



Historical working definitions and primary actions for SARS-CoV-2 variants

Given the continuous evolution of the SARS-CoV-2 virus and the constant developments in our understanding of the impacts of variants, the working definitions are periodically adjusted. Below are the previous working definitions used by WHO for variants of concern (VOC), variants of interest (VOI) and variants under monitoring (VUM). The new definitions (as of 15 March 2023) can be found here[link].

Variants of concern (VOC)

Previous 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.

Previously circulating VOCs:

WHO label	Pango lineage*	GISAID clade	Nextstrain clade	Earliest documented samples	Date of designation
Alpha	B.1.1.7	GRY	20I (V1)	United Kingdom, Sep-2020	VOC: 18-Dec-2020 Previous VOC: 09-Mar-2022
Beta	B.1.351	GH/501Y.V2	20H (V2)	South Africa, May-2020	VOC: 18-Dec-2020

WHO label	Pango lineage*	GISAID clade	Nextstrain clade	Earliest documented samples	Date of designation
					Previous VOC: 09-Mar-2022
Gamma	P.1	GR/501Y.V3	20J (V3)	Brazil, Nov-2020	VOC: 11-Jan-2021 Previous VOC: 09-Mar-2022
Delta	B.1.617.2	G/478K.V1	21A, 21I, 21J	India, Oct-2020	VOI: 4-Apr-2021 VOC: 11-May-2021 Previous VOC: 7-Jun-2022
Omicron parent lineage	B.1.1.529	GR/484A	21K	Multiple countries, Nov-2021	VUM: 24-Nov-2021 VOC: 26-Nov-2021 Previous VOC: 14-Mar-2023

*includes all descendent lineages.

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.
- Facilitate sharing of virus isolates via WHO Biohub.

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;
- Share virus isolates via WHO Biohub and/or other virus sharing initiatives.

VOC subvariant under monitoring

Previous working definition:

- A variant that, according to phylogenetic analysis, belongs to a currently circulating VOC;
AND
- shows signals of transmission advantage compared to other circulating VOC lineages;
AND
- has additional amino acid changes that are known or suspected to confer the observed change in epidemiology and fitness advantage as compared to other circulating variants.

Omicron subvariants under monitoring (as of 14 March 2023)

Pango lineage#(+ mutation)	GISAID clade	Nextstrain clade	Relationship to circulating VOC lineages	Spike genetic features	Earliest documented samples
BF.7*	GRA	22B	BA.5 sublineage	BA.5 + S:R346T	24-01-2022
BQ.1 [§]	GRA	22E	BA.5 sublineage	BQ.1 and BQ.1.1: BA.5 + S:R346T, S:K444T, S:N460K	07-02-2022
BA.2.75 [§]	GRA	22D	BA.2 sublineage	BA.2.75: BA.2 + S:K147E, S:W152R, S:F157L, S:I210V, S:G257S, S:D339H, S:G446S, S:N460K, S:Q493R reversion	31-12-2021
CH.1.1 [§]	GRA	22D	BA.2 sublineage	BA.2.75 + S:L452R, S:F486S	27-07-2022
XBB ^μ	GRA	22F	Recombinant of BA.2.10.1 and BA.2.75 sublineages, i.e. BJ1 and BM.1.1.1, with a breakpoint in S1	BA.2+ S:V83A, S:Y144-, S:H146Q, S:Q183E, S:V213E, S:G252V, S:G339H, S:R346T, S:L368I, S:V445P, S:G446S,	13-08-2022

Pango lineage#(+ mutation)	GISAID clade	Nextstrain clade	Relationship to circulating VOC lineages	Spike genetic features	Earliest documented samples
				S:N460K, S:F486S, S:F490S	
XBB.1.5	GRA	23A	Recombinant of BA.2.10.1 and BA.2.75 sublineages, i.e. BJ1 and BM.1.1.1, with a breakpoint in S1	XBB + S:F486P (see rapid risk assessment)	05-01-2022
XBF	GRA		Recombinant of BA.5.2.3 and CJ.1 (BA.2.75.3 sublineage)	BA.5 + S:K147E, S:W152R, S:F157L, S:I210V, S:G257S, S:G339H, S:R346T, S:G446S, S:N460K, S:F486P, S:F490S	27-07-2022

includes descendent lineages

* additional mutations outside of the spike protein: **N:** G30-, S33F, **ORF9b:** M26-, A29I, V30L

\$ additional mutation outside the spike protein: **ORF1a:** Q556K, L3829F, **ORF1b:** Y264H, M1156I, N1191S, **N:**E136D, **ORF9b:** P10F

§ additional mutations outside of the spike protein: **ORF1a:** S1221L, P1640S, N4060S, **ORF1b:** G662S, **E:** T11A

µ additional mutations outside of the spike protein: **ORF1a:** K47R, **ORF1b:** G662S, S959P, **E:** T11A, **ORF8:** G8*

Actions taken by WHO and Member States:

Primary actions by WHO for a VOC-subvariant under monitoring

- Review global epidemiology of VOC-subvariant under monitoring;
- Monitor and track global spread of VOC-subvariant under monitoring;
- If determined necessary, coordinate additional laboratory investigations with Member States and partners;
- Facilitate sharing of virus isolates via WHO Biohub;
- In consultation with the TAG-VE, review characteristics of the VOC-subvariant under monitoring as compared to the VOC it belongs to, and provide a separate label in case those are substantially different.

