

# Genomic surveillance of SARS-CoV-2 in Belgium

Report of the National Reference Laboratory (UZ Leuven & KU Leuven)

Situation update – 22 of June 2021  
(report 2021\_33)

## Executive summary

27.528 Belgian sequences of SARS-CoV-2 are now publicly available on GISAID.

Among these, 676 sequences of positive SARS-CoV-2 samples collected between 7 June and 20 June were reported,

- B.1.1.7 (*Alpha*) represented 71,3% (compared to 80,4% in the last report) ↘
- B.1.617.2 (*Delta*) represented 15,7% (compared to 6,1% in the last report) ↗
- P.1 (*Gamma*) represented 9,7% (compared to 9,9% in the last report) =
- B.1.351 (*Beta*) represented 1,2% (compared to 1,4% in the last report) =

Other points of attention:

- The NRC performed 103 VOC PCRs on unselected positive samples analyzed during the last 9 days. B.1.1.7, P.1 and B.1.617.1/.2 represented respectively 49,5%, 17,4% and 28,1% (↗) of the results.

- The decreasing epidemiological trend observed in Belgium is a very positive element as it will help mitigate the impact of the rapid viral population replacement currently taking place. It should be noted that the absolute number of infections caused by B.1.617.2 is currently relatively stable (even though the percentage increases), but that this fragile equilibrium could be disrupted if the relaxation of measures or the importation of numerous strains through travels cannot be compensated by a proportional effort with regard to testing, tracing and isolation measures.

Authors (National Reference Laboratory – UZ Leuven and KU Leuven):

*Lize Cuypers, Guy Baele, Piet Maes, Simon Dellicour, Els Keyaerts, Sunita Janssenswillen, Marc Van Ranst, Emmanuel André.*

*With the collaboration of Tom Wenseleers (KU Leuven)*

With the collaboration of the laboratories of UCL, ULB, UMONS, UNAMUR, ULiège, UGent, UZA/UAntwerpen, JESSA ZH, AZ Delta, AZ Klina, IPG, AZ St Lucas Gent, OLVA Aalst, Briant network, ZNA, AZ St Jan Brugge, and UZ Leuven/KU Leuven.

Previous reports can be downloaded using the following link:

<https://www.uzleuven.be/nl/laboratoriumgeneeskunde/genomic-surveillance-sars-cov-2-belgium>

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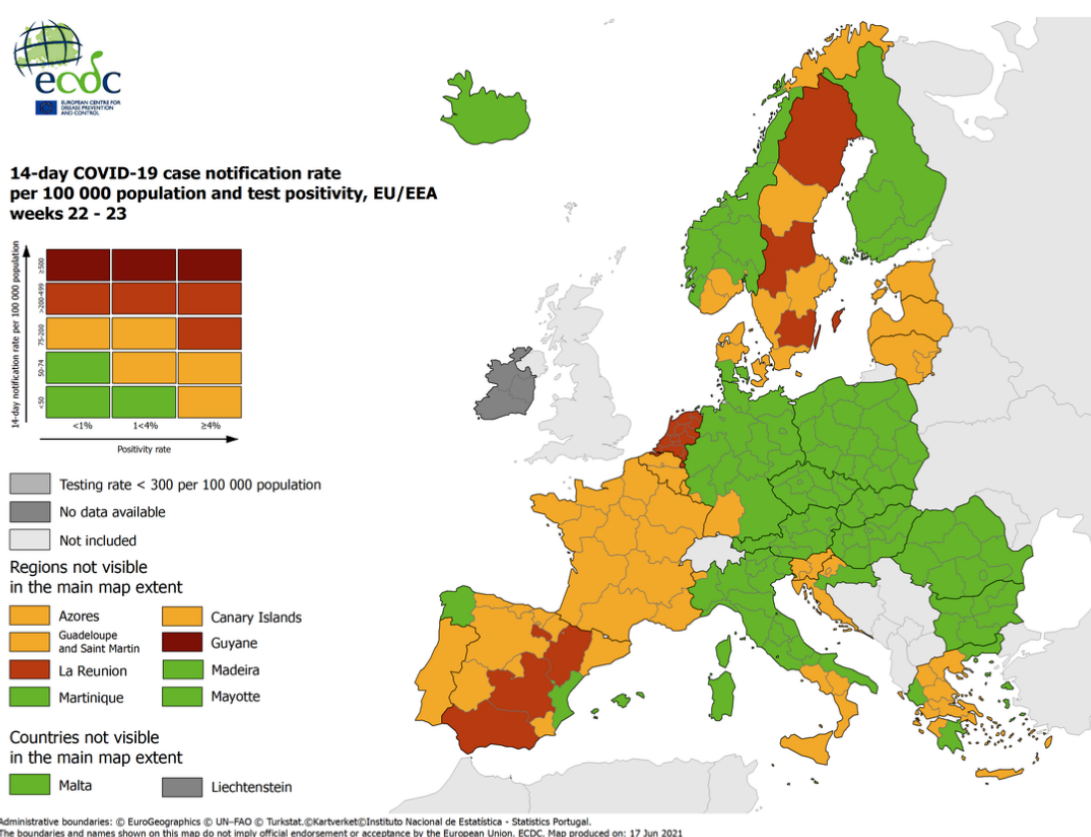
## 1. Monitoring of VOCs

