

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

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Situation Report

March 12th, 2024

The National Institute of Health Doutor Ricardo Jorge, I.P. (INSA) has analysed **49167** SARS-CoV-2 genome sequences so far.

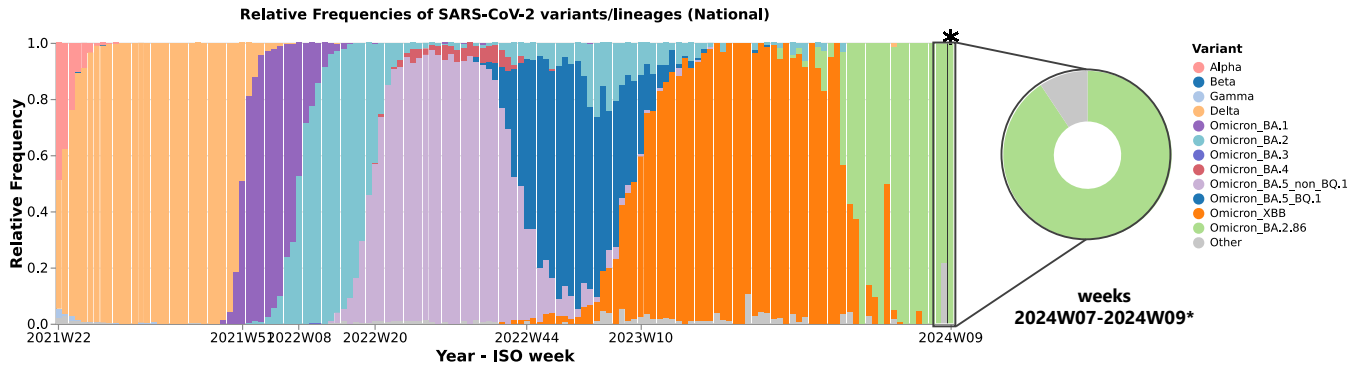


Figure 1: Evolution of the weekly relative frequency of the SARS-CoV-2 variants circulating in Portugal between ISO weeks 22/2021 (31/05/21 - 06/06/21) and 09/2024 (26/02/24 a 03/03/24), with emphasis on the latest weeks. *The interpretation of the presented relative frequencies during this period (ISO weeks 07/2024 to 09/2024) should take into account the current low sampling. *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 03/2024 to 05/2024), no sequences of this lineage were detected (**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 90.6%** in the latest sampling between weeks 07/2024 and 09/2024 (**Figure 2**). Its sub-lineage JN.1 and descendants are predominantly circulating in Portugal (**Figure 2**).
- In the latest sampling (weeks 07/2024 to 09/2024) (**Figure 2**), we highlight the detection of a recently described **recombinant lineage, XDS**, reflecting a **genomic mosaic between the XBB and BA.2.86 sub-lineages**. Although representing ~10% of the analyzed sequences and detected in more than one geographic region, the current low sampling hinders more definitive conclusions about the extent of its circulation in Portugal at this stage. To date, XDS has been reported in only 9 countries, making its international impact also uncertain.
- All lineages detected in this latest sampling (i.e., sub-lineages BA.2.86 and the recombinant XDS) 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.

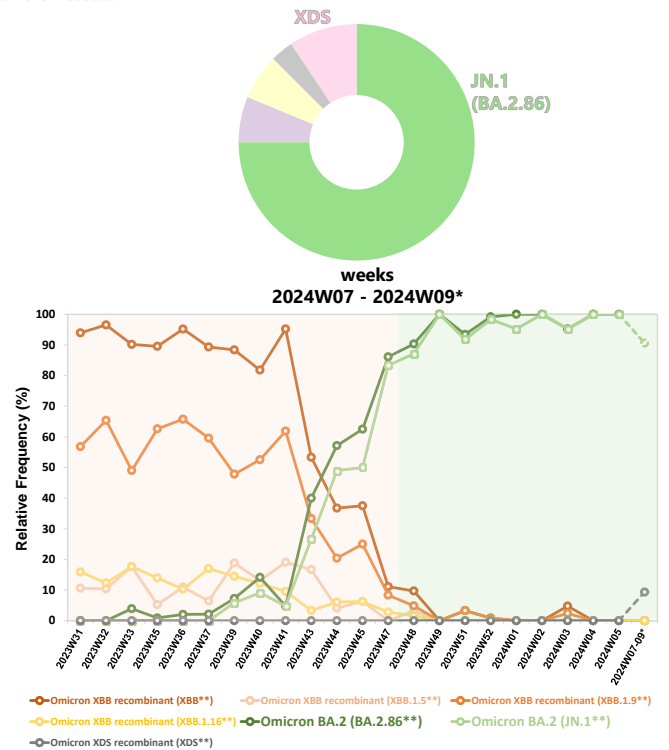


Figure 2: Evolution of the relative frequency of some sub-lineages of interest circulating in Portugal. The circular graph shows the distribution of the relative frequencies of SARS-CoV-2 sub-lineages in the period of ISO weeks 07/2024 and 09/2024 (12/02/24 - 03/03/24). The evolution of XBB, XBB.1.5, XBB.1.9, XBB.1.16, BA.2.86, JN.1 and XDS relative frequencies during the last weeks is shown in the line plot. *The interpretation of the presented relative frequency during this period (ISO weeks 07/2024 to 09/2024) 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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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/>