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Genomic surveillance report

Update for Belgium, 01/03/2022

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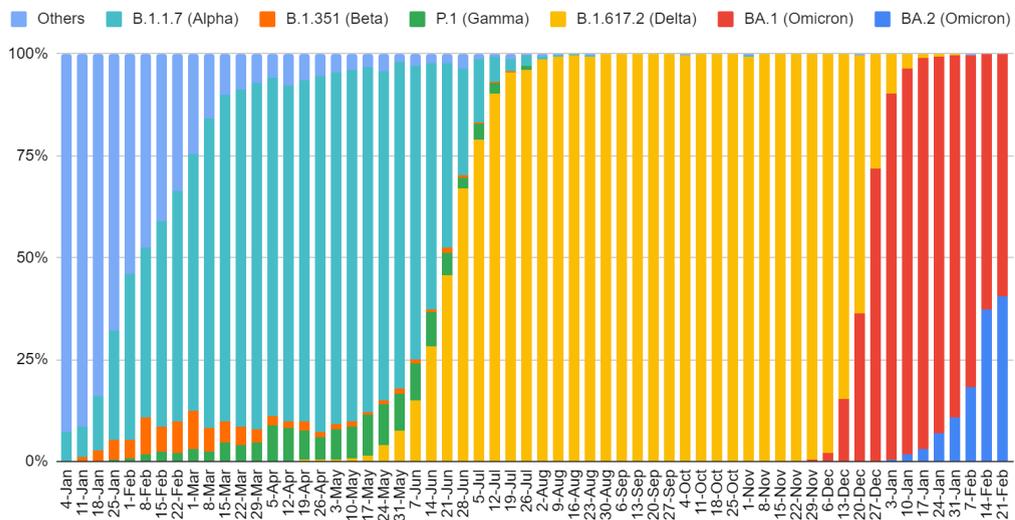
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Executive summary

The share of BA.2 has reached 50% of new cases diagnosed during the last weekend, as confirmed by the share of SGTF among positive qPCR results (data federal platform labs). This phenomenon is not yet visible through sequencing-based surveillance, a delay explained by the turn-around-time of this surveillance system.

Between 14/2/2022 and 27/2/2022 (1473 sequences collected at this stage), BA.1 and BA.1.1 jointly represented 62.3% (↘) of the circulating strains, while BA.2 represented 37.7% (↗) of the strains sequenced as part of the baseline surveillance. No Delta sequence was reported for the last two weeks.



This viral population replacement still seems at this stage to be linked to a sharp decrease in BA.1 infections rather than a tangible increase in the total number of BA.2 infections. The latter has become dominant and will continue to increase its share, but we observe no sign that this phenomenon will lead to an immediate new significant surge of infections.

1 Epidemiological context and indicators related to diagnostic activities

The recent decline in the reported number of infections has been associated with a continued decline in the positivity rate among diagnostic PCR tests performed at the Federal Platform Laboratories, from 50% more than one month ago to currently less than 30% (Figure 1). This positivity rate remains high and did not significantly decrease during the last week (30%). Of note, considering that a significant share of the samples referred for PCR aim to confirm a positive rapid antigen test, the positivity rate will remain artificially high in the future.

