KU LEUVEN

DEPARTMENT OF MICROBIOLOGY, IMMUNOLOGY AND TRANSPLANTATION

UZ LEUVEN | LABORATORIUMGENEESKUNDE

Genomic surveillance report

Update for Belgium, 10/05/2022

Lize Cuypers, Guy Baele, Simon Dellicour, Piet Maes, Emmanuel André

See page 2 for full list of authors and participating laboratories

May 2022

Content

This rapport was written in collaboration with:

Louis Nevejan, Tom Wenseleers, Bram Slechten, Johan Van Weyenbergh, Els Keyaerts, Joren Raymenants, Barney Potter, Sunita Janssenswillen, Elke Wollants, Marc Van Ranst and the Belgian Sequencing Consortium.

Corresponding author: lize.cuypers@uzleuven.be (National Reference Center for Coronaviruses, UZ Leuven)

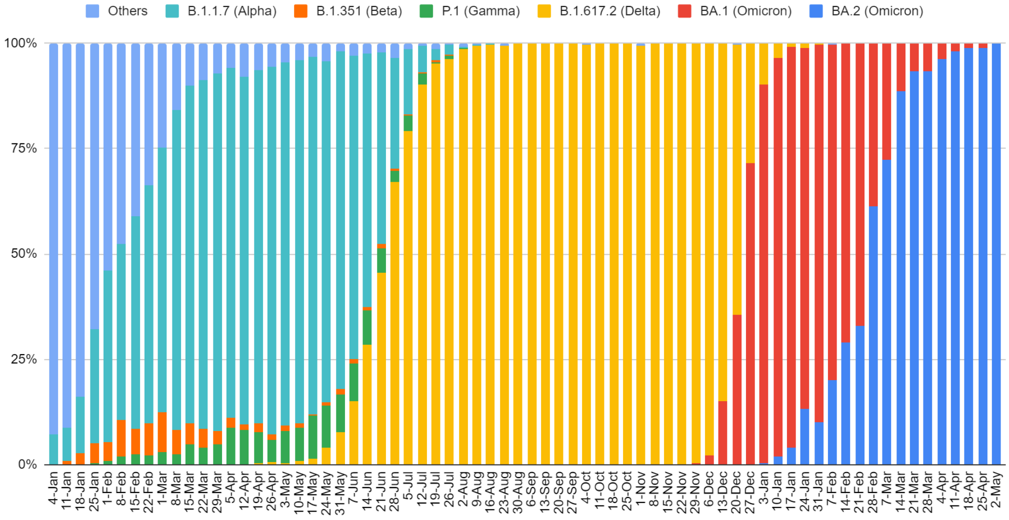
Belgian Sequencing Consortium:

Cliniques Universitaires Saint-Luc, Centre Hospitalier CHU UCL Namur, 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, UZ Leuven/KU Leuven and Sciensano HealthData.

Previous reports are available online using this link.

Executive summary

The Omicron BA.2 lineage currently represent 93-96% of new infections diagnosed in Belgium, and this situation is currently associated with a high but declining circulation of the virus (reported incidence during the last 14 days: 559 cases/100.000 habitants).



Worldwide, the number of reported BA.4 (1107, including 19 from Belgium), BA.5 (612, including 7 cases detected in Belgium) and BA.2.12.1 (16343, including 3 cases detected in Belgium) cases continues to increase. We continue to monitor these trends over the coming weeks.

At this stage, there is no indication that these emerging variants will lead to more severe disease compared to other Omicron sublineages but, as it has been the case with previous variants, the efficacy of monoclonal antibodies used for the treatment of high risk patients may be affected.

1 Epidemiological context and indicators related to diagnostic activities

Since the Alpha wave, the federal platform laboratories have been used for genomic surveillance purposes in addition to their diagnostic function to monitor real-life viral population replacement dynamics. We therefore used the share of positive samples (Cq <25) presenting or not an S gene target failure (SGTF) to reflect in real time rapidly evolving situations. This approach has been particularly efficient thanks to the very high number of samples referred to these laboratories and to the chronological sequence of the different variants of concern which have emerged in Belgium: Alpha (SGTF), Delta (no SGTF), Omicron BA.1 & BA.1.1 (SGTF), Omicron BA.2 (no SGTG). The upcoming BA.4 and BA.5 present again the deletion 69/70 in the S gene and therefore are characterized by an SGFT.

Samples without SGTF (most likely to be BA.2 infections) currently represent up to 93-96% of positive samples tested in the federal platform laboratories. However, recently, Omicron BA.2 genomes characterized by the deletion 69/70 in the spike protein (causing SGTF) have been reported as well, therefore caution is warranted when interpreting samples with SGTF as Omicron BA.4 and BA.5 only. Moreover, Omicron BA.1 infections are still sporadically detected.

