As of May 11, genomic surveillance data will be reported biweekly, based on the availability of positive test specimens. You can find archived genomic surveillance data at data.cdc.gov.

United States At a Glance	Total Hospitalizations 6,143,551	Total Deaths 1,127,928	17.0% of People with Updated Booster Dose
	Trend in Hospital Admissions -6.5% in past week	Trend in % COVID-19 Deaths -5.3% in past week	

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Variants & Genomic Surveillance

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Variant Proportions

Monitoring Variant Proportions

SARS-CoV-2, the virus that causes COVID-19, is constantly changing and accumulating mutations in its genetic code over time. New variants of SARS-CoV-2 are expected to continue to emerge. Some variants will emerge and disappear, while others will emerge and continue to spread and may replace previous variants.

To identify and track SARS-CoV-2 variants, CDC uses genomic surveillance. CDC's national genomic surveillance system collects SARS-CoV-2 specimens for sequencing through the National SARS-CoV-2 Strain Surveillance (NS3) program, as well as SARS-CoV-2 sequences generated by commercial or academic laboratories contracted by CDC and state or local public health laboratories. Virus genetic sequences are analyzed and classified as a particular lineage. The proportions of SARS-CoV-2 variants in a population are calculated nationally, by HHS region, and by jurisdiction. The sequences analyzed through CDC's national genomic sequencing and bioinformatics efforts fuel the comprehensive and population-based U.S. surveillance system established to identify and monitor the spread of variants.

Rapid virus genomic sequencing data combined with phenotypic data are further used to determine whether COVID-19 tests, treatments, and vaccines authorized or approved for use in the United States will work against emerging variants.

Types of Variant Proportion Data

CDC provides estimates of variant proportions for two-week periods. These proportions are calculated in two ways: weighted estimates and Nowcast estimates.

Weighted estimates (provided for all two-week periods except the most recent two, two-week periods) are variant proportions that are based on empirical (observed) genomic sequencing data. These estimates are not available for the most recent two-week periods because of the time it takes to generate the sequencing data, including sample collection, specimen treatment, shipping, analysis, and upload into public databases.

Lineages with weighted estimates less than 1% of all circulating variants are combined with their parent lineage. When the weighted estimate of a lineage crosses the 1% threshold and has substitutions in the spike protein that could affect vaccine efficacy, transmission, or severity, it may be separated from its parent lineage and displayed on its own in the variant proportions data.

Nowcast estimates (provided for the most recent two two-week periods when the "Nowcast on" option is selected below) are model-based projections of variant proportions for the most recent two-week periods to enable timely public health action. CDC uses the Nowcast to forecast variant proportions before the weighted estimates are available for a given two-week period.

Projections for an emerging lineage with a high growth rate may have a higher degree of uncertainty (wider predictive interval) when it is just beginning to spread and still has low weighted estimates. Projections may also be biased during times of delayed reporting (e.g., around holidays). CDC performs frequent evaluations of Nowcast to inform performance improvements.

Nowcast estimates for a parent lineage include projected changes in its child lineages until a child lineage's weighted estimate crosses the 1% threshold. Once the weighted estimate crosses the 1% threshold for the two-week period with sequences available, the initial Nowcast projections for the child lineage proportion for the two recent two-week periods may be substantially higher than 1%.

CDC provides updated variant proportions for weighted estimates and Nowcast estimates every other week on Friday.

