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

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

Situation Report

2nd March 2022

The **National Institute of Health Doutor Ricardo Jorge, I.P. (INSA)** has analysed **28907 SARS-CoV-2 genome sequences** so far, obtained from positive samples collected in more than 100 laboratories/hospitals/institutions, accross 304 municipalities.

The genetic diversity of SARS-CoV-2 has been monitored based on an average of 523 sequences/week, since the beginning of June, 2021. These sequences have been obtained from positive samples collected randomly throughout the 18 Districts of Portugal Mainland and the Autonomous Regions of the Azores and Madeira, covering an average of 136 municipalities per week (**Figures 1 e 2**).

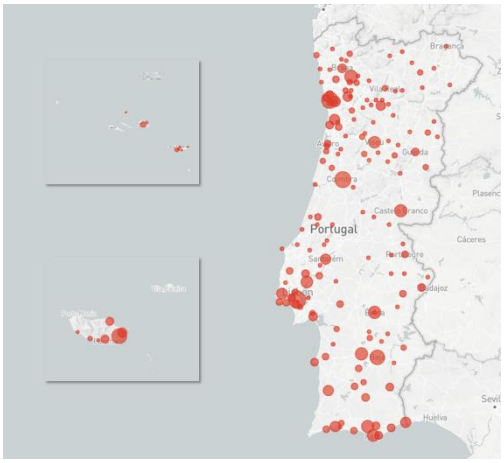

Figure 1. Geographic coverage (at the municipality level) of the last weekly nationwide sequencing survey, which resulted in 542 new SARS-CoV-2 genome sequences from 168 municipalities.

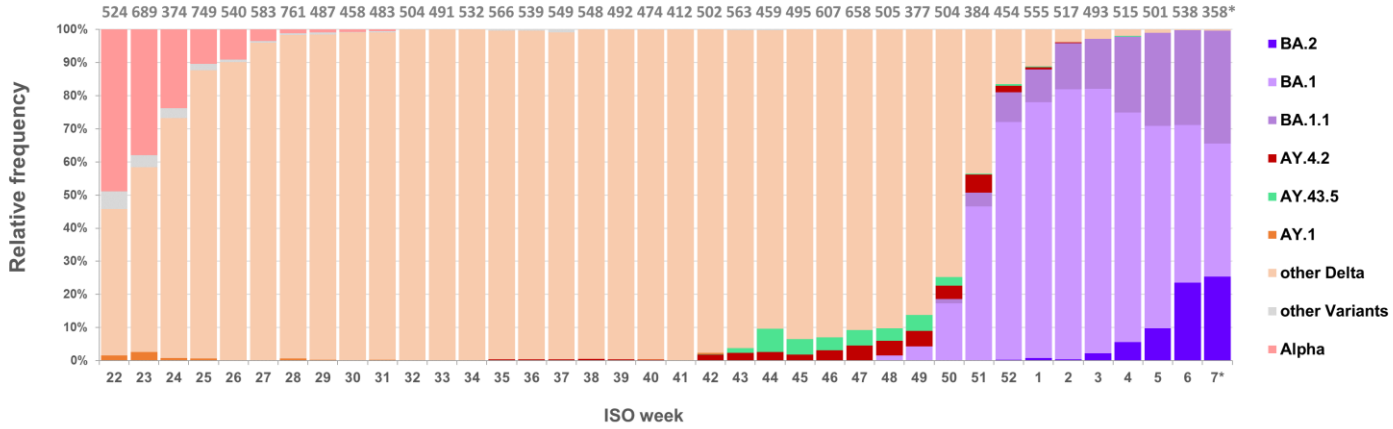

Figura 2. Evolution of the weekly relative frequency of the SARS-CoV-2 (sub-)lineages circulating in Portugal between ISO weeks 22 (31st May – 6th June, 2021) and 7 (14th – 20th February, 2022). The values on top of each bar indicate the number of sequences analysed per week in the context of the weekly random nationwide surveys. The plot highlights: i) the BA.1, BA.1.1 e BA.2 (sub)lineages (classified as *Omicron* by the WHO) and ii) *Delta* sublineages of interest (AY.1, AY.4.2 e AY.43.5). *The frequencies presented for the last week under analysis (ISO week 6) might change in the next report, given that some data from that period is still being processed.

