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

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

Situation Report

22nd March 2022

The **National Institute of Health Doutor Ricardo Jorge, I.P. (INSA)** has analysed **30315 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 520 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 137 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 510 new SARS-CoV-2 genome sequences from 139 municipalities**.

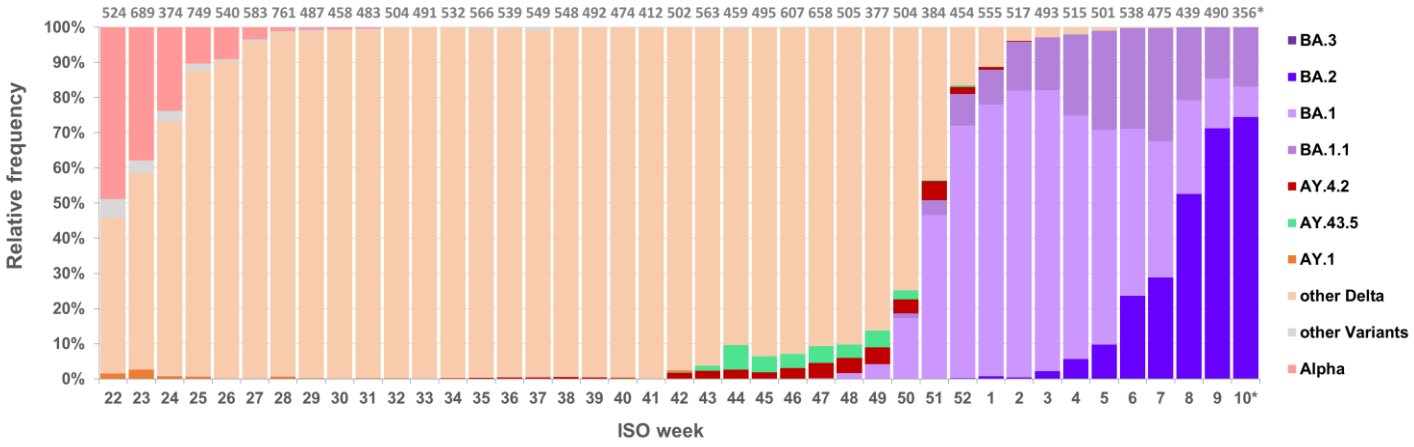

Figura 2. **Evolution of the weekly relative frequency of the SARS-CoV-2 (sub-)lineages circulating in Portugal between ISO weeks 22 (31st May – 6th June, 2021) and 10 (7th -13th March, 2022).** The values on top of each bar indicate the number of sequences analysed per week in the context of the weekly random nationwide surveys. The plot highlights: i) the BA.1, BA.1.1, BA.2 and BA.3 (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 10) 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), all of them already detected in Portugal.**

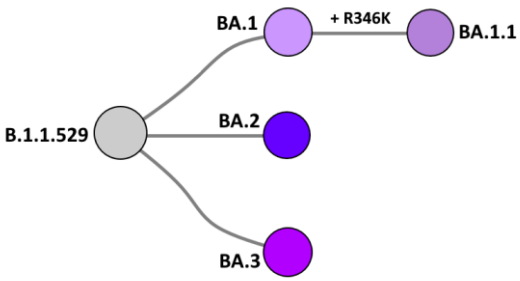

Figure 3. Simplified overview of the genetic relatedness of the several *Omicron* (sub)lineages.

- **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 (22nd-28th 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%, 10th-16th 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 11.3% (21st March 2022)** (Figure 4).

  - **BA.1.1 sublineage**, which is characterized by the additional mutation **R346K in the host receptor-binding domain of Spike protein** (Figure 3) has been circulating in Portugal since early December 2021 and its relative frequency increased gradually until ISO week 7 (Figures 2 and 5), where it represented around 30% of the sequences analysed (Figure 2). Its relative frequency has shown a decreasing trend, **representing 16.9% of the sequences analysed in ISO week 10 (7th-13th March, 2022;** *preliminary data***)**.

