



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

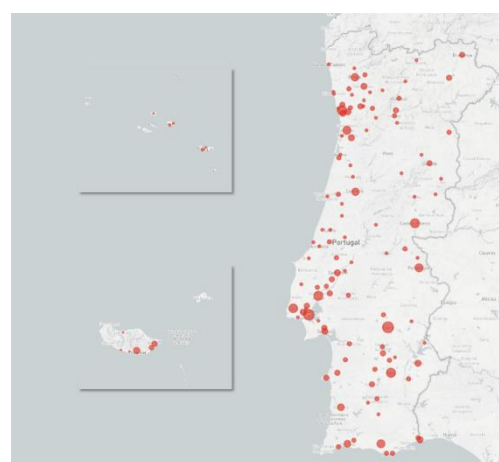
More information at <https://insaflu.insa.pt/covid19/>

## Situation Report

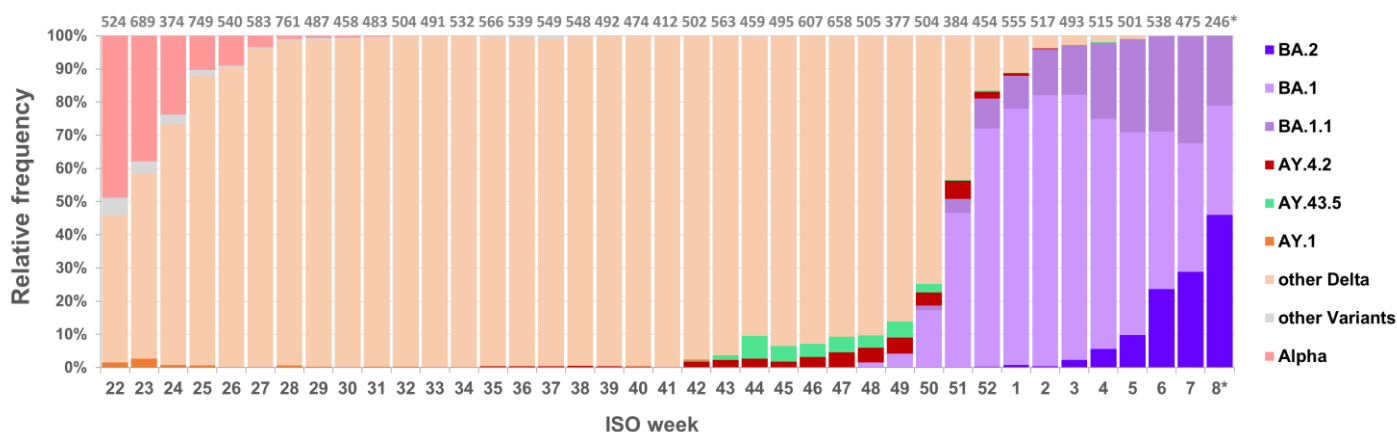
8<sup>th</sup> March 2022

The **National Institute of Health Doutor Ricardo Jorge, I.P. (INSA)** has analysed **29270 SARS-CoV-2 genome sequences** so far, obtained from positive samples collected in more than 100 laboratories/hospitals/institutions, across 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 139 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 363 new SARS-CoV-2 genome sequences from 128 municipalities.**

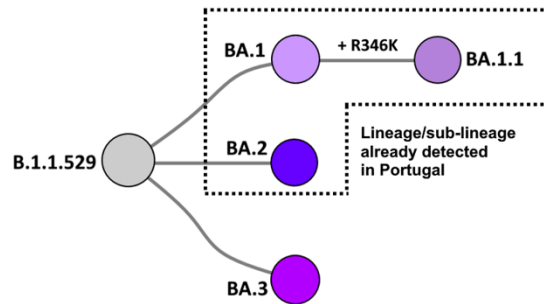


**Figura 2. Evolution of the weekly relative frequency of the SARS-CoV-2 (sub-)lineages circulating in Portugal between ISO weeks 22 (31<sup>st</sup> May – 6<sup>th</sup> June, 2021) and 8 (21<sup>st</sup> – 27<sup>th</sup> February, 2022).** The values on top of each bar indicate the number of sequences 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 8) might change in the next report, given that some data from that period is still being processed.



