World Health Organization

Tracking SARS-CoV-2 variants

All viruses, including SARS-CoV-2, the virus that causes COVID-19, change over time. Most changes have little to no impact on the virus' properties. However, some changes may affect the virus's properties, such as how easily it spreads, the associated disease severity, or the performance of vaccines, therapeutic medicines, diagnostic tools, or other public health and social measures.

WHO, in collaboration with partners, expert networks, national authorities, institutions and researchers have been monitoring and assessing the evolution of SARS-CoV-2 since January 2020. During late 2020, the emergence of variants that posed an increased risk to global public health prompted the characterisation of specific Variants of Interest (VOIs) and Variants of Concern (VOCs), in order to prioritise global monitoring and research, and ultimately to inform the ongoing response to the COVID-19 pandemic.

WHO and its international networks of experts are monitoring changes to the virus so that if significant amino acid substitutions are identified, we can inform countries and the public about any changes that may be needed to respond to the variant, and prevent its spread. Globally, systems have been established and are being strengthened to detect “signals” of potential VOIs or VOCs and assess these based on the risk posed to global public health. National authorities may choose to designate other variants of local interest/concern.

Reducing transmission through established and proven disease control methods/measures, as well as avoiding introductions into animal populations, are crucial aspects of the global strategy to reduce the occurrence of mutations that have negative public health implications.

Current strategies and measures recommended by WHO continue to work against virus variants identified since the start of the pandemic. Evidence from multiple countries with extensive transmission of VOCs has indicated that public health and social measures (PHSM), including infection prevention and control (IPC) measures, have been effective in reducing COVID-19 cases, hospitalizations and deaths. National and local authorities are encouraged to continue strengthening existing PHSM and IPC measures. Authorities are also encouraged to strengthen surveillance and sequencing capacities and apply a systematic approach to provide a representative indication of the extent of transmission of SARS-CoV-2 variants based on the local context, and to detect unusual epidemiological events.

This content is last updated on 29 November 2021.

Naming SARS-CoV-2 variants

The established nomenclature systems for naming and tracking SARS-CoV-2 genetic lineages by GISAID, Nextstrain and Pango are currently and will remain in use by scientists and in scientific research. To assist with public discussions of variants, WHO convened a group of scientists from the WHO Virus Evolution Working Group (now called the Technical Advisory Group on Virus Evolution), the WHO COVID-19 reference laboratory network, representatives from GISAID, Nextstrain, Pango and additional experts in virological, microbial nomenclature and communication from several countries and agencies to consider easy-to-pronounce and non-stigmatising labels for VOI and VOC. At the present time, this expert group convened by WHO has recommended using letters of the Greek Alphabet, i.e., Alpha, Beta, Gamma, Delta which will be easier and more practical to be discussed by non-scientific audiences.

31 May 2021 | Departmental news

WHO announces simple, easy-to-say labels for SARS-CoV-2 Variants of Interest and Concern

SARS-CoV-2 Variants, Working Definitions and Actions Taken

Given the continuous evolution of the virus that leads to SARS-CoV-2 and the constant developments in our understanding of the impacts of variants, these working definitions may be periodically adjusted. When necessary, variants not otherwise meeting all criteria outlined in these definitions may be designated as VOCs/VOIs/VUMs, and those posing a diminishing risk relative to other circulating variants may be reclassified, in consultation with the Technical Advisory Group on Virus Evolution (formally called the Virus Evolution Working Group).

Updates on SARS-CoV-2 classifications, the geographic distribution of VOCs, and summaries of their phenotypic characteristics (transmissibility, disease severity, risk of reinfection, and impacts on diagnostics and vaccine performance) based on published studies, are regularly provided in the WHO Weekly Epidemiological Updates.

Variants of Concern (VOC)

Working definition:

A SARS-CoV-2 variant that meets the definition of a VOI (see below) and, through a comparative assessment, has been demonstrated to be associated with one or more of the following changes at a degree of global public health significance:

- **Increase in transmissibility or detrimental change in COVID-19 epidemiology; OR**
- **Increase in virulence or change in clinical disease presentation; OR**

- **Decrease in effectiveness of public health and social measures or available diagnostics, vaccines, therapeutics.**

Currently designated Variants of Concern (VOCs)[+]:

WHO label	Pango lineage•	GISAID clade	Nextstrain clade	Additional amino acid changes monitored°	Earliest documented samples	Date of
Alpha	B.1.1.7	GRY	20I (V1)	+S:484K +S:452R	United Kingdom, Sep-2020	18-Dec
Beta	B.1.351	GH/501Y.V2	20H (V2)	+S:L18F	South Africa, May-2020	18-Dec
Gamma	P.1	GR/501Y.V3	20J (V3)	+S:681H	Brazil, Nov-2020	11-Jan-
Delta	B.1.617.2	G/478K.V1	21A, 21I, 21J	+S:417N +S:484K	India, Oct-2020	VOI: 4- VOC: 1
Omicron*	B.1.1.529	GR/484A	21K	-	Multiple countries, Nov-2021	VUM: 2 VOC: 2

• Includes all descendent lineages. See the cov-lineages.org and the Pango network websites for further details.

