# Genomic surveillance of SARS-CoV-2 in Belgium

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

**Situation update – 12 of October 2021**
**(report 2021_49)**


**Executive summary**

51,160 Belgian sequences of SARS-CoV-2 are now publicly available on GISAID.

526 sequences of positive SARS-CoV-2 samples collected between 27/09/2021 and 10/10/2021 have at this stage been analysed in the context of baseline surveillance. Among these, B.1.617.2 and its sublineages (*Delta*) represented 100% of the circulating strains.

The genomic diversity of SARS-CoV-2 in Belgium is comparable with the situation described over the last 10 weeks.



Authors (National Reference Laboratory – UZ Leuven and KU Leuven):
*Lize Cuypers, Piet Maes, Els Keyaerts, Guy Baele, Simon Dellicour, Tom Wenseleers, Barney Potter, Sunita Janssenswillen, Elke Wollants, Marc Van Ranst, Emmanuel André.*

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, OLVZ Aalst, Briant network, ZNA, AZ St Jan Brugge, UZ Brussel, LHUB-ULB, and UZ Leuven/KU Leuven; and Sciensano HealthData.


Previous reports can be downloaded using the following link:
https://www.uzleuven.be/nl/laboratoriumgeneeskunde/genomic-surveillance-sars-cov-2-belgium

**Table of contents**


1. Monitoring of VOCs in Belgium
2. Testing of travellers
3. Update on re-infections: which variants do we observe?
4. Update on hospitalisations: which variants do we observe?
5. Update on post-vaccination infections: which variants do we observe?

## 1. Monitoring of VOCs in Belgium

While first identified on 6 April 2021 in Belgium, the B.1.617.2 Variant of Concern (Delta) is now the dominant lineage in the country, representing 100% of the surveillance samples sequenced.

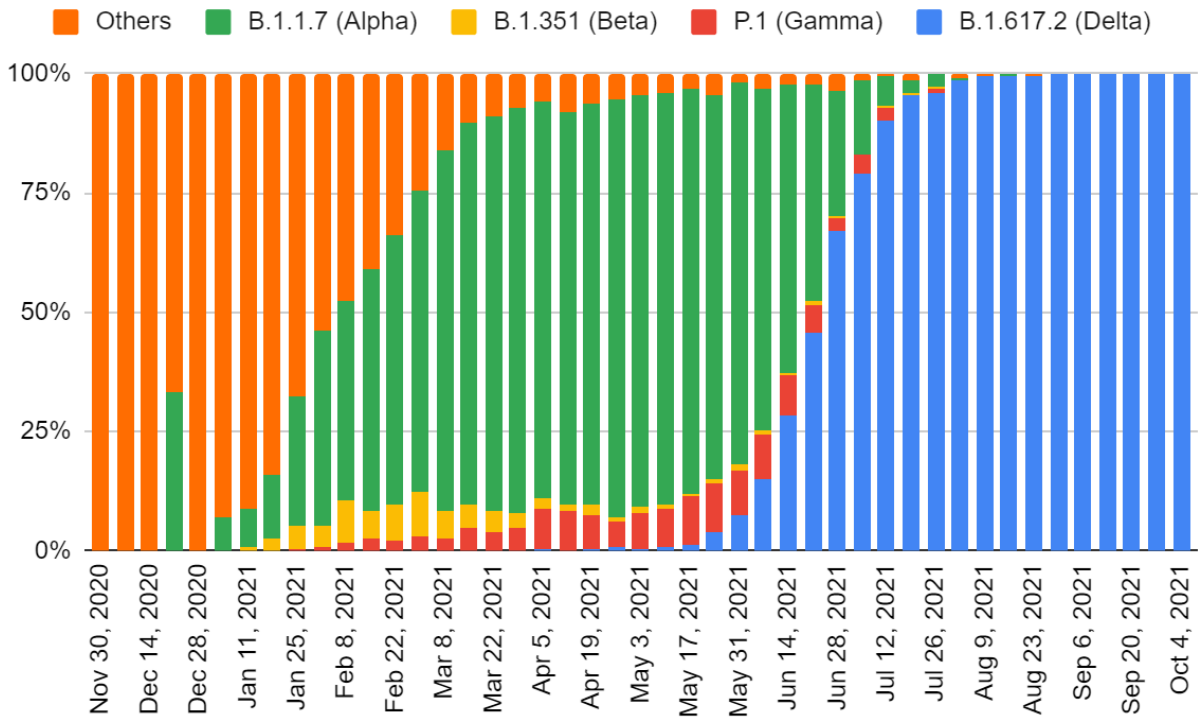


***Figure 1:*** *Weekly evolution of the frequency of variants of concern reported by the baseline surveillance network using a whole genome sequencing (WGS) approach.*

## 2. Testing of travellers

According to data provided by Sciensano, at the Belgian level and during the last 8 weeks (weeks 33-40), 98.6% of the travellers who tested positive upon return were infected with the Delta variant (548 out of 556 infections). During this same period, 16.5% (548/3322) of the people tested positive for the variant Delta were returning travellers. Of note, 53.3% of the people tested positive for the variant Alpha were returning travellers (8/15 infections), and therefore accounting for 1.4% of the travellers who tested positive upon return. To calculate these numbers, only positive persons for which travel history status and variant information is known, were considered.

