

Update on the emergence of SARS-CoV-2 Omicron sublineages and recombination events

18 November 2022

Key messages

In the context of the continuous emergence of additional Omicron sublineages, PAHO/WHO reiterates that the nomenclature established to address the potential public health impacts of variants and based on Greek letter labels has not changed. Nomenclatures based on phylogenetic analysis (ie, Pango Network, GISAID, and Nextstrain) can also be used to designate lineages or sublineages. However, other nomenclatures or nicknames are not official and should not be used.

PAHO/WHO regularly assesses new Omicron sublineages. To date, there is no evidence of significant changes in the public health impact of these sublineages and no justification of the assignment of a new variant label.

The occurrence of mutations is a natural and expected event within the evolutionary process of viruses. Since the emergence of SARS-CoV-2, this virus has been divided into different genetic groups or clades. In fact, some specific mutations define the viral genetic groups (also called lineages) that are currently circulating globally. Due to various microevolution processes and selection pressures, some additional mutations may appear, generating differences within each genetic group (called variants). Additionally, recombination between lineages might occur and give rise to recombinant lineages.

SARS-CoV-2 variant classification

SARS-CoV-2 lineage classification includes the Pango Network nomenclature which is solely based on the analysis of the genetic composition of the virus (phylogenetics). This nomenclature assigns a letter or combination of letters followed by numbers to each lineage (e.g., B.1.1.529). More importantly, the WHO nomenclature established to address the potential public health impacts of variants has not changed and is based on Greek letters as designated based on risk assessments conducted by the WHO Technical Advisory Group on SARS-CoV-2 virus evolution (TAG-VE)¹. This classification includes the variants of concern (VOC) and of interest (VOI). Currently, the only circulating VOC or VOI is the Omicron VOC. Five main sublineages of Omicron classified as BA.1, BA.2, BA.3, BA.4 and BA.5 in the Pango nomenclature, have been reported globally.

As expected, the high transmission and reinfection patterns demonstrated for Omicron have facilitated the occurrence of additional mutations driving the emergence of multiple sublineages within the Omicron VOC. Thus, a new category of “Omicron subvariants under monitoring” was established to identify lineages that may require prioritized monitoring because they carry additional mutations that might confer some fitness advantage. Currently, this category includes BA.5 subvariants carrying additional mutations (including BQ.1), BA.2.75, BJ.1 (a BA.2 sublineage), BA.4.6, BA.2.3.20, and XBB (a recombinant between two BA.2 sublineages).

¹ WHO. Tracking SARS-CoV-2 variants. Available at: <https://www.who.int/en/activities/tracking-SARS-CoV-2-variants/>

However, the inclusion of a particular subvariant in this category does not mean that the subvariant poses an additional public health threat. In fact, recent assessments of BQ.1 and XBB by the TAG-VE found that their overall phenotype of did not diverge sufficiently to justify the designation of a new VOC and the assignment of a new label². Thus, all “Omicron subvariants under monitoring” remain part of Omicron. Risk assessments of these and newly emerging sublineages are updated periodically.

In summary, no significant changes in public health impact regarding the Omicron sublineages have been demonstrated, besides the high transmission capacity already demonstrated by Omicron. Although some treatments based on monoclonal antibodies might be affected by specific structural changes in the virus, vaccination and non-pharmacological measures, including the appropriate use of masks, remain extremely useful to control virus transmission and surges of cases.

Circulation of Omicron sublineages in the PAHO Region

Omicron was introduced in the Americas at the end of 2021 and rapidly replaced Delta and other lineages throughout the Region and globally. Omicron has been officially reported by 54 countries or territories and has been predominant in all PAHO countries since the beginning of 2022. The BA.1 sublineage circulated at the end of 2021 and the beginning of 2022 and was replaced by BA.2 between weeks 12 and 15 of 2022. BA.2 was then largely replaced by a combination of BA.4 and BA.5 sublineages between weeks 25 and 34 (Figure 1). Notably, in the past four weeks, the BA.4 and BA.5 (and sublineages) combined represent 96%, 99%, 96%, and 96% of the characterized samples in North America, the Caribbean, Central America, and South America, respectively.

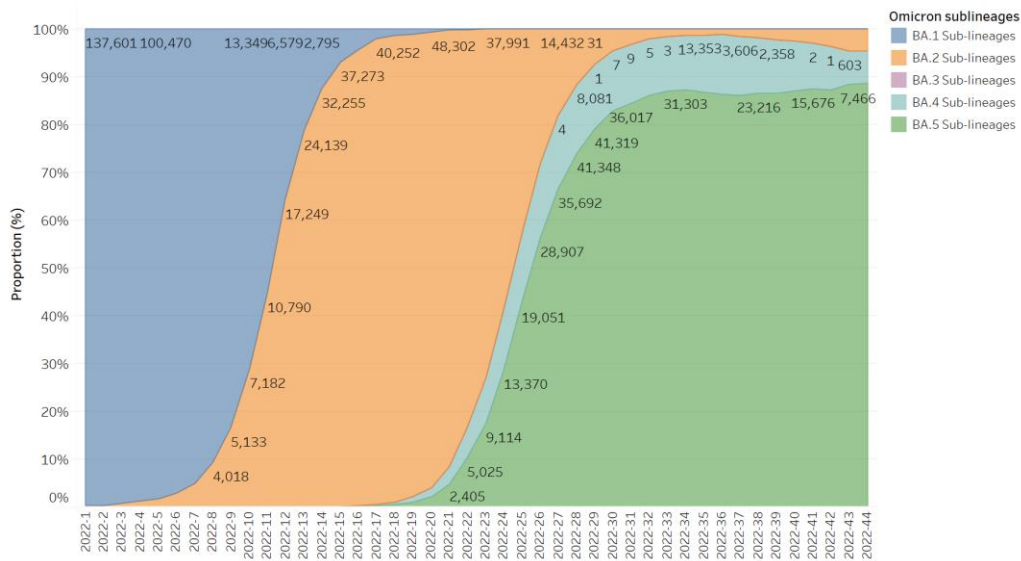


Figure 1. Proportions of VOC Omicron sublineages identified by the countries in the Region of the Americas (January- November 2022). Source: GISAID.

² WHO. TAG-VE statement on Omicron sublineages BQ.1 and XBB. 27 October 2022. Available at: <https://www.who.int/news/item/27-10-2022-tag-ve-statement-on-omicron-sublineages-bq.1-and-xbb>

Additional information on SARS-CoV-2 variant circulation in the Americas can be found in PAHO's Weekly COVID-19 Epidemiological Update³.

Guidance for national authorities

PAHO/WHO reiterates to Member States the need to: (i) maintain SARS-CoV-2 genomic surveillance activities in accordance with PAHO⁴ and WHO guidance⁵; (ii) ensure the immediate publication of genomic sequences produced on the GISAID platform; and (iii) utilize the WHO SARS-CoV-2 variant classification when communicating to the public.

³ PAHO. Weekly COVID-19 Epidemiological Update – Region of the Americas. Available at: <https://www.paho.org/en/covid-19-weekly-updates-region-america>

⁴ PAHO. Guidance for SARS-CoV-2 samples selection for genomic characterization and surveillance. 1 February 2021. Available at: <https://www.paho.org/en/documents/guidance-sars-cov-2-samples-selection-genomic-characterization-and-surveillance>

⁵ WHO. Genomic sequencing of SARS-CoV-2: a guide to implementation for maximum impact on public health. 8 January 2021. Available at: <https://www.who.int/publications/i/item/9789240018440>