### 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).

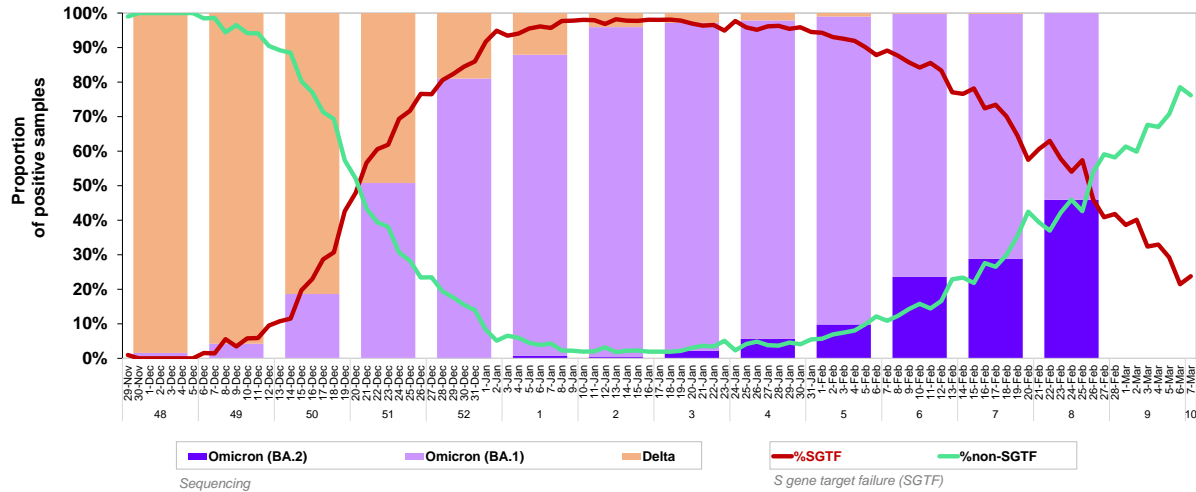


**Figure 3.** Simplified overview of the genetic relatedness of the several *Omicron* (sub)lineages.

- **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 23,8% (7 March 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 increased gradually until ISO week 7 (Figures 2 and 5), where it represented around 30% of the sequences analysed (Figure 2).** However, following the decreasing trend observed for the relative frequency of lineage BA.1, **lineage BA.1.1 represented around 20% of the sequences analysed in ISO week 8 (21<sup>st</sup> – 27<sup>th</sup> February, 2022; preliminary data).**



