



Genomic surveillance report

Update for Belgium, 07/06/2022

Lize Cuypers, Guy Baele, Simon Dellicour, Piet Maes, Emmanuel André
See page 2 for full list of authors and participating laboratories

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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)

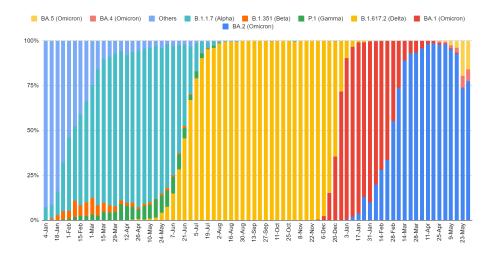
Belgian Sequencing Consortium:

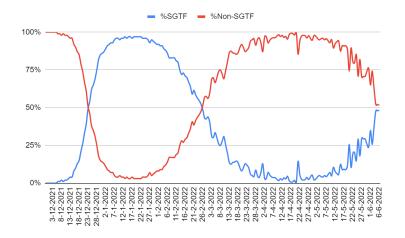
Cliniques Universitaires Saint-Luc, Centre Hospitalier CHU UCL Namur, ULB, UMons, UNamur, ULiège, UGent, UZA/UAntwerpen, Jessa ZH, AZ Delta, AZ Klina, IPG, AZ St Lucas Gent, OLVZ Aalst, Briant network, ZNA, AZ St Jan Brugge, UZ Brussel, LHUB-ULB, UZ Leuven/KU Leuven and Sciensano HealthData.

Previous reports are available online using this <u>link</u>.

Executive summary

Omicron BA.2 remains the dominant lineage in Belgium (52-63% of new infections), although both BA.4 and BA.5 represent an increasing share of infections, accounting for almost half of all new infections. This distribution of variants is concomitant with a declining incidence of COVID-19 (reported incidence during the last 14 days: 204 cases/100.000 habitants). The decreasing incidence associated with a lower testing intensity has an impact on the number of recent genomes available for genomic surveillance. Therefore, the latest estimates are based on SGTF reported by federal PCR testing laboratories, who however analyze a smaller share of the samples compared to all analyzes performed on a national level compared to earlier waves.





Based on current genomic trends, it is expected that BA.4 and BA.5 will altogether become the dominant lineages during the upcoming week.

1 Epidemiological context and indicators related to diagnostic activities

Omicron BA.2 can be distinguished from BA.4 and BA.5 using some specific diagnostic PCR kits as the latter variants present the deletion 69/70 in the S gene and therefore are characterized by an SGFT.

In the current epidemiological context, samples without SGTF are most likely to be BA.2 infections (including BA.2.12.1). These samples currently represent up to 52-63% of positive tests in the country (declining share week by week). SGTF samples are presumed to be predominantly Omicron BA.4 and BA.5, since Omicron BA.1 infections have been rarely detected for the last month by the baseline surveillance effort conducted by the sequencing consortium.

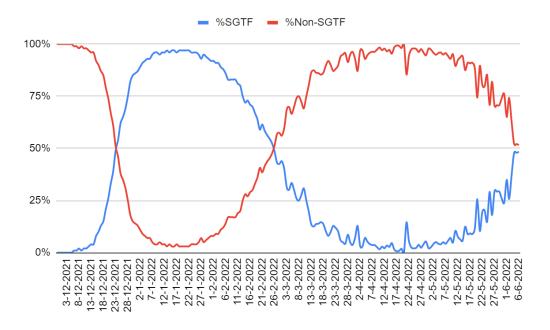


Figure 1: S gene target failure (SGTF; blue: BA.1 & BA.1.1, BA.4 and BA.5, and potentially BA.2 with 69/70 deletion) and others (red: currently considered predominantly BA.2) among positive samples reported by the federal platform laboratories.

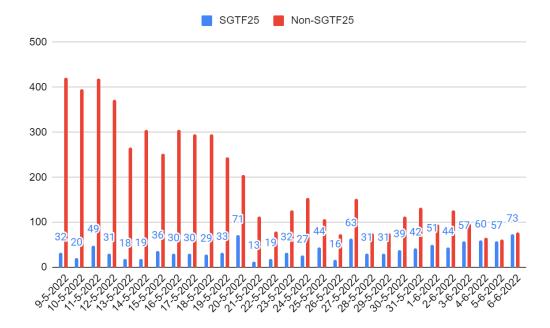


Figure 2: S gene target failure (SGTF; BA.4 and BA.5, and potentially BA.2 with 69/70 deletion) and others (red: currently considered predominantly BA.2) among positive samples reported by the federal platform laboratories.

2 Monitoring of Variants of Concern in Belgium

During the last two weeks of baseline surveillance - 23/05/2022 and 06/06/2022 - (402 sequences collected at this stage), One BA.1 strain was reported, while BA.2 represented 74.4% (\searrow) of the circulating strains (Figure 3). Overall, 124 BA.4 and 125 BA.5 genomes have so far been detected in our country, respectively representing 6.5% and 17.9% of the genomes (\nearrow) for the last two weeks. Based on the latter, it seems that BA.5 has an advantage over BA.4 and will most likely become the dominant lineage in the upcoming weeks in Belgium.

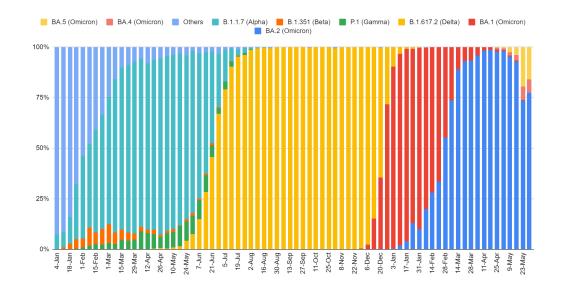


Figure 3: Share of variants of concern per week in Belgium