



Genomic surveillance report

Update for Belgium, 09/08/2022

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

See page 2 for full list of authors and participating laboratories

Content

Executive summary	3
Epidemiological context and indicators related to diagnostic activities	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: reile.janssen@uzleuven.be (National Reference Center for Coronaviruses, UZ Leuven)

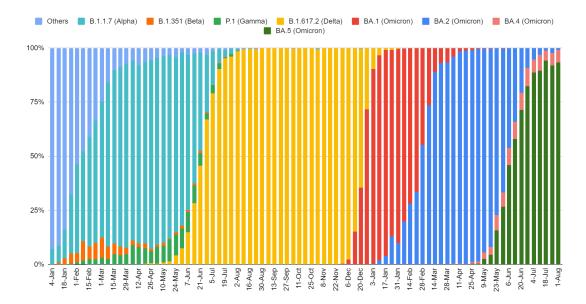
Belgian Sequencing Consortium:

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.5 is the dominant lineage in Belgium and accounts for around 90% of the most recent infections. The epidemic resurgence associated with the latest viral shift (BA.2 -> BA.5) has reached a peak, as highlighted by a decreasing number of infections (Rt = 0.80). Hospital admissions are declining and also the number of deaths is now going down.



No BA.2.75 have yet been detected through the national genomic surveillance program. This does not mean that this variant has not yet been introduced or is not currently circulating at low level in Belgium. The latest international estimates tend to support that BA.2.75 will replace BA.5 in the future. Nevertheless, considering the limited growth advantage of BA.2.75 against BA.5, the upcoming viral population replacement is not expected to occur in Belgium before the fall.

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 using 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) represent 95-98% of the most recent samples analyzed (Figure 1).

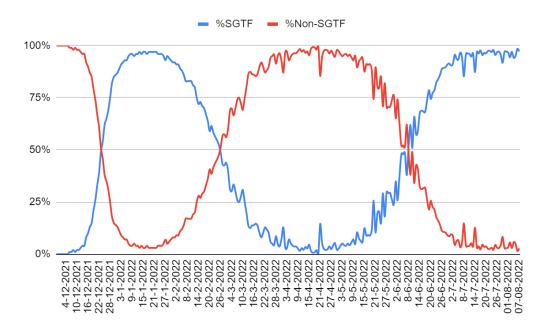


Figure 1: S gene target failure (SGTF, in blue: BA.4 and BA.5) and others (red: currently considered predominantly BA.2, but also possibly BA.2.75) among positive samples reported by the federal platform laboratories.

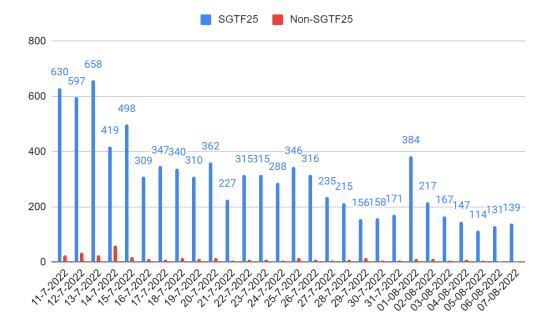


Figure 2: S gene target failure (SGTF, in blue: BA.4 and BA.5) and others (red: currently considered predominantly BA.2, but also possibly BA.2.75) among positive samples reported by the federal platform laboratories.

2 Monitoring of Variants of Concern in Belgium

During the last two weeks of baseline surveillance - 25/07/2022 to 07/08/2022 - (739 sequences collected at this stage), BA.5 represented 92%, BA.4 represented 6% and BA.2 represented 2%. No BA.2.75 have been identified at this stage. In the meantime, we keep monitoring the situation abroad and state of knowledge regarding the emergence and spread of BA.2.75 (currently classified as a variant of interest by the ECDC).

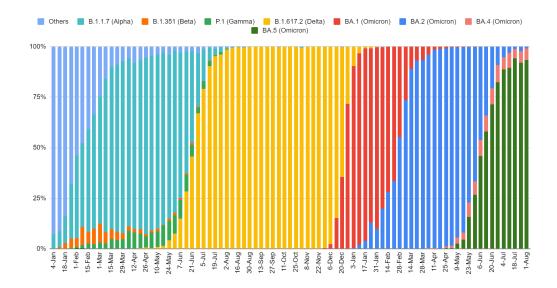


Figure 3: Share of variants of concern per week in Belgium since January 2021