KU LEUVEN

DEPARTMENT OF MICROBIOLOGY, IMMUNOLOGY AND TRANSPLANTATION

UZ LEUVEN | LABORATORIUMGENEESKUNDE

Genomic surveillance report

Update for Belgium, 19/04/2022

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April 2022

Content

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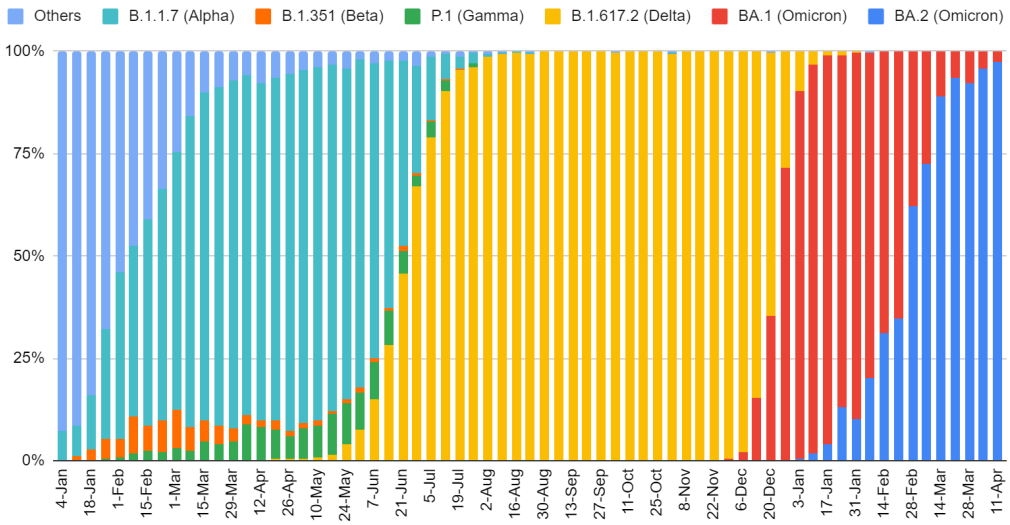
Previous reports are available online using this link.

Executive summary

The share of BA.2 has reached up to 99% of new infections diagnosed in Belgium, as suggested by the share of SGTF among positive qPCR results (data federal platform labs), and supported by sequencing-based surveillance (BA.2 was responsible for 96.0% (↗) of the infections diagnosed between 4/4/2022 and 17/4/2022 - 871 sequences analyzed at this stage in the context of baseline surveillance).
During this same period, BA.1 and BA.1.1 jointly represented 4.0% (↘) of the circulating strains. No Delta case was reported during the last four weeks.



Due to the current 'stable' epidemiological situation, a report will be written every two weeks instead of every week. The next report can therefore be expected on May 3rd, at least when no important changes in genomic surveillance are noted. In case of the emergence of a new variant or any other important change in the epidemiological or genomic context, additional reports will be written and published.

1 Epidemiological context and indicators related to diagnostic activities

The share of positive samples (Cq <25) presenting an S gene target failure (SGTF) reflects the share of BA.1 and BA.1.1 samples circulating in the country. Samples which are negative for this marker can be Delta or BA.2, although from genomic baseline surveillance we know that Delta is only sporadically detected for more than two months (one genome for the last month through the baseline surveillance initiative). Samples without SGTF (most likely to be BA.2 infections) have taken over, now representing up to 99% of positive samples diagnosed (Figure 1).

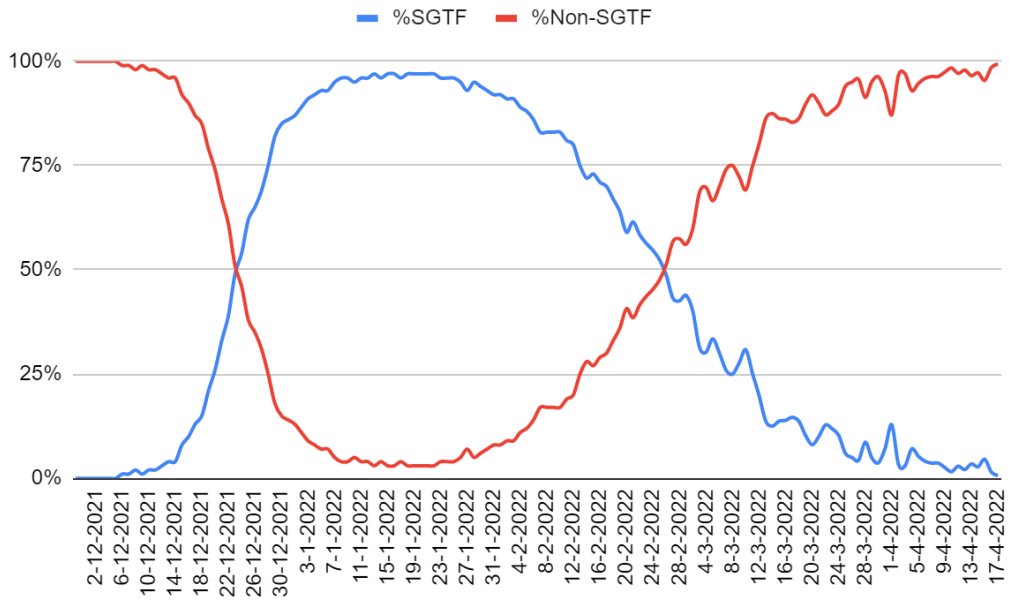


Figure 1: *S gene target failure (SGTF; blue: BA.1 & BA.1.1) and others (red: currently considered predominantly BA.2) among positive samples reported by the federal platform laboratories.*

As shown in Figure 2, the increasing share of non-SGTF positive PCR results was first associated with a steep decrease in SGTF samples (BA.1, BA.1.1, and BA.3). More recently, and despite de-intensification of PCR testing at national level, we observe a rise in the number of non-SGTF infections (BA.2).