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Main highlights:

- **The Variant of Concern (VOC) *Omicron*, according to the WHO classification, currently includes several (sub)lineages identified by the "BA" prefix (Figure 3).**

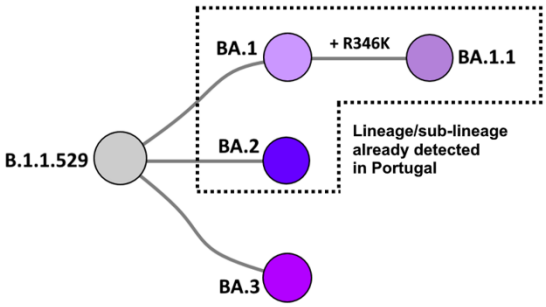

Figure 3. Simplified overview of the genetic relatedness of the several *Omicron* (sub)lineages.

- **Lineage BA.1**

  BA.1 has been firstly identified in Southern Africa countries in November 2021, and in over 100 countries since then. It is characterized by a large number of mutations of interest in the Spike protein, including mutations known by their role in binding to human cell receptors and/or antibody recognition.

  - **BA.1 has been firstly identified in Portugal by mid November, 2021 and has been detected in all weekly nationwide sequencing surveys since ISO week 47 (22-28 November), 2021** (Figure 2). These surveys, together with the real-time monitoring of the proportion of positive samples with S gene target failure (SGTF), using the *TaqPath* diagnostic kit (proxy for *Omicron* BA.1), has allowed us to monitor its circulation in Portugal (Figures 2 and 4). According to the sequencing data, **the relative frequency of BA.1 reached a maximum in ISO week 2 (95,6%, 10-16 January, 2022) and then started a decreasing trend** (Figures 2 and 4)**.** SGTF data shows a concordant trend in the proportion of SGTF positive samples, with a **current estimated frequency of 41,8% (28th February 2022)** (Figure 4).
  - Recently, part of the *Omicron* BA.1 sequences were reclassified internationally, constituting the BA.1.1 sublineage, which is characterized by the additional mutation **R346K in the receptor-binding domain of Spike protein** (Figure 3). This sub-classification was due to the increase in the frequency of cases associated with BA.1 with this mutational profile (BA.1 + Spike R346K) in some countries. The **BA.1.1** sublineage **has been circulating in Portugal since early December 2021 and its relative frequency has been gradually increasing** (Figures 2 and 5), **representing around 30% of the sequences analysed in the ISO weeks 6 and 7** (**7th – 20th February**), **2022** (Figure 2).

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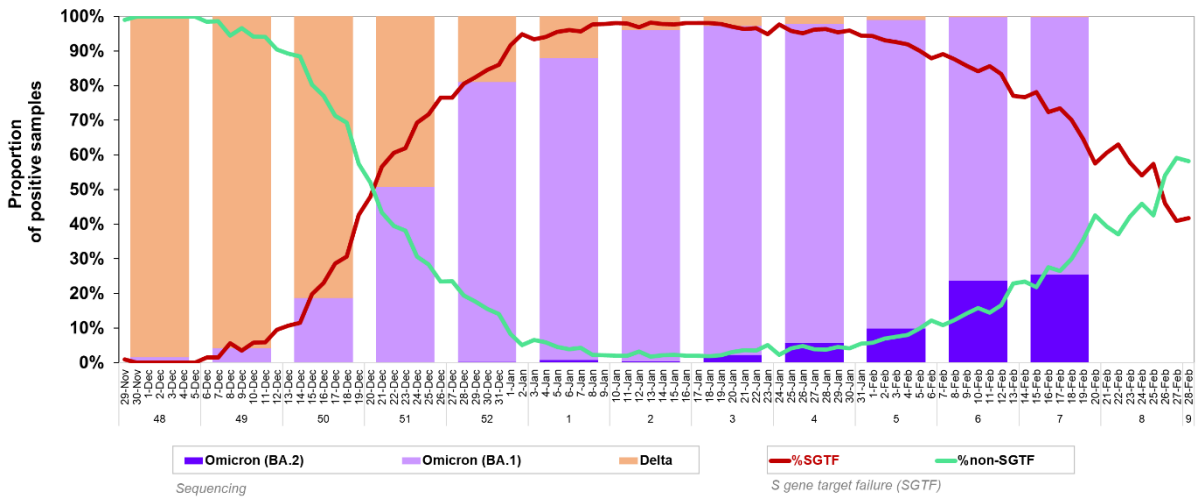

