

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

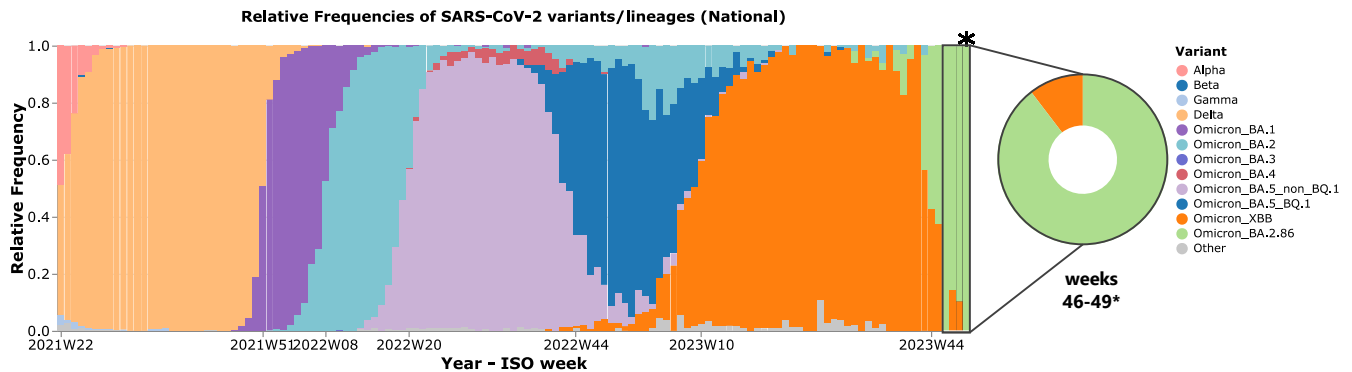
More information at <https://insaflu.insa.pt/covid19>



## Situation Report

December 19<sup>th</sup>, 2023

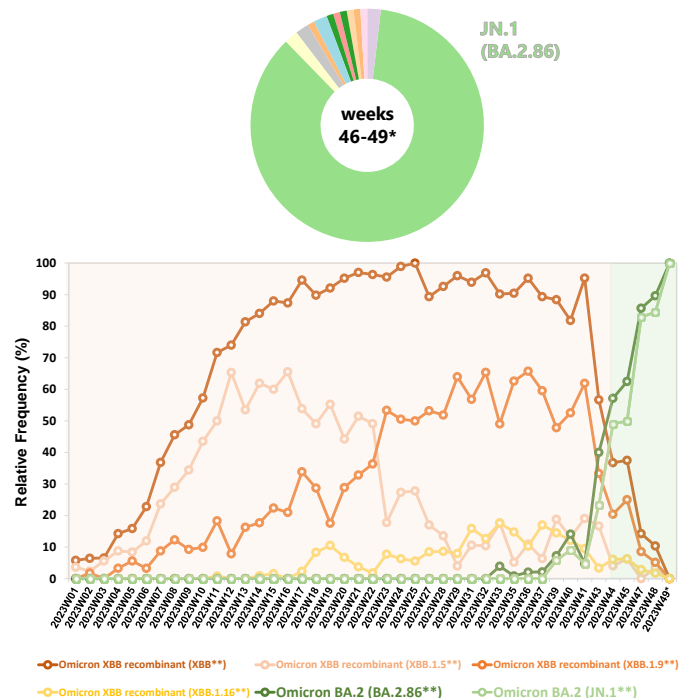
The National Institute of Health Doutor Ricardo Jorge, I.P. (INSA) has analysed **48842** SARS-CoV-2 genome sequences so far.



**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 49/2023 (04/12/23 a 10/12/23), with emphasis on the latest weeks. \*The interpretation of the presented relative frequencies during this period (ISO weeks 46 to 49) should take into account the current low sampling. *This and other graphs can be explored interactively on the website.*

## Main highlights

- The **recombinant lineage XBB** (and its descendants) was **dominant in Portugal, from week 10 of 2023 up to week 43** (Figure 1). In the latest survey (weeks 46 to 49), XBB presented a **relative frequency of 10%**, mainly due to its **XBB.1.5, XBB.1.9 and XBB.1.16 sub-lineages** (and its descendants) (Figure 2).
- The **lineage BA.2** of variant Omicron was dominant in Portugal in the first months of 2022, having maintained a discreet circulation since then, until the emergence of its **sub-lineage BA.2.86**, detected for the first in Portugal in week 33 / 2023 (14-20 august). **BA.2.86 (and its descendants) has shown a relative frequency with a strongly growing tendency, reaching 90% of all sequences analyzed in weeks 46 and 49**, mainly due to the circulation of its JN.1 sub-lineage (Figure 2).
- Although the presented relative frequencies should be interpreted with caution due to the current low sampling, **lineage BA.2.86 is already clearly dominant in Portugal**, replacing the recombinant XBB lineages, similarly to what is being observed internationally. The BA.2.86 lineage has been detected in several countries and has been a focus of international 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). These mutations endow BA2.86 lineage a greater ability to escape the immune system and, potentially, a greater transmissibility.



**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 46 and 49 (13/11/23 - 10/12/23), highlighting sub-lineages representing >5% of the sequences analyzed in this period. The evolution of XBB, XBB.1.5, XBB.1.9, XBB.1.16, BA.2.86 and JN.1 relative frequencies during the last weeks is shown in the line plot. \*The interpretation of the presented relative frequencies during this period (ISO weeks 46 to 49) should take into account the current low sampling. \*\*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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### 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/>