KU LEUVEN

DEPARTMENT OF MICROBIOLOGY, IMMUNOLOGY AND TRANSPLANTATION

UZ LEUVEN | LABORATORIUMGENEESKUNDE

Genomic surveillance report

Update for Belgium, 24/05/2022

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)

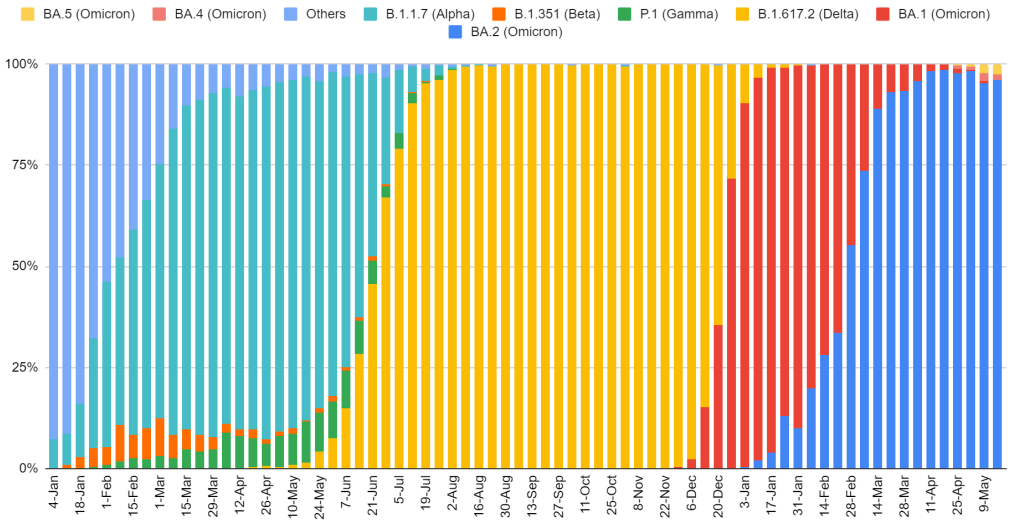
Belgian Sequencing Consortium:

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 represents 74-91% of new infections diagnosed in Belgium, and this situation is currently associated with a declining circulation of the virus (reported incidence during the last 14 days: 371 cases/100.000 habitants).



Worldwide, using the international database GISAID, the number of reported BA.4 (2424, including 64 from Belgium), BA.5 (2056, including 39 cases detected in Belgium) and BA.2.12.1 (42036, including 19 cases detected in Belgium) cases continue to increase. BA.4 and BA.5 have been recognized as variants of concern by the WHO.

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. The National Reference Center UZ/KULeuven has been able to culture BA.4 and BA.5 isolates and will shortly initiate a series of studies that should allow better describing the eventual intrinsic resistance mechanisms and immune escape characteristics of these variants.

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 74-91% of positive tests in the country (declining share week by week). SGTF samples are presumed to be mainly Omicron BA.4 and BA.5, since Omicron BA.1 infections have only been rarely detected over the last few weeks. .

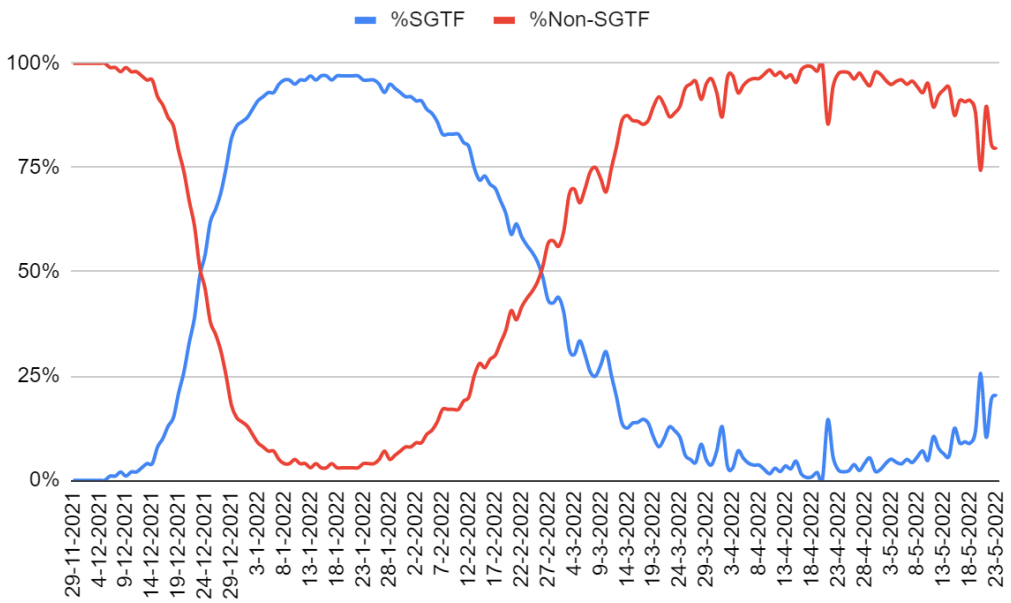


Figure 1: *S gene target failure (SGTF; blue: BA.1 & BA.1.1, BA.4 and BA.5, and potentially BA.2 with 69/70 deletion) and others (red: currently considered predominantly BA.2) among positive samples reported by the federal platform laboratories.*

2 Monitoring of Variants of Concern in Belgium

During the last two weeks of baseline surveillance - 09/05/2022 and 22/05/2022 - (775 sequences collected at this stage), BA.1 and BA.1.1 jointly represented 0.4% (=) of the circulating strains, while BA.2 represented 95.0% (↘) of the strains (Figure 3). Overall, 64 BA.4 and 39 BA.5 genomes have been detected in Belgium, respectively representing 1.9% and 2.2% of the genomes for the last two weeks.

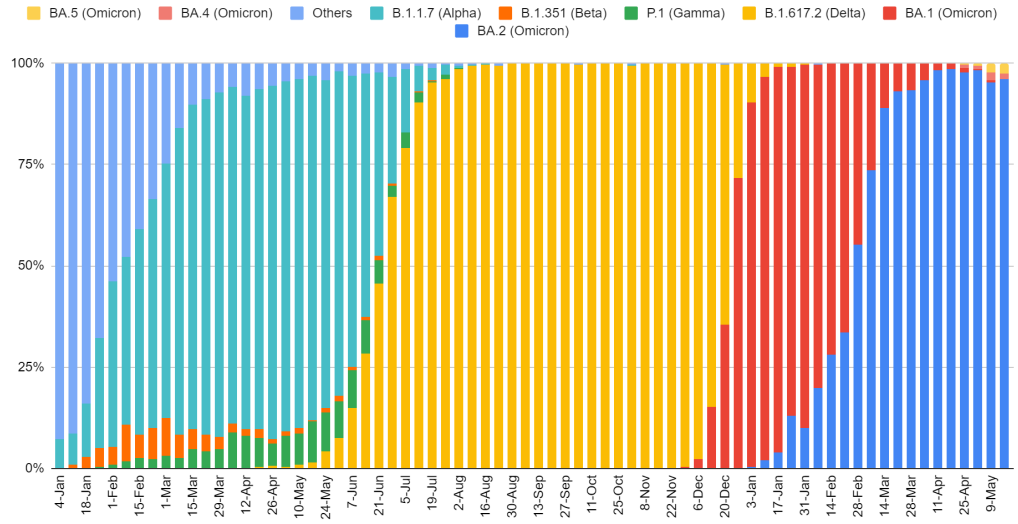


Figure 2: *Share of variants of concern per week in Belgium*