Figure 4. Evolution of the daily proportion of positive samples with and without S gene target failure (SGTF) in parallel with the relative frequency of the variants/lineages in circulation as assessed by the random nationwide sequencing surveys, since ISO week 48, 2021 (collection date). An **SGTF positive** sample is indicative of a probable case of ***Omicron* BA.1 (including its BA.1.1 sublineage)**. A **non-SGTF positive** sample is indicative of a probable case of ***Omicron* BA.2 or *Delta***. The SGTF data analysis includes only positive samples tested with *TaqPath – ThermoFisher* with a *Cycle threshold* (Ct) ≤30 for the N and ORF1ab genes. The data relative to the most recents days (SGTF) or week (Sequencing) are provisional.

Source of SGTF data: laboratories using the kit TaqPath – ThermoFisher (UNILABS, a Cruz Vermelha Portuguesa, o Algarve Biomedical Center, SYNLAB, Hospital de Santo Espírito da Ilha Terceira e Universidade do Porto); See here the table with the data presented in the Figure.

Technical note: The %SGTF data has been revised and updated retrospectively from 1st January 2022 in the report released on 8th February 2022. This revision corrected a technical artefact that was detected in the automatic computation of data since 10th January, which underestimated the proportion of SGTF. The estimates of the relative frequency of the BA.1 lineage obtained by sequencing and by %SGTF are again concordant, similarly to what was observed previously.

- **Lineage BA.2**
  - When the BA.1 was firstly identified in mid November 2021, another lineage (BA.2) sharing several genetic traits was also identified. In particular, both lineages descend from the same ancestral lineage (designated "B.1.1.529") (**Figure 3**) and both present an "excess" of mutations in the Spike protein, with many being shared between them. However, contrarily to BA.1 lineage, **BA.2 lineage does not harbor the del69-70 deletion in the Spike protein, and hence does not present S gene target failure (SGTF)** with the kit *TaqPath – ThermoFisher*. This lineage has already been detected in multiple countries, with special highlight to its high prevalence in Denmark.
  - **In Portugal, BA.2 has been firstly detected in random nationwide sequencing surveys in ISO week 52** (27 December 2021 – 2 January 2022) (**Figure 2**). **Its relative frequency has been slowly increasing since then**, representing about 25,4% of the samples subjected to sequencing in ISO week 7 (14– 20 February**;** *ongoing analysis*) (**Figure 2**). Similarly to the *Delta* variant, BA.2 can be indirectly monitored through the proportion of non-SGTF positive samples. Since the circulation of *Delta* is now residual (<1% since week 5), the predictive value of this indicator to identify BA.2 suspected cases is currently robust. Hence, it is estimated that **BA.2 is now dominant in Portugal, representing 58.2% of the positive samples on 28 February 2022** (**Figures 2 e 4**).
  - Sequencing data shows that BA.2 has been increasing its relative frequency in all Regions, representing ≥15% of all sequences analysed per Region in ISO week 7, with exception of the Autonomous Region of the Azores, where BA.2 dissemination in the community started later (**Figure 5**).

