

Genomic surveillance of SARS-CoV-2 in Belgium

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

**Situation update – 7 of December 2021
(report 2021_58)**

Executive summary

68,279 Belgian sequences of SARS-CoV-2 are now publicly available on GISAID; compared to last week's report, 1,301 sequences have been added.

1,459 sequences of positive SARS-CoV-2 samples collected between 22/11/2021 and 05/12/2021 have at this stage been analysed in the context of baseline surveillance. Among these, B.1.617.2 (*Delta*) and its sublineages represented 99.7% of the circulating strains. We estimate that during the week of 29/11/2021, Omicron (B.1.1.259) represented 0.3% of the circulating strains.

In addition to the baseline genomic surveillance, the evolution of the Omicron variant is followed-up on a daily basis through the percentage of diagnostic PCRs harboring the S gene target failure (rate estimated between 0.6% and 0.7% during the last 48 hours) and a complementary active investigation of local transmission clusters. At this stage, we could extensively circumscribe 3 out of the 4 clusters of local Omicron transmission. An active collaboration with the federal authorities and the regional disease control services has been initiated to define an adequate strategy, taking into account that this variant will probably become dominant across Europe in the coming weeks.

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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) remains the dominant lineage in the country, representing 99.7% of the baseline surveillance samples sequenced (see Figure 1). Four Omicron infections were reported through the baseline surveillance system during the week of November 29, representing 0.3% of all sequences reported during that week.

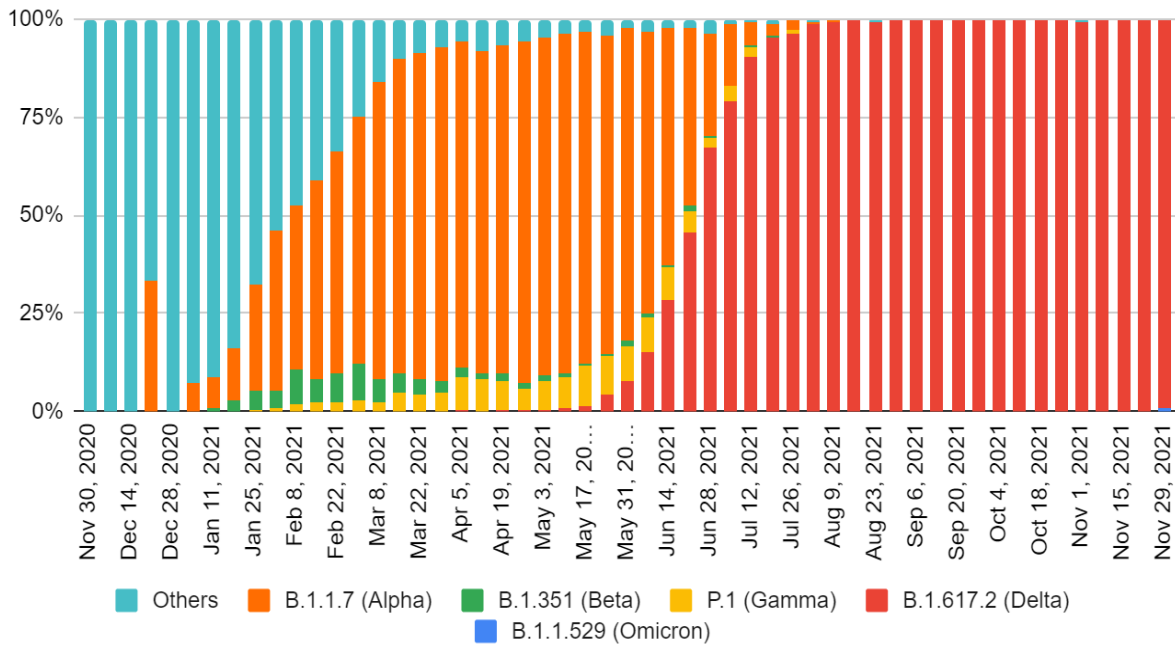


Figure 1: Weekly evolution of the frequency of variants of concern reported by the baseline surveillance network using a whole genome sequencing (WGS) approach.