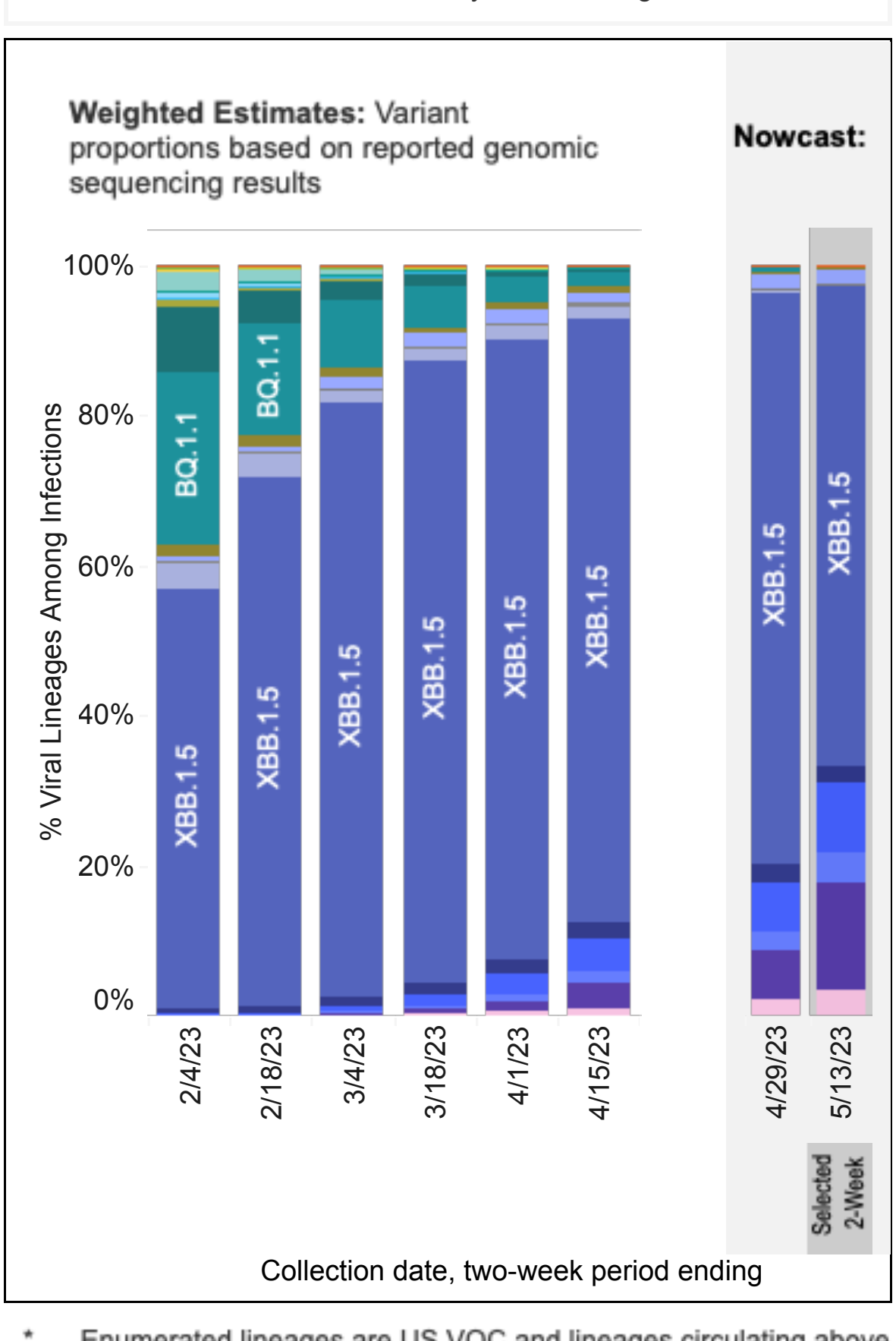
On This Page

HHS Region: USA | Data for the 2-Week Period Ending on: 5/13/2023 (Nowcast) | View: Nowcast and Weighted Estimates / Weighted Estimates Only

This shows weighted and Nowcast estimates for the United States. The table and map show estimates for the 2-week period ending on 5/13/2023 (Nowcast).

Weighted and Nowcast Estimates in United States for 2-Week Periods in 1/2..

Hover over (or tap in mobile) any lineage of interest to see the amount of uncertainty in that lineage's estimate.



