

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

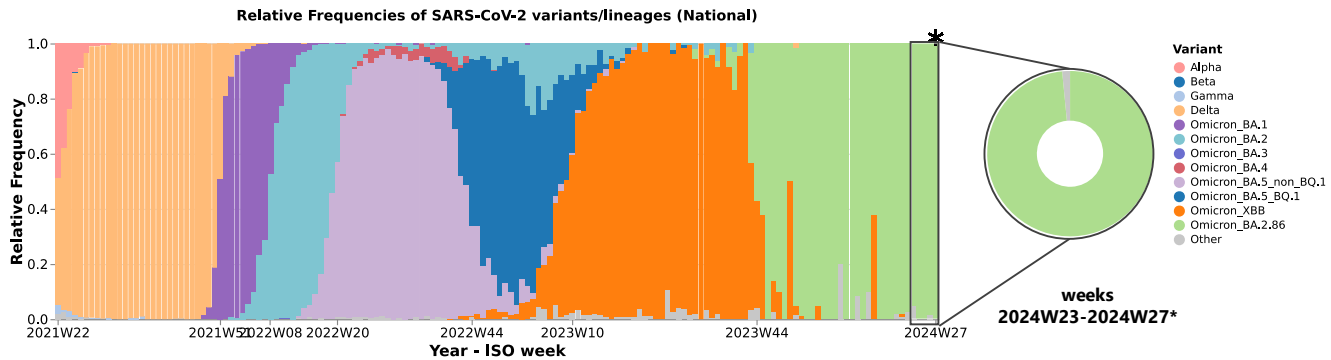
More information at <https://insaflu.insa.pt/covid19>



## Situation Report

July 16<sup>th</sup>, 2024

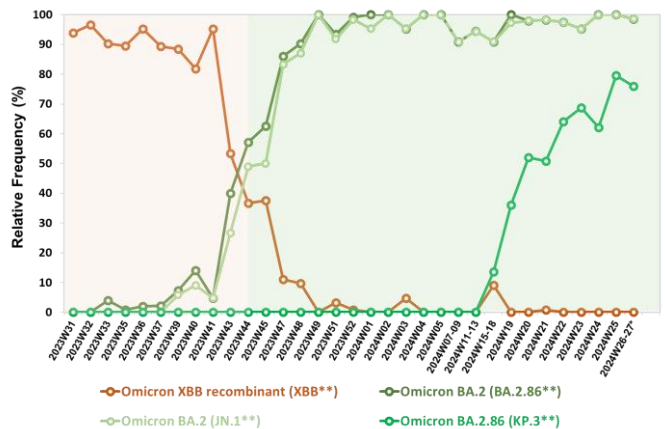
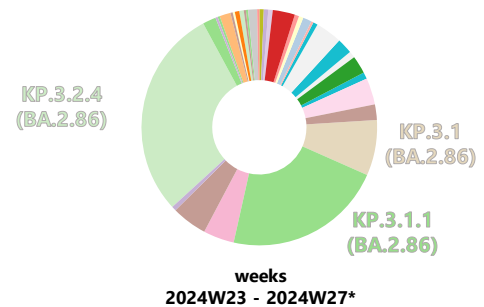
The National Institute of Health Doutor Ricardo Jorge, I.P. (INSA) has analysed **49800** SARS-CoV-2 genome sequences so far.



**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 27/2024 (01/07/24 - 07/07/24), with emphasis on the latest weeks. \*The presented relative frequencies refer to the period of ISO weeks 23/2024 to 27/2024. **This and other graphs can be explored interactively on the website.**

## Main highlights

- The **XBB lineage** (and its descendants) **was dominant in Portugal, from week 10 of 2023 up to week 43 (Figure 1)**, presenting a decreasing trend since then. In the latest survey (weeks 23/2024 and 27/2024), we did not detect any sequences from this lineage (Figure 2).
- The **BA.2 lineage** 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**. This sub-lineage **is dominant in Portugal since week 44 of 2023**, with a **relative frequency of 98.5%** in the latest sampling between weeks 23/2024 and 27/2024 (Figure 1). Its sub-lineage JN.1 and descendants are predominantly circulating in Portugal (Figure 2). Within the latter, we highlight the **considerable increase in circulation of sub-lineage KP.3**, which accounted for **72%** of the sequences analyzed between weeks 23/2024 and 27/2024. The sub-lineage KP.3, as well as other sub-lineages in circulation (e.g., KP.1 and KP.2), belongs to the list of variants under monitoring by ECDC (<https://www.ecdc.europa.eu/en/covid-19/variants-concern>) (Figure 2).
- Most of the lineages detected in this latest sampling exhibit a similar mutational profile in the Spike protein ("BA.2.86-like"), which is considerably divergent from the former dominant main lineage (XBB). This profile endows them a higher potential for immune system evasion and, potentially, increased 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 23/2024 and 27/2024 (03/06/24 - 07/07/24) highlighting sub-lineages representing >5% of the sequences analysed in this period. The evolution of XBB, BA.2.86, JN.1 and KP.3 relative frequencies during the last weeks is shown in the line plot. \*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/>