

DEPARTMENT OF MICROBIOLOGY, IMMUNOLOGY AND TRANSPLANTATION



Genomic surveillance report

Update for Belgium, 16/08/2022

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

See page 2 for full list of authors and participating laboratories

August 2022

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 remains 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 = 0.88). Hospital admissions and ICU beds are also declining.



surveillance program. BA.2.75 has now become the dominant variant in India and is being found in more and more countries around the world. Also in Belgium, it is likely that the percentage of BA.2.75 strains will continue to go up and that BA.2.75 and BA.5 will cocirculate over the coming weeks. If BA.2.75 will rapidly become dominant in countries that had a large BA.5 outbreak remains to be established.

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 93-97% 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 - 01/08/2022 to 14/08/2022 - (491 sequences collected at this stage), BA.5 represented 92%, BA.4 represented 5%, BA.2 represented 1% and BA.2.75 represented 2%. Nine BA.2.75 samples have been identified at this stage. The first BA.2.75-positive patient in this surveillance was sampled in Belgium on 31/7/2022.

BA.2.75-positive samples have also been isolated in 28 other countries. In India, BA.2.75 now accounts for more than 50% of the genotyped strains, but with limited impact on hospitalisations.

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. If BA.2.75 will rapidly become dominant in countries that had a large BA.5 outbreak remains to be established.



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