### International evolution

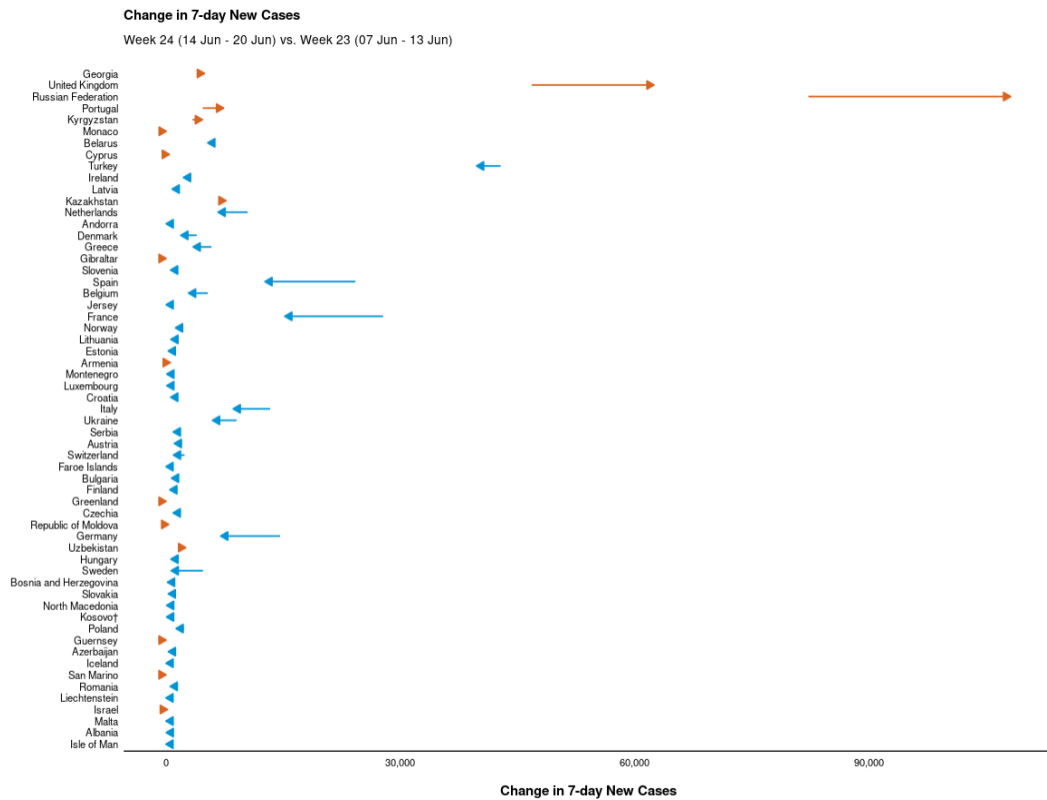
The Delta variant (B.1.617.2) has continued to spread globally, including in the UK, with a proportion of cases associated with more severe disease and hospitalisation.

