

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

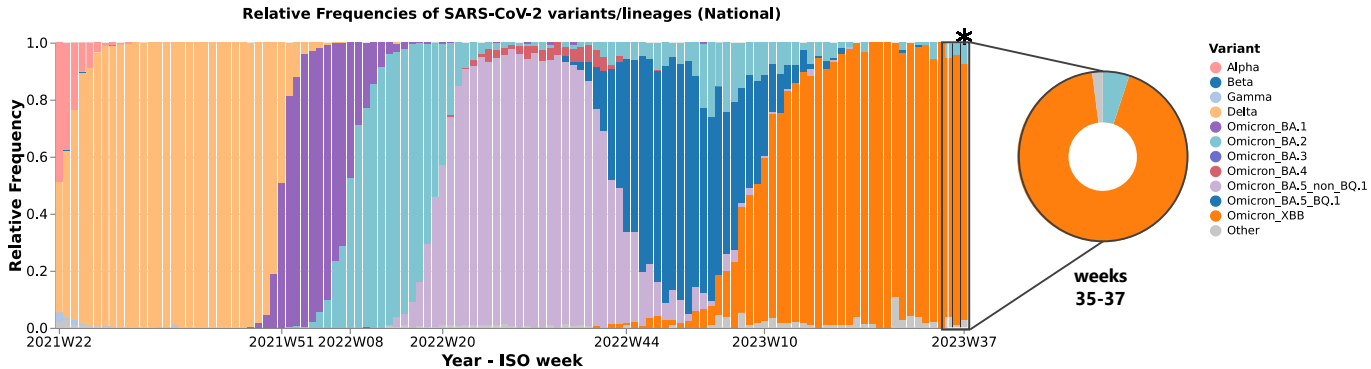
More information at <https://insaflu.insa.pt/covid19>



## Situation Report

September 26<sup>st</sup>, 2023

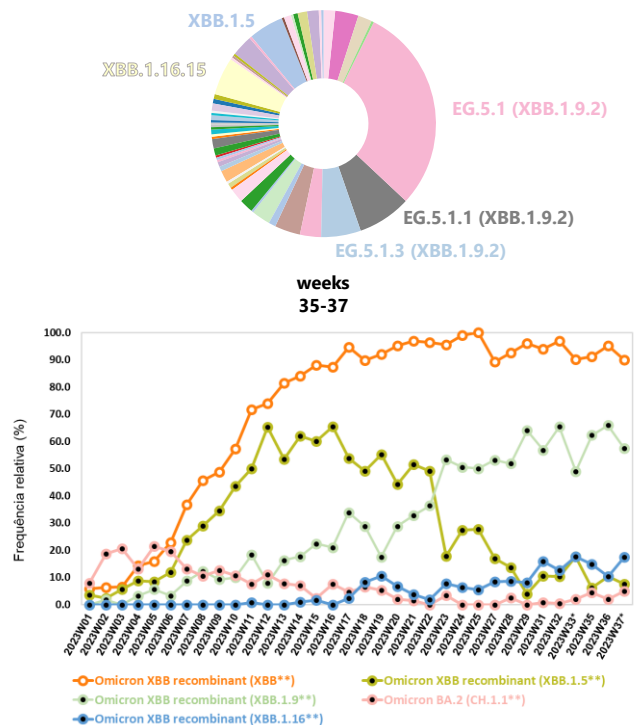
The National Institute of Health Doutor Ricardo Jorge, I.P. (INSA) has analysed **48429** SARS-CoV-2 genome sequences so far.



**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 37/2023 (11/09/23 - 17/09/23), with emphasis on the latest weeks. The frequencies presented for the last week under analysis (ISO week 37\*) 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 92.95%** (weeks 35 to 37), 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 50.7% of all sequences analysed in the last three weeks (weeks 35 and 37).
- 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 **5.03% between weeks 35 and 37**.
- To date, we have detected **7 sequences of BA.2.86** in Portugal between weeks 33 and 37. This sublineage has already been detected in several 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 35 and 37 (28/08/23 - 17/09/23), highlighting sub-lineages representing >5% 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 37\*) 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://cov-lineages.org/lineage_list.html)  
<https://outbreak.info/>  
<https://www.gisaid.org/>