Primary actions by a Member State, if a VOC-subvariant under monitoring is identified:

- Inform WHO through established WHO Country or Regional Office reporting channels with supporting information;
- 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 VOC-subvariant under monitoring 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 VOC-subvariant under monitoring on relevant virus characteristics;
- Share virus isolates via WHO Biohub and/or other virus sharing initiatives.

Variants of interest (VOI)

Previous 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.

WHO label	Pango lineage*	GISAID clade	Nextstrain clade	Earliest documented samples	Date of designation
Epsilon	B.1.427 B.1.429	GH/452R.V1	21C	United States of America, Mar-2020	VOI: 5-Mar-2021 Previous VOI: 6-Jul-2021
Zeta	P.2	GR/484K.V2	20B/S.484K	Brazil, Apr-2020	VOI: 17-Mar-2021 Previous VOI: 6-Jul-2021
Eta	B.1.525	G/484K.V3	21D	Multiple countries, Dec-2020	VOI: 17-Mar-2021 Previous VOI: 20-Sep-2021
Theta	P.3	GR/1092K.V1	21E	Philippines, Jan-2021	VOI: 24-Mar-2021 Previous VOI: 6-Jul-2021
Iota	B.1.526	GH/253G.V1	21F	United States of America, Nov-2020	VOI: 24-Mar-2021 Previous VOI: 20-Sep-2021
Kappa	B.1.617.1	G/452R.V3	21B	India, Oct-2020	VOI: 4-Aprl-2021 Previous VOI: 20-Sep-2021
Lambda	C.37	GR/452Q.V1	21G	Peru, Dec-2020	VOI: 14-Jun-2021

					Previous VOI: 9-Mar-2022
Mu	B.1.621	GH	21H	Colombia, Jan-2021	VOI: 30-Aug- 2021 Previous VOI: 9-Mar-2022

*Includes all descendent lineages.

Actions taken by WHO and Member States:

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;
- Facilitate sharing of virus isolates via WHO Biohub.

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;
- Share virus isolates via WHO Biohub and/or other virus sharing initiatives.

Variants under monitoring (VUM)

Previous 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.

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;
- Share virus isolates via WHO Biohub and/or other virus sharing initiatives.

WHO Actions:

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

Formerly monitored variants:

Pango lineage*	GISAID clade	Nextstrain clade	Earliest documented samples	Date of designation
AV.1	GR	-	United Kingdom, Mar-2021	VUM: 26-May-2021 FMV: 21-Jul-2021
AT.1	GR	-	Russian Federation, Jan-2021	VUM: 09-Jun-2021 FMV: 21-Jul-2021
R.1	GR	-	Multiple countries, Jan-2021	VUM: 07-Apr-2021 FMV: 9-Nov-2021

Pango lineage*	GISAID clade	Nextstrain clade	Earliest documented samples	Date of designation
B.1.466.2	GH	-	Indonesia, Nov-2020	VUM: 28-Apr-2021 FMV: 9-Nov-2021
B.1.1.519	GR	20B/S.732A	Multiple countries, Nov-2020	VUM: 02-Jun-2021 FMV: 9-Nov-2021
C.36.3	GR	-	Multiple countries, Jan-2021	VUM: 16-Jun-2021 FMV: 9-Nov-2021
B.1.214.2	G	-	Multiple countries, Nov-2020	VUM: 30-Jun-2021 FMV: 9-Nov-2021
B.1.1.523	GR	-	Multiple countries, May 2020	VUM: 14-July-2021 FMV: 9-Nov-2021
B.1.619	G	20A/S.126A	Multiple countries, May 2020	VUM: 14-July-2021 FMV: 9-Nov-2021
B.1.620	G	-	Multiple countries, Nov-2020	VUM: 14-July-2021 FMV: 9-Nov-2021
B.1.630	GH	-	Dominican Republic, Mar-2021	VUM: 12-Oct-2021 FMV: 29-Dec-2021
B.1.1.318	GR	-	Multiple countries, Jan-2021	VUM: 02-Jun-2021

Pango lineage*	GISAID clade	Nextstrain clade	Earliest documented samples	Date of designation
				FMV: 11-Mar-2022
C.1.2	GR	-	South Africa, May 2021	VUM: 01-Sep-2021 FMV: 11-Mar-2022
B.1.640	GH/490R	-	Multiple countries, Sep-2021	VUM: 22-Nov-2021 FMV: 25-May-2022
XD	-	-	France, Jan-2022	VUM: 09-Mar-2021 FMV: 25-May-2022

*Includes all descendent lineages.