The UK recorded 11,625 new Covid-19 cases in the past 24 hours, the highest daily total since mid-February. The country also reported 27 daily coronavirus deaths, a 44 per cent increase on last week.

- In the **European Region**, the number of infections is rising in Russia, the United Kingdom, Portugal and Monaco. In other countries, the number of infections is stable or declining (Figures 1 and 2), but it should be noted that in these countries, B.1.617.2 is not yet dominant and that the situation will most probably evolve over the next few weeks.

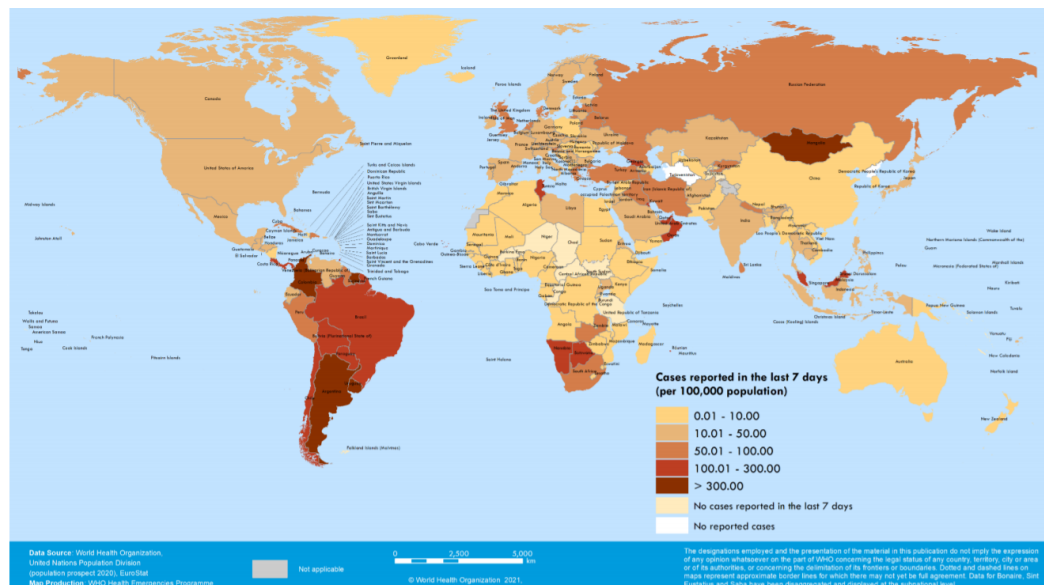


**Figure 1.** 14-day COVID-19 case notification rate per 100,000 inhabitants and test positivity rate. An increasing number of regions across Europe are seen to lower their overall risk.



**Figure 2.** The United Kingdom and The Russian Federation are reporting a strong increase in new cases, whereas Belgium and its surrounding countries see a decrease in new cases (Source: WHO).

- In other regions of the world, the situation is still rapidly evolving in continents where vaccination coverage is very low (Africa, Latin America, Asia; Figure 3), a phenomenon which can be widely underestimated due to the limited diagnostic capacity in low-income countries.



