



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

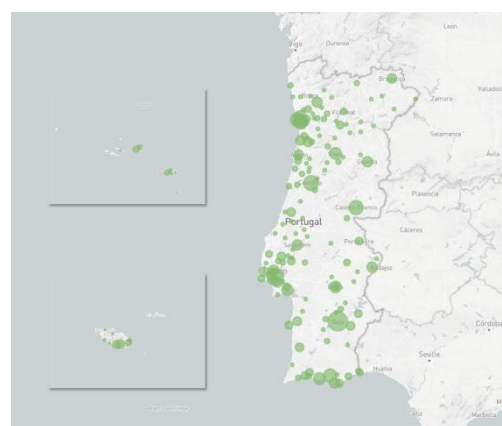
More information at <https://insaflu.insa.pt/covid19/>

## Situation Report

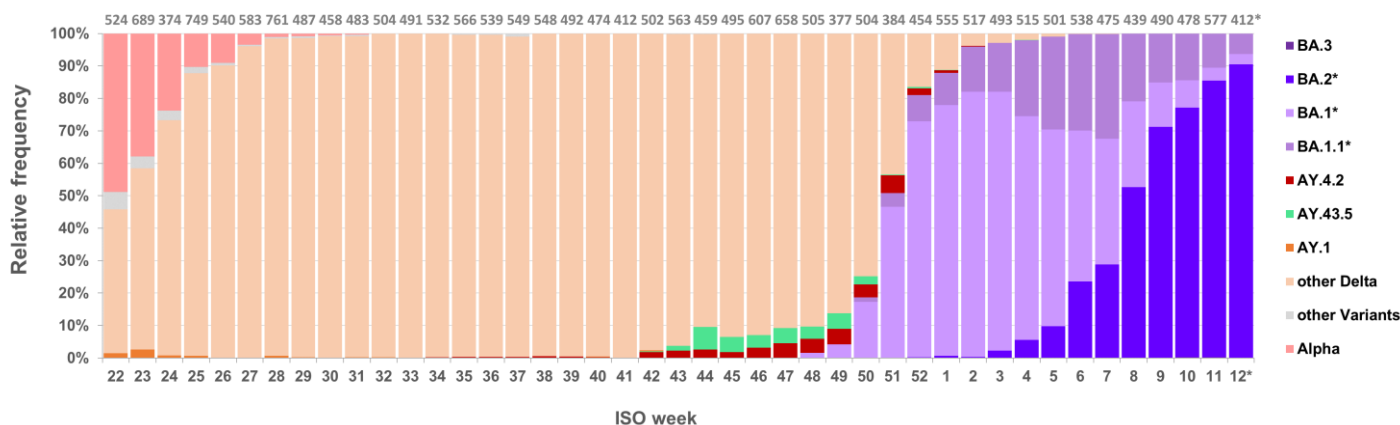
5<sup>th</sup> April 2022

The **National Institute of Health Doutor Ricardo Jorge, I.P. (INSA)** has analysed **31428 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 **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 558 new SARS-CoV-2 genome sequences from 156 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 12 (21<sup>st</sup> - 27<sup>th</sup> 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 12) might change in the next report, given that some data from that period is still being processed. BA.1.1 = BA.1.1 and sub-lineages; BA.2 = BA.2 and sub-lineages; BA.1 = BA.1 and sub-lineages (with exception of BA.1.1 and sub-lineages).