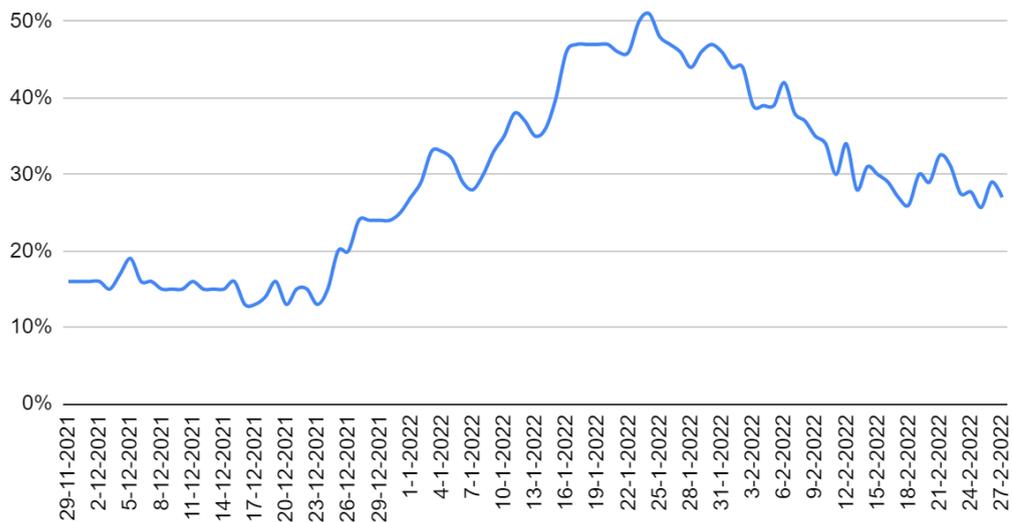


Figure 1: Positivity rate among the Federal Platform Laboratories.

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 the large majority can be attributed to BA.2 infections. Samples presenting SGTF currently represent 43% (compared to 59% last week) of positive samples diagnosed (Figure 2). Samples without SGTF (most likely considered to be BA.2 infections) have taken over, now representing 57% of positive samples diagnosed.

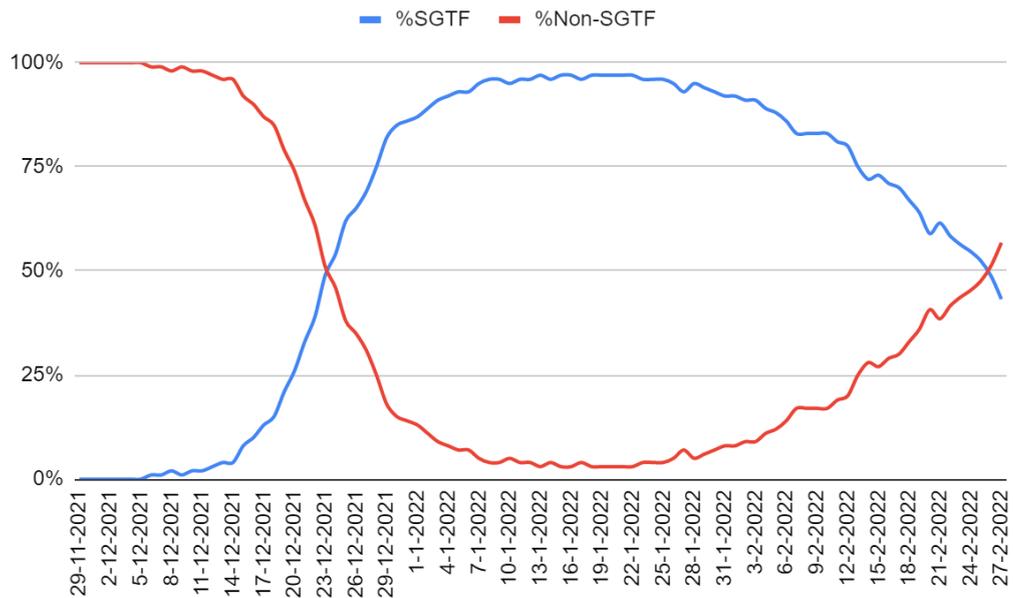


Figure 2: S Gene Target failure (blue: BA.1 & BA.1.1) and others (red: BA.2 and Delta) among positive samples reported by the Federal Platform laboratories.

As shown in Figure 3, the increasing share of non-SGTF positive PCR results continue to look to be due to a steep decrease of SGTF samples, rather than to an increase of non-SGTF samples. This implies that there is currently no marked absolute increase of BA.2 infections in the population and that the epidemiological situation should therefore not be profoundly modified (new wave of infections) despite BA.2 became dominant.