**Figure 3 :** COVID-19 cases per 100.000 population reported by country (7-13 June, 2021). Source: WHO

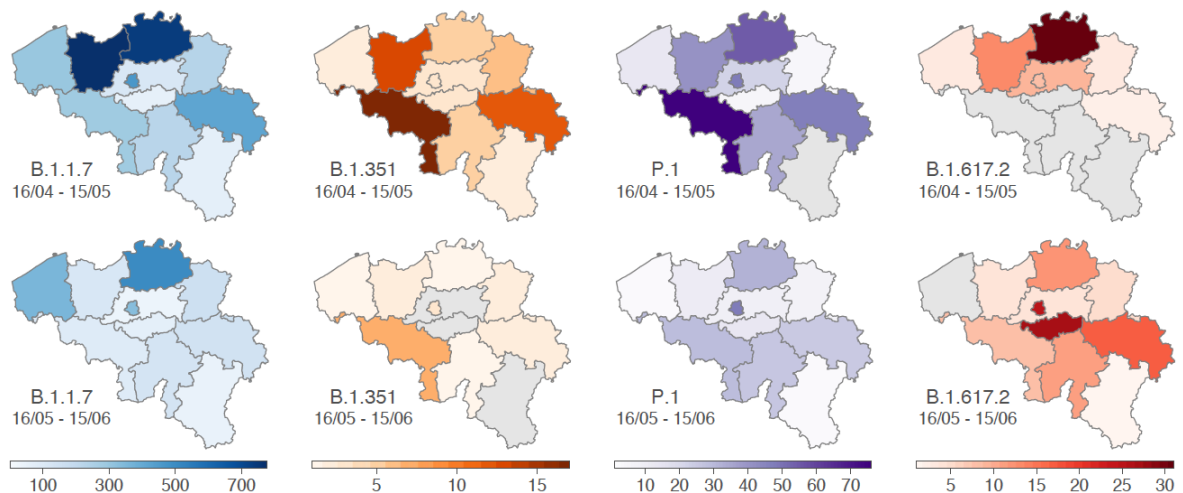
## Situation in Belgium

While it was first identified on 6 April 2021 in Belgium, the B.1.617.2 Variant of Concern (Delta) has now outpaced P.1 (Gamma), and will very probably become the dominant lineage in the country in the coming weeks (early July 2021).

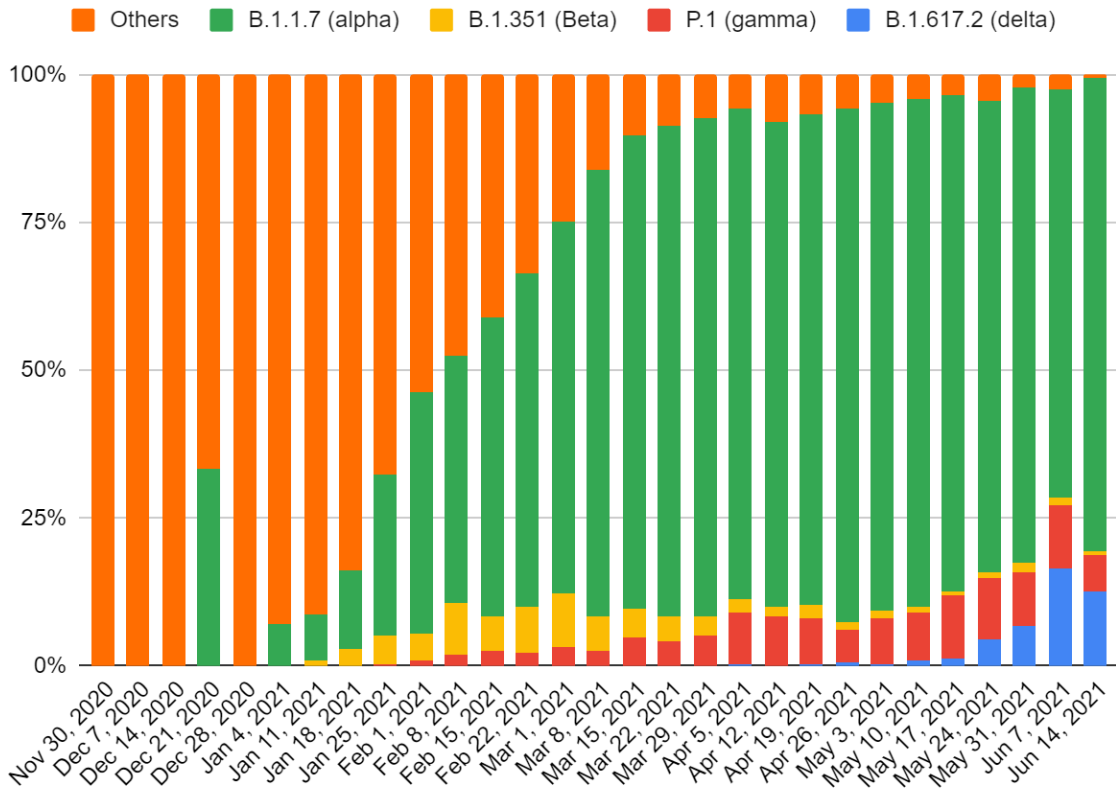
Between 7/6/2021 and 20/6/2021 (676 genomes available to date)