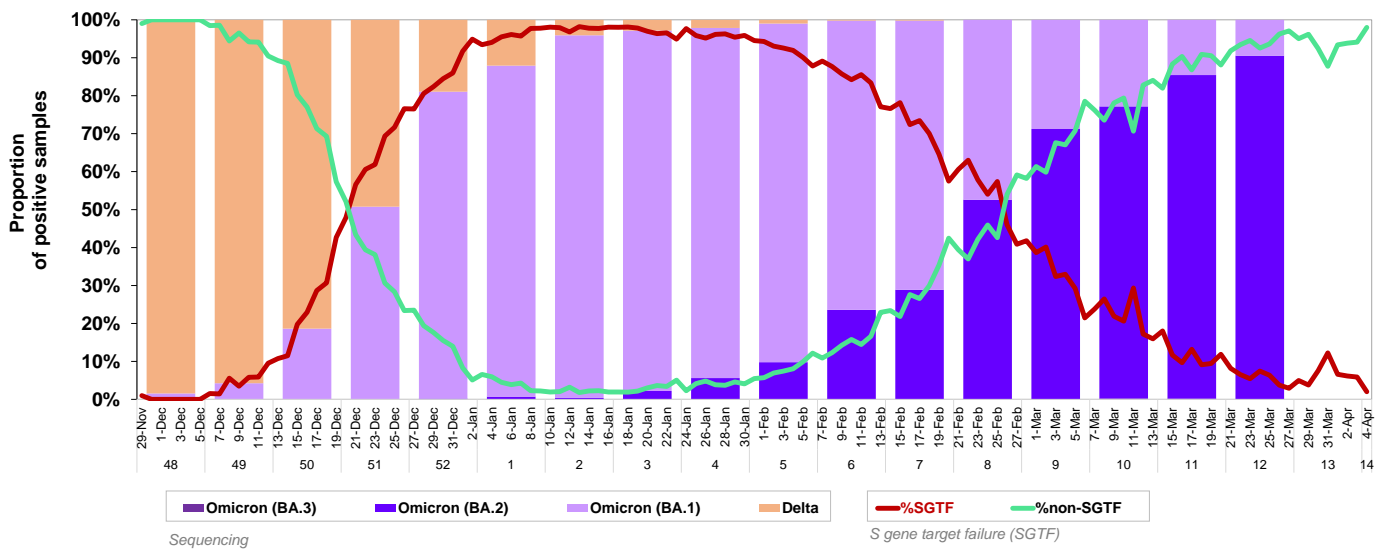
## Main highlights:

The Variant of Concern (VOC) *Omicron*, according to the [WHO](https://www.who.int/) classification, currently includes several (sub)lineages identified by the “BA” prefix. The nomenclature of the various sub-lineages is under constant review and refinement (<https://www.pango.network/>). The sequences identified in Portugal are reclassified weekly and the result are available on our website <https://insaflu.insa.pt/covid19/>. Whenever relevant, some of these sub-lineages will be highlighted in this report.

### 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<sup>nd</sup>-28<sup>th</sup> 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 3). According to the sequencing data, the relative frequency of BA.1 reached a maximum in ISO week 2 (95,6%, 10<sup>th</sup>-16<sup>th</sup> January, 2022) and then started a decreasing trend (Figures 2 and 3). SGTF data shows a concordant trend in the proportion of SGTF positive samples, with a current estimated frequency of 2% (4<sup>th</sup> April, 2022) (Figure 3).

