

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

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



Situation Report

May 2nd, 2023

The National Institute of Health Doutor Ricardo Jorge, I.P. (INSA) has analysed **46589** SARS-CoV-2 genome sequences so far.

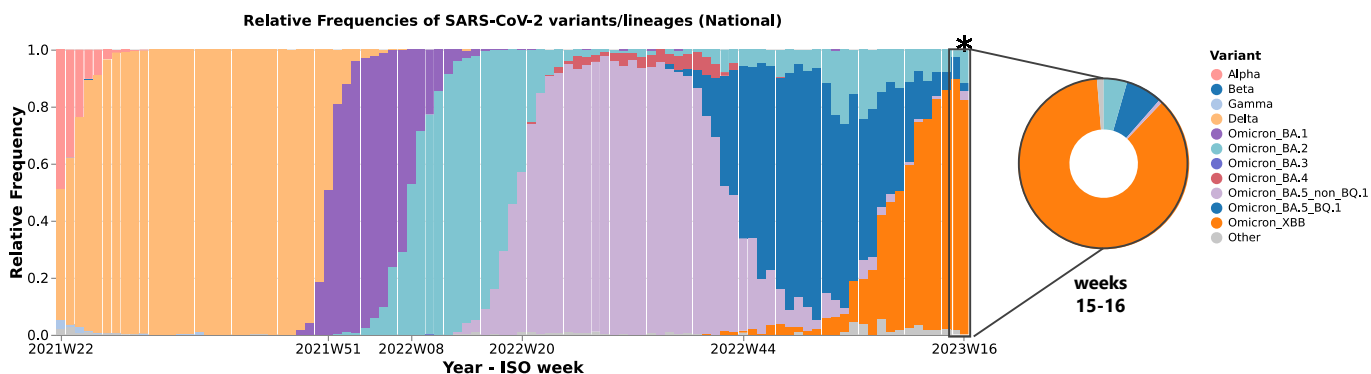


Figure 1: Evolution of the weekly relative frequency of the SARS-CoV-2 variants circulating in Portugal between ISO weeks 22 (31/05/21 - 06/06/21) and 16 (17/04/23 - 23/04/23). The frequencies presented for the last week under analysis (ISO week 16*) might change in the next report, given that some data from that period is still being processed. *This and other graphs can be explored interactively on the website.*

Main highlights

- 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, in particular BQ.1.1)** (Figure 1 and Figure 2). Lineage BA.5 has shown a decrease in frequency since 52 of 2022, presenting a **relative frequency of 7.7%** in the period of weeks 15 and 16 (10/04/23 - 23/04/23) (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), maintaining a residual frequency during the period of BA.5 dominance. 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 2). Since this period, lineage BA.2 has shown a decrease in frequency, presenting **4.5% between weeks 15 and 16**.
- Since week 1 of 2023, a marked increase in circulation of the **recombinant sub-lineage XBB** (and its descendants) has been observed, leading to its dominance in Portugal by week 10 (Figure 1). In latest survey, XBB presented a **relative frequency of 86.6%** (weeks 15 and 16), mainly due to its **XBB.1.5 and XBB.1.9 sub-lineages (and its descendants)** (Figure 2).
- 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.

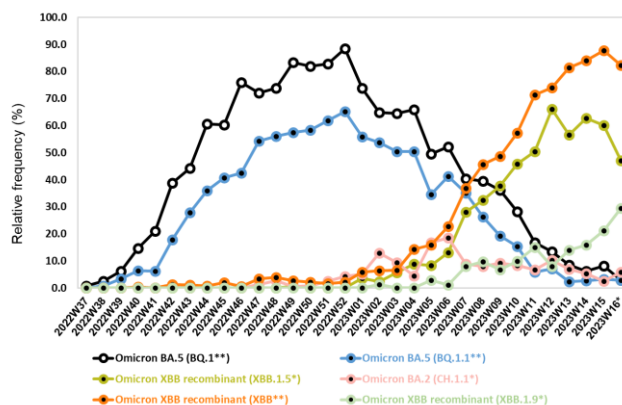
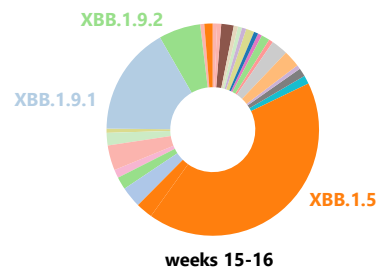


Figure 2: Evolution of the relative frequency of some sub-lineages of interest circulating in Portugal. The circular graph shows the distribution of the relative frequencies of SARS-CoV-2 sub-lineages in the period of ISO weeks 15 and 16 (10/04/23 - 23/04/23), highlighting sub-lineages representing >5% of the sequences analysed in this period. The evolution of BQ.1**, BQ.1.1**, CH.1.1**, XBB** and XBB.1.5* 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 16*) 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_list.html
<https://outbreak.info/>
<https://www.gisaid.org/>