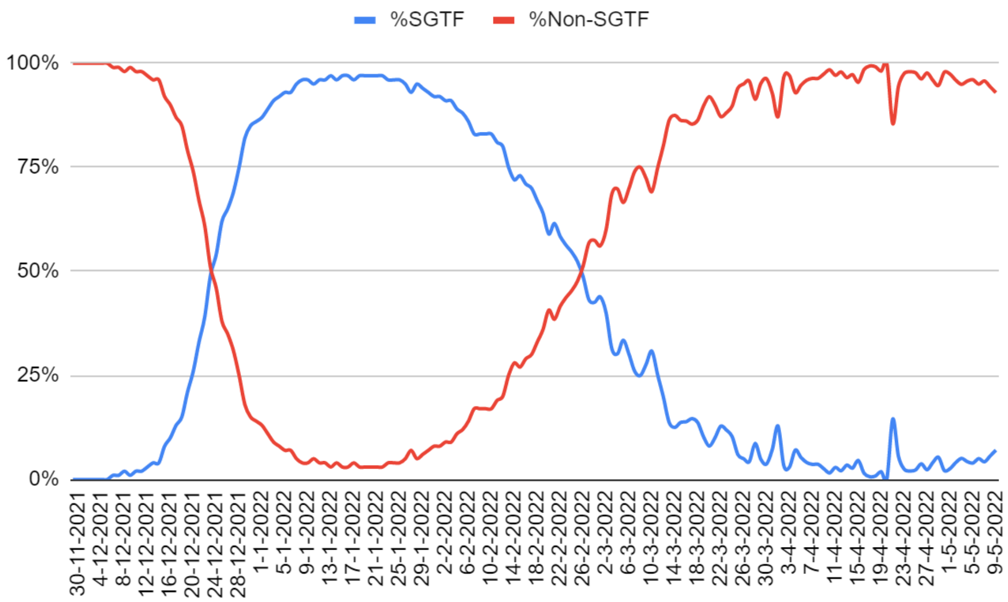


Figure 1: *S gene target failure (SGTF; blue: BA.1 & BA.1.1, BA.4 and BA.5, and potentially BA.2 with 69/70 deletion) and others (red: currently considered predominantly BA.2) among positive samples reported by the federal platform laboratories.*

Figure 2 highlights the total number of positive cases tested in the federal platform laboratories based on the presence or absence of SGTF for the last four weeks. BA.4 has been identified in Belgium since 29/03/2022 (so far 10 genomes), and BA.5 since 24/04/2022 (the first two cases have been identified), with both lineages presenting an SGTF.

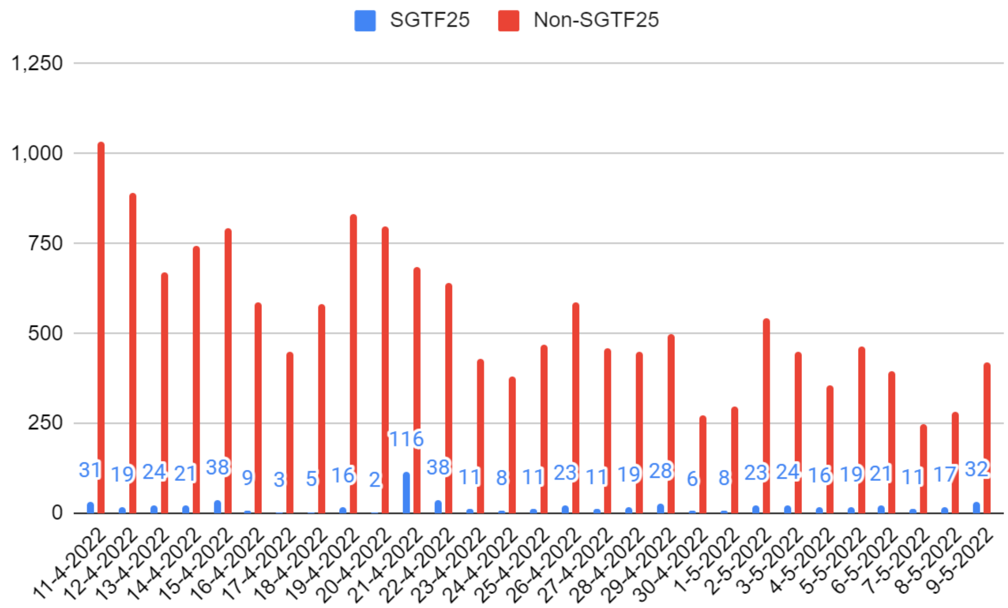


Figure 2: *Number of samples tested positive in the federal platform laboratories with S gene target failure (SGTF; blue, compatible with BA.4 and BA.5) and without SGTF (non-SGTF; red, compatible with BA.2). The absolute numbers are less representative of the actual epidemiology since a couple of weeks, as a result of a change in testing indications and a lower testing intensity. Therefore, only the last four weeks are visualized in the graph.*

2 Monitoring of Variants of Concern in Belgium

During the last two weeks of baseline surveillance - 25/04/2022 and 08/05/2022 - (598 sequences collected at this stage), BA.1 and BA.1.1 jointly represented 0.8% (↘) of the circulating strains, while BA.2 represented 98.8% (=) of the strains (Figure 3). So far, 19 BA.4 genomes and 7 BA.5 genomes have been detected in Belgium; a separate graph visualizes the progress of the cases over time (Figure 4).