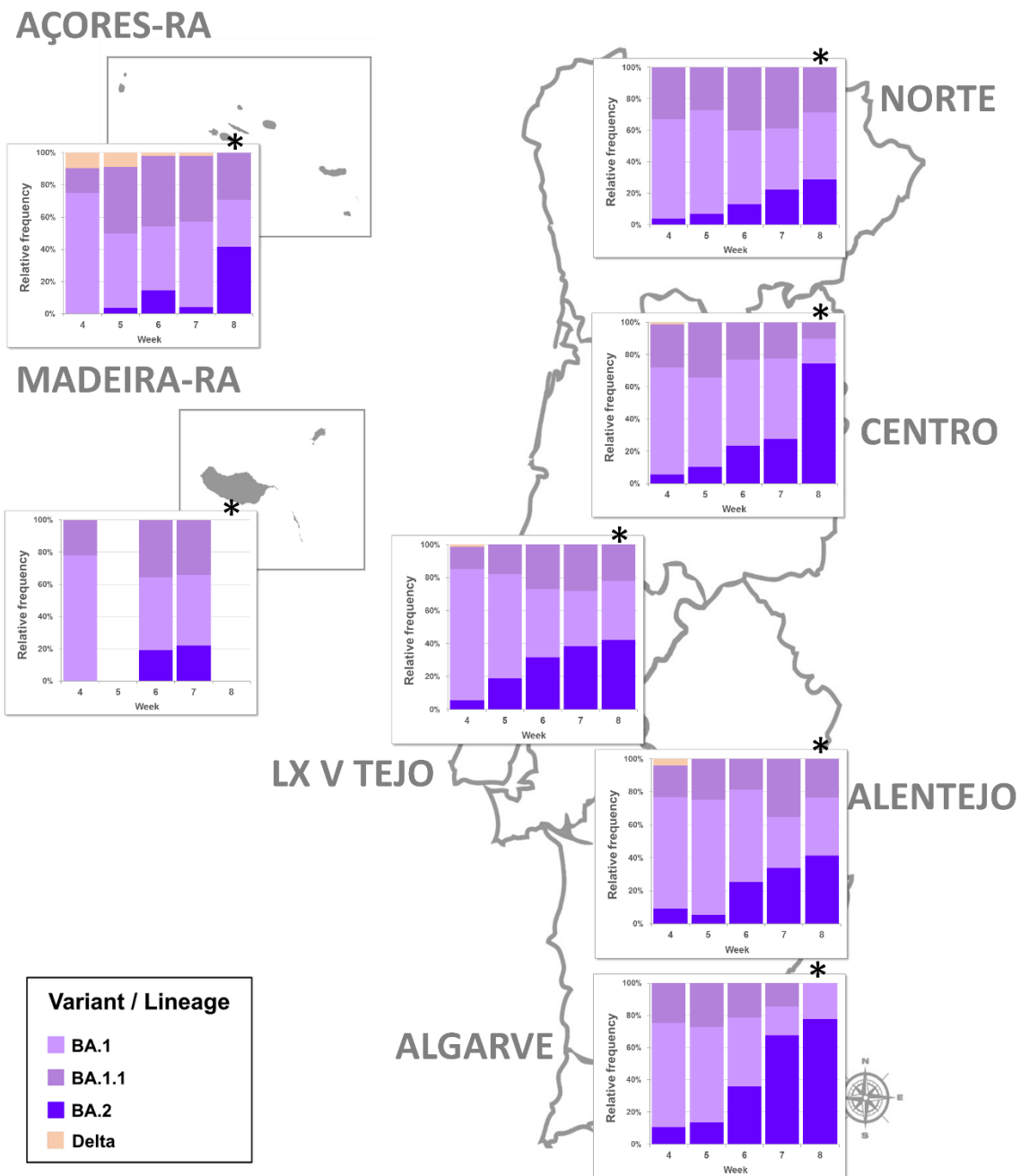
**Figure 4. Evolution of the daily proportion of positive samples with and without S gene target failure (SGTF) in parallel with the relative frequency of the variants/lineages in circulation as assessed by the random nationwide sequencing surveys, since ISO week 48, 2021 (collection date).** An **SGTF 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)*  $\leq 30$  for the N and ORF1ab genes. The data relative to the most recent 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 1<sup>st</sup> January 2022 in the report released on 8<sup>th</sup> February 2022. This revision corrected a technical artefact that was detected in the automatic computation of data since 10<sup>th</sup> 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 45,9% of the samples subjected to sequencing in ISO week 8 (21-27 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 clearly dominant in Portugal, representing 76.2% of the positive samples on 7 March 2022 (Figures 2 e 4).**
- Sequencing data shows that BA.2 has been increasing its relative frequency in all Regions, representing  $\geq 20\%$  of all sequences analysed per Region in ISO week 8 (**Figure 5**).



**Figure 5. Evolution of the weekly relative frequency of SARS-CoV-2 lineages in each Health Region, between ISO weeks 4 (24-30 January) and 8 (21 - 27 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 8) 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](#).