KU LEUVEN

DEPARTMENT OF MICROBIOLOGY, IMMUNOLOGY AND TRANSPLANTATION

UZ LEUVEN | LABORATORIUMGENEESKUNDE

Genomic surveillance report

Update for Belgium, 28/06/2022

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Content

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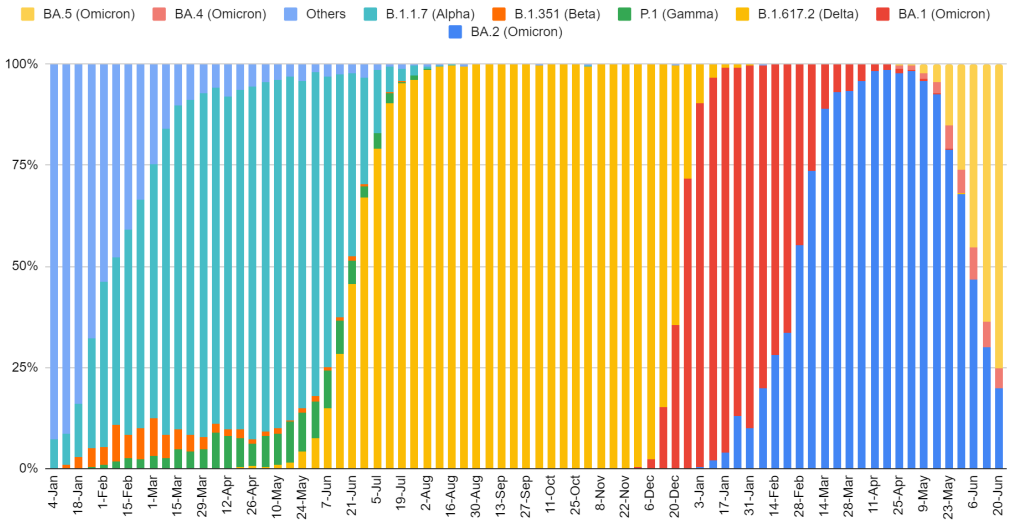
Previous reports are available online using this link.

Executive summary

Omicron BA.5 is now the dominant lineage in Belgium. This recent shift is associated with an increase in the number of infections (Rt 1.), increasing positivity rate despite an increased testing intensity and an increase in the number of hospital admissions (Rt > 1).



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 11-14% of positive tests in the country (declining share week by week). SGTF samples are presumed to be predominantly Omicron BA.5 and, to a lesser extent, BA.4. These samples represent 86-89% of the most recent samples analyzed. (Figure 1)

Although the current testing policies do not allow precise estimations, the current doubling time of BA.5/BA.4 positive samples observed at the level of federal platform laboratories is between 7 and 10 days.

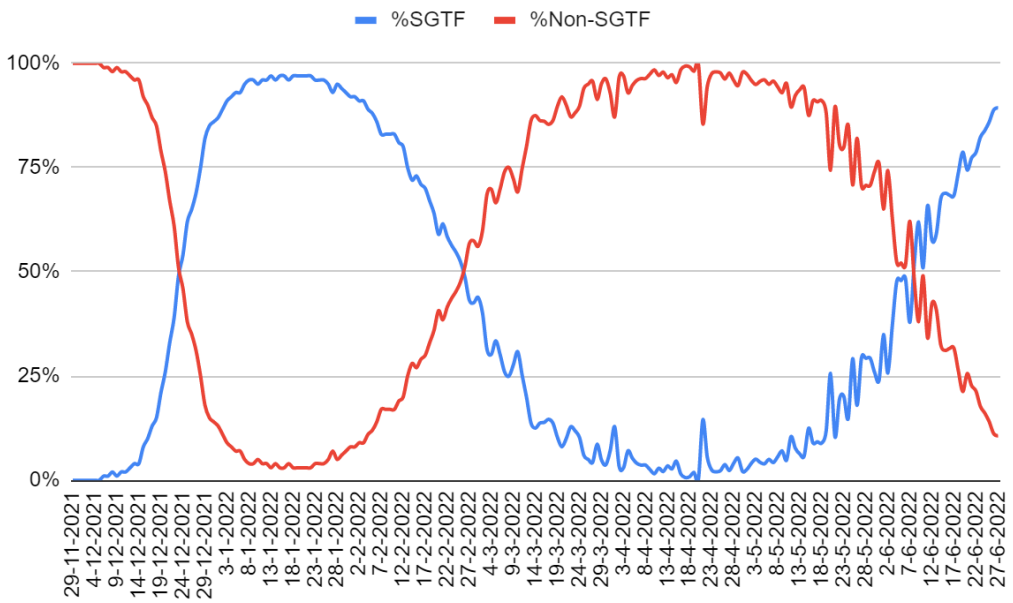


Figure 1: *S gene target failure (SGTF, in blue: BA.1 & BA.1.1, BA.4 and BA.5, and potentially BA.2 with 69/70 deletion) and others (red: currently considered predominantly BA.2) among positive samples reported by the federal platform laboratories.*