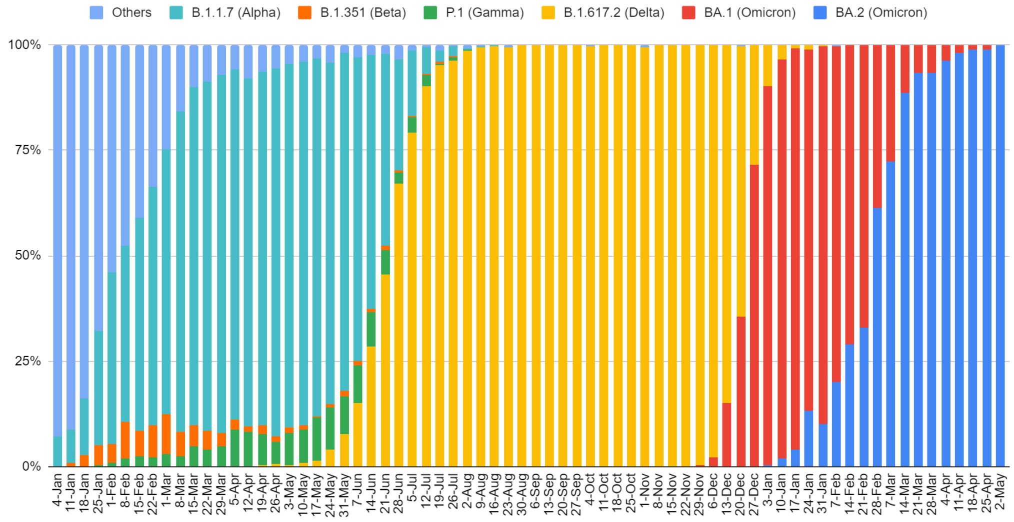


Figure 3: *Share of variants of concern per week in Belgium*

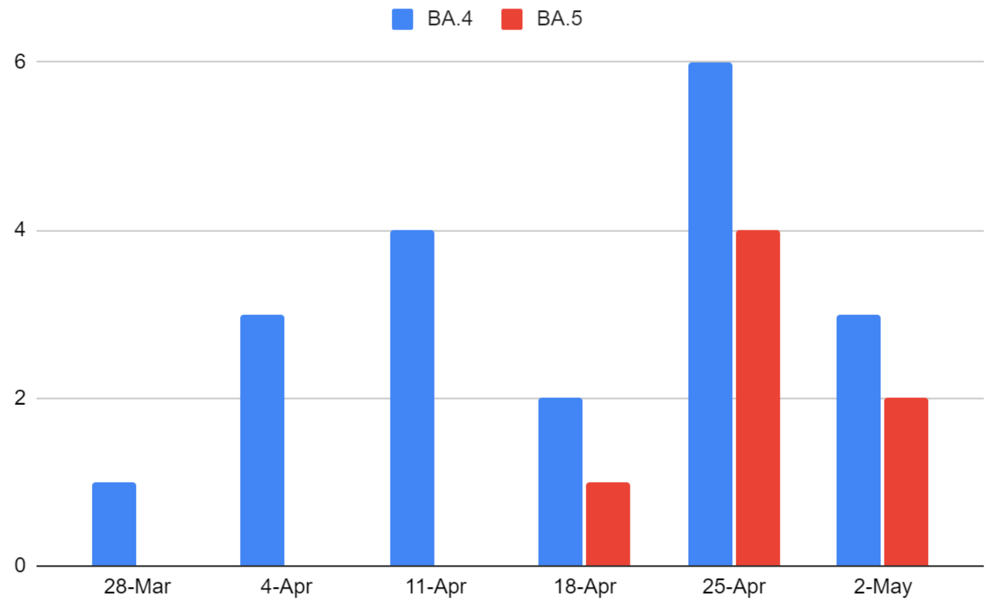


Figure 4: *Number of BA.4 and BA.5 cases reported on GISAID in Belgium per week. The first detection of BA.4 in Belgium dates from 29/03/2022 (in blue), while the first BA.5 case was sequenced on 24/04/2022 (in red). In total, 19 BA.4 and 7 BA.5 genomes from Belgium have been deposited to GISAID, respectively with the most recent infections dating from May 4th and 5th, stressing the close follow-up of infections and sequences by the national genomic surveillance consortium.*