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

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

Situation Report

November 22nd, 2022

The National Institute of Health Doutor Ricardo Jorge, I.P. (INSA) has analysed **43536** SARS-CoV-2 genome sequences so far.

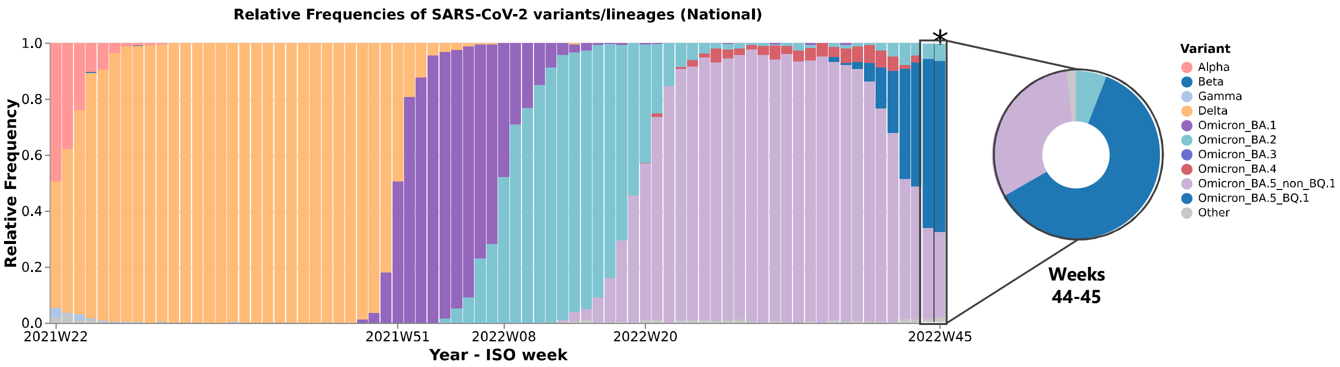

Figure 1: **Evolution of the weekly relative frequency of the SARS-CoV-2 variants circulating in Portugal between ISO weeks 22 (31/05/21 - 06/06/21) and 45 (07/11/22 – 13/11/22).** The frequencies presented for the last week under analysis (ISO week 45*) might change in the next report, given that some 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 91.6%** according to the most recent national sequencing survey on week 45 (07/11/22 - 13/11/22) (**Figure 1**).

- **Lineage BA.4 of the variant Omicron was not detected in weeks 44 and 45**.

- **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, representing **5,9% of the sequences in weeks 44 and 45**.

- 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 sub-lineages 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), **BA.4** (e.g., BA.4.6) **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 sub-lineages, **in particular BQ.1.1), and BN.1** (and its sub-lineages, in particular BN.1.3.1) (**Figure 2**). To date, seven 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.

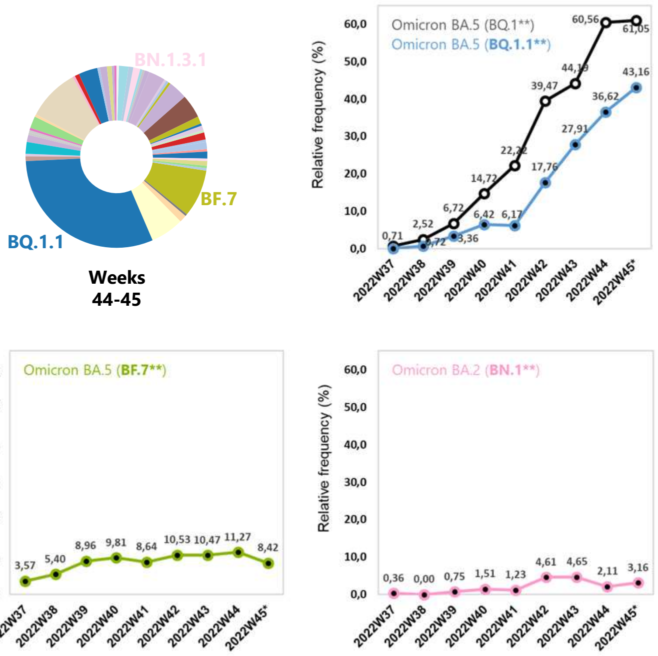

Figure 2: **Sub-lineages of interest circulating in Portugal.** The circular graph shows the distribution of the relative frequencies of SARS-CoV-2 sub-lineages in the period of ISO weeks 44 and 45 (31/10/22 – 13/11/22), **highlighting sub-lineages of interest** (see the evolution of their relative frequencies during the last 9 weeks in the line plots). It is expected that the frequencies presented for the last week under analysis (ISO week 45*) 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

Genomics and Bioinformatics Unit
Department of Infectious Diseases
NATIONAL INSTITUTE OF HEALTH DOUTOR RICARDO JORGE
Avenida Padre Cruz, 1649-016 Lisboa, PORTUGAL

Recommended citation

National Institute of Health (INSA) Doutor Ricardo Jorge. Genetic diversity of the novel coronavirus SARS-CoV-2 (COVID-19) in Portugal. Lisbon, Portugal INSA; 2022. Available at: https://insaflu.insa.pt/covid19

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/

REPÚBLICA PORTUGUESA
SAÚDE
SNS SERVIÇO NACIONAL DE SAÚDE
Instituto Nacional de Saúde Doutor Ricardo Jorge