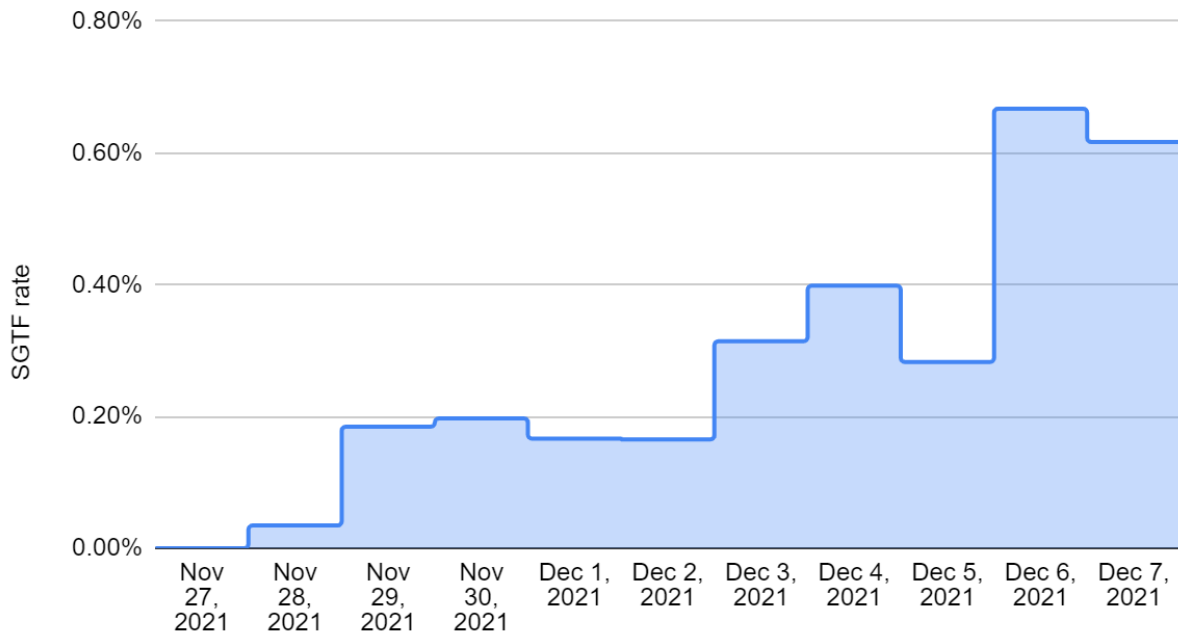


Figure 2: SGTF (S dropout with $C_q < 25$) rate over the past 11 days in Belgium. Data for the last 2 days are preliminary and may still evolve as all data may not yet be uploaded. Analysis performed from 37,725 positive samples tested by the Federal Platform laboratories.

2. Current status with regard to Omicron in the world

As of 6/12/2021 (source: ECDC), 17 EU/EEA countries reported a total of 201 confirmed B.1.1.529 cases. In total, 23 countries confirmed the presence of this new variant of concern.

