

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

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



Situation Report

November 21st, 2023

The National Institute of Health Doutor Ricardo Jorge, I.P. (INSA) has analysed **48723** SARS-CoV-2 genome sequences so far.

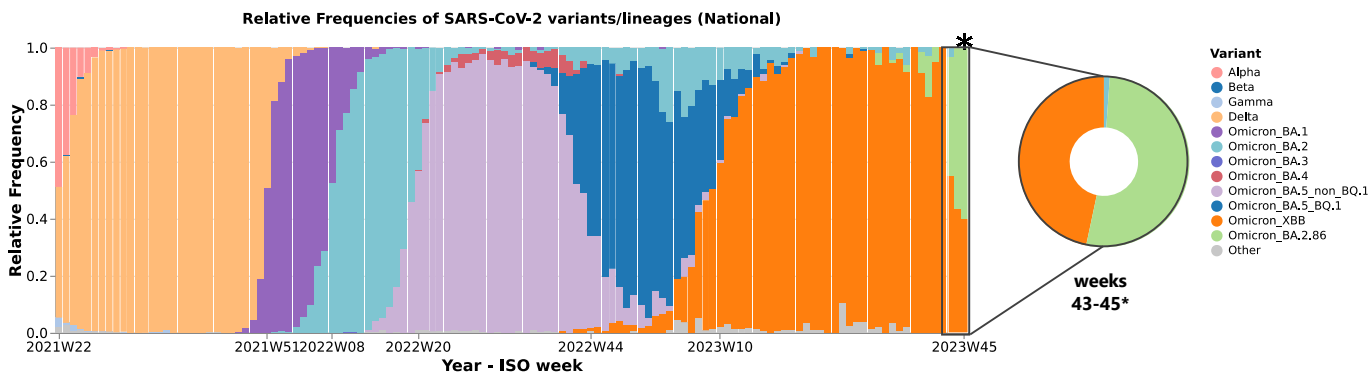


Figure 1: Evolution of the weekly relative frequency of the SARS-CoV-2 variants circulating in Portugal from ISO weeks 22/2021 (31/05/21 - 06/06/21) and 45/2023 (06/11/23 a 12/11/23), with emphasis on the latest weeks. *The interpretation of the presented relative frequencies during this period (ISO weeks 43 to 45) should take into account the current low sampling. *This and other graphs can be explored interactively on the website.*

Main highlights

- The **recombinant lineage XBB** (and its descendants) was **dominant in Portugal**, from week 10 of 2023 up to week 41 (Figure 1). In the latest survey, XBB presented a **relative frequency of 46.7%** (weeks 43 to 45), mainly due to its **XBB.1.5, XBB.1.9 and XBB.1.16** sub-lineages (and its descendants) (Figure 2).
- 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 has resurfaced, mainly due to the emergence of the **lineage BA.2.86 (and its descendants)**. Its **relative frequency represented 52.2%** of all sequences analyzed in **weeks 43 and 45**, in particular due to the circulation of its **JN.1** sub-lineage.
- Although the presented relative frequencies should be interpreted with caution due to the current low sampling, **lineage BA.2.86 has shown an increasing trend in frequency**, replacing the recombinant XBB lineages, similarly to what is being observed internationally. 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 BA.2.86 lineage a greater ability to escape the immune system and, potentially, a greater transmissibility.

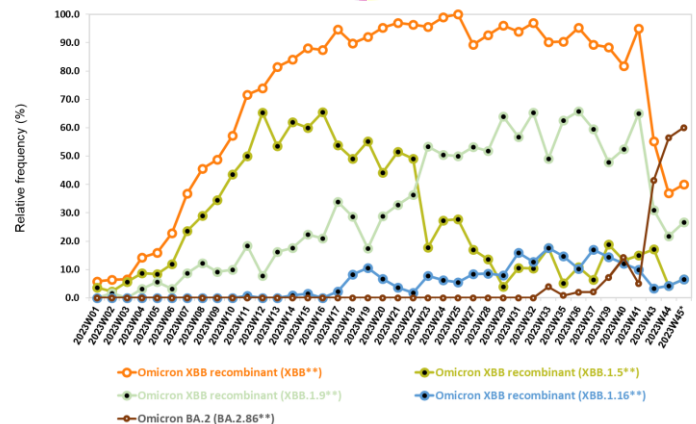
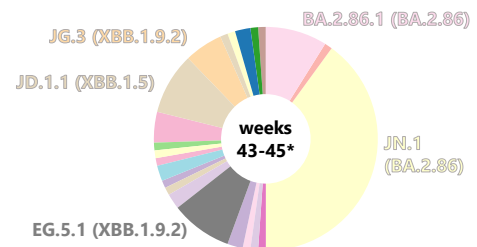


Figure 2: Evolution of the relative frequency of some sub-lineages of interest circulating in Portugal. The circular graph shows the distribution of the relative frequencies of SARS-CoV-2 sub-lineages in the period of ISO weeks 43 and 45 (23/10/23 - 12/11/23), highlighting sub-lineages representing >5% 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. *The interpretation of the presented relative frequencies during this period (ISO weeks 43 to 45) should take into account the current low sampling. **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://covid19.gisaid.org/>
<https://www.gisaid.org/>