

# Genomic surveillance of SARS-CoV-2 in Belgium

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

**Situation update – 2nd of November 2021  
(report 2021\_52)**

## Executive summary

60,760 Belgian sequences of SARS-CoV-2 are now publicly available on GISAID; compared to last week's report 2,199 sequences have been added.

887 sequences of positive SARS-CoV-2 samples collected between 18/10/2021 and 31/10/2021 have at this stage been analysed in the context of baseline surveillance. Among these, B.1.617.2 (*Delta*) and its sublineages represented 99,9% of the circulating strains..

The genomic diversity of SARS-CoV-2 in Belgium is comparable with the situation described over the last 13 weeks.

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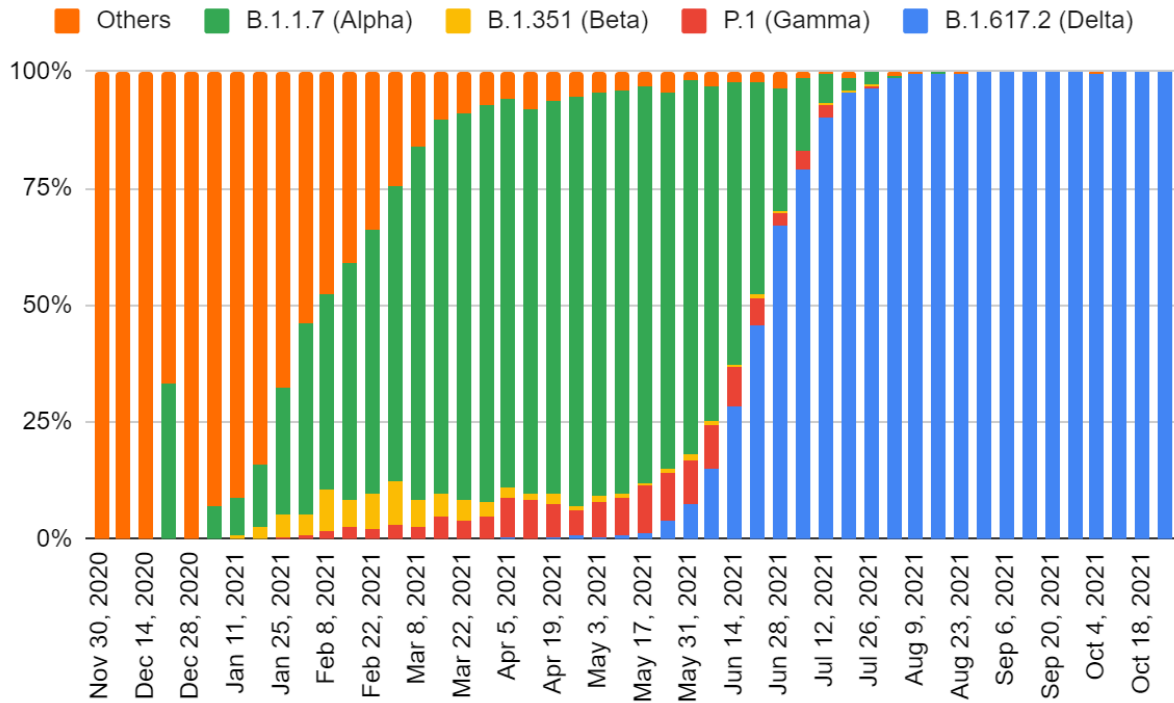
With the collaboration of the laboratories of UCL, ULB, UMons, UNamur, ULiège, UGent, UZA/UAntwerpen, Jessa ZH, AZ Delta, AZ Klina, IPG, AZ St Lucas Gent, OLVZ Aalst, Briant network, ZNA, AZ St Jan Brugge, UZ Brussel, LHUB-ULB, and UZ Leuven/KU Leuven; and Sciensano HealthData.

Previous reports can be downloaded using the following link:

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

## 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 baseline surveillance samples sequenced (see Figure 1).



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