



COVID-19

SARS-CoV-2 Variant Classifications and Definitions

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What You Need to Know

- Viruses like SARS-CoV-2 continuously evolve as changes in the genetic code (caused by genetic mutations or viral recombination) occur during replication of the genome.
- SARS-CoV-2 has consistently mutated over the course of the pandemic, resulting in variants that are different from the original SARS-CoV-2 virus.
- Throughout the COVID-19 pandemic, many variants of SARS-CoV-2 have been found in the [United States](#) and [globally](#).
- Scientists use multiple [classification systems](#) to describe and communicate similarities and differences between SARS-CoV-2 viruses.

Key Definitions

- **Mutation:** A mutation refers to a single change in a virus's genome (genetic code). Mutations happen frequently, but only sometimes change the characteristics of the virus.
- **Lineage:** A lineage is a group of closely related viruses with a common ancestor. SARS-CoV-2 has many lineages; all cause COVID-19.
- **Sublineage:** A term used to define a lineage as it relates to being a direct descendent of a parent lineage. For example, BA.2.75 is a sublineage of BA.2.
- **Variant:** A variant is a viral genome (genetic code) that may contain one or more mutations. In some cases, a lineage or group of lineages with similar genetic changes, may be designated by the World Health Organization (WHO) or the U.S. SARS-CoV-2 Interagency Group (SIG) as a Variant of Interest (VOI), Variant of Concern (VOC), Variant of High Consequence (VOHC) or Variant Being Monitored (VBM) due to shared attributes and characteristics that may require public health action.
- **Recombination:** A process in which the genomes of two SARS-CoV-2 variants combine during the viral replication process to form a new variant that is different from both parent lineages. This may occur when a person is infected with two variants at the same time. The lineage that results from recombination is called a "recombinant."

Types of Classification

There are multiple ways in which SARS-CoV-2 viruses are classified. Each classification type can be appropriate, depending on the context in which SARS-CoV-2 is being communicated. SARS-CoV-2 is often discussed in the context of lineages (and sublineages). The most commonly used classification system for lineages is Pango. [Nextclade](#) may also be used in this context. In a larger context, lineages or groups of related lineages may be classified using Greek letters (such as Omicron) by the World Health Organization (WHO). These classification methods enable scientists to communicate similarities and differences between SARS-CoV-2 viruses.

Variant Classification

The U.S. Department of Health and Human Services (HHS) established a SARS-CoV-2 Interagency Group (SIG) to enhance coordination among CDC, National Institutes of Health (NIH), Food and Drug Administration (FDA), Biomedical Advanced Research and Development Authority (BARDA), and Department of Defense (DoD). This interagency group characterizes emerging variants and monitors their potential impact on vaccines, therapeutics, and diagnostics.

The SIG meets regularly to evaluate SARS-CoV-2 variants and lineages circulating in the United States and to make recommendations about the classification of variants and lineages. A group of experts assess the available data on variant proportion at the national and regional level. This information is shared with local and state public health officials to aid in their decision-making for community-level guidance. They also assess how these changes may affect vaccines, therapeutics, and diagnostics, as well as transmission and severity of disease. Variants may be reclassified as more information becomes available.

The SIG has updated its classification system and working definitions for variants of SARS-CoV-2, the virus that causes COVID-19, to better reflect the current variant landscape. The previous system classified all Omicron sublineages as part of the Omicron VOC and therefore did not provide the distinction needed to compare new descendent lineages with altered phenotypic characteristics to the Omicron parent lineages (BA.1, BA.2). These classification updates allow for independent evaluation and tracking of Omicron sublineages and forthcoming new variants when required.

The SIG uses [four types of classifications](#):

- Variant of high consequence (VOHC)
- Variant of concern (VOC)
- Variant of interest (VOI)
- Variants being monitored (VBM)

Notes: Each variant classification includes the possible attributes of lower classes (for example, VOC includes the possible attributes of VOI). This page will be updated as needed to show the variants that belong to each class. U.S. classifications may differ from the WHO classifications because the impact of variants may differ by location. The labels assigned to each variant are provided in the [List of Variants Table](#).

