

Genomic surveillance of SARS-CoV-2 in Belgium

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

Situation update – 24th of August 2021
(report 2021_42)

Executive summary

38,838 Belgian sequences of SARS-CoV-2 are now publicly available on GISAID.

Among these, 943 sequences of positive SARS-CoV-2 samples collected between 9th and 22nd of August were reported in the context of baseline surveillance,

- B.1.617.2 (*Delta*) represented 99.4% (compared to 98.9% in the last report)

Other variants currently represent less than 1% of the circulating strains.

Other points of attention:

- The NRC performed 2181 tests among departing travellers and 2137 tests among returning travellers during the week of August 16. The positivity rate among returning travellers was 4.2 times higher compared to departing travellers (2.1% against 0.5%). This difference **highlights the risk of infection associated with travels** and the potential benefits of extending testing criteria among returning travellers. The current restrictive testing indications and financial barriers for testing could contribute to a continuous importation of undetected infections associated with secondary clusters.

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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 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.

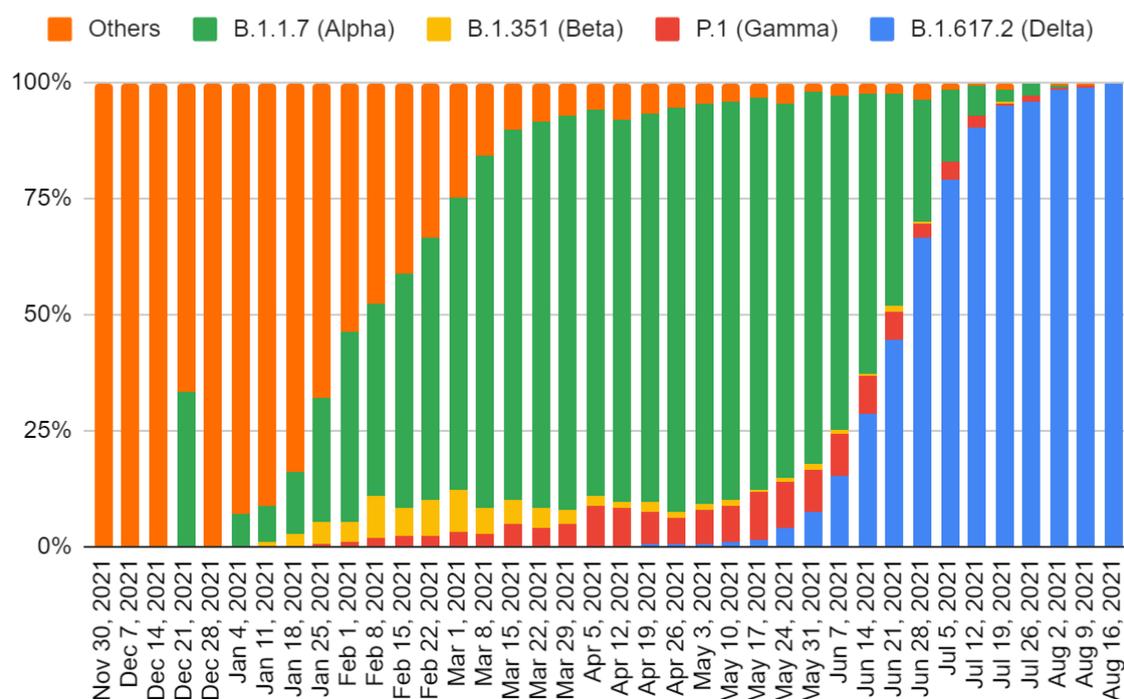


Figure 1: Weekly evolution of the frequency of variants of concern reported by the baseline surveillance network using a whole genome sequencing (WGS) approach.

Subclassification within the Delta (B.1.617.2) variant according to Pangolin

Recently, twelve different sublineages (AY.1 to AY.12) have been assigned as subclades within the large group of B.1.617.2 genomes. All these lineages have been and remain classified as the Delta variant, since no functional biological difference is implied compared to the parental classification of B.1.617.2. This more detailed subclassification has been specifically designated to track the virus on a fine-scale, now that the Delta variant is widespread across the world and that it is the predominant lineage in many countries, such as in Belgium. It is anticipated that more AY lineages will follow soon, although most likely they should all be treated as the Delta variant.

2. Testing of travellers

Departing travellers

During the last 8 full weeks (June 28 to August 22), the National Reference Center in Leuven has tested 48,138 departing travellers, among which 311 were tested positive (0.65%). The positivity rate increased from 0.28% during the first week to 0.90% during the week of August 2, while it has decreased in the meantime to 0.46% in the last week. The Delta variant represented 100% of the positive samples tested during the last week.

Returning travellers

For the last 8 full weeks (June 28 to August 22),

- Among the travellers returning from abroad to the region of Leuven, 6,539 people were tested, among which 180 were tested positive (2.8%). The Delta variant represented 96.7% of the positive samples tested during the last week.
- Currently, incomplete data is available to calculate the positivity rate, and associated distribution of SARS-CoV-2 variants, according to the countries from which travellers return to Belgium. Sciensano HealthData is looking into the possibility to perform such an analysis.

According to data provided by Sciensano, at the Belgian level and during the last 8 weeks, 92% of the travellers who tested positive upon return were infected with the Delta variant. During this same period, 12.8% of the people tested positive for the variant Delta were returning travellers (Table 1).