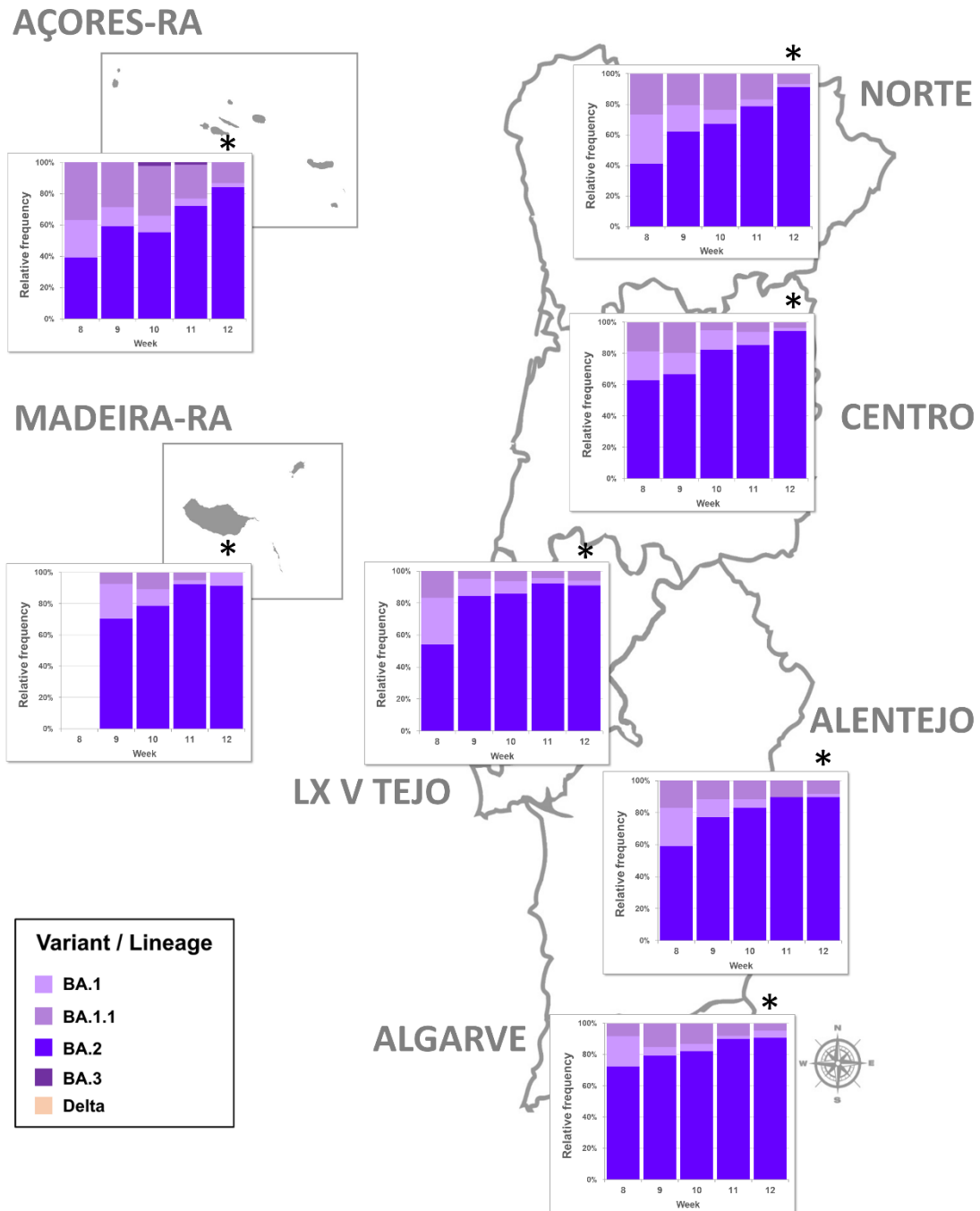


**Figure 3. Evolution of the daily proportion of positive samples with and without S gene target failure (SGTF) in parallel with the relative frequency of the variants/lineages in circulation as assessed by the random nationwide sequencing surveys, since ISO week 48, 2021 (collection date).** Currently, 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 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.



- **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”) 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<sup>th</sup> December 2021 – 2<sup>nd</sup> January 2022) (**Figure 2**). **Its relative frequency has been slowly increasing since then**, representing 90.5% of the samples subjected to sequencing in ISO week 12 (21<sup>st</sup>-27<sup>th</sup> 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 98% of the positive samples on 4<sup>th</sup> April 2022** (**Figures 2, 3 and 4**).
- **Lineage BA.3**
  - This lineage, firstly identified in South Africa, shares genetic similarities to both BA.1 and BA.2 *Omicron* lineages, and has been detected sporadically worldwide. In Portugal, BA.3 was only detected in two cases in the random surveys of ISO weeks 10 and 11 (7<sup>th</sup>-20<sup>th</sup> March, 2022) in the **Autonomous Region of the Azores** (**Figure 4**), with the phylogenetic analysis suggesting that they might be epidemiologically linked. So far, none BA.3 case was detected in week 12 (*ongoing analysis*).
- **Recombinants**
  - The co-circulation of several lineages/variants in the community increases the possibility of the occurrence of mixed infections, i.e., the same individual is simultaneously infected by more than one of them. In this context, mixture of their genetic material might occur, resulting in a hybrid genetic profile, commonly designated as “recombinant”. To date, several recombinant SARS-CoV-2 have been detected at a global scale (e.g., Delta+Omicron BA.1 or BA.1+BA.2), with novel designations being assigned to the recombinants with epidemiological/functional relevance. The few recombinant viruses identified so far in Portugal were detected in sporadic cases and do not correspond to the genetic profiles that are under special international monitoring.
- 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](#).



**Figure 4. Evolution of the weekly relative frequency of SARS-CoV-2 lineages in each Health Region, between ISO weeks 7 (14<sup>th</sup>-20<sup>th</sup> February) and 17 (21<sup>st</sup>-27<sup>th</sup> March) 2022.** The plots highlight the BA.1 (including its sublineage BA.1.1), BA.2 and BA.3 (classified as *Omicron* by [WHO](https://www.who.int)), as well as the *Delta* variant. BA.1.1 = BA.1.1 and sub-lineages; BA.2 = BA.2 and sub-lineages; BA.1 = BA.1 and sub-lineages (with exception of BA.1.1 and descendent sub-lineages).

\*It is expected that the frequencies presented for the last week under analysis (ISO week 12) 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 8 were available from the Autonomous Region of Madeira.