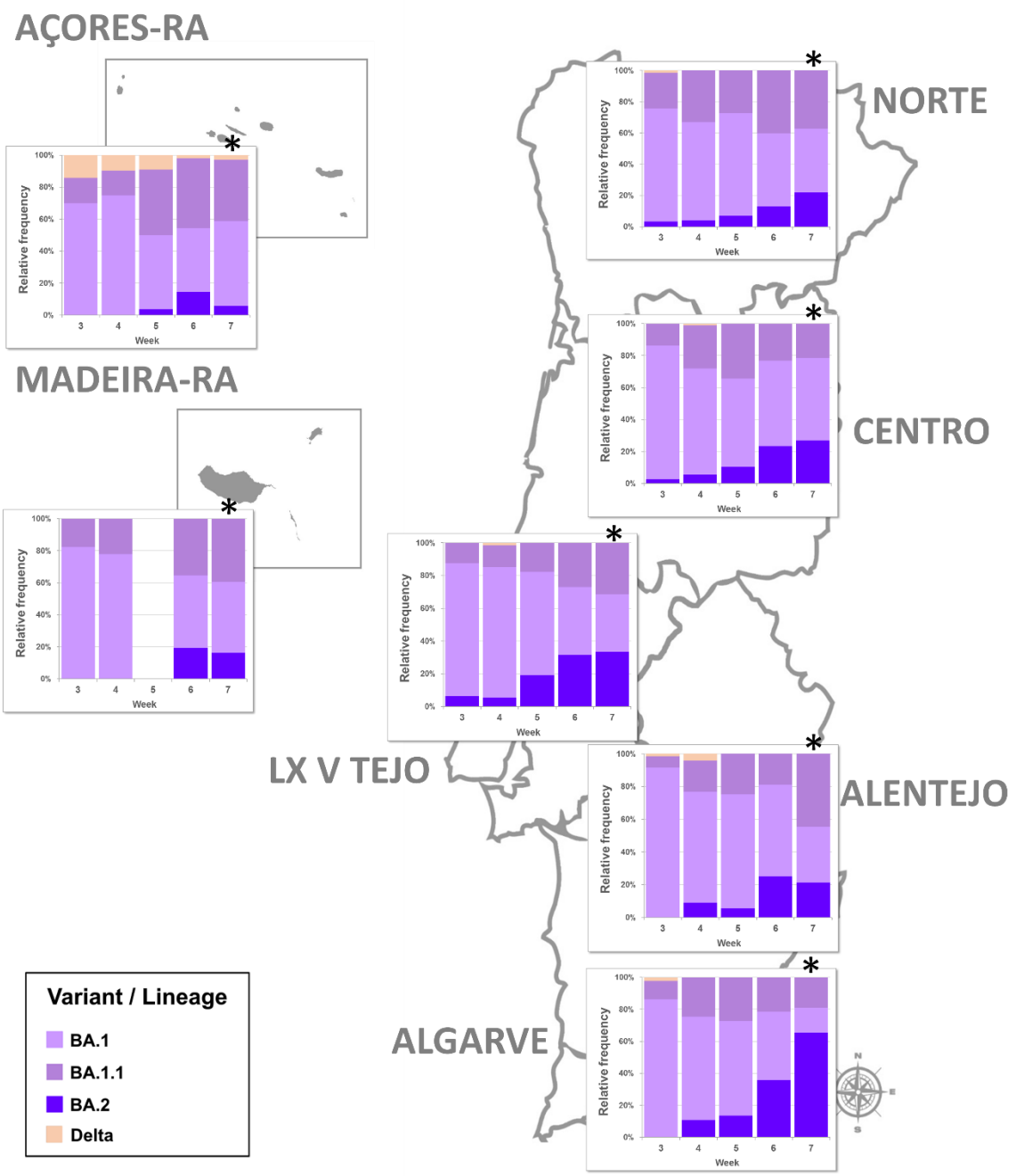

Figure 5. Evolution of the weekly relative frequency of SARS-CoV-2 lineages in each Health Region, between ISO weeks 2 (10-16 January) **and 7** (14 - 20 February)**, 2022**. The plots highlight the BA.1 (including its sublineage BA.1.1) and BA.2 (classified as *Omicron* by WHO), as well as the *Delta* variant.

**It is expected that the frequencies presented for the last week under analysis (ISO week 7) might change in the next report, given that some data from that period is still being processed. Of note, as of the date of publication of this report, no samples from ISO week 5 were available from the Autonomous Region of Madeira.*

- Dynamic tables summarizing the **frequency and geotemporal spread of the variants/lineages identified so far as well as the mutations of interest in protein Spike** in each of them are available in the website.