	% of returning travelers among persons positive for the considered VOC*	% of persons positive for the considered VOC among all positive returning travelers**
Alpha	11,7% (68/580)	7,6% (68/900)
Beta	8,3% (1/12)	0,1% (1/900)
Gamma	2,5% (3/120)	0,3% (3/900)
Delta	12,8% (828/6484)	92,0% (828/900)

Table 1: (*) Ratio between the number of returning travelers tested positive for a given VOC and the total number of persons tested positive for that VOC; (**) Ratio between the number of returning travelers tested positive for a given VOC and the total number of returning travelers tested positive for one of the four VOCs. N.B.: We only considered positive persons for which the travel history status is known (estimated for the last 8 weeks, i.e. weeks 26-33).

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 is provided by Sciensano.

Table 2 highlights for the last two months the number of re-infection cases (with one of the four listed VOCs) documented. Of the 5.930 infections reported (only considering cases for which pre-infection status is known), 104 re-infections were observed (1.8% of total).

	% of re-infections among persons positive for the considered VOC*
Alpha	1,9% (9/466)
Beta	0,0% (0/9)
Gamma	1,2% (1/82)
Delta	1,7% (94/5373)

Table 2: Percentage of re-infections among persons tested positive for each VOC (only considering positive persons for which the pre-infection status is known) during the last 8 weeks (W26-33).

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.

Table 3 highlights for the last two months the number of hospital admissions documented. Of the 87 COVID-19 patients that were hospitalised and for which variant data is available, the large majority (80.5%) was reported to be infected with the Delta variant. The low number of hospitalized patients for which variant data is available can be explained by the fact that disease severity is currently 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.

	Share (%) of VOCs represented in hospital admissions*
Alpha	6,9% (6/87)
Beta	0,0% (0/87)
Gamma	2,3% (2/87)
Delta	80,5% (70/87)

Table 3: Share of VOCs among hospital admissions (only considering approximately 60% of all hospitalised COVID-19 patients in Belgium) during the last 8 weeks (W26-33).

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 will receive an automatic message from HealthData notifying them that a particular sample meets the criteria of a post-vaccination breakthrough case. Following the communication and report of last week, such samples can be transferred to any of the sequencing laboratories, preferentially geographically the closest or for which logistic flows already are in place.

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. Details on age category, gender and vaccine brand are available, however, these are not yet included in this week's report as they are highly influenced by the design and roll out of the vaccination campaign in Belgium, which in priority targeted elderly persons and healthcare workers and hence resulted in an overrepresentation of the female gender and the BioNTech/Pfizer (Comirnaty) vaccine. To avoid misinterpretation, the data will be evaluated in more detail before sharing it in this report.

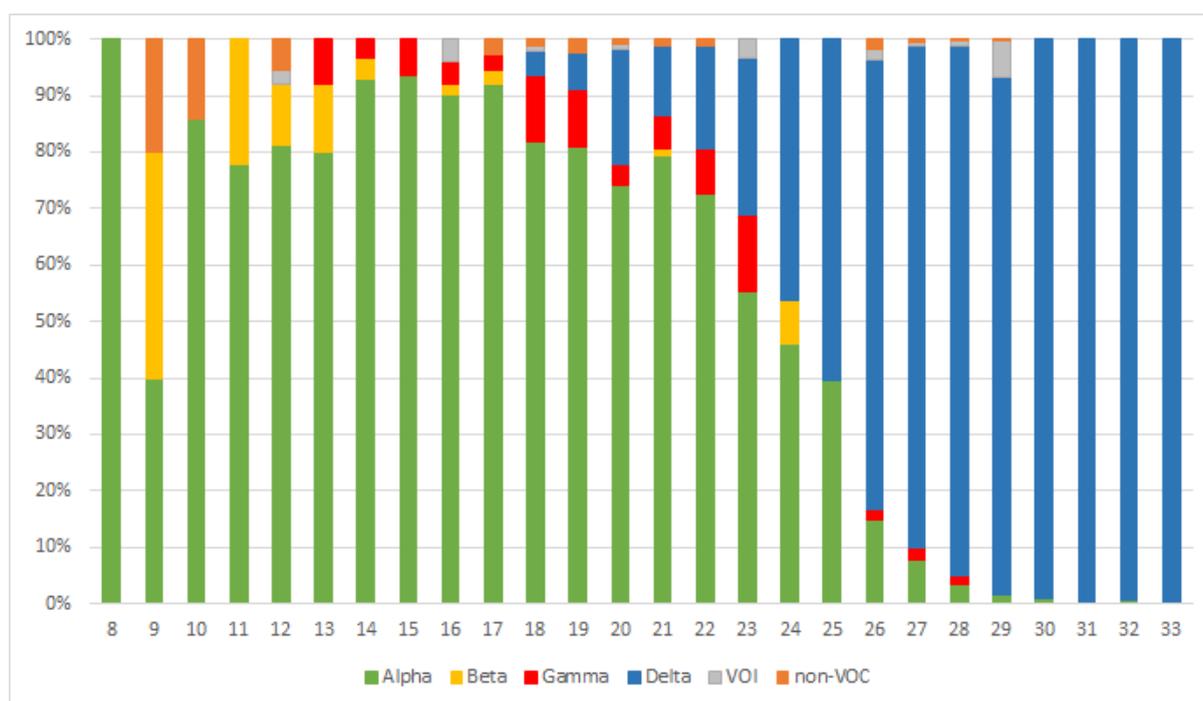


Figure 2: Weekly evolution of the frequency of variants of concern reported for post-vaccination infections using a WGS approach (source: HealthData).