- B.1.1.7 (Alpha) represented 71,3%
- B.1.617.2 (Delta) represented 15,7%
- P.1 (Gamma) represented 9,7%
- B.1.351 (Beta) represented 1,2%

The recent evolution of the different variants of concern is represented in figure 4 for the different provinces of the country.

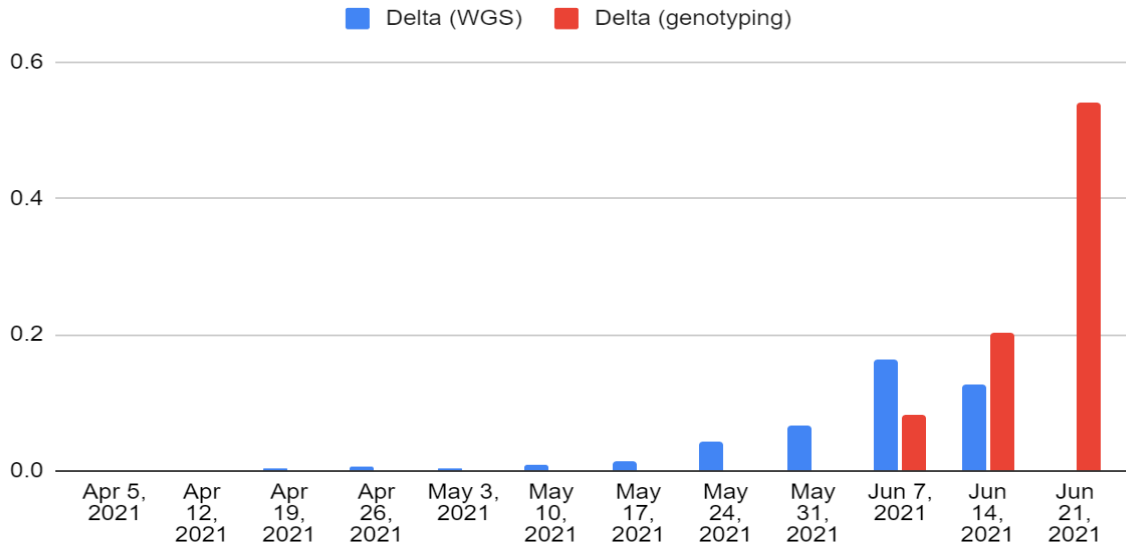


**Figure 4:** Evolution of the number of variants of concern identified in each province since April 16, 2021. Of note, the numbers represented here are collected from GISAID and combine both baseline surveillance and active surveillance.

