

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

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



Situation Report

June 12th, 2023

The National Institute of Health Doutor Ricardo Jorge, I.P. (INSA) has analysed **47270** SARS-CoV-2 genome sequences so far.

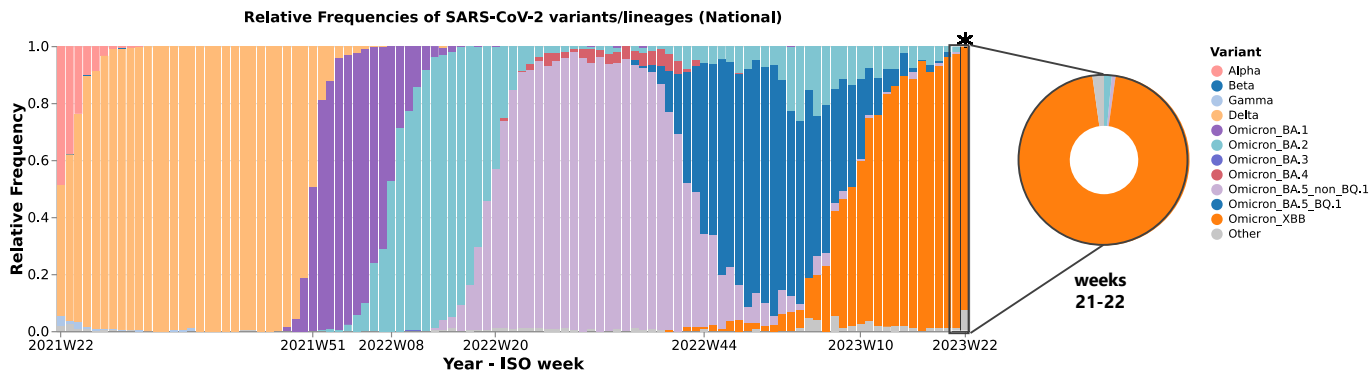


Figure 1: Evolution of the weekly relative frequency of the SARS-CoV-2 variants circulating in Portugal between ISO weeks 22 (31/05/21 – 06/06/21) and 22 (29/05/23 – 04/06/23). The frequencies presented for the last week under analysis (ISO week 22*) might change in the next report, given that some data 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 92.8%** (weeks 19 and 20), mainly due to its **XBB.1.5, XBB.1.9 and XBB.1.16 sub-lineages (and its descendants)** (Figure 2). XBB.1.16 has roused recent interest due to its expansion in some countries, reaching 4.4% in the last two weeks (weeks 21 and 22).
- Lineage BA.5 of variant Omicron** (including its multiple sub-lineages) **was dominant in Portugal** between the weeks 19 of 2022 (09-15/05/22) and 7 of 2023 (13-19/02/23). Since week 44 of 2022, its circulation was mainly due to its **sub-lineage BQ.1 (and its descendants)** (Figure 1 and Figure 2). In the last few weeks it has displayed a residual frequency, with no sequence being detected in the period of weeks 21 and 22 (22/05/23 – 04/06/23) (Figure 1).
- 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 **1.5% between weeks 21 and 22**.
- The sub-lineages with the highest relative frequency in Portugal (such as XBB and their descendants) present constellations of mutations potentially associated with resistance to neutralizing antibodies. Thus, their higher transmissibility may be due to a higher immune evasion capacity.

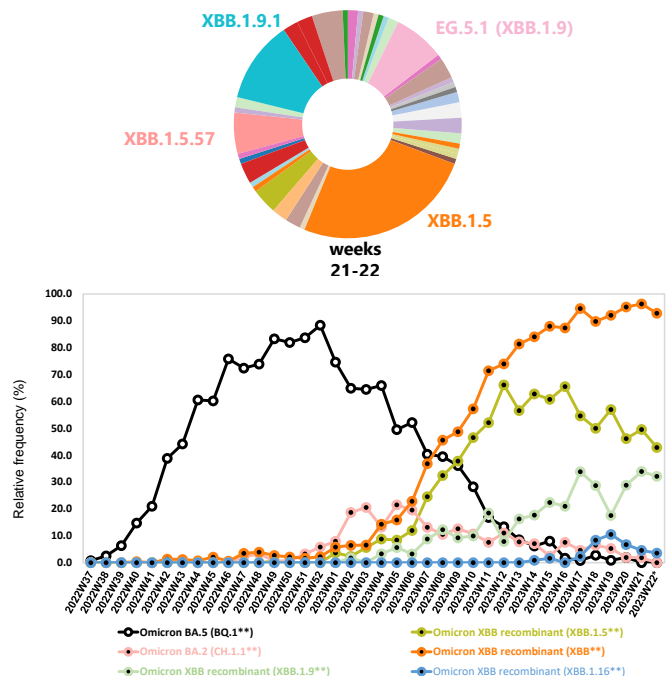


Figure 2: Evolution of the relative frequency of some sub-lineages of interest circulating in Portugal. The circular graph shows the distribution of the relative frequencies of SARS-CoV-2 sub-lineages in the period of ISO weeks 21 and 22 (22/05/23 – 04/06/23), highlighting sub-lineages representing >5% of the sequences analysed in this period. The evolution of BQ.1**, 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 22*) 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.*

Autorship

Genomics and Bioinformatics Unit
Department of Infectious Diseases
NATIONAL INSTITUTE OF HEALTH DOUTOR RICARDO JORGE
Avenida Padre Cruz, 1649-016 Lisboa, PORTUGAL

Recommended citation

National Institute of Health (INSA) Doutor Ricardo Jorge. Genetic diversity of the novel coronavirus SARS-CoV-2 (COVID-19) in Portugal. Lisbon, Portugal INSA; 2022. Available at: <https://insaflu.insa.pt/covid19>

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-plot.html>
<https://outbreak.info/>
<https://www.gisaid.org/>