* See TAG-VE statement issued on 26 November 2021

° Only found in a subset of sequences

Enhancing Readiness for Omicron (B.1.1.529): Technical Brief and Priority Actions for Member States

Actions taken by WHO and Member States:

Primary actions by WHO for a potential VOC:

- **Comparative assessment of variant characteristics and public health risks by WHO and the Technical advisory Group on Virus Evolution.**
- **If determined necessary, coordinate additional laboratory investigations with Member States and partners.**
- **Communicate new designations and findings with Member States and public through established mechanisms.**
- **Evaluate WHO guidance through established WHO mechanisms and update, if necessary.**

Primary actions by a Member State, if a VOC is identified:

- **Submit complete genome sequences and associated metadata to a publicly available database, such as GISAID.**
- **Report initial cases/clusters associated with VOC infection to WHO through the IHR mechanism.**
- **Where capacity exists and in coordination with the international community, perform field investigations and laboratory assessments to improve understanding of the potential impacts of the VOC on COVID-19 epidemiology, severity, effectiveness of public health and social measures, diagnostic methods, immune responses, antibody neutralization, or other relevant characteristics.**

Variants of Interest (VOI)

Working definition

A SARS-CoV-2 variant :

- **with genetic changes that are predicted or known to affect virus characteristics such as transmissibility, disease severity, immune escape, diagnostic or therapeutic escape; AND**
- **Identified to cause significant community transmission or multiple COVID-19 clusters, in multiple countries with increasing relative prevalence alongside increasing number of cases over time, or other apparent epidemiological impacts to suggest an emerging risk to global public health.**

Currently designated Variants of Interest (VOIs):

WHO label	Pango lineage*	GISAID clade	Nextstrain clade	Earliest documented samples	Date of designati
Lambda	C.37	GR/452Q.V1	21G	Peru, Dec-2020	14-Jun-20
Mu	B.1.621	GH	21H	Colombia, Jan-2021	30-Aug-2(

*Includes all descendent lineages. See the cov-lineages.org and the Pango network websites for further details.

Actions taken by WHO and Member States:

Primary actions by a Member State, if a new potential VOI is identified:

- **Inform WHO through established WHO Country or Regional Office reporting channels with supporting information about VOI-associated cases (person, place, time, clinical and other relevant characteristics).**

- **Submit complete genome sequences and associated metadata to a publicly available database, such as GISAID.**
- **Perform field investigations to improve understanding of the potential impacts of the VOI on COVID-19 epidemiology, severity, effectiveness of public health and social measures, or other relevant characteristics.**
- **Perform laboratory assessments according to capacity or contact WHO for support to conduct laboratory assessments on the impact of the VOI on relevant topics.**

Primary actions by WHO for a potential VOI:

- **Comparative assessment of variant characteristics and public health risks by WHO.**
- **If determined necessary, coordinated laboratory investigations with Member States and partners.**
- **Review global epidemiology of VOI.**
- **Monitor and track global spread of VOI**

Reclassifying VOIs/ VOCs

A previously designated Variant of Interest (VOI) or Variant of Concern (VOC) which has conclusively demonstrated to no longer pose a major added risk to global public health compared to other circulating SARS-CoV-2 variants, can be reclassified.

This is undertaken through a critical expert assessment, in collaboration with the Technical Advisory Group on Virus Evolution of several criteria, such as the observed incidence/relative prevalence of variant detections among sequenced samples over time and between geographical locations, the presence/absence of other risk factors, and any ongoing impact on control measures.

Mutation Profiles of VOC/VOIs

As part of WHO's assessment of circulating variants, a clear understanding of the amino acid substitutions that are characteristic of each variant is needed. In collaboration with Erasmus Medical Centre the below table was assembled to summarize the spike protein amino acid changes for the current VOCs and VOIs. For each variant, the profile of amino acid changes in the Spike protein was created based on the first 1,000 genomes available in GISAID (genomes with less than 29,000 nucleotides and >5% Ns were excluded). Amino acid changes that are present in ≥ 85% of the sequences are shown. Of note, relevant amino acid changes may be present in other regions of the SARS-CoV-2 genome, and not all amino acid changes in the spike protein are associated to potential changes in the characteristics of the virus variant.

VOI/VOC profiles of Spike amino acid changes

Variants Under Monitoring (VUM)

Working definition

A SARS-CoV-2 variant with genetic changes that are suspected to affect virus characteristics with some indication that it may pose a future risk, but evidence of phenotypic or epidemiological impact is currently unclear, requiring enhanced monitoring and repeat assessment pending new evidence.