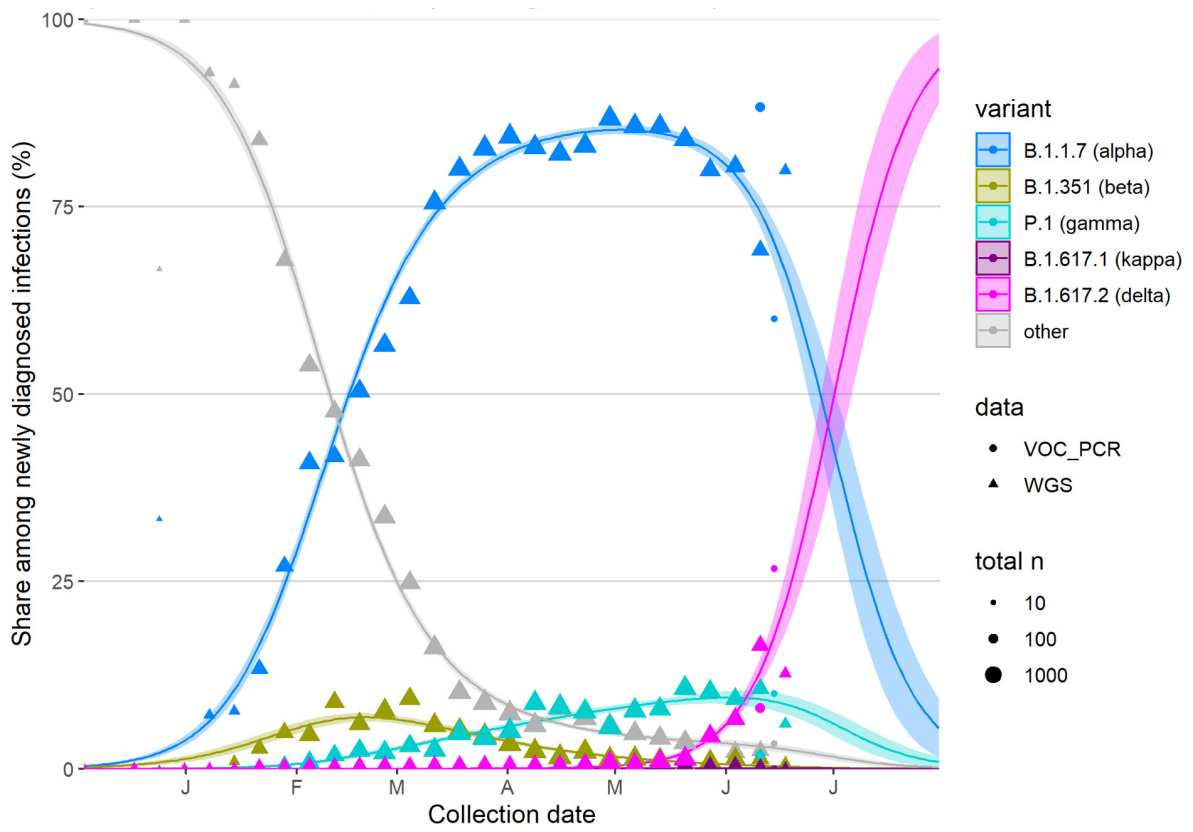


**Figure 5:** Weekly evolution of the frequency of variants of concern reported by the baseline surveillance network using a whole genome sequencing (WGS) approach.

### Delta (WGS) and Delta (genotyping)



**Figure 6:** Weekly evolution of the frequency of variants of concern reported by the baseline national surveillance network using a whole genome sequencing (blue) and rapid VOC PCRs performed among all positive cases received at the national reference laboratory (red : mainly unbiased sampling, but limited geographical representativeness). Numbers for week 21 June are still limited (only 2 days reported for this week), and the final figure may thus be revised.



