

Update on the evolution and circulation of SARS-CoV-2 sublineages

16 January 2024

Key messages

In the context of the constant evolution and spread of additional SARS-CoV-2 sublineages, PAHO/WHO reiterates that the nomenclature established to address the potential public health impacts of variants has not changed. Circulating sublineages are regularly assessed and might be designated as variants of concern (VOC), variants of interest (VOI), or variants under monitoring (VUM) based on their assessed potential for expansion and replacement of prior variants, for causing new waves with increased circulation, and for the need for adjustments to public health actions. 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 SARS-CoV-2 sublineages. At the moment, no circulating sublineage is classified as VOC; five are classified as VOIs and five more as VUMs. The most recent designations include VOIs **BA.2.86** and **JN.1**. However, based on the available information, the **public health risk posed by these variants is currently evaluated as low at the global level and no increased severity or virulence has been documented**. Vaccines remain effective and vaccination should be maintained as part of the control measures.

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 belong to 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

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

circulating” VOCs². The working definitions for these variants were also updated recently³. Greek letters are only assigned to sublineages classified as currently circulating VOCs. However, at present, no sublineage is classified as such.

Currently, five Omicron sublineages are classified as circulating VOIs: XBB.1.5, XBB.1.16, EG.5, BA.2.86, and JN.1. Since the last PAHO update on SARS-CoV-2 sublineages⁴, two additional VOIs have been designated:

- BA.2.86 was designated on 21 November 2023 but had previously been designated as VUM on 17 August 2023 due to a large number of mutations in the spike protein.
- JN.1 is a sublineage of BA.2.86 (BA.2.86.1.1) and was designated as a VOI on 18 December 2023.

As for other VOIs, the TAG-VE has conducted risk evaluations for BA.2.86⁵ and JN.1⁶. These risk evaluations take into consideration available information on three indicators: growth advantage, antibody escape, and severity and clinical/diagnostic considerations. The risk evaluations note that JN.1 has shown a growth advantage in all WHO regions and that both BA.2.68 and JN.1 might have increased immune escape properties. Thus, these variants may be associated with an increase in case incidence in some countries⁷ and become dominant. However, there are no reports of increase severity associated with these variants. Thus, based on the available evidence, **the public health risk posed by BA.2.68 and JN.1 was evaluated as low at the global level, aligning with the risk associated with other currently circulating VOIs.**

Additionally, five Omicron sublineages are classified as circulating VUMs: XBB.1.9.1, XBB.1.9.2, XBB.2.3, DV.7, and XBB sublineages not included in other VOIs or VUMs. The last designation in this category was DV.7 on 23 October 2023. These variants, as well as other circulating or emerging sublineages, are continuously monitored by the TAG-VE, and risk evaluations are published/updated as new information becomes available.

Circulation of Omicron sublineages in the Americas

Since the introduction of Omicron in the Americas at the end of 2021, different sublineages have been predominant and have then progressively been replaced by new sublineages. In 2023, the Region has seen the increase and subsequent decrease in the circulation of VOIs XBB.1.5, XBB.1.16, and EG.5 (Figure 1). These variants largely cocirculated peaking at different times: late March for XBB.1.5 (maximum weekly proportion of 73% of the sequences), end of August for XBB.1.16 (at 25%), and mid-November for EG.5 (at 45%). The past last months of 2023 have also seen the expansion of VOIs BA.2.86 (since end of September) and JN.1 (since end of October). The proportions of BA.2.86 and JN.1 sequences in the week of 17 December 2023

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>

³ WHO. Updated working definitions and primary actions for SARS-CoV-2 variants, 4 October 2023. Available at: <https://www.who.int/publications/m/item/updated-working-definitions-and-primary-actions-for--sars-cov-2-variants>

⁴ PAHO. Update on the emergence of SARS-CoV-2 Omicron sublineages. 22 August 2023. Available at: <https://www.paho.org/en/documents/update-emergence-sars-cov-2-omicron-sublineages-22-august-2023>

⁵ WHO. BA.2.86 Initial Risk Evaluation. 21 November 2023. Available at: https://www.who.int/docs/default-source/coronaviruse/21112023_ba.2.86_ire.pdf

⁶ WHO. JN.1 Initial Risk Evaluation. 18 December 2023. https://www.who.int/docs/default-source/coronaviruse/18122023_jn.1_ire_clean.pdf

⁷ PAHO. Epidemiological Update: SARS-CoV-2 and Other Respiratory Viruses in the Americas Region. 8 January 2024. Available at: <https://www.paho.org/en/documents/epidemiological-update-sars-cov-2-and-other-respiratory-viruses-americas-region-8-january>

were 7% and 30%, respectively. As noted above, these proportions are likely to increase, in particular for JN.1.

