

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

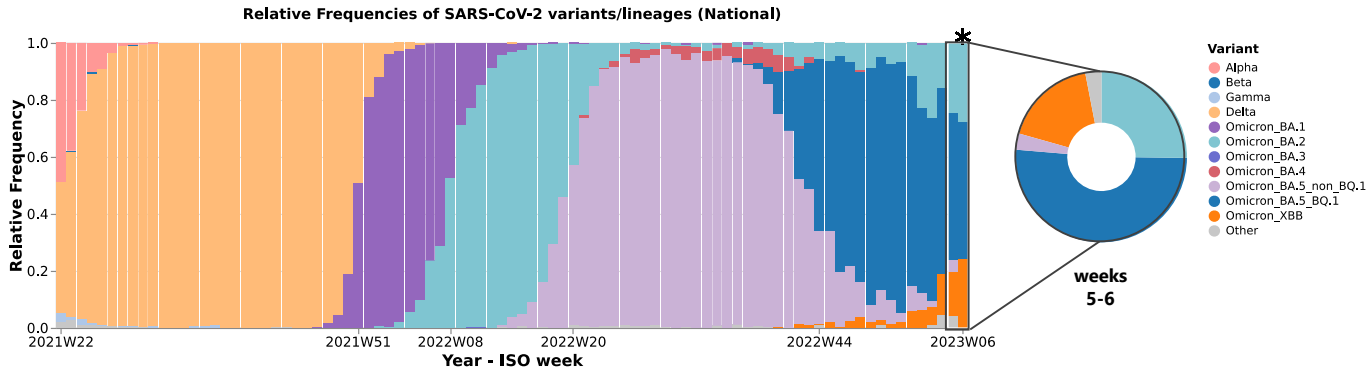
More information at <https://insaflu.insa.pt/covid19>



## Situation Report

February 20<sup>th</sup>, 2023

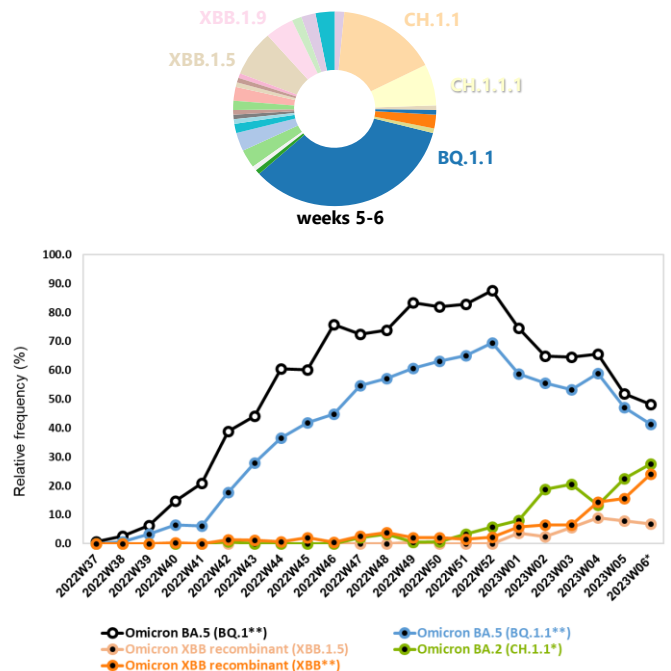
The National Institute of Health Doutor Ricardo Jorge, I.P. (INSA) has analysed **45388** SARS-CoV-2 genome sequences so far.



**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 6 (06/02/23 - 12/02/23). The frequencies presented for the last week under analysis (ISO week 6\*) 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 the variant Omicron** (including its multiple sub-lineages) **is dominant in Portugal** since week 19 (09/05/22 - 15/05/22). From week 44 onwards, its intense circulation is mainly due to its **sub-lineage BQ.1 (and its descendants, in particular BQ.1.1)** (Figure 1 and Figure 2). A continuous decrease in frequency has been observed since week 52 (26/02/22 - 01/01/23). Lineage BA.5 presents a **relative frequency of 54.2%** according to the most recent national sequencing survey, relative to the period of weeks 5 and 6 (30/01/23 - 12/02/23) (Figure 1).
- **Lineage BA.2 of the variant Omicron was dominant in Portugal between weeks 8 (21/02/22 - 27/02/22) and 19 (09/05/22 - 15/05/22)**, maintaining a residual frequency during the period of BA.5 dominance. Nevertheless, a considerable increase in frequency has been observed since week 51 (19/12/22 - 25/12/22) mainly due to the circulation of its **lineage CH.1.1 (and its sub-lineages)**, with relative frequency of 23.7%, in the period of weeks 5 and 6 (Figure 2).
- Since week 1 of 2023, it is highlighted the increase in circulation of the **recombinant sub-lineage XBB** (and its descendants), **with a relative frequency of 17.6%** in the period of weeks 5 and 6 (Figure 1). In particular, we underline the circulation in Portugal of its **XBB.1.5 sub-lineage since week 49** (Figure 2).
- The sub-lineages with the highest relative frequency in Portugal (BQ.1, CH.1.1, 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 5 and 6 (30/01/23 - 12/02/23), highlighting sub-lineages representing >4% of the sequences analysed in this period. The evolution of BQ.1\*\*, CH.1.1\*\*, XBB\*\* and XBB.1.5 relative frequencies during the last 22 weeks is shown in the line plot. It is expected that the frequencies presented for the last week under analysis (ISO week 6\*) 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

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### Recommended citation

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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://cov-lineages.org/lineage_list.html)  
<https://outbreak.info/>  
<https://www.gisaid.org/>