Pango Lineage System

The Pango lineage system is hierarchical—like a family tree. Lineages are evolutionarily descendants of a "parent" lineage. A lineage may be described as a "sublineage" when it is being discussed in relation to its parent lineage.

Lineages are named using an alphabetical prefix (such as B or BA) and numerical suffix (such as “.1” or “.1.1.5”). When a new lineage is defined, the Pango system assigns an additional number to the name of its parent lineage (e.g., BA.2.75 is a sublineage of BA.2). As the virus continues to change, the Pango lineage names can become very long. Lineages with longer names may be given alphabetic aliases and numbering continues (e.g., “BA” stands for “B.1.1.529,” thus BA.2 is the same as B.1.1.529.2).

For more information on the Pango lineage system and its nomenclature, see the [Pango Network](#). For a full list of the current Pango lineages, see [cov-lineages.org](#).

Nextclade

Nextclade is a tool that is used to classify SARS-CoV-2 sequences according to their genetic relatedness. Potentially important branches of the SARS-CoV-2 family tree are given names, indicating members of that branch are a “clade” and are thought to arise from a common ancestor.

Members of a clade will share many features with each other, reflecting their common ancestry. Not every SARS-CoV-2 virus is assigned its own clade by Nextclade. Each potential clade must circulate at a certain frequency for a period of time, show consistent growth in a region, or be assigned a WHO classification. The Nextclade team outlines their clade designation rubric in this [publication](#). These broader definitions offer an alternative naming solution that is meant to reflect significant differences in biology or circulation.

Nextclade clade names consist of the two-digit year of assignment followed by a letter indicating the order of assignment within the year. For example, “22A” is the first clade designated in 2022 and corresponds to the group of Pango lineages that descended from BA.4, which was circulating in early 2022. More information about the various clades and their relationship to the various Pango lineages is detailed at [covariants.org](#).

Recombinants

All coronaviruses have the potential to undergo a natural process called “recombination”. This can occur when two different lineages infect the same cell in someone at the same time. This rare phenomenon may affect the characteristics of the virus – including its ability to spread, cause severe disease or make treatments or vaccines less effective. In many cases, recombinant viruses do not have competitive advantages that help them rise.

CDC’s genomic surveillance systems can reliably detect and monitor the spread of variants, including recombinants. When a recombinant does emerge, CDC scientists evaluate and monitor the new recombinant just like any other variant lineage – including how it might be classified or when it should be presented on CDC’s COVID Data Tracker.

Summary of Variant Classifications

Variant of High Consequence (VOHC)

A VOHC has clear evidence that prevention measures or medical countermeasures (MCMs) have significantly reduced effectiveness relative to previously circulating variants. CDC monitors all variants circulating in the United States. In addition to the possible attributes of a variant of concern, variants designated as VOHC include impact on MCMs such as:

- demonstrated failure of diagnostic test targets.
- evidence to suggest a significant reduction in vaccine effectiveness, a disproportionately high number of infections in vaccinated persons, or very low vaccine-induced protection against severe disease.
- significantly reduced susceptibility to multiple EUA or approved therapeutics.
- more severe clinical disease and increased hospitalizations.

A variant of high consequence would require notification to WHO under the International Health Regulations, reporting to CDC, an announcement of strategies to prevent or contain transmission, and recommendations to update treatments and vaccines.

Currently, no SARS-CoV-2 variants are designated as VOHC. Classifications may change over time, based on the information available.

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Variant of Concern (VOC)

CDC monitors all variants circulating in the United States. In addition to the possible attributes of a variant of interest, variants designated as VOC include:

- increase in transmissibility.
- more severe disease (for example, increased hospitalizations or deaths).
- significant reduction in neutralization by antibodies generated during previous infection or vaccination.
- reduced effectiveness of treatments or vaccines, or diagnostic detection failures.

Variants of concern might require one or more appropriate public health actions such as:

- notify WHO under the International Health Regulations.
- report to CDC, local or regional efforts.
- increase preventative measures, such as masking, testing or physical distancing.
- conduct research to determine the effectiveness of vaccines and treatments against the variant.