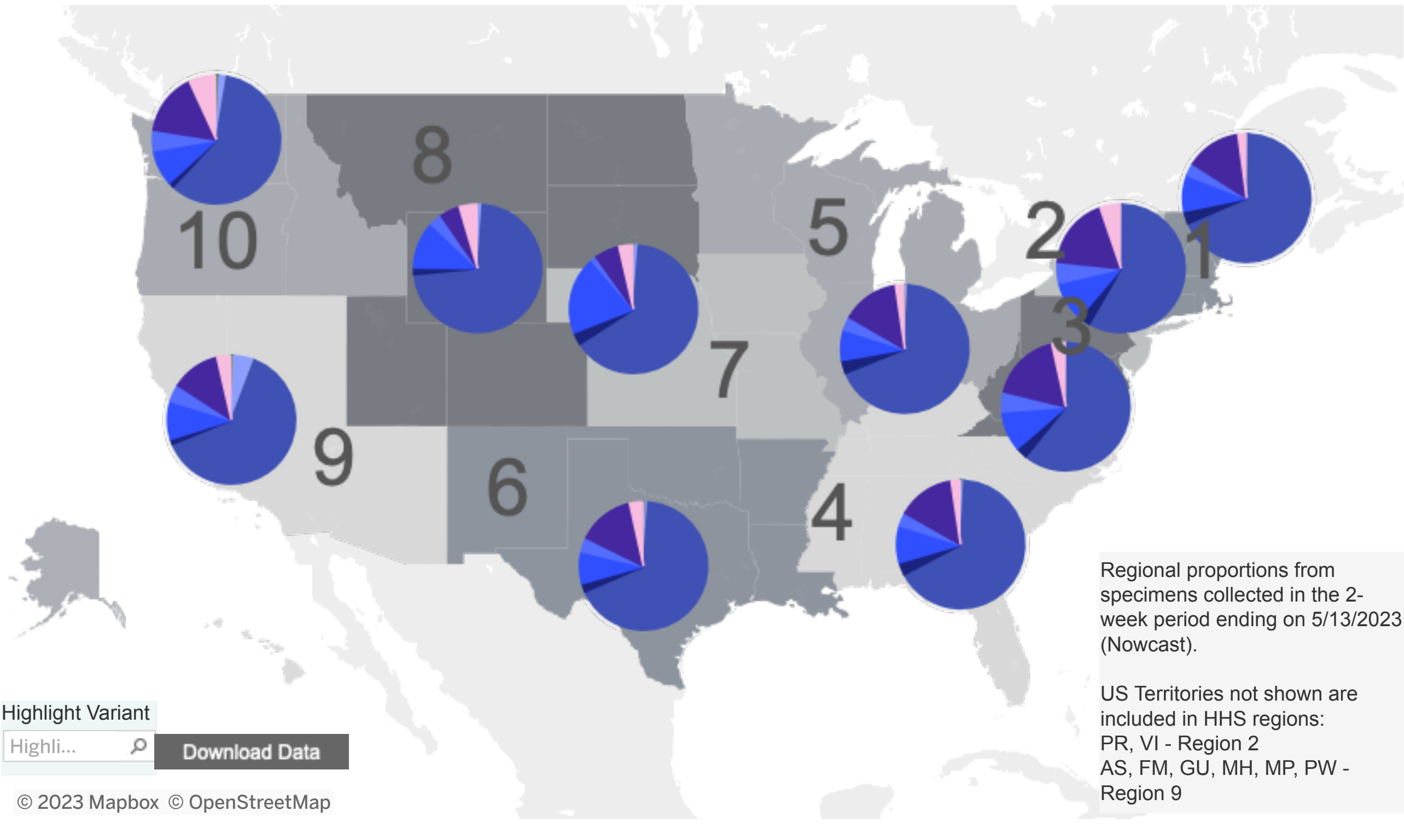
Nowcast Estimates in United States for 4/30/2023 – 5/13/2023

USA

WHO label	Lineage #	US Class	%Total	95%PI
Omicron	XBB.1.5	VOC	64.0%	59.1-68.6%
	XBB.1.16	VOC	14.3%	11.1-18.1%
	XBB.1.9.1	VOC	9.2%	8.0-10.6%
	XBB.1.9.2	VOC	4.0%	3.2-5.1%
	XBB.2.3	VOC	3.5%	1.9-6.3%
	XBB.1.5.1	VOC	2.4%	1.9-3.0%
	FD.2	VOC	1.8%	0.8-4.0%
	BQ.1.1	VOC	0.3%	0.1-0.5%
	CH.1.1	VOC	0.2%	0.2-0.4%
	XBB	VOC	0.2%	0.1-0.4%
	BQ.1	VOC	0.0%	0.0-0.1%
	BN.1	VOC	0.0%	0.0-0.0%
	BA.5	VOC	0.0%	0.0-0.0%
	BA.2.12.1	VOC	0.0%	0.0-0.1%
	BA.2	VOC	0.0%	0.0-0.0%
	BA.2.75	VOC	0.0%	0.0-0.0%
	BF.7	VOC	0.0%	0.0-0.0%
	BA.5.2.6	VOC	0.0%	0.0-0.0%
Other	Other*		0.0%	0.0-0.0%

* Enumerated lineages are US VOC and lineages circulating above 1% nationally in at least one 2-week period. "Other" represents the aggregation of lineages which are circulating <1% nationally during all 2-week periods displayed.
# BA.1, BA.3 and their sublineages (except BA.1.1 and its sublineages) are aggregated with B.1.1.529. Except BA.2.12.1, BA.2.75, XBB and their sublineages, BA.2 sublineages are aggregated with BA.2. Except BA.2.75.2, CH.1.1 and BN.1, BA.2.75 sublineages are aggregated with BA.2.75. Except BA.4.6, sublineages of BA.4 are aggregated to BA.4. Except BF.7, BF.11, BA.5.2.6, BQ.1 and BQ.1.1, sublineages of BA.5 are aggregated to BA.5. Except the lineages shown and their sublineages, sublineages of XBB are aggregated to XBB. Except XBB.1.5.1 and FD.2, sublineages of XBB.1.5 are aggregated to XBB.1.5. For all the other lineages listed, their sublineages are aggregated to the listed parental lineages respectively. Previously, XBB.2.3 and XBB.1.16 were aggregated to XBB. Lineages BA.2.75.2, XBB, XBB.1.5, XBB.1.5.1, FD.2, XBB.1.9.1, XBB.1.9.2, XBB.1.16, XBB.2.3, BN.1, BA.4.6, B..