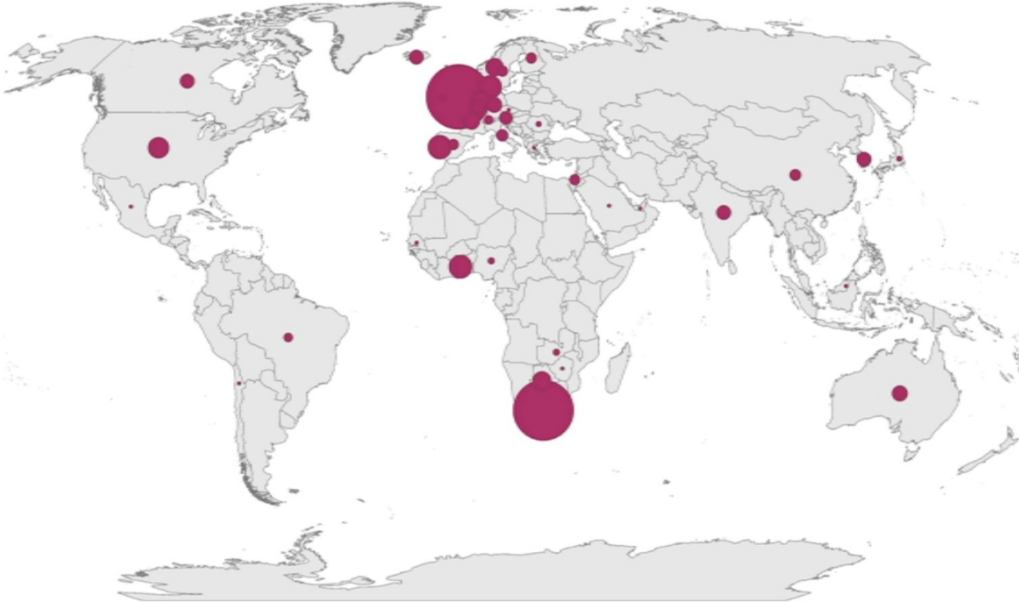


Figure 3: Countries reporting confirmed B.1.1.529 cases. Many countries, particularly in the African continent where genomic surveillance capacity is limited, probably currently under-report the real number of infections (source: ECDC).

3. Current status with regard to Omicron in Belgium

Currently, the National Reference Laboratory has sequenced or been informed of 30 confirmed Omicron cases confirmed by sequencing in Belgium. The actual number is probably higher, as several probable Omicron infections are currently being confirmed and several clusters of local transmission could not be fully circumscribed.

Using the available Omicron genomic sequences on GISAID on Tuesday December 7th, of which 12 were generated by different labs in Belgium, we performed a detailed phylogenetic analysis to investigate how these Belgian cases are linked. This analysis currently - **based on available data and subject to change if more data become available** - reveals the presence of three Belgian transmission clusters, which we discuss and illustrate below. A fourth cluster, for which sequencing data is not yet available on GISAID, is also briefly discussed hereunder.

Cluster 1 (probably contained, to be followed-up)

First off, two people that returned from Egypt via Turkey (and have identical genomes) cluster within a multifurcation that does not reveal much information about the origin of their infection (see Figure 4). These genomes do not cluster with other Belgian Omicron genomes. As there are currently no Omicron genomes from Egypt nor Turkey, the origin of these infections cannot at this stage be formally confirmed. Importantly, at the moment no other Omicron infections are known to stem from these two infected patients.

hCoV-19/Hong_Kong/HKU-211129-002/2021|EPI_ISL_6841981|2021-11-21
hCoV-19/Hong_Kong/HKU-211129-001/2021|EPI_ISL_6841980|2021-11-14
hCoV-19/USA/NY-PRL-2021_1126_01D05/2021|EPI_ISL_7129869|2021-11-22
hCoV-19/Hong_Kong/HKU-691/2021|EPI_ISL_7138045|2021-11-14
hCoV-19/South_Africa/NICD-N21650/2021|EPI_ISL_6914029|2021-11-17
hCoV-19/South_Korea/KDCA18125/2021|EPI_ISL_6959935|2021-11-25
hCoV-19/South_Africa/CERI-KRISP-K032355/2021|EPI_ISL_6825395|2021-11-16
hCoV-19/Brazil/SP-HIAE-ID990/2021|EPI_ISL_6901961|2021-11-25
hCoV-19/Belgium/regal-20472/2021|EPI_ISL_6989250|2021-11-29
hCoV-19/Belgium/regal-20174/2021|EPI_ISL_6794907|2021-11-24
hCoV-19/Hong_Kong/VM21044713-1/2021|EPI_ISL_6590782|2021-11-13
hCoV-19/Brazil/SP-HIAE-ID989/2021|EPI_ISL_6901960|2021-11-25

Figure 4. Phylogenetic analysis of the two Belgian patients first infected with Omicron. At the time of writing, their source / location of infection can not be reliably determined.

Cluster 2 (Circumscribed at the Belgian level ; probably uncontained at international level)

Second, three genomes which are currently available on GISAID originate from Belgian travellers returning from an international congress which took place at the end of November. More than 100 nationalities were represented in this congress. The genomes of the 8 returning travellers are part of a wider belgian cluster comprising at this stage 11 confirmed Omicron cases, among 3 household members of these returning travellers. Three of these genomes have been sequenced so far, cluster together (see Figure 5) and seem to stem from South Africa (uncertain and subject to change when more data become available). No Omicron genomes from Dubai were available at the time of writing.