At the subregional level, the trends in **North America and the Caribbean** are similar to the regional trends (Figure 2). The expansion of JN.1 is notable in these subregions, and model-based projections estimate that JN.1 represents 62% (95% CI: 55-68%) of the US sequences in the two-week period ending 6 January 2024⁸. VUM DV.7 has also been circulating in North America, notably, in Canada. However, the proportion of DV.7 in Canada peaked at 2.6% on the week of 19 November 2023 and model-based estimates for the week of 31 December were at 0.2% (95%CI: 0.1-0.3%)⁹.

In **South America**, the circulation of XBB.1.5 has been more extensive while XBB.1.6 and EG.5 have circulated to a lesser extent than in North America and the Caribbean. Also, the expansion of JN.1 appears to have started later in South America and there are few reported BA.2.86 sequences.

In **Central America**, XBB.1.5, XBB.1.16, and EG.5 have accounted for most of the characterized sequences through 2023. Trends in recent months are difficult to evaluate owing to the low number of sequences available. There are few reported sequences for BA.2.86 and JN.1.

It is important to note that the number of SARS-CoV-2 sequences deposited in GISAID by PAHO Member States has significantly decreased since early 2023 (Figures 1 and 2). This decrease, which is in part linked to decreases in the number of cases, the integration with influenza and other respiratory viruses, and the migration from universal to sentinel surveillance, might bias in the sublineage prevalence estimates reported above and reduces our collective ability to timely identify new emerging lineages or new variants. In this context, PAHO strongly encourages all countries in the Region to continue collecting representative samples for sequencing, ensuring sample quality and cold-chain during sample transport, and to strengthen COVID-19 genomic surveillance.

Information on the COVID-19 situation in the Americas including SARS-CoV-2 variant circulation (based on the sequences reported to GISAID) is compiled weekly and available at: <https://www.paho.org/en/covid-19-weekly-updates-region-americas>.

⁸ US CDC. COVID Data Tracker - Variant Proportions. Available at: <https://covid.cdc.gov/covid-data-tracker/#variant-proportions>

⁹ Public Health Agency Canada. Variants in Canada. Available at: <https://health-infobase.canada.ca/covid-19/testing-variants.html>

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)¹⁰. In particular, PAHO/WHO reiterates to Member States the need to: (i) maintain SARS-CoV-2 genomic surveillance activities in accordance with PAHO¹¹ and WHO guidance¹²; (ii) ensure the timely publication of genomic data on the GISAID platform; and (iii) utilize the WHO SARS-CoV-2 variant classification when communicating to the public.

¹⁰ 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-\(2005\)-\(ihr\)](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))