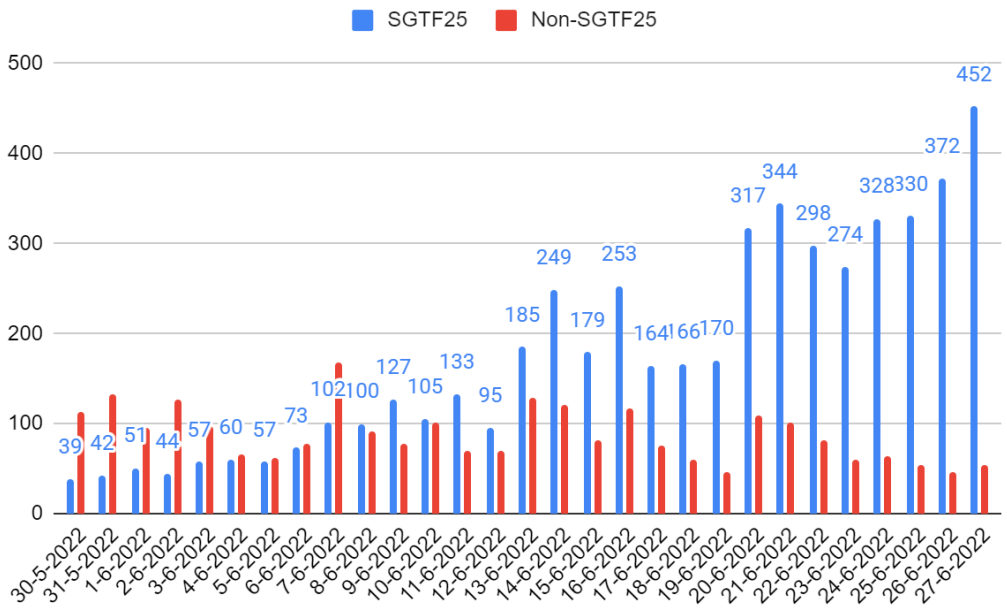


Figure 2: *S gene target failure (SGTF, in blue: BA.4 and BA.5, and potentially BA.2 with 69/70 deletion) and others (red: currently considered predominantly BA.2) among positive samples reported by the federal platform laboratories.*

2 Monitoring of Variants of Concern in Belgium

During the last two weeks of baseline surveillance - 13/06/2022 to 26/06/2022 - (994 sequences collected at this stage), BA.5 represented 67% (increasing trend), BA.2 represented 27% (decreasing trend) and BA.4 represented 6% (stable trend).

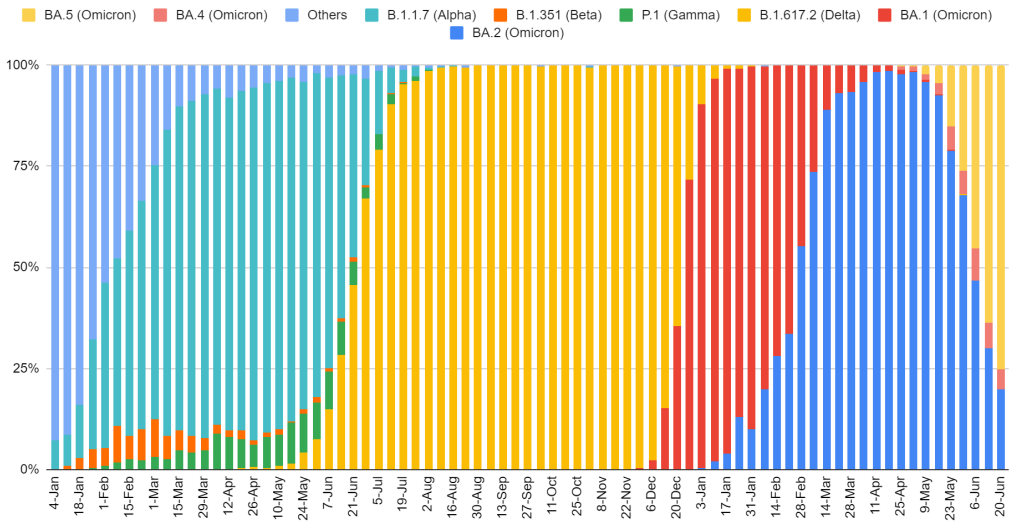


Figure 3: *Share of variants of concern per week in Belgium*

3 Implementation of a genomic surveillance program for antiviral resistance

It is expected that the increased usage of antiviral treatments will progressively lead to the emergence of drug resistance against antivirals.

Until now resistance to therapeutic monoclonal antibodies has been mainly driven by variant-specific antigenic properties associated with genetic polymorphisms in the Spike protein. A summary of the current knowledge in this regard is available on https://covdb.stanford.edu/susceptibility-data/table-mab-susc/ .

At this stage, there is less evidence of the emergence of resistance to antivirals, in particular Paxlovid (nirmatrelvir and ritonavir). Concern is mainly driven by *in vitro* observations of mutations in the protease gene leading to decreased susceptibility to the drug (3CLpro : L50F, E166A and L167F; reference https://www.biorxiv.org/content/10.1101/2022.06.07.495116v1), and observations of disease relapse (rebound) following Paxlovid treatment. Until now, these rebounds have not been associated with specific mutations, but a close monitoring is required as utilization of antivirals is expected to increase in the future.

For these reasons, the National Reference Center recommends that, in a first period of active surveillance, all patients eligible for antiviral therapy would get a systematic genotyping (baseline whole genome sequencing) before initiation of treatment. In case of treatment failure or rebound, a second strain should be referred for genotyping and comparative analysis. During this evaluation period, we ask laboratories to refer these samples to the reference laboratory in order to allow systematic analysis using constantly updated databases of resistance-associated mutations and to allow comparative analysis between sequential samples of patients.