

DEPARTMENT OF MICROBIOLOGY, IMMUNOLOGY AND TRANSPLANTATION



# Genomic surveillance report

## Update for Belgium, 13/09/2022

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

September 2022

#### Content

Executive summary Epidemiological context and indicators related to diagnostic activities	3
	4
Monitoring of Variants of Concern in Belgium	6

This report was written in collaboration with:

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

*Corresponding author: lies.laenen@uzleuven.be (National Reference Center for Coronaviruses, UZ Leuven)* 

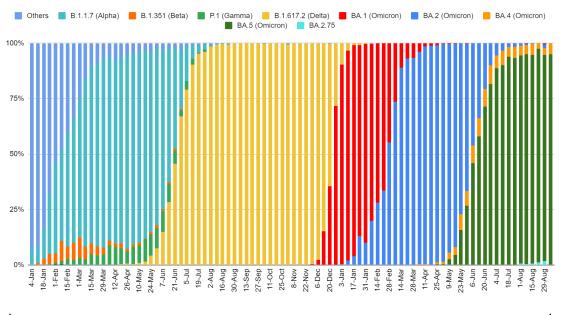
Belgian Sequencing Consortium:

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**

Omicron BA.5 remains the dominant lineage in Belgium and accounts for around 93% of the most recent infections. The genomic situation is currently stable.

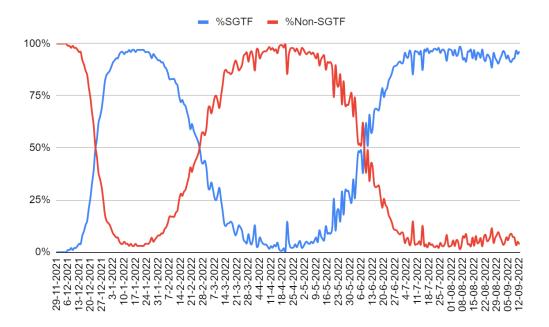


To date, thirty-three BA.2.75 samples have been detected through the national genomic surveillance program and account for approximately 1% of the circulating strains.

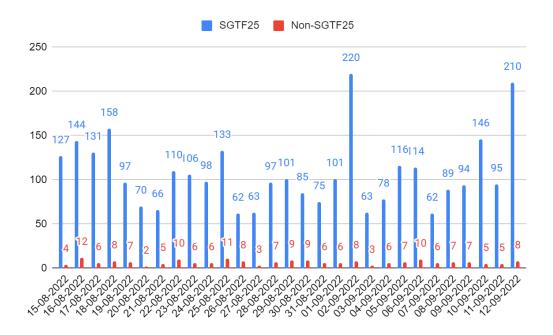
### 1 Epidemiological context and indicators related to diagnostic activities

Omicron BA.2 and BA.2.75 can be distinguished from BA.4 and BA.5 as the latter variants present a deletion 69/70 in the Spike gene (S gene target failure, SGTF).

At this stage, SGTF samples (BA.5 and BA.4) still represent the vast majority of the most recent infections, but a slow decline in favor of non-SGTF samples (including BA.2.75) may have started since a couple of weeks (Figure 1). These recent changes must be interpreted with caution as there is currently a low number of samples analyzed by the federal PCR platform (figure 2). This signal will nevertheless be followed-up carefully in the coming weeks.



*Figure 1:* S gene target failure (SGTF, in blue: BA.4 and BA.5) and others (red: currently considered predominantly BA.2 and BA.2.75) among positive samples reported by the federal platform laboratories.



*Figure 2:* S gene target failure (SGTF, in blue: BA.4 and BA.5) and others (red: currently considered predominantly BA.2 and BA.2.75) 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 - 29/08/2022 to 11/09/2022 - (405 sequences collected at this stage), BA.5 represented 93%, BA.4 represented 4% and BA.2.75 represented 1% of the samples sequenced. Thirty-three BA.2.75 samples have been identified at this stage. The BA.2.75 subvariant is currently classified as a variant of interest (VOI) by the ECDC, and seems to have a (modest) transmission advantage over BA.5. It is likely that the percentage of BA.2.75 strains will continue to go up in Belgium and that BA.2.75 and BA.5 will cocirculate over the coming weeks.

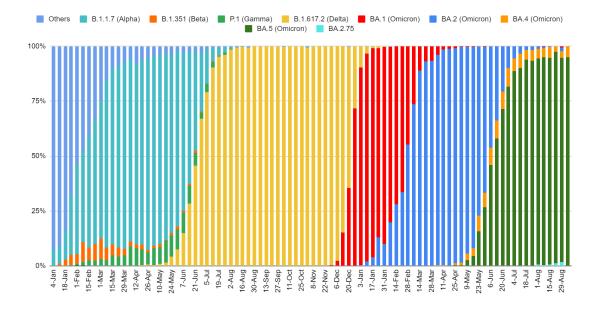


Figure 3: Share of variants of concern per week in Belgium since January 2021.