KU LEUVEN

DEPARTMENT OF MICROBIOLOGY, IMMUNOLOGY AND TRANSPLANTATION

UZ LEUVEN | LABORATORIUMGENEESKUNDE

Genomic surveillance report

Update for Belgium, 31/05/2022

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Content

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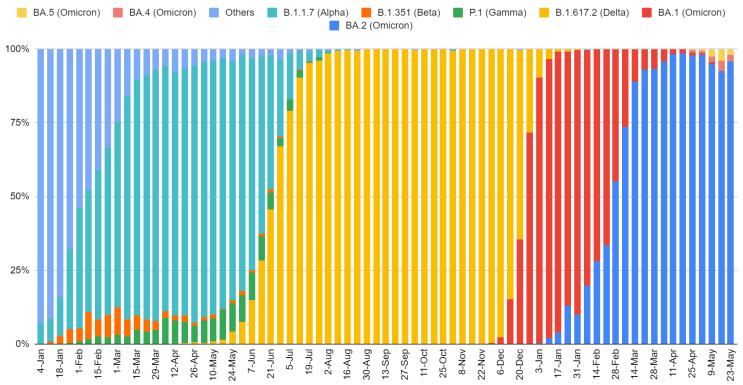
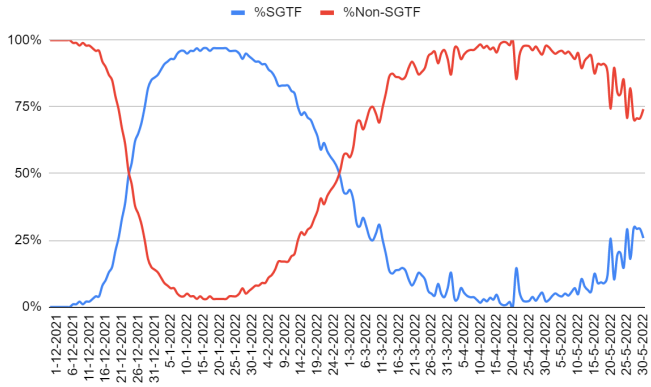
Executive summary

Omicron BA.2 remains the dominant lineage in Belgium (71-82% of new infections), although both BA.4 and BA.5 represent an increasing share of infections. This distribution of variants is concomitant with a declining incidence of COVID-19 (reported incidence during the last 14 days: 227 cases/100.000 habitants). The decreasing incidence associated with a lower testing intensity has an impact on the number of recent genomes available for genomic surveillance. Therefore, the latest estimates are based on SGTF reported by federal PCR testing laboratories.





Based on current genomic trends, it is expected that BA.4 and BA.5 will altogether become the dominant lineages in the coming weeks. This shift in viral populations will most probably occur during a low-incidence phase and should therefore have a contained impact on the general epidemiology in the short term.

Current literature suggests that these emerging variants will negatively impact the efficacy of vaccines and most monoclonal antibodies, similarly to what has been reported with previous Omicron sublineages.

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 71-82% of positive tests in the country (declining share week by week). SGTF samples are presumed to be predominantly Omicron BA.4 and BA.5, since Omicron BA.1 infections have not been detected for the last two weeks by the baseline surveillance effort conducted by the sequencing consortium..

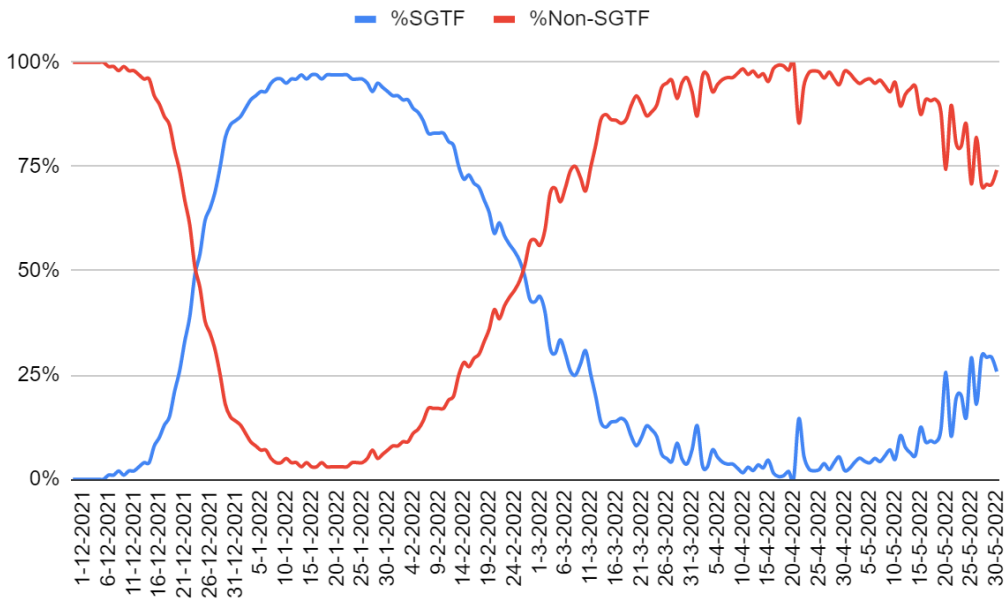


Figure 1: *S gene target failure (SGTF; blue: BA.1 & BA.1.1, BA.4 and BA.5, and potentially BA.2 with 69/70 deletion) and others (red: currently considered predominantly BA.2) among positive samples reported by the federal platform laboratories.*