**Figure 7:** Evolution and foreseen evolution of the different variants of concern in Belgium (figure by Tom Wenseleers, KU Leuven)

| Lineage               | Number of Belgian cases reported on GISAID | First reported |
|-----------------------|--|----------------|
| B.1.1.7 (Alpha)       | 16.764                                     | 30/11/2020     |
| B.1.351 (Beta)        | 954  | 20/12/2020     |
| P.1 (Gamma) and P.1.1 | 1.339                                      | 29/1/2021      |
| B.1.617.2 (Delta)     | 309  | 6/4/2021       |
| B.1.1.7 +S:E484K      | 25   | 31/3/2021      |
| B.1.1.7 +S:S477R      | 31   | 15/3/2021      |
| B.1.214.2             | 698  | 3/1/2021       |
| B.1.525 (Eta)         | 71   | 30/1/2021      |
| B.1.620               | 19   | 31/3/2021      |
| B.1.1.318             | 52   | 3/3/2021       |
| A.27                  | 19   | 11/1/2021      |
| B.1.617.1 (Kappa)     | 10   | 25/3/2021      |

**Table 1:** List of VOCs (red) and VOIs (orange) identified in Belgium to date and cumulative number of sequences available on GISAID (total of 25,921 sequences).

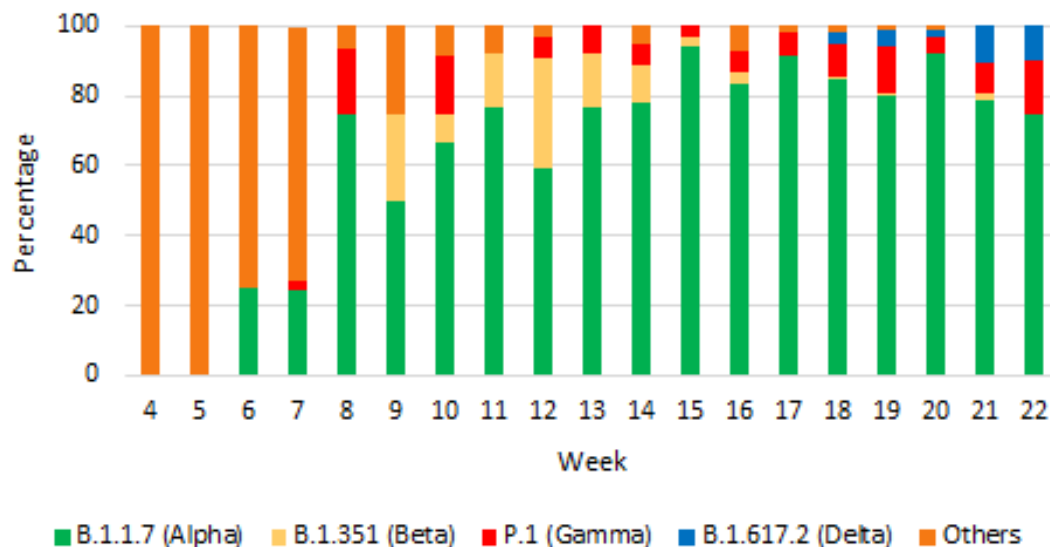
## 2. Update on post-vaccination breakthrough infections: circulation of VOCs

### Surveillance methodology

A breakthrough infection is defined as a positive SARS-CoV-2 test at least 7 days after the full completion of a vaccination scheme. To facilitate the transfer of samples that meet the definition to the sequencing lab in Leuven, laboratories that submit RT-PCR test results to HealthData, will receive an automatic message from HealthData notifying them that a particular sample meets the criteria of a post-vaccination breakthrough case. It remains the responsibility of each lab to verify whether the sample meets the criteria for sequencing (viral load is sufficiently high, corresponding to a Ct value <25) and if so, to send the sample accompanied with the completed application form (see the website of Sciensano) to the NRC UZ/KU Leuven.

### Intermediate results

The NRC is actively collecting information on post-vaccination infections, of which to date, 710 samples could be typed. All 710 samples were sampled between January 28 and June 5, 2021. In parallel to baseline surveillance, the evolution of the four main VOCs (B.1.1.7, B.1.351, P.1 and B.1.617.2) are currently being followed over time.



**Figure 8:** Share of the different variants of concern among post-vaccination breakthrough infections over the time.