



## COVID-19



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# Variant Proportions in the U.S.

Updated Mar. 24, 2021

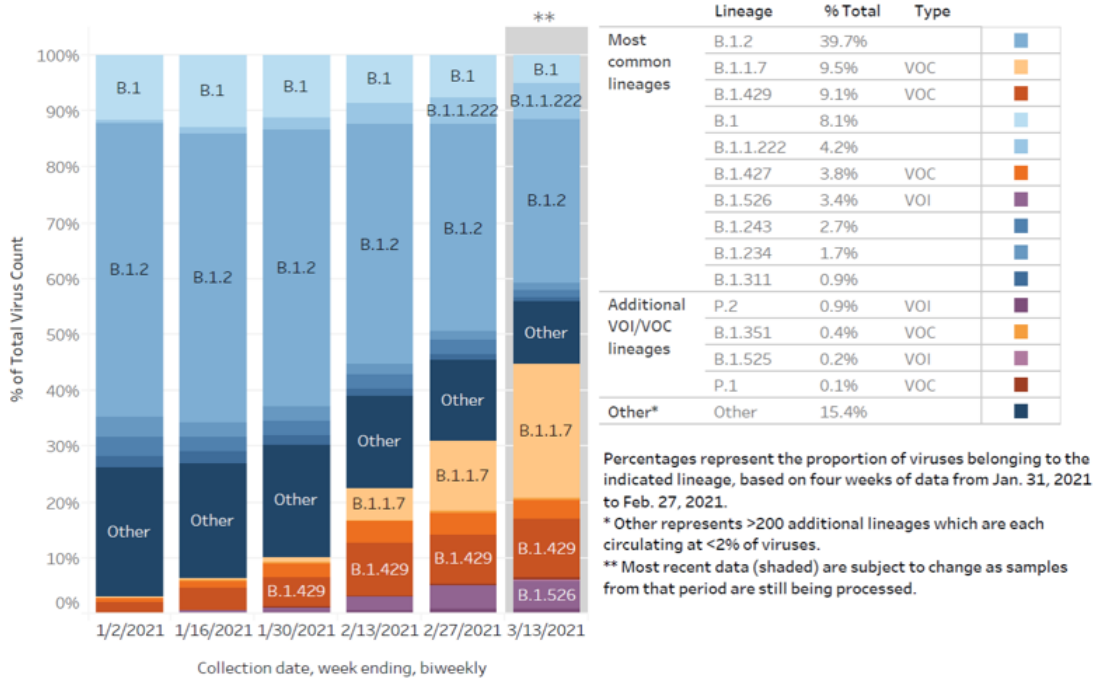
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CDC's [national genomic surveillance](#) program identifies new and emerging SARS-CoV-2 variants to determine implications for COVID-19 diagnostics, treatments, or vaccines authorized for use in the United States. Monitoring the spread of emerging variants in the United States relies on widespread, rapid sequencing. To accelerate sequencing in the United States, CDC has contracted with commercial diagnostic laboratories, and, in partnership with the Association of Public Health Laboratories (APHL), has 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\*, and the proportion of lineages circulating in the United States are tracked and characterized to determine if they are considered [variants of concern \(VOC\)](#) or [variants of interest \(VOI\)](#). Most of the lineages identified through genomic surveillance do not fall into either of these categories. These data, along with data from many other sources, are used to inform national and state public health actions related to variants.

\*A viral lineage is a group of viruses defined by a founding variant and its descendants. Names are assigned to SARS-CoV-2 lineages using manual and automated methods. Lineage designations are based on phylogenetic grouping followed by the identification of shared, common mutations.

## SARS-CoV-2 Variants Circulating in the United States



[Download Data](#) [CSV - 12 KB]

**Above left:**

The chart above shows the biweekly proportions of the most common SARS-CoV-2 lineages circulating in the United States, based on > 25,000 sequences collected through CDC national genomic surveillance since Dec 20, 2020 and grouped in two-week intervals. Proportions are calculated using empirical data which are subject to change over time and will be updated as more data becomes available.

The most recent data, shown in the rightmost column and highlighted in gray, are subject to change as specimens from that period are still being processed.

B.1.526, P.2, and B.1.525 are currently characterized as Variants of Interest (VOI). B.1.429, B.1.427, B.1.1.7, B.1.351, and P.1 are currently characterized as Variants of Concern (VOC). The most common circulating variants, B.1.2, B.1, B.1.1.222, B.1.243, B.1.234, B.1.311, are neither VOIs nor VOCs. Other variants are labeled as "Other" and represent >200 additional lineages which are each circulating at <2% of viruses during the period analyzed.

**Above, right:**

The table above lists the current VOIs and VOCs and the most common co-circulating SARS-CoV-2 lineages in the United States based on proportion. Percentages are based on CDC surveillance samples collected during the four-week period ending February 27, 2021.

Additional work is underway to produce model-based estimates of the prevalence of SARS-CoV-2 variants. These estimates are expected to be reported on this page in the near future.

## Proportions of SARS-CoV-2 Variants of Concern by State

State	B.1.1.7	B.1.351	B.1.427/B.1.429	P.1	Other lineages
Arizona	1.2%		25.7%		73.1%
California	1.7%		52.3%		46.0%
Connecticut	3.2%	0.3%	6.9%		89.7%
Florida	13.2%	0.1%	8.7%	0.4%	77.7%
Georgia	6.2%	0.2%	3.1%		90.6%
Illinois	2.2%	0.3%	4.9%	0.3%	92.5%
Indiana	3.2%		4.3%		92.4%
Louisiana	3.5%		2.8%		93.7%
Maryland	3.7%	0.5%	3.9%		92.0%
Massachusetts	5.9%	0.3%	1.5%		92.3%
Missouri	0.3%		5.8%		93.9%
Nevada	2.7%	0.4%	41.3%		55.6%
New Jersey	9.4%		3.4%		87.2%
New York	3.7%	0.2%	5.6%		90.5%
North Carolina	1.3%	0.7%	2.2%		95.8%
Ohio	2.2%		3.8%		94.0%
Pennsylvania	3.0%		3.6%		93.4%
Texas	7.1%		6.6%		86.3%
Virginia	0.3%	0.2%	3.1%		96.4%

Variant proportions are based on representative CDC sequence data (NS3 + CDC-funded contract sequencing) collected over a four-week period ending February 27, 2021. Proportions are only shown for states for which CDC has 300 sequences from specimens collected during this timeframe. Proportions are calculated using empirical data which are subject to change over time and will be updated as more data becomes 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 period. Data are based on the four-week period ending February 27, 2021, excluding data received within the last week.

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### More Information on Variants

- [Variants of the Virus that Causes COVID-19](#)
- [US COVID-19 Cases Caused by Variants](#)
- [Genomic Surveillance for SARS-CoV-2 Variants](#)
- [SARS-CoV-2 Variant Classifications and Definitions](#)
- [How CDC is Responding to SARS-CoV-2 Variants Globally](#)

#### Footnote

Rambaut A, Holmes EC, et. al. A dynamic nomenclature proposal for SARS-CoV-2 lineages to assist genomic epidemiology. (2020) *Nature Microbiology*  
DOI:10.1038/s41564-020-0770-5 [↗](#)

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Content source: [National Center for Immunization and Respiratory Diseases \(NCIRD\), Division of Viral Diseases](#)