Genomic surveillance of SARS-CoV-2 in Belgium

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

Situation update – 3rd of August 2021 (report 2021_39)

Executive summary

35,691 Belgian sequences of SARS-CoV-2 are now publicly available on GISAID.

Among these, 985 sequences of positive SARS-CoV-2 samples collected between 19 July and 1st of August July were reported in the context of baseline surveillance in the context of baseline surveillance,

- B.1.617.2 (Delta) represented 94.6% (compared to 89% in the last report) ✓
- B.1.1.7 (*Alpha*) represented 3.7% (compared to 8.4% in the last report) \> Other variants currently represent less than 1% of the circulating strains.

Other points of attention:

- The NRC performed 6089 tests among departing travellers and 489 tests among returning travellers during the week of July 26. The positivity rate among returning travellers was 4.7 times higher compared to departing travellers (4% against 0.87%). 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.
- The NRC is involved in the investigation of 3 post-vaccination outbreaks in elderly care facilities associated with a high proportion of fatal infections. These outbreaks involve the Delta variant, the Gamma variant and the B.1.621 variant (with S:K417N mutation). The latter will be very closely monitored in the coming weeks, and the NRC recommends to consider this variant as a variant of concern until more information is collected.

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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.

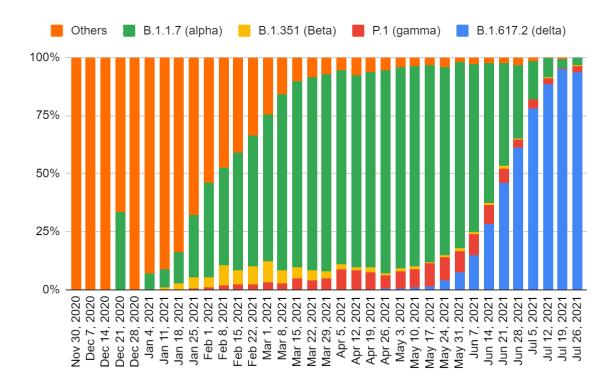


Figure 1: Weekly evolution of the frequency of variants of concern reported by the baseline surveillance network using a whole genome sequencing (WGS) approach.

The recent introduction of the lineage B.1.621 /B.1.621.1, with the additions S:K417N mutation, is of concern considering that this lineage harbours a number of mutations of concern (R346K, K417N, E484K, N501Y and P681H) and that at least one post-vaccination outbreak with several fatalities is ongoing in the country. Until more information can be collected with regard to this variant, we recommend intensifying testing, tracing and outbreak management efforts when this variant is highlighted.

Lineage	Number of Belgian cases reported on GISAID	First reported
B.1.1.7 (Alpha)	20,840	30/11/2020
B.1.351 (Beta) and B.1.351.2	1121	20/12/2020
P.1 (Gamma) and P.1.1	1970	29/1/2021
B.1.617.2 (Delta)	3385	6/4/2021
B.1.621 B1.621.1	18 11	24/6/2021 22/5/2021
B.1.214.2	756	
A.27	20	11/1/2021
B.1.427 (Epsilon)	1	18/1/2021
B.1.525 (Eta)	84	30/1/2021
P.2 (Zeta)	2	9/2/2021
B.1.526 (lota)	3	24/2/2021
B.1.1.318	61	3/3/2021
C.36.3	29	23/3/2021
B.1.617.1 (Kappa)	18	25/3/2021
B.1.619 B.1.619.1	121 11	23/1/2021 11/6/2021
B.1.620	36	31/3/2021
C.37 (Lambda)	7	20/6/2021
P.3 (Theta)	3	27/6/2021

Table 2: List of VOCs (red) and VOIs (orange) identified in Belgium to date and cumulative number of sequences available on GISAID (total of 35,691 sequences).

2. Testing of travellers

Departing travellers

During the last 5 full weeks (June 28 to August 1), the National Reference Center in Leuven has tested 38,299 departing travellers, among which 235 were tested positive (0.6%). The positivity rate increased from 0.28% during the first week to 0.87% during the last two weeks. The Delta variant represented 95% of the positive samples tested during the last week.

Returning travellers

For the last 5 full weeks (June 28 to August 1),

- Among the travellers returning from abroad to the region of Leuven, 1,038 people were tested, among which 39 were tested positive (3.7%). The Delta variant represented 72.7% of the positive samples tested during the last week.