Note: It is expected that our understanding of the impacts of these variants may fast evolve, and designated Variants under Monitoring may be readily added/removed; therefore, WHO labels will not be assigned at this time. Former VOIs/VOCs may, however, be monitored for an extended period under this category, and will maintain their assigned WHO label until further notice.

Currently designated Variants Under Monitoring

Pango lineage*	GISAID clade	Nextstrain clade	Earliest document samples

Pango lineage*	GISAID clade	Nextstrain clade	Earliest document samples
AZ.5[#]	GR	-	Multiple countries, Jan-2021
C.1.2	GR	-	South Africa, May 2(
B.1.617.1[§]	G/452R.V3	21B	India, Oct-2020
B.1.526[§]	GH/253G.V1	21F	United States of Am Nov-2020
B.1.525[§]	G/484K.V3	21D	Multiple countries, Dec-2020
B.1.630	GH	-	Dominican Republic 2021
B.1.640	GH/490R	-	Republic of Congo,

*Includes all descendent lineages. See the cov-lineages.org and the Pango network websites for further details.

[#]formerly tracked under parent lineage B.1.1.318

[§]Former VOIs: Kappa: B.1.617.1; Iota: B.1.526; Eta: B.1.525

Member State Actions:

- **Enhance efforts towards a more representative picture of circulating variants in the country. Submit complete genome sequences and associated metadata to a publicly available database, such as GISAID.**
- **Perform field investigations to improve understanding of the characteristics of the VUM on COVID-19 epidemiology (infectivity, neutralization, severity etc.).**
- **Conduct laboratory investigations to understand the phenotypic implications of the VUM**

- **Monitor spread of VUM and interaction with other circulating variants for potential to outcompeting or thrive in the presence of a known dominant VOC/VOI**

WHO Actions:

- **Comparative assessment of variant characteristics and public health risks by WHO.**
- **Monitor and track global spread of VUM.**

Formerly monitored variants

Former VOCs/VOIs/VUMs, including their descendent lineages, that have been reclassified based on at least one the following criteria: (1) the variant is no longer circulating at levels of global public health significance, (2) the variant has been circulating for a long time without any impact on the overall epidemiological situation, or (3) scientific evidence demonstrates that the variant is not associated with any concerning properties.

Formerly monitored variants

Pango lineage*	GISAID clade	Nextstrain clade	Earliest document samples
AV.1	GR	-	United Kingdom, M
AT.1	GR	-	Russian Federation,
P.2§	GR/484K.V2	20B/S.484K	Brazil, Apr-2020
P.3§	GR/1092K.V1	21E	Philippines, Jan-2021

Pango lineage*	GISAID clade	Nextstrain clade	Earliest document samples
R.1	GR	-	Multiple countries, J
B.1.466.2	GH	-	Indonesia, Nov-202
B.1.1.519	GR	20B/S.732A	Multiple countries, N
C.36.3	GR	-	Multiple countries, J
B.1.214.2	G	-	Multiple countries, N
B.1.427 B.1.429§	GH/452R.V1	21C	United States of Am 2020
B.1.1.523	GR	-	Multiple countries, N
B.1.619	G	20A/S.126A	Multiple countries, N
B.1.620	G	-	Multiple countries, N

*Includes all descendent lineages. See the cov-lineages.org and the Pango network websites for further details.

§ Former VOIs: Epsilon: B.1.427/B.1.429 ; Zeta: P.2; Theta: P.3

Technical Advisory Groups

[Technical Advisory Group on SARS-CoV-2 Virus Evolution]

Publications

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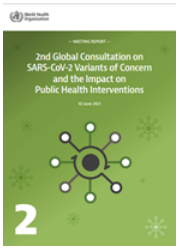

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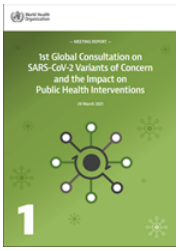

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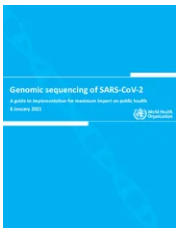

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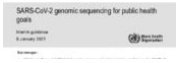

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SARS-CoV-2 genomic sequencing for public health goals: Interim guidance, 8 January 2021

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9 August 2021

Guidance for surveillance of SARS-CoV-2 variants: Interim guidance, 9 August 2021

This document aims to describe a minimum set of surveillance activities recommended at the national level to detect and monitor SARS-CoV-2 variants. It is primarily intended for national and sub-national public health authorities and partners who support implementation of surveillance for SARS-CoV-2 variants, and complements the interim guidance on public health surveillance for COVID-19, which provides overall guidance for public health surveillance of coronavirus disease 2019 (COVID-19) in humans.

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SARS-CoV-2 mink-associated variant strain – Denmark, 3 December 2020

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