Update on the emergence of SARS-CoV-2 Omicron sublineages

22 August 2023

Key messages

In the context of the emergence of additional Omicron sublineages, PAHO/WHO reiterates that the nomenclature established to address the potential public health impacts of variants has not changed. Nomenclatures based on phylogenetic analysis (e.g., Pango Network 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. Two new variants have recently been identified: EG.5, classified as a variant of interest (VOI), and BA.2.86, classified as a variant under monitoring (VUM). Based on the available evidence, the public health risk posed by EG.5 has been evaluated as low and it is similar to other circulating variants of interest. Limited information is available for BA.2.86; and the initial risk assessment will be generated soon. To date, there is no evidence of significant changes in the public health impact of these sublineages and there is no justification for the assignment of a new "variant of concern".

COVID-19 recommendations remain unchanged. In particular, PAHO **strongly encourages** all countries in the Region to continue collecting representative samples for sequencing and to maintain appropriate SARS-CoV-2 genomic surveillance.

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). The WHO nomenclature established to address the potential public health impacts of variants 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].

The vast majority of SARS-CoV-2 viruses circulating globally are sublineages of Omicron. Thus, since March 2023, the WHO variant tracking system considers the classification of Omicron sublineages independently as **variants under monitoring** (VUM), **variants of interest** (VOIs), or **variants of concern** (VOCs), while Alpha, Beta, Gamma, Delta and the Omicron original lineages are classified as "previously circulating" VOCs[2]. Greek letters are only assigned to sublineages classified as currently circulating VOCs. However, at present, no Omicron sublineage is classified as such.

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

[2] WHO. Statement on the update of WHO's working definitions and tracking system for SARS-CoV-2 variants of concern and variants of interest. 16 March 2023. Available at: https://www.who.int/news/item/16-03-2023-statement-on-the-update-of-who-s-working-definitions-and-tracking-system-for-sars-cov-2-variants-of-concern-and-variants-of-interest

The recombinant sublineages XBB.1.5 and XBB.1.16 were classified as currently circulating VOIs in January and April 2023, respectively, while the **recombinant EG.5 was classified as VOI on 9 August 2023**. Additionally, BA.2.75 and CH.1.1 (two BA.2 sublineages), and recombinants XBB, XBB.1.9.1, XBB.1.9.2, and XBB.2.3 were included in the list of currently circulating VUMs before Augst 2023, while **BA.2.86 was classified as VUM on 17 August 2023**. This update focuses on EG.5 and BA.2.86.

Variant of interest EG.5

EG.5 is a descendent lineage of XBB.1.9.2 and was first reported in February of 2023. The spike protein of EG.5 is similar to XBB.1.5. Globally, there has been a steady increase in the proportion of EG.5 reported. This trend has also been observed in some countries in the Region of the Americas, including, Canada, Colombia, Costa Rica, Dominican Republic, and the United States.

Based on the available evidence, **the public health risk posed by EG.5 is evaluated as low at the global level[3], aligning with the risk associated with other currently circulating VOIs**. While EG.5 has shown increased prevalence, growth advantage, and is likely to have increased immune escape properties, there have been no reported changes in disease severity to date. Concurrent increases in the proportion of EG.5 and COVID-19 hospitalizations have been observed in countries such as Japan and the Republic of Korea; however, the hospitalization increase has been lower than during previous waves and no associations have been made between these hospitalizations and EG.5. Due to its growth advantage, EG.5 may cause a rise in case incidence in some countries and become dominant.

Variant under monitoring BA.2.86

This variant was initially reported in a sample collected in Denmark at the end of July 2023. It has since been detected in Israel, the United Kingdom, and the United States, but only seven sequences in total have been reported. It carries a significant number (over 30) of mutations in the spike protein and has been called BA.2.86 in the Pango Network nomenclature. WHO has designated BA.2.86 as a VUM due to the large number of mutations it carries but limited additional information is available at this time.

Presently there is no known epidemiological link between the identified cases. However, the fact that BA.2.86 has been identified in distant countries suggests it is present elsewhere. Given the low number of cases, **it is currently not possible to determine whether BA.2.86 is associated with any changes in transmissibility, immune escape or severity**. It is also difficult to infer whether the large number of mutations identified will increase or decrease viral fitness. Additional sequence data and epidemiological characterization of the cases are required to understand the significance of this variant.

In summary, for EG.5, no significant changes in public health impact have been demonstrated, besides the high transmission capacity already demonstrated by Omicron. For **BA.2.86**, additional information is required to better characterize this variant in terms of transmissibility, immune escape, and severity. Both variants, as well as other circulating or emerging sublineages, are continuously monitored by the TAG-VE, and risk assessments will be published/updated as new information becomes available.

[3] WHO. EG.5 Initial Risk Evaluation. 9 August 2023. Available at: https://www.who.int/docs/default-source/coronaviruse/09082023eg.5_ire_final.pdf

Guidance for national authorities

General guidance related to COVID-19 can be found in the Standing recommendations for COVID-19 issued by WHO in accordance with the International Health Regulations (2005) (IHR)[4]. In particular, PAHO/WHO reiterates to Member States the need to: (i) maintain SARS-CoV-2 genomic surveillance activities in accordance with PAHO[5] and WHO guidance[6]; (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.

[4] WHO. Standing recommendations for COVID-19 issued by the Director-General of the World Health Organization (WHO) in accordance with the International Health Regulations (2005) (IHR). 9 August 2023. Available at: https://www.who.int/publications/m/item/standing-recommendations-for-covid-19-issued-by-the-director-general-of-the-world-health-organization-(who)-in-accordance-with-the-international-health-regulations-(2005)-(ihr)

[5] 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

[6] 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