## 3. Update on re-infections: which variants do we observe?

A re-infection is defined as a distinct clinical episode of SARS-CoV-2 infection after a first positive SARS-CoV-2 test. Data are provided by Sciensano. To facilitate the identification of re-infections, a similar alert message has been set up by HealthData notifying the lab that a particular sample meets the criteria of a re-infection case. Such samples can be transferred to the NRC.

For the last two months, of the 2,588 infections reported (only considering cases for which pre-infection status and variant information is known), 50 re-infections were observed (1.9% of total). Of those 50 re-infections, two can be attributed to Alpha (2 reinfections out of 11 infections with Alpha reported during that time period) and 48 to Delta (48/2577). Both for Beta and Gamma, no infections were reported in the last 8 weeks.

## 4. Update on hospitalisations: which variants do we observe?

For the hospitalised cases, the reported numbers are purely descriptive as the data were derived from COVID-19 patients who were hospitalized and registered by the hospitals in the Clinical Hospital Survey (CHS) coordinated by Sciensano. The CHS is not exhaustive and covers approximately 60% of all hospitalized COVID-19 patients in Belgium. As a consequence, absence of a link between variant data and registration in the CHS does not automatically imply that this patient did not require hospitalization. Approximately 40% of hospitalized COVID-19 patients are not registered in the CHS.

For the last two months, of the 206 COVID-19 patients that were hospitalised and for which variant data is available, the large majority (72.8%) was reported to be infected with the Delta variant. Of note, for the other 56 records (27.2%), no details were specified with respect to the Pangolin lineage that was identified. Most probably, a large share of these records can be attributed to Delta or one of its sublineages. However, no cases were identified for Alpha, Beta or Gamma.

The low number of hospitalized patients for which variant data is available can be explained by the fact that disease severity was until recently not considered as a prioritized indication to perform SARS-CoV-2 WGS, complemented by the limitation of the viral load that needs to be sufficiently high to be able to perform detailed typing. According to a recent RAG advice (revision date 30/8/2021), a more representative and systematic sample of infections in hospitalized patients should be targeted.

## 5. Update on post-vaccination infections: which variants do we observe?

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 a sequencing lab, laboratories that submit RT-PCR test results to HealthData receive an automatic message from HealthData notifying them that a particular sample meets the criteria of a post-vaccination breakthrough case. According to a recent RAG advice, there is no longer a need to systematically sequence all breakthrough cases. It was agreed that only samples of infections of fully vaccinated persons with a severe disease course (hospitalisation) should be systematically sequenced, as well as samples of fully vaccinated residents of nursing homes.

According to data provided by Sciensano, the weekly evolution of the frequency of variants of concern is summarized in Figure 2 for the post-vaccination breakthrough infections, showing the same trends as visualized in Figure 1 in the context of baseline surveillance.

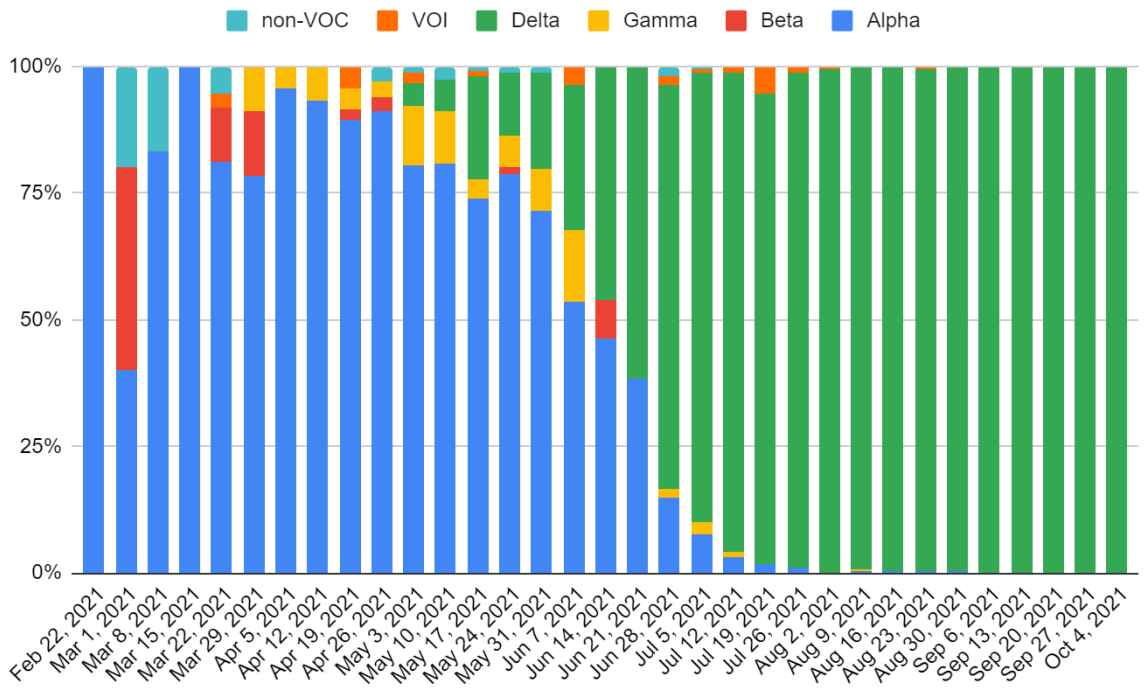


***Figure 2:*** *Weekly evolution of the frequency of variants of concern reported for post-vaccination infections using a WGS approach (source: HealthData).*