Figure 5. Three Belgian travellers returning from an international congress tested positive for the Omicron variant and are currently estimated to be part of the same transmission cluster.

Cluster 3 (Circumscribed at the Belgian level ; probably uncontained at international level)

We identify a cluster of five Belgian Omicron genomes within a larger European cluster (see Figure 6). The possible origin of this cluster is an international sport competition which took place in the Czech Republic mid-November and where several European countries were represented in addition to a team from South Africa. This possible source of infection (i.e. the competition in the Czech Republic) is currently under investigation and is therefore to be considered as unconfirmed at this stage, as no genomic data from participants were available or identified as such at the time of writing.

Nevertheless, the clustering of the sequences of two roommates with no travel history (EPI_ISL_6929785 and EPI_ISL_7021517), among which one had a high risk contact with one participant to this competition with other genomes for which a direct epidemiological link could be made with another participant to this competition tend to support this hypothesis. Among the 7 confirmed or very probable secondary & tertiary Belgian Omicron cases linked to this cluster, transmission possibly occurred within the household (3), at work (2), at school (1) or during a small-scale social event (1).

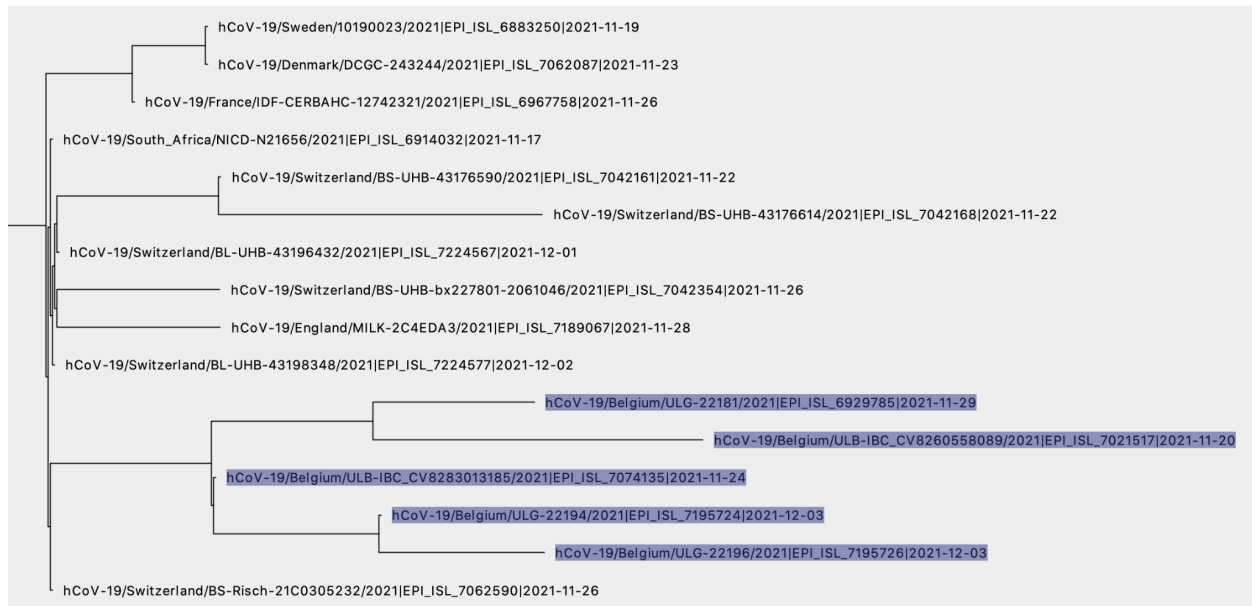


Figure 6. Phylogenetic analysis currently places 5 Belgian Omicron infections in connection with one another. Additional Belgian samples presumably related to this cluster are being sequenced and will be analysed in a future report.

Cluster 4 (not circumscribed, origin unclear at this stage)

A new cluster of 3 Omicron infections has been described on 7/12/2021 in one school, where the children did not report a recent international trip. Contact tracing is ongoing to investigate the possible origin of this cluster. Phylogenetic analysis could not yet be performed and further analysis will be provided in the next report.

Other cases (direction introduction)

All other confirmed cases are currently related to a personal travel to an African country.