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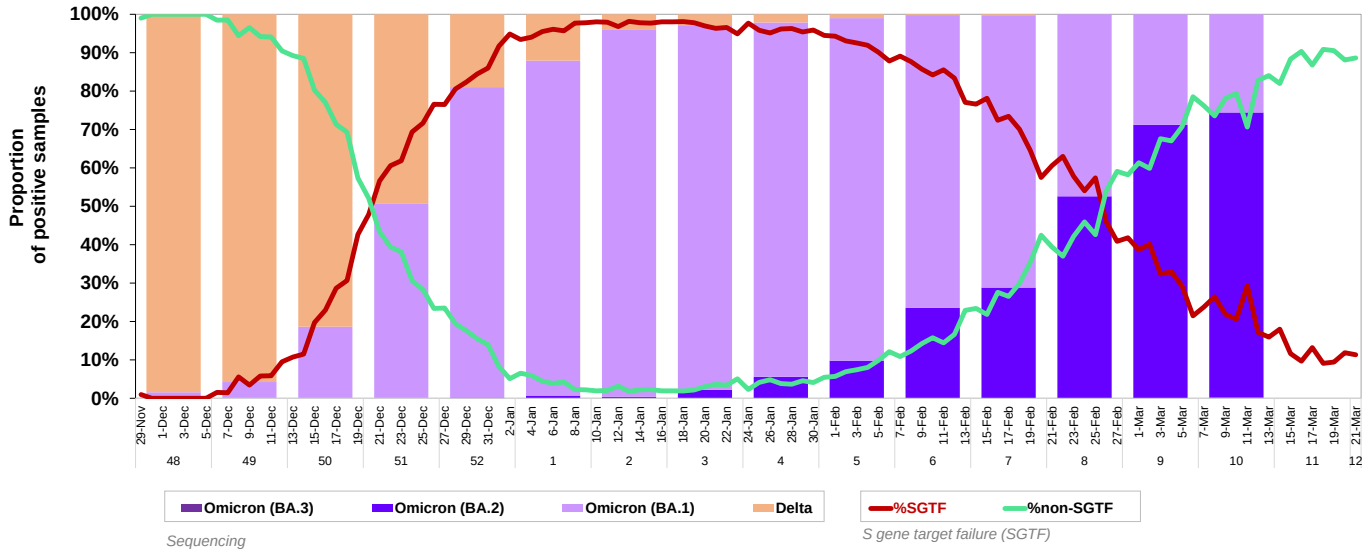

Figure 4. Evolution of the daily proportion of positive samples with and without S gene target failure (SGTF) in parallel with the relative frequency of the variants/lineages in circulation as assessed by the random nationwide sequencing surveys, since ISO week 48, 2021 (collection date). Currently, a **SGTF positive** sample is indicative of a probable case of ***Omicron* BA.1 (including its BA.1.1 sublineage)**, since BA.3 (also "SGTF") has been detected at a relative frequency <0.5%. A **non-SGTF positive** sample is indicative of a probable case of ***Omicron* BA.2**, since *Delta* (also "non-SGTF") is now residual (<1% since week 5). 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.

- **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** (27th December 2021 – 2nd January 2022) (**Figure 2**). **Its relative frequency has been slowly increasing since then**, representing 74.2% of the samples subjected to sequencing in ISO week 10 (7th-13th March; *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, **BA.2 is clearly dominant in Portugal, representing 88.7% of the positive samples on 21st March 2022** (**Figures 2, 4** and **5**).

- **Lineage BA.3**
  - This lineage, firstly identified in South Africa, shares genetic similarities to both BA.1 and BA.2 *Omicron* lineages (**Figure 3**), and has been detected sporadically worldwide. In Portugal, BA.3 was only detected in the random survey of ISO week 10 (7th-13th March, 2022) in the Autonomous Region of the Azores (**Figure 5**), representing a travel-associated case, with no current evidence of community transmission.