Nowcast Estimates in for 4/30/2023 – 5/13/2023 by HHS Region

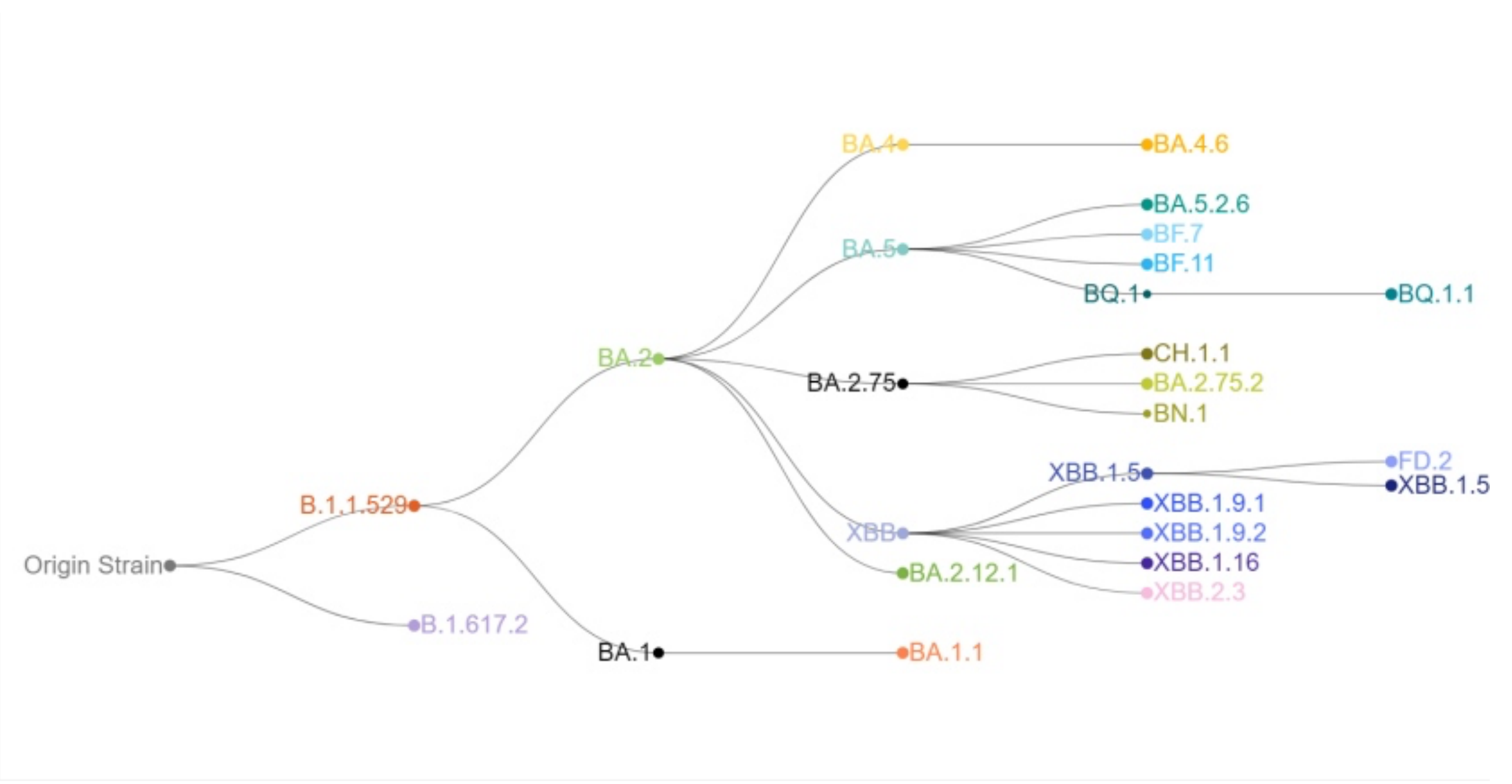


Lineages called using pangolin v4.2, pangolin-data v1.19 and usher v0.6.2.

