Variant Proportions in the U.S.

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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 U.S. surveillance system.

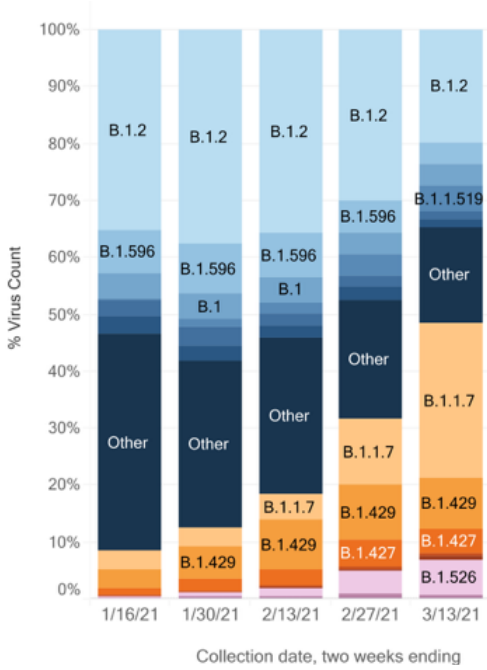
Based on these data, sequences with similar genetic changes associated with important epidemiological and biological events are grouped into lineages* and the proportion of lineages circulating in the United Stated are tracked and characterized to determine if they are considered variants of interest (VOI), variants of concern (VOC), or variants of high consequence (VOHC). These data, along with data from many other sources, are used to inform national and state public health actions related to variants. Most of the lineages identified through genomic surveillance are neither VOI nor VOC, and there are currently none that rise to the level of high consequence.

*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 the identification of shared mutations, followed by a phylogenetic analysis, which determines genetic or evolutionary relatedness.

Estimates of SARS-CoV-2 Prevalence

Figure 1 below shows the estimated biweekly prevalence of the most common SARS-CoV-2 lineages circulating in the United States, based on >40,000 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 in Figure 1 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.

Figure 1. SARS-CoV-2 Variants Circulating in the United States, January 2 – March 13, 2021†



	Lineage	% Total	95%CI	Type
Most common lineages	B.1.1.7	27.2%	24.6-29.9%	VOC
	B.1.2	19.8%	17.3-22.6%	
	B.1.429	9.1%	6.8-12.1%	VOC
	B.1.526	6.2%	4.3-8.8%	VOI
	B.1.1.519	4.7%	3.8-5.8%	
	B.1.427	4.3%	3.3-5.6%	VOC
	B.1.596	3.9%	3.2-4.7%	
	B.1	3.7%	2.9-4.6%	
	B.1.234	1.4%	1.0-1.9%	
	B.1.243	1.4%	1.1-1.8%	
Additional VOI/VOC lineages	P.2	0.5%	0.3-0.7%	VOI
	P.1	0.5%	0.3-0.8%	VOC
	B.1.351	0.5%	0.3-0.7%	VOC
	B.1.525	0.3%	0.2-0.4%	VOI
Other*	Other	16.6%	14.4-19.2%	

Percentages represent the proportion of viruses belonging to the indicated lineage, based on two weeks of data with collection dates ending March 13, 2021.

* Other represents >200 additional lineages, which are each circulating at <2% of viruses.

† Estimated weights come from laboratory data providing the number of reverse transcription polymerase chain reaction (RT-PCR) tests and number of positive RT-PCR test results stratified by state, specimen collection date, and by genomic surveillance data source, using a survey-design-based approach. COVID-19 laboratory data sources include commercial and reference laboratories, public health laboratories, hospital laboratories, and other testing locations. Summary data that appear in the table include specimen collection dates from February 28 through March 13, 2021. Methods for sub-national estimation are being developed as more data are received.

Download Data [XLS – 658 KB]

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

Alabama	14.6%	0.2%	2.6%		82.6%
Arizona	4.3%		31.3%	0.2%	64.2%
Arkansas	1.6%		5.7%		92.7%
California	10.3%	0.1%	56.1%	0.7%	32.6%
Colorado	16.6%		25.9%	0.3%	57.3%
Connecticut	16.1%	0.8%	7.4%	0.4%	75.4%
District of Columbia	16.2%	0.8%	5.9%		77.1%
Florida	34.5%	0.3%	9.4%	1.2%	54.6%
Georgia	22.1%	1.0%	4.8%	0.1%	72.1%
Illinois	13.1%	0.2%	13.2%	3.8%	69.7%
Indiana	10.4%	0.1%	6.2%	0.2%	83.1%
Kansas	0.5%		8.6%		90.9%
Kentucky	4.5%		3.9%		91.6%
Louisiana	13.4%		6.8%		79.8%
Maine	3.1%	0.9	6.0%		90.0%
Maryland	20.4%	1.6%	4.0%		74.0%
Massachusetts	18.6%	0.2%	3.6%	1.4%	76.3%
Michigan	39.0%	0.1%	7.2%	0.1%	53.6%
Minnesota	25.5%	0.2%	10.9%		63.5%
Mississippi	7.7%	0.3%	6.2%		85.8%
Missouri	7.4%	0.2%	6.0%		86.5%
Nevada	4.8%	0.2%	46.0%		49.1%

New Hampshire	13.0%		2.5%	0.2%	84.3%
New Jersey	22.8%		2.7%	0.2%	74.3%
New Mexico	3.3%		21.3%		75.5%
New York	15.7%	0.1%	5.3%		78.9%
North Carolina	8.3%	1.6%	4.4%		85.8%
Ohio	11.4%	0.4%	5.8%	0.4%	82.0%
Oregon	5.5%	0.3%	31.3%	0.6%	62.4%
Pennsylvania	14.1%	0.3%	4.8%		80.9%
Rhode Island	11.9%		7.4%	0.3%	80.5%
South Carolina	9.2%	2.8%	6.0%	0.3%	81.7%
Tennessee	35.0%		4.9%		60.2%
Texas	25.2%	0.2%	8.0%	0.1%	66.5%
Utah	4.6%		20.8%	0.5%	74.2%
Virginia	11.5%	1.7%	6.7%		80.1%
Washington	2.2%		27.0%		70.8%
West Virginia	11.3%		9.1%		79.6%
Wisconsin	9.5%	1.0%	8.5%	0.2%	80.8%

Variant proportions are based on representative CDC sequence data (NS3 + CDC-funded contract sequencing) collected over a 4-week period ending March 13, 2021. Proportions in Table 1 are only shown for states 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 period.

More Information on Variants

- Science Brief: Emerging SARS-CoV-2 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, O'Toole A, et. al. A dynamic nomenclature proposal for SARS-CoV-2 lineages to assist genomic epidemiology. *Nature Microbiology* 2020; 5(11)1403–1407.

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