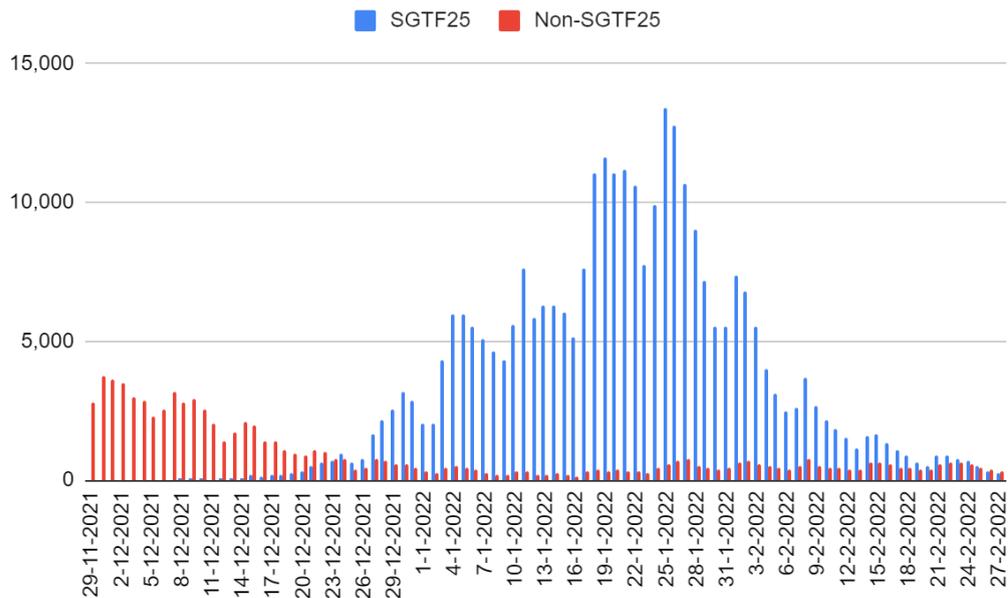


Figure 3: Number of samples tested positive in the Federal Platform Laboratories with S Gene target failure (SGTF, blue) and without SGTF (non-SGTF, red).

2 Monitoring of Variants of Concern in Belgium

During the last two weeks of surveillance (14/2/2022 - 27/2/2022), BA.1 and BA.1.1 jointly represented 62.3% of the circulating strains, while BA.2 represented 37.7%.

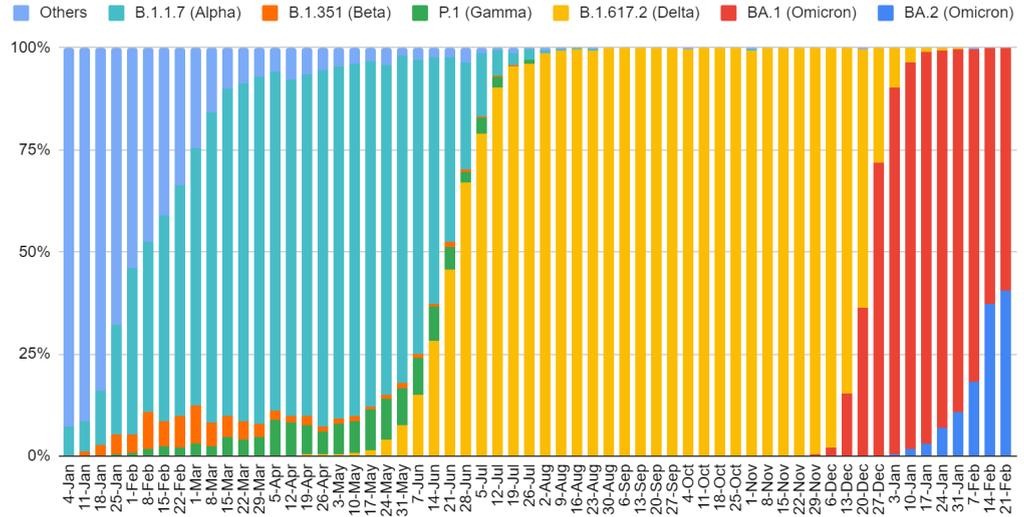


Figure 4: Share of variants of concern per week in Belgium