¹¹ 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>

¹² 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>

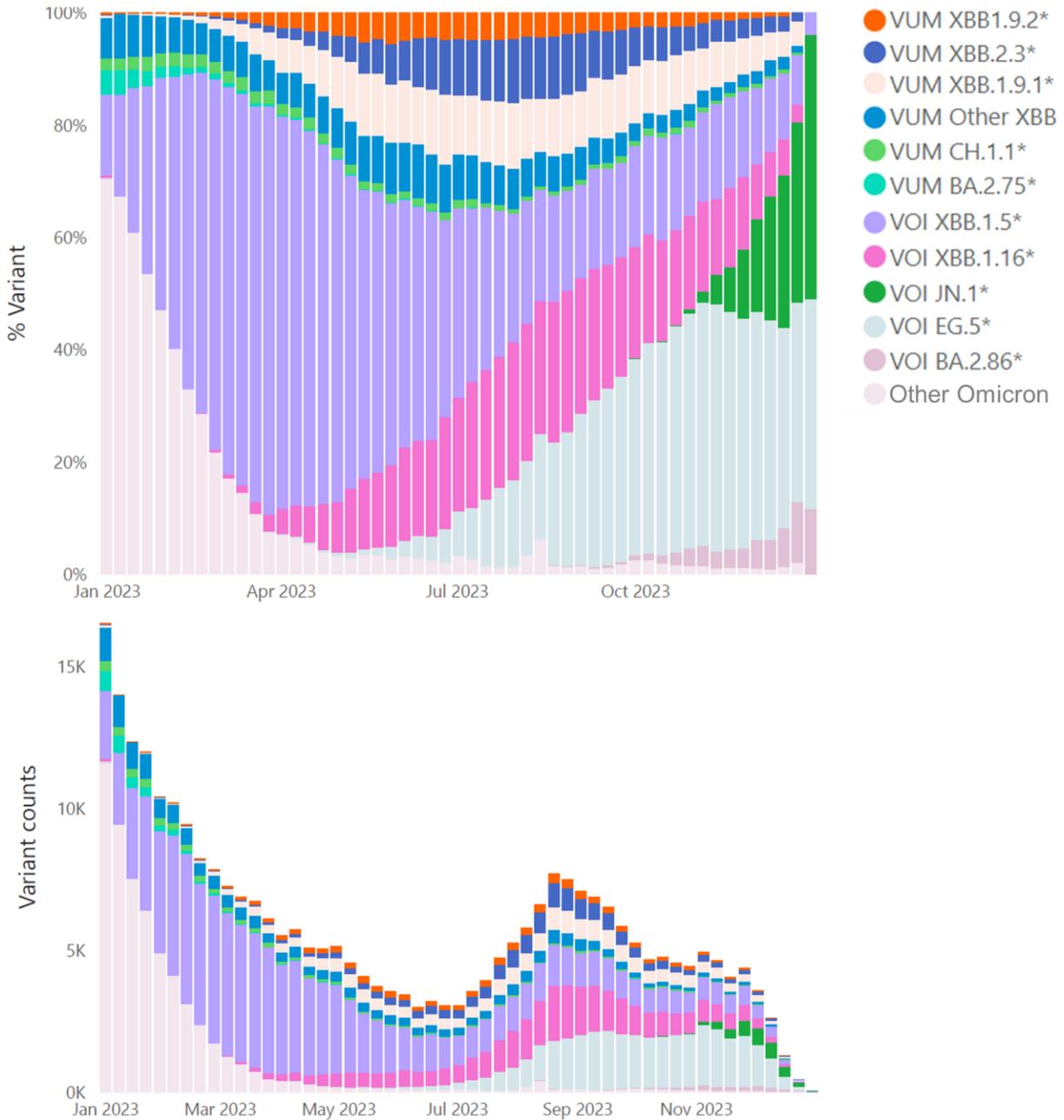


Figure 1. Proportions and counts of variants of interest (VOI) and variants under monitoring (VUM) identified by the countries in the Region of the Americas (January – December 2023). Omicron sequences not classified as VOIs or VUMs are grouped together under “Other Omicron”. Data: GISAID.

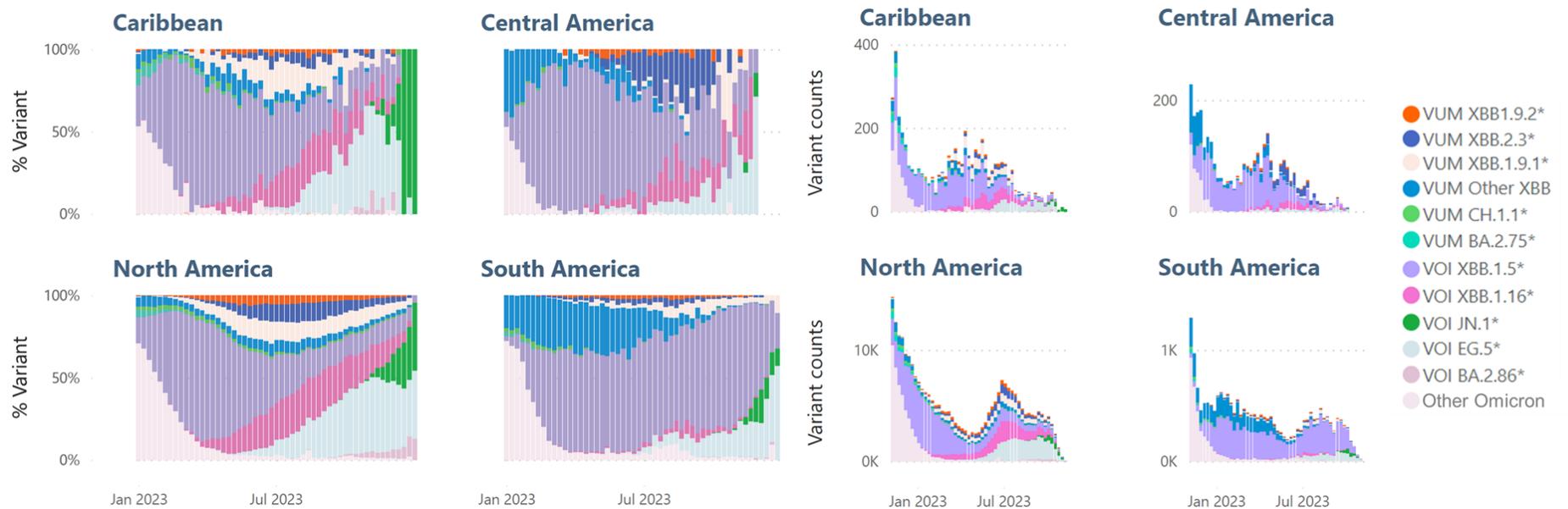


Figure 2. Proportions and counts of variants of interest (VOI) and variants under monitoring (VUM) identified by subregion (January – December 2023). Omicron sequences not classified as VOIs or VUMs are grouped together under “Other Omicron”. Data: GISAID.