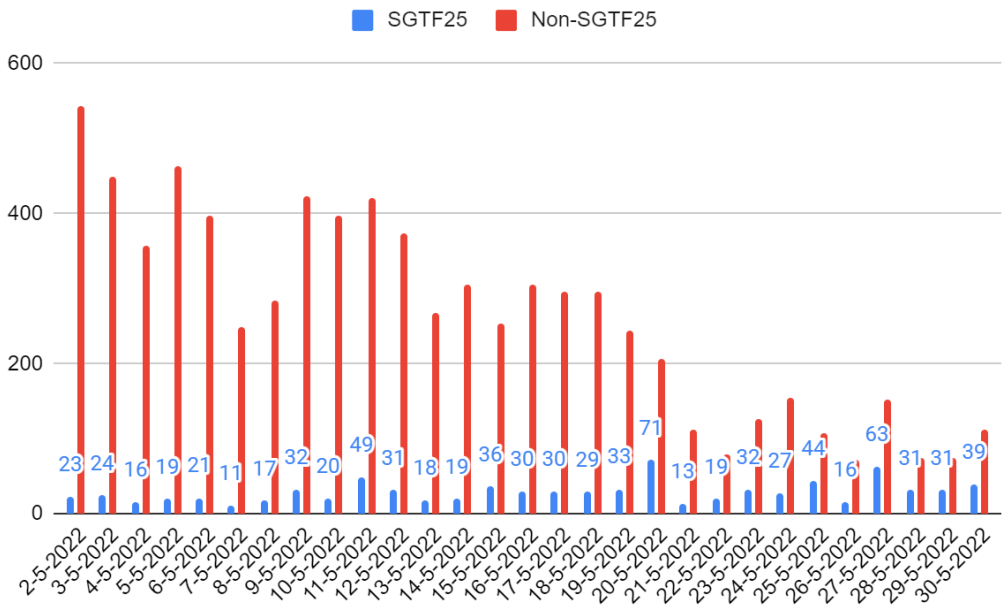


Figure 2: *S gene target failure (SGTF; BA.4 and BA.5, and potentially BA.2 with 69/70 deletion) and others (red: currently considered predominantly BA.2) among positive samples reported by the federal platform laboratories.*

2 Monitoring of Variants of Concern in Belgium

During the last two weeks of baseline surveillance - 16/05/2022 and 29/05/2022 - (277 sequences collected at this stage), No BA.1 and BA.1.1 strains were reported, while BA.2 represented 93.1% (↘) of the circulating strains (Figure 3). Overall, 86 BA.4 and 61 BA.5 genomes have been detected in Belgium, respectively representing 3.2% and 3.6% of the genomes (↗) for the last two weeks.

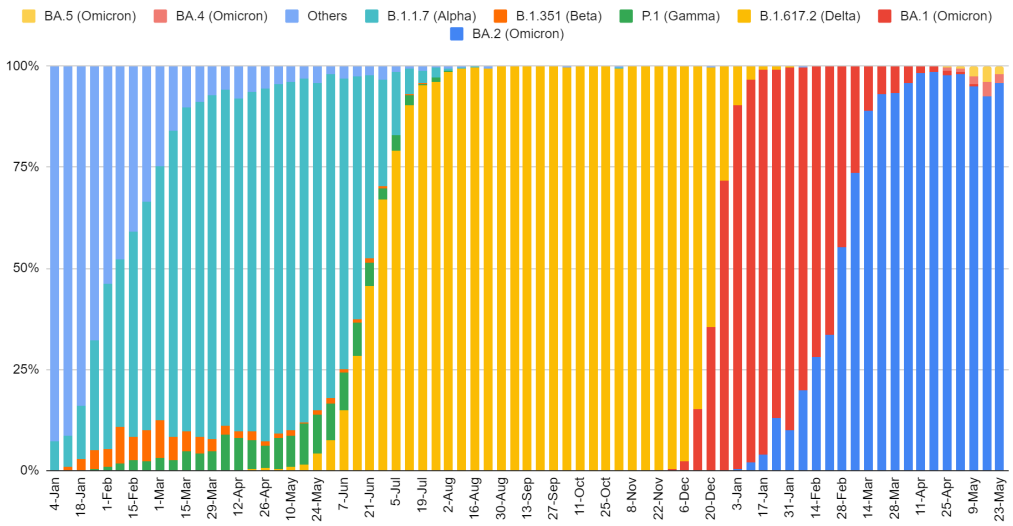


Figure 3: *Share of variants of concern per week in Belgium*