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

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Situation Report

December 27th, 2022

The National Institute of Health Doutor Ricardo Jorge, I.P. (INSA) has analysed 44385 SARS-CoV-2 genome sequences so far.

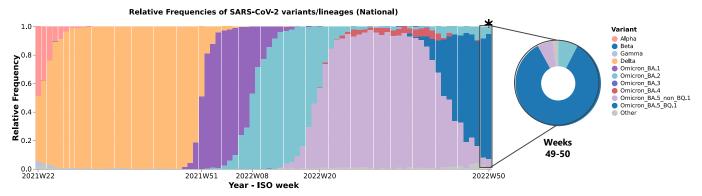


Figure 1: Evolution of the weekly relative frequency of the SARS-CoV-2 variants circulating in Portugal between ISO weeks 22 (31/05/21 - 06/06/21) and 50 (13/12/22 - 19/12/22). The frequencies presented for the last week under analysis (ISO week 50*) might change in the next report, given that some data 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) and presents a relative frequency of 94,6% according to the most recent national sequencing survey on week 50 (13/12/22 19/12/22) (Figure 1).
- The relative frequency of **lineage BA.4 of the variant Omicron** has been residual, with **no sequence detected in the last 2 weeks (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). Since then, its relative frequency is residual, being represented mainly by **lineage BN.1 (and its sub-lineages)**, with relative frequencies of 3,7% and 3,6% in weeks 49 and 50, respectively.
- On behalf of the continuous monitoring of the introduction and circulation of (new) SARS-CoV-2 (sub-)lineages in Portugal, we have been observing the emergence of sublineages of interest, with novel constellations of mutations potentially associated with resistance to neutralizing antibodies. Among these, we highlight the sub-lineages of BA.2 (e.g., BN.1 and CA.7) and BA.5 (e.g., BF.7 and BQ.1), some of them showing considerable increase of circulation in some countries, particularly in Europe. In Portugal, it is highlighted the increase of the relative frequencies of BQ.1 (and its sublineages, in particular BQ.1.1), which is dominant since week 44 (Figure 2). To date, 29 sequences of the recombinant sub-lineage XBB have been detected in Portugal. XBB has been a focus of interest due to its immune evasion capacity.

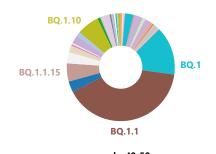




Figure 2: Evolution of the relative frequency of sub-lineage BQ.1 and its descendants BQ.1.1 in Portugal. The circular graph shows the distribution of the relative frequencies of SARS-CoV-2 sub-lineages in the period of ISO weeks 49 and 50 (06/12/22 – 19/12/22), highlighting sub-lineages representing >5% of the sequences analysed in this period. The evolution of BQ.1** and BQ.1.1** relative frequencies during the last 14 weeks is shown in the line plot. It is expected that the frequencies presented for the last week under analysis (ISO week 50°) 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

;//www.ecdc.europa.eu/en/covid-19/situation-updates/variants-dashboard ;//www.who.int/activities/tracking-SARS-CoV-2-variants ;//cov-lineages.org/lineage_list.html







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