

Genomic surveillance of SARS-CoV-2 in Belgium

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

**Situation update – 28 of September 2021
(report 2021_47)**

Executive summary

47,484 Belgian sequences of SARS-CoV-2 are now publicly available on GISAID.

404 sequences of positive SARS-CoV-2 samples collected between 16/09/2021 and 26/09/2021 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 8 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>

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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.

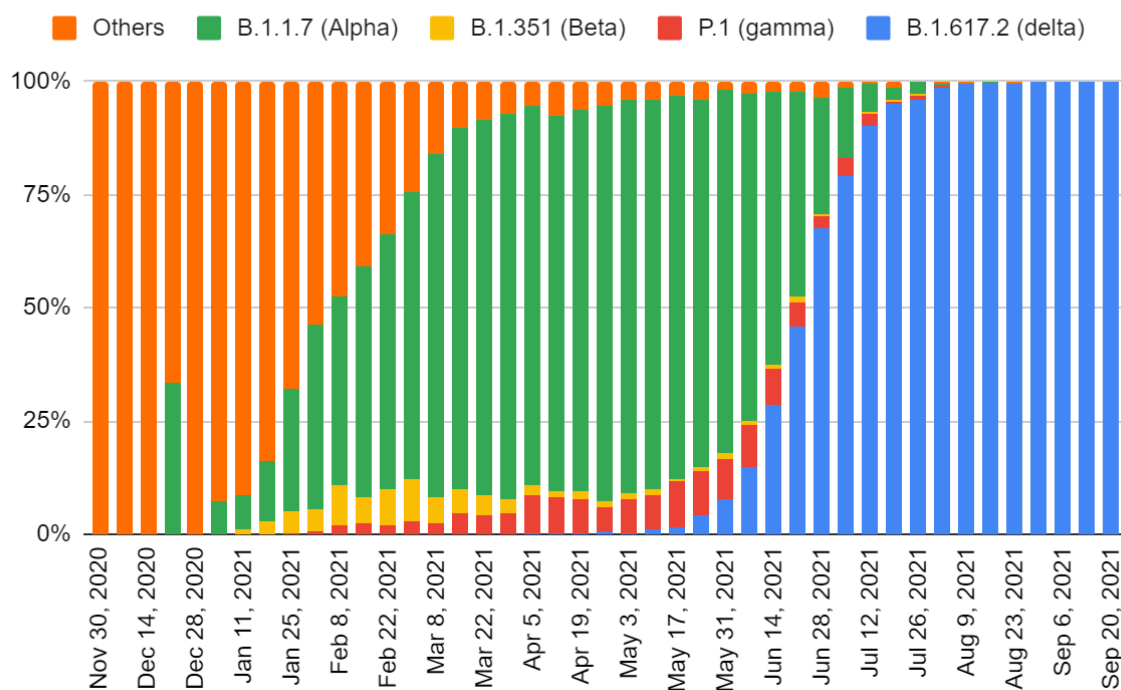


Figure 1: Weekly evolution of the frequency of variants of concern reported by the baseline surveillance network using a whole genome sequencing (WGS) approach.

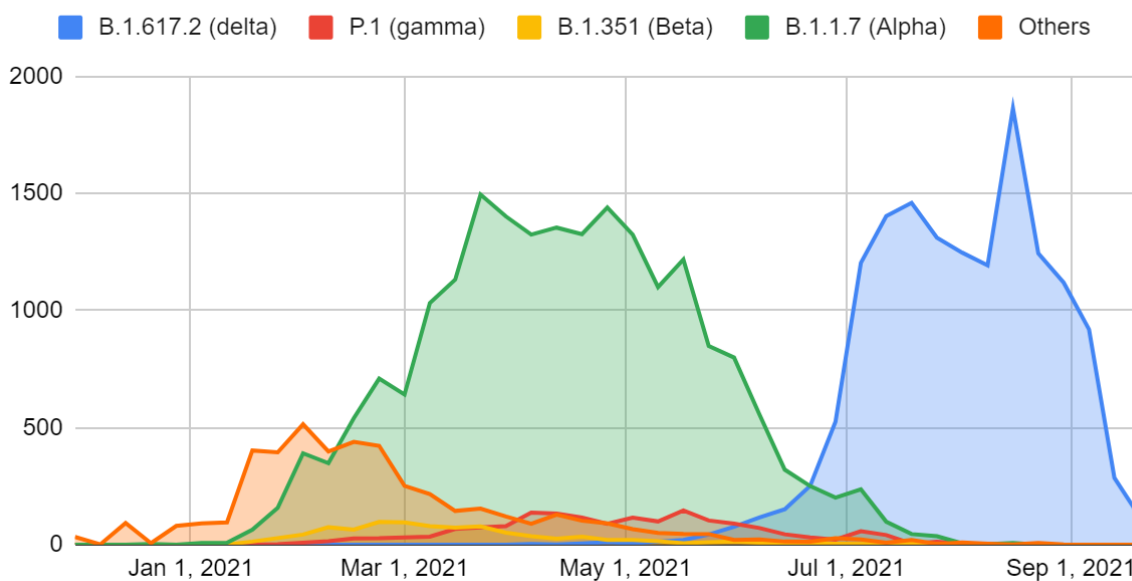


Figure 2: Evolution of the number of sequenced COVID-19 samples per variant since January 2021.