actions related to variants.

Estimated Proportions of SARS-CoV-2 Lineages

The data below show the estimated biweekly proportions of the most common SARS-CoV-2 lineages circulating in the United States, based on greater than 175,000 sequences collected through CDC's national genomic surveillance since Dec 20, 2020 and grouped in 2-week intervals. Data are subject to change over time and will be updated as more data become available. Variant proportions are adjusted using statistical weighting to correct for the non-random sampling of sequencing data over time and across states and to provide more representative national estimates.

Nowcast weighted estimates that predict proportions for more recent time intervals are added when "Nowcast On" is selected in the dashboard controls below.

Seroprevalence +

People at Increased Risk +

Prevention Measures and Social Impact +

Additional COVID-related Data

Communications Resources

COVID-19 Home

The interactive dashboard default setting is “Nowcast Off” and in this mode the data shown include the following:

Bar Charts:

The bar charts present point estimates of weighted proportions of the most common SARS-CoV-2 lineages grouped into selected 2-week intervals at the national-level or selected U.S. Department of Health & Human Services (HHS) region.

Table:

The table presents point estimates and associated 95% confidence intervals for the weighted proportions of the most common SARS-CoV-2 lineages per selected 2-week interval at the national-level or selected HHS region.

Pie Charts:

Each pie chart represents the point estimates of weighted proportions of the most common SARS-CoV-2 lineages within the selected 2-week interval based on sequences collected from each HHS region.

Statistical weighting:

The estimates of weighted variant proportions shown in the bar charts, pie charts, and table above are adjusted to correct for the potential non-random sampling of sequencing data over time and across states in order to provide more representative national and regional estimates. Using a survey-design-based approach, statistical weights for these estimates are based on the number of reverse transcription polymerase chain reaction (RT-PCR) tests and number of positive RT-PCR test results received, stratified by state, specimen collection date, and by genomic surveillance data source. Genomic surveillance data sources include commercial and reference laboratories, public health laboratories, hospital laboratories, and other testing locations. Estimates of weighted variant proportions from the most recent two-week interval are subject to change as specimens from that period are still being processed. Regional proportions are based on the number of sequences from each jurisdiction. Different jurisdictions may provide different numbers of sequences, and lower sequence numbers can produce greater uncertainty in the weighted proportion estimates.

Nowcast Weighted Estimates

When “Nowcast On” is selected, nowcast predicted proportions for the most recent 2-week interval are added to the bar chart and indicated by a double asterisk (**). The ** differentiates nowcast predictions from the weighted estimates shown for the earlier intervals in the same bar chart. To show nowcast prediction proportions, the most recent 2-week interval will need to be selected in the bar chart or in the dashboard controls, then the data table and map with pie charts will update as indicated by gray headers. The nowcast estimates use a multinomial regression model of weighted sequencing data to estimate variant proportions and prediction intervals. The nowcast provides timely estimates while accounting for limited sequence data availability, as specimens from that interval are still being processed. Nowcast estimates are projections and may differ from weighted estimates generated at later dates.

Bar Chart:

The bar(s) marked with a double asterisk (**) in the bar chart represents nowcast proportions of the most common SARS-CoV-2 lineages grouped at the national-level or selected HHS region. The nowcast uses all available weighted sequencing data and a mathematical model to project current SARS-CoV-2 lineage proportions for the most recent 2-week interval.

Table:

When “Nowcast On” and a nowcasted 2-week interval (denoted by **) are selected in the

dashboard controls, the table presents point estimates and associated 95% prediction intervals for nowcast variant proportions of the most common SARS-CoV-2 lineages for the most recent 2-week interval at the national-level or selected HHS region.

Pie Charts:

When “Nowcast On” and a nowcasted 2-week interval (denoted by **) are selected in the dashboard controls, each pie chart represents the point estimates and associated 95% prediction intervals of nowcast variant proportions of the most common SARS-CoV-2 lineages for the selected interval in each HHS region.

Unweighted Proportions of Variants of Concern and Other Lineages by State or Jurisdiction

Updated June 29, 2021

Variant proportions are based on representative CDC sequence data (NS3 + CDC-funded contract sequencing) collected over a 4-week period ending June 5, 2021 for states with at least 300 sequences.

State	B.1.1.7	B.1.351	B.1.617.2	P.1	Other lineages	Gra
Arizona	64.3%		7.2%	16.8%	10.7%	
California	56.3%	0.2%	8.5%	10.9%	20.2%	
Colorado						
Connecticut						
Florida						
Georgia						
Illinois						
Indiana						
Maryland						
Massachusetts						
Michigan						
Minnesota						
Missouri						
New Jersey						
New York						
North Carolina						
Ohio						
Oregon						
Pennsylvania						
Rhode Island						
Tennessee						
Texas						
Virginia						
Washington						
West Virginia						

Proportions in the table above are only shown for states, or jurisdictions, for which CDC has at least 300 sequences from specimens collected during this timeframe. Proportions are calculated using empirical (unweighted) data, which are subject to change over time and will

be updated as more data become available. Proportions of variants do not represent the total number that may be circulating in the United States and may not match cases reported by states, territories, tribes, and local officials. For states and jurisdictions not listed, CDC has insufficient genomic surveillance data for the specified time interval.

Data are subject to change over time and will be updated as more data become available. Sequences are assigned to a jurisdiction based on where the specimen was collected. Data are updated weekly.

More Information on Variants

- Substitutions of Concern for SARS-CoV-2 Monoclonal Antibody Therapies
- Variants of the Virus that Causes COVID-19
- Published SARS-CoV-2 Variants
- Genomic Surveillance for SARS-CoV-2 Variants
- SARS-CoV-2 Variant Classifications and Definitions
- Global Variants Report
- Science Brief: Emerging SARS-CoV-2 Variants

Why do we use genomic surveillance to monitor SARS-CoV-2 variants?

Visit the Genomic Surveillance for SARS-CoV-2 Variants page to learn more

Want to know more about variants of the virus that causes COVID-19?

Visit the About Variants of the Virus that Causes COVID-19 page to learn more

What SARS-CoV-2 variants are being monitored?

Visit the SARS-CoV-2 Variant Classifications and Definitions page to learn more about variant attributes and their classifications.

View and Download COVID-19 Case Surveillance Public Use Data