

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

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



Situation Report

August 29st, 2023

The National Institute of Health Doutor Ricardo Jorge, I.P. (INSA) has analysed **48120** SARS-CoV-2 genome sequences so far.

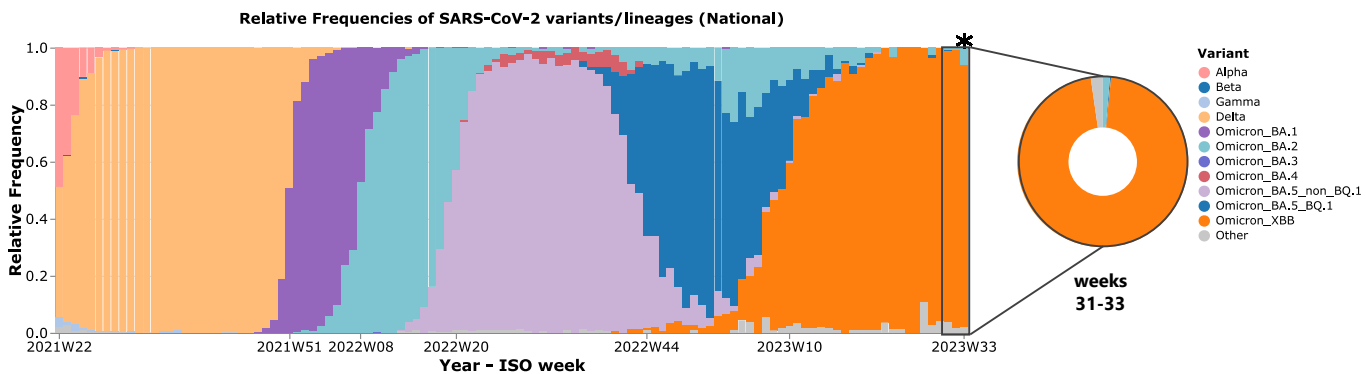


Figure 1: Evolution of the weekly relative frequency of the SARS-CoV-2 variants circulating in Portugal between ISO weeks 22/2021 (31/05/21 - 06/06/21) and 33/2023 (14/08/23 - 20/08/23), with emphasis on the latest weeks. The frequencies presented for the last week under analysis (ISO week 33*) might 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 96.15%** (weeks 31 to 33), mainly due to its **XBB.1.5, XBB.1.9 and XBB.1.16 sub-lineages (and its descendants)** (Figure 2). It is highlighted that XBB.1.9 (in particular its descendant EG.5.1 and its sublineages) has revealed a considerable increase in frequency in Portugal, representing around 50.3% of all sequences analysed in the last three weeks (weeks 31 and 33).
- In 2022, **lineage BA.2 of variant Omicron was dominant in Portugal between weeks 8 (21-27/02/22) and 19 (09-15/05/22)**. An increase in frequency was observed between week 51 of 2022 and week 3 of 2023, mainly due to the circulation of its **lineage CH.1.1 (and its sub-lineages)** (Figure 1 and Figure 2). Since this period, lineage BA.2 has shown a decrease in frequency, presenting **1.36% between weeks 31 and 33**.
- We highlight the **detection of 2 sequences of BA.2.86** in Portugal in week 33. This sublineage has already been detected in a few countries and has been a focus of 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). The impact of these mutations in transmissibility and/or disease severity is still unclear.

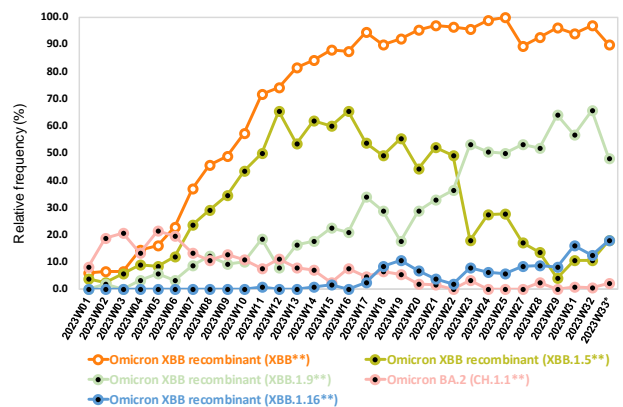
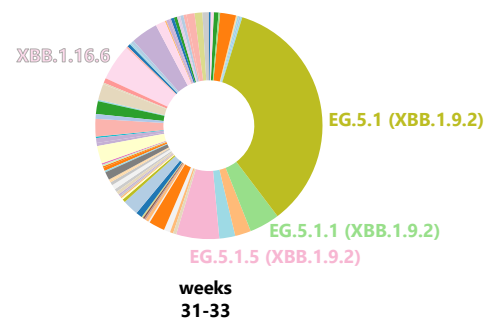


Figure 2: Evolution of the relative frequency of some sub-lineages of interest circulating in Portugal. The circular graph shows the distribution of the relative frequencies of SARS-CoV-2 sub-lineages in the period of ISO weeks 31 and 33 (31/07/23 - 20/08/23), highlighting sub-lineages representing >4% of the sequences analyzed in this period. The evolution of CH.1.1**, XBB**, XBB.1.5**, XBB.1.9** and XBB.1.16** 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 33*) 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.gisaid.org/>