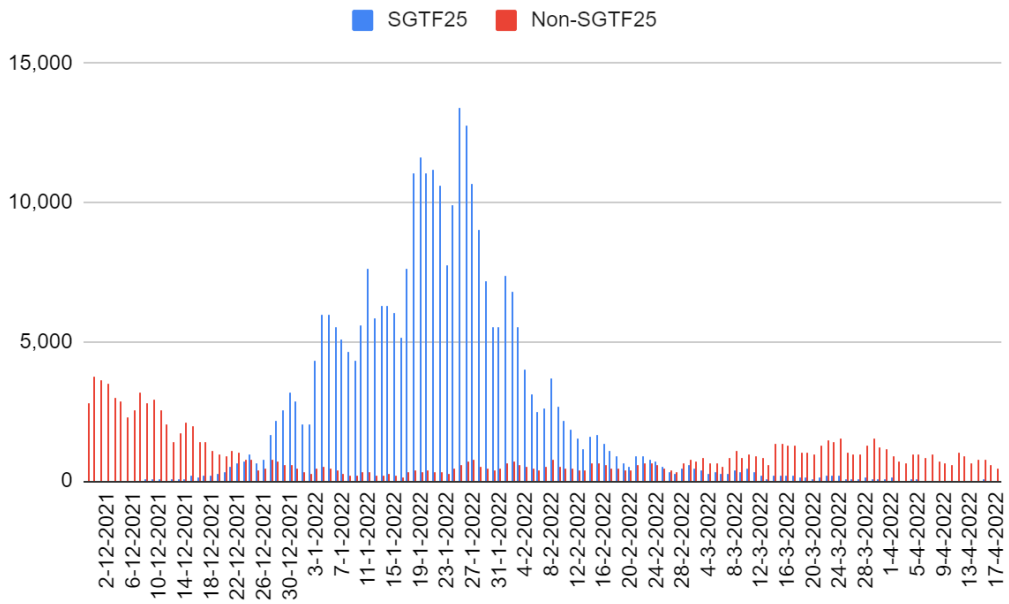


Figure 2: *Number of samples tested positive in the federal platform laboratories with S gene target failure (SGTF; blue) and without SGTF (non-SGTF; red). The absolute numbers are less representative of the actual epidemiology since a couple of weeks, as a result of a change in testing indications and a lower testing intensity.*

2 Monitoring of Variants of Concern in Belgium

During the last two weeks of baseline surveillance - 4/4/2022 and 17/4/2022 - (871 sequences collected at this stage), BA.1 and BA.1.1 jointly represented 4.0% (↘) of the circulating strains, while BA.2 represented 96.0% (↗) of the strains. No Delta sequence was reported for the last four weeks (Figure 3).

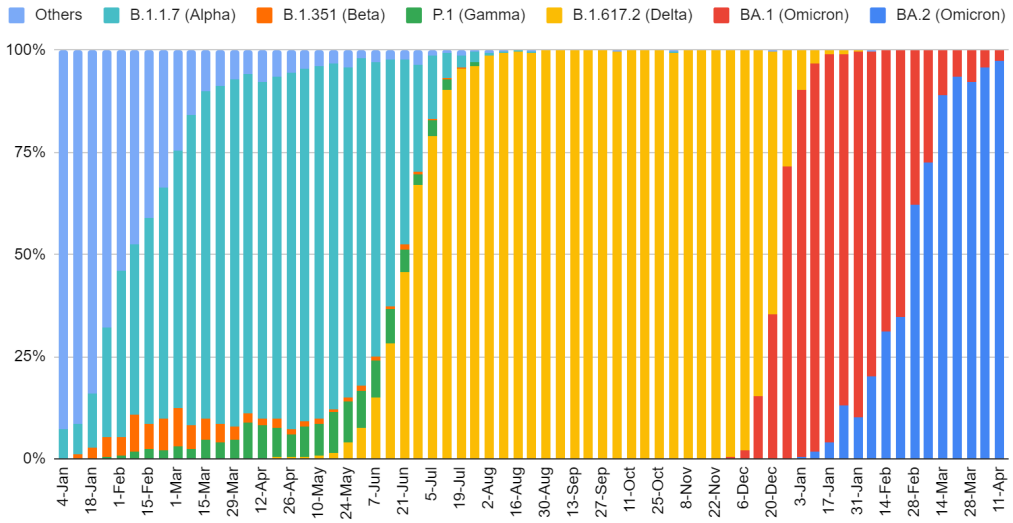


Figure 3: *Share of variants of concern per week in Belgium*

Recently, the variant of concern Omicron can be subdivided in five different sublineages, BA.1, BA.2, BA.3, BA.4 and BA.5. Both Pangolin designations BA.4 and BA.5 have been assigned since April 6, and have been first detected in South Africa, following their detection in other countries across the world (e.g. Botswana, Denmark, the United Kingdom, Portugal, Germany, the United States, …). Although the mutational profiles of these two new sublineages are somewhat concerning (characterized by the mutations L452R and F486V; and the 69-70 deletion in the spike protein (causing SGTF) - with mutation L452R so far being a signature mutation of the Delta variant), the number of genomes published for both BA.4 and BA.5 remains limited until today and so far there is no associated concerning epidemiological situation in South Africa (source: ECDC assessment of April 6). In Belgium, so far, two BA.4 genomes have been identified and have been published on GISAID (sampled on 29/3 and 7/4 respectively), while no BA.5 was detected.