

Genetic diversity of the novel coronavirus SARS-CoV-2 (COVID-19) in Portugal

More information at <https://insaflu.insa.pt/covid19>



Situation Report

October 24th, 2023

The National Institute of Health Doutor Ricardo Jorge, I.P. (INSA) has analysed **48617** SARS-CoV-2 genome sequences so far.

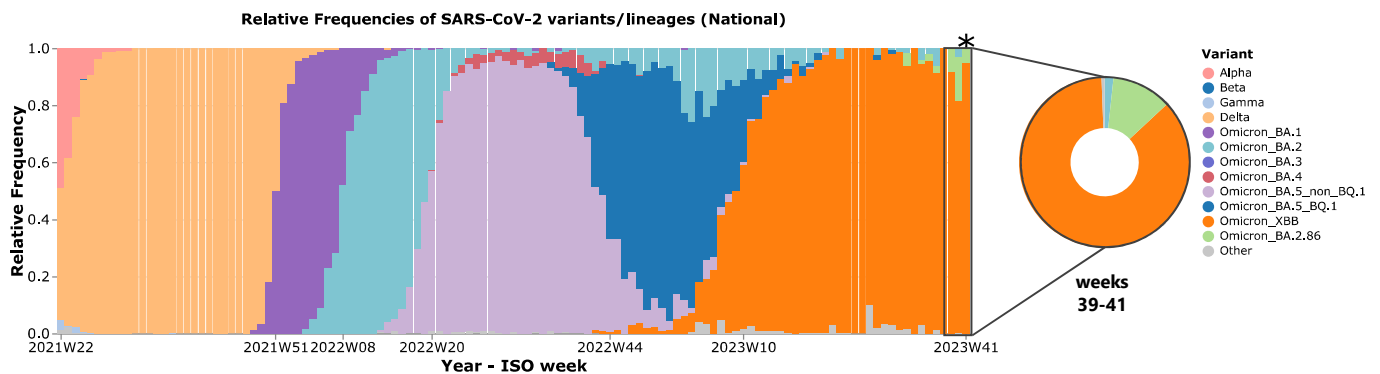


Figure 1: Evolution of the weekly relative frequency of the SARS-CoV-2 variants circulating in Portugal between ISO weeks 22/2021 (31/05/21 - 06/06/21) and 41/2023 (09/10/23 a 15/10/23), with emphasis on the latest weeks. The frequencies presented for the last week under analysis (ISO week 41*) might change in the next report, given that some data from that period is still being processed. This and other graphs can be explored interactively on the website.

Main highlights

- The **recombinant lineage XBB** (and its descendants) has been increasing in circulation since the beginning of 2023, leading to its **dominance in Portugal by week 10 (Figure 1)**. In the latest survey, XBB presented a **relative frequency of 86.36%** (weeks 39 to 41), mainly due to its **XBB.1.5, XBB.1.9 and XBB.1.16 sub-lineages (and its descendants) (Figure 2)**. Of note, XBB.1.9 (in particular, its descendant EG.5.1 and its sublineages) has displaying a relative frequency above 50% since week 23. Among the descendants of EG.5.1, it is highlighted the recent detection of HV.1 in Portugal, which has shown a strongly increasing trend in some countries.
- The **lineage BA.2 of variant Omicron was dominant in Portugal** in the first months of 2022, having maintained a discreet circulation since then. Recently, an increasing trend in relative frequency was seen again, mainly due to the emergence of the **lineage BA.2.86 (and its descendants)**. Its **relative frequency represented 11.4%** of all sequences analyzed in **weeks 39 and 41**, in particular due to the circulation of its JN.1 sub-lineage. The BA.2.86 lineage has been detected in several countries and has been a focus of international interest due to its mutational profile, which represents an “evolutionary jump” to its ancestral BA.2, and due to its divergent antigenic profile in relation to the currently dominant variant (XBB). These mutations endow BA2.86 lineage a greater ability to escape the immune system and, potentially, a greater transmissibility.

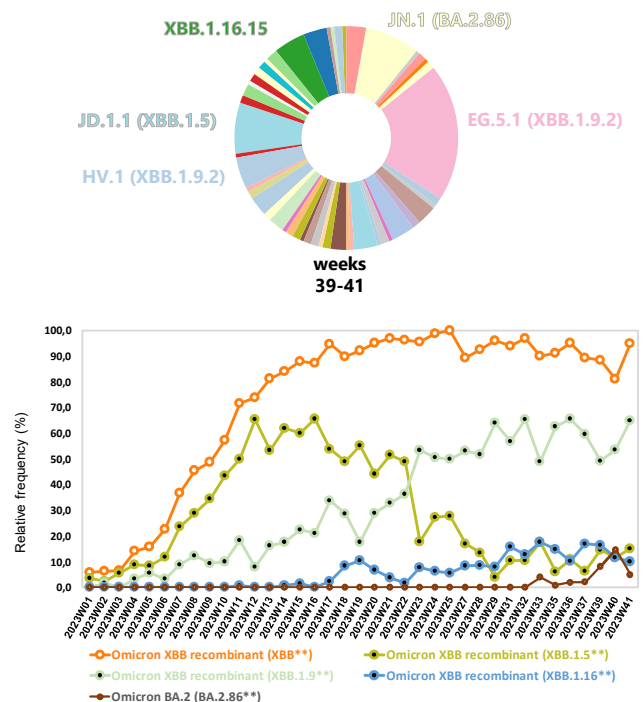


Figure 2: Evolution of the relative frequency of some sub-lineages of interest circulating in Portugal. The circular graph shows the distribution of the relative frequencies of SARS-CoV-2 sub-lineages in the period of ISO weeks 39 and 41 (25/09/23 – 15/10/23), **highlighting sub-lineages representing >4% of the sequences analyzed in this period.** The evolution of XBB**, XBB.1.5**, XBB.1.9**, XBB.1.16** and BA.2.86** relative frequencies during the last weeks is shown in the line plot. It is expected that the frequencies presented for the last week under analysis (ISO week 41*) might change in the next report, given that some data from that period is still being processed. **the presented relative frequencies correspond to the sub-lineages and their descendants. Other graphs can be explored interactively on the website.

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Useful links

<https://www.ecdc.europa.eu/en/covid-19/situation-updates/variants-dashboard>
<https://www.who.int/activities/tracking-SARS-CoV-2-variants>
https://cov-lineages.org/lineage_list.html
<https://outbreak.info/>
<https://www.gtsaid.org/>