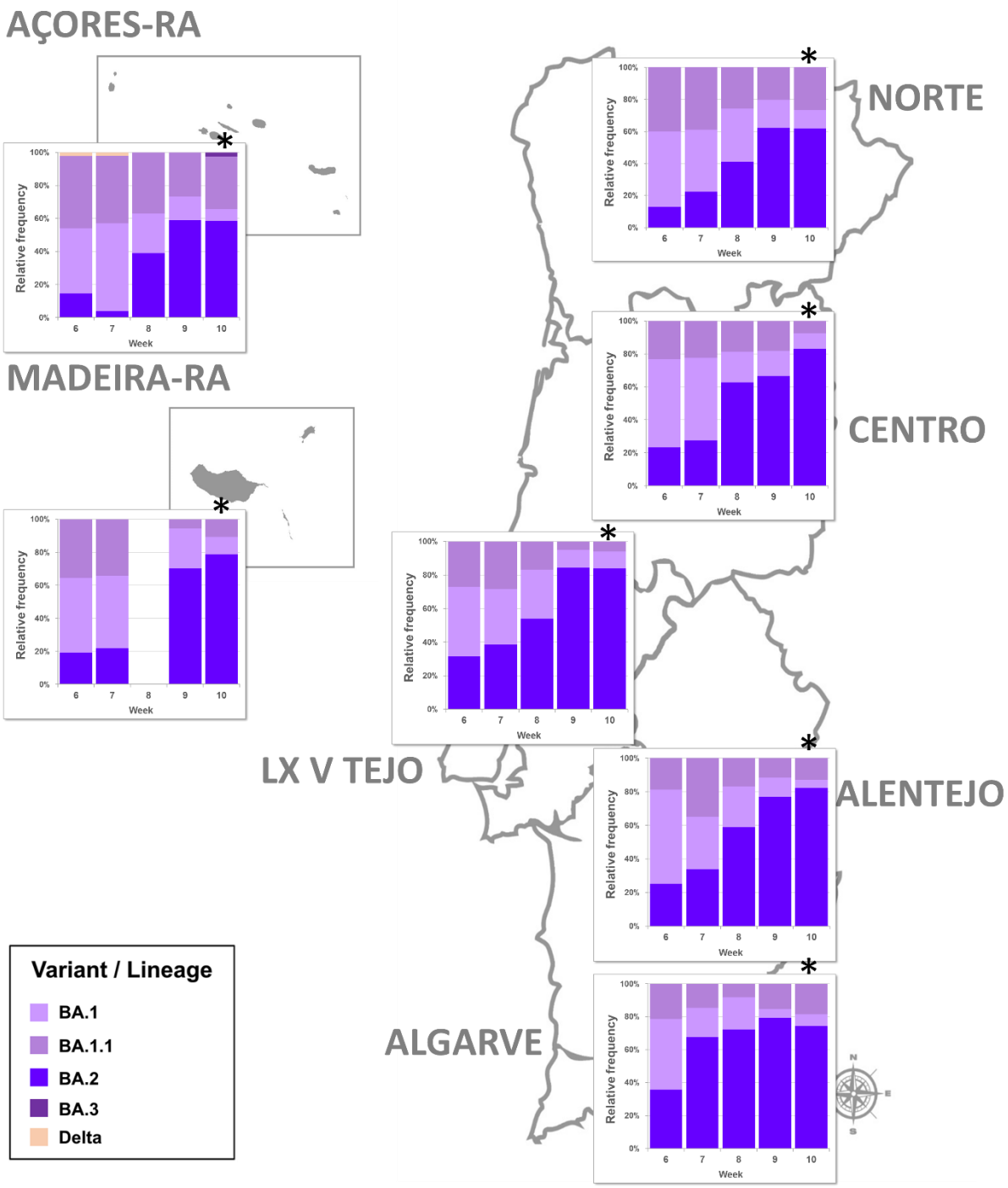

Figure 5. Evolution of the weekly relative frequency of SARS-CoV-2 lineages in each Health Region, between ISO weeks 5 (31st January – 6th February) **2021 and 10** (7th-13th March) **2022**. The plots highlight the BA.1 (including its sublineage BA.1.1), BA.2 and BA.3 (classified as *Omicron* by WHO), as well as the *Delta* variant.

**It is expected that the frequencies presented for the last week under analysis (ISO week 9) 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 weeks 5 and 8 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.