Diagnostic tests, vaccines or treatments may be adapted to increase efficacy against circulating variants of concern.

Currently, no SARS-CoV-2 variants are designated as VOC. Classifications may change over time, based on the information available.

Variant of Interest (VOI)

CDC monitors all variants circulating in the United States. Variants designated as VOI include variants that have:

- reduced neutralization by antibodies generated against previous infection or vaccination.
- reduced efficacy of FDA approved treatments, or diagnostic tests.
- predicted increase in transmissibility or disease severity.

Possible attributes of a Variant of Interest include:

- specific genetic markers that are predicted to affect transmission, diagnostics, therapeutics, or immune escape.
- evidence that it is the cause of an increased proportion of cases or unique outbreak clusters.

A Variant of Interest may have limited prevalence in the United States, but potentially expanding in other countries. It might require one or more public health actions. CDC may increase surveillance or epidemiologic investigations to evaluate the risk a VOI may have on the United States.

Variants Being Monitored (VBM) ^

CDC monitors all variants circulating in the United States. Variants designated as VBM include:

- lineages with potential impact on available medical countermeasures based on analysis of genetic sequence data.
- lineages that previously caused more severe disease or increased transmission but that are no longer detected.
- lineage with an unusually large number of antigenic mutations AND presence in multiple countries with collection dates within 4 weeks.
- lineages previously designated as a VOI, VOC, or VOHC that are currently circulating at very low levels in the United States.

A Variant of Interest or a Variant of Concern may be downgraded to this list after it is no longer circulating at sustained levels and no longer poses significant risk to public health in the United States. Classifications may change over time, based on the evolving situation and information available.

List of Variants

WHO Label	Pango Lineage	Current Status	Date of Designation
N/A	Variants containing the F456L spike mutations*	VOI	VOI: September 1, 2023
Omicron	BA.2.86	VBM	VBM: September 1, 2023
Omicron	XBB.1.9.1	VBM	VBM: September 1, 2023
Omicron	XBB.1.9.2	VBM	VBM: September 1, 2023
Omicron	XBB.2.3	VBM	VBM: September 1, 2023
Omicron	XBB.1.16	VBM	VBM: September 1, 2023
Omicron	XBB.1.5	VBM	VBM: September 1, 2023
Omicron	CH.1.1	VBM	VBM: September 1, 2023
Omicron	BA.2.74	VBM	VBM: September 1, 2023
Alpha	B.1.1.7 and Q lineages	VBM	VOC: December 29, 2020 VBM: September 21, 2021
Beta	B.1.351 and descendent lineages	VBM	VOC: December 29, 2020 VBM: September 21, 2021
Gamma	P.1 and descendent lineages	VBM	VOC: December 29, 2020 VBM: September 21, 2021
Delta	B.1.617.2 and descendant lineages	VBM	VOC: June 15, 2021 VBM: April 14, 2022
Epsilon	B.1.427 and B.1.429	VBM	VOC: March 19, 2021 VOI: February 26, 2021 VOI: June 29, 2021 VBM: September 21, 2021
Eta	B.1.525	VBM	VOI: February 26, 2021 VBM: September 21, 2021
Iota	B.1.526	VBM	VOI: February 26, 2021

Kappa	B.1.617.1	VBM	VBM: September 21, 2021 VOI: May 7, 2021
N/A	B.1.617.3	VBM	VBM: September 21, 2021 VOI: May 7, 2021
Omicron (parent lineages)**	B.1.1.529 and descendant lineages	VOC	VOC: November 26, 2021
Zeta	P.2	VBM	VOI: February 26, 2021 VBM: September 21, 2021
Mu	B.1.621, B.1.621.1	VBM	VBM: September 21, 2021

* Many lineages have acquired the F456L mutation and common examples include EG.5, FL.1.5.1, and XBB.1.16.6.

** Omicron parent lineages include BA.1 or similar.

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*Non-peer-reviewed

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