Updated May 12, 2023

tableau

The diagram below shows how the Pango lineages on COVID Data Tracker are related to each other. For a full list of the current Pango lineages see https://cov-lineages.org/lineage_list.html.
CDC monitors SARS CoV-2 viruses from every lineage, but COVID Data Tracker only includes the lineages whose weighted estimates are above 1%. Some lineages have key differences in spike protein sequence that may reduce the effectiveness of some treatments or increase the virus's ability to spread. These lineages may be separated from their parent lineage on COVID Data Tracker when their biweekly proportion reaches more than 1%.



tableau

More About Variants

Understanding Variants

- What You Need to Know about Variants
- Understanding Variants

Variants and Genomic Surveillance

- Genomic Surveillance for SARS-CoV-2 Variants
- SARS-CoV-2 Variant Classifications and Definitions
- CDC's Role in Tracking Variants
- Published SARS-CoV-2 Sequences
- Global Variants Report
- Science Brief: Emerging SARS-CoV-2 Variants

About These Data

All Variants in the United States

Instructions: Data in the chart and table show the estimated variant proportions for the most common variants and timeframe. The U.S. map shows the estimated biweekly proportions of the most common SARS-CoV-2 variants circulating in the United States, divided by HHS regions. Data can be filtered by timeframe (two-week periods), and national or HHS region from the drop-down controls on the top. If a specific timeframe is selected in the chart, the data will change in the table and map to reflect the selected timeframe. If a specific region is selected in the U.S. map, the data will change in the table and map to reflect the selected region. For example, if Region 4 is selected, data will reflect estimates based on reported results from MS, GA, AL, TN, KY, NC, SC, and FL. Data for a specific variant can be highlighted in all figures by selecting it in the "Highlight Variant" box in the left bottom corner of U.S. map, or in the chart, table or pie chart in the U.S. map. To see the proportions and their confidence intervals/prediction intervals for all the common variants in the specific timeframe, hover pointer over a bar (timeframe) in the chart. To see the change of the proportion of a variant in different timeframes in a specific region, hover pointer to that variant in the specific region in U.S. map (a table showing proportions of other variants will also show up).

Nowcasting: The default setting for the chart, table, and U.S. map is to display CDC's Nowcast estimates. Because it can take 2-3 weeks from the time a specimen is collected to when its sequence data is available for analysis, Nowcast is an important tool that can estimate variant proportions for more recent time intervals. Nowcast does not predict future spread of the virus, but it does help estimate current prevalence of variants, based on genomic surveillance data from previous weeks. Estimates of variant proportions for previous two-week period may change as more data are reported. Nowcast estimates consistently align with the weighted proportions based on reported sequencing data, which are published 2-3 weeks later.

Weighted Proportions

To provide more representative national, regional, and jurisdiction-level estimates of variant proportions, calculations are included to account for sampling of data over time and across or within states. For example, sequences generated from outbreak investigations are often from a very narrow geographical region (such as a school) and may skew proportions within its larger jurisdiction. Using a survey-design-based approach, CDC uses statistical weights for these estimates that are based on the total number of reverse transcription polymerase chain reaction (RT-PCR) tests and number of SARS-CoV-2-positive RT-PCR test results received, stratified by state, specimen collection date, and by genomic surveillance data source. Variant proportions are estimated based on genomic sequences obtained through CDC (NS3 and CDC-funded sequencing contracts) and tagged baseline surveillance sequencing submitted to public repositories by state, local, academic, or commercial laboratories. Sequences used in this analysis are intended to be a representative sample of all cases during the selected timeframe and location. They may not match cases reported by states, territorial, tribal, and local officials. Estimates of weighted variant proportions are subject to change, as sequence data from specimens previously collected continues to increase over time.

The variant data reported for the jurisdiction-level estimates are limited to those designated as a variant of concern (VOC), variant of interest (VOI), or variant being monitored (VBM) by the U.S. government SARS-CoV-2 Interagency Group (SIG). Differences in the number of SARS-CoV-2 positive RT-PCR tests, sources of sequence data, and number of sequences available during a period affects the degree of certainty in the weighted proportion estimates. Confidence intervals are provided to describe these uncertainties. These data will be updated every other week on Friday.

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

How is CDC using genomic sequencing to track SARS-CoV-2 variants?
Visit CDC's Role in Tracking 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.

Cite COVID Data Tracker

Centers for Disease Control and Prevention. COVID Data Tracker. Atlanta, GA: US Department of Health and Human Services, CDC; 2023, May 13. https://covid.cdc.gov/covid-data-tracker