KU LEUVEN

DEPARTMENT OF MICROBIOLOGY, IMMUNOLOGY AND TRANSPLANTATION

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Genomic surveillance report

Update for Belgium, 08/03/2022

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March 2022

Content

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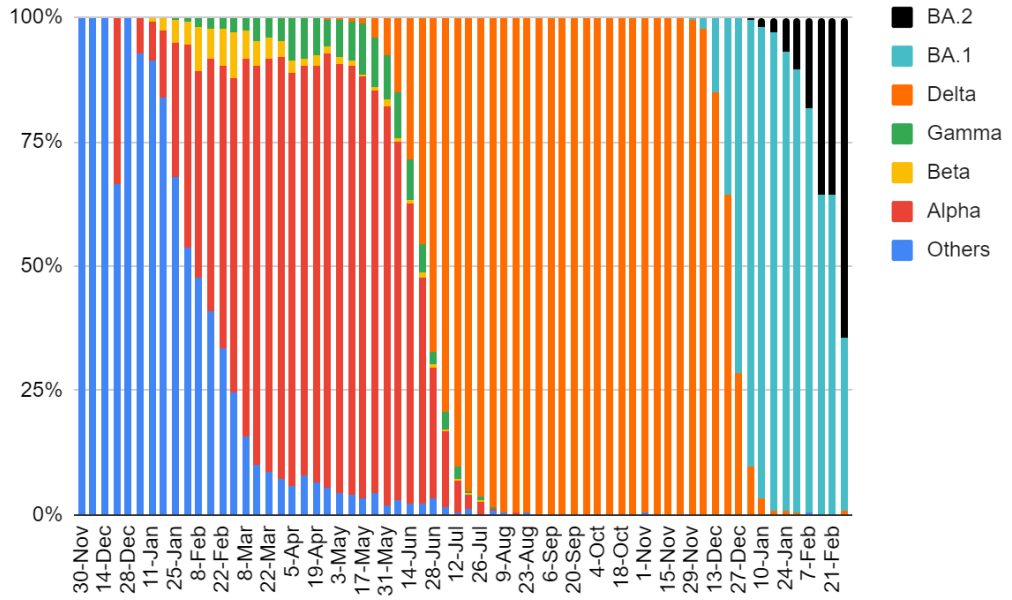
Executive summary

The share of BA.2 has reached 75% of new cases diagnosed during the last few days, 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 21/2/2022 and 6/3/2022 (494 sequences collected at this stage), BA.1 and BA.1.1 jointly represented 57.9% (↘) of the circulating strains, while BA.2 represented 41.9% (↗) of the strains sequenced as part of the baseline surveillance. Only one Delta sequence was reported during the last two weeks.



In this report, we identify the risks associated with reduced PCR testing strategies in the general population for the quality of the genomic surveillance in Belgium. We therefore suggest maintaining active qPCR testing in selected populations which are typically the first affected during a resurgence of infections or during the early spread of a new variant of concern. This strategy should allow maintaining the early warning function intrinsic to the functions of genomic surveillance.

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 the very large majority can be attributed to BA.2 infections since one month. Samples without SGTF (most likely considered to be BA.2 infections) have taken over, now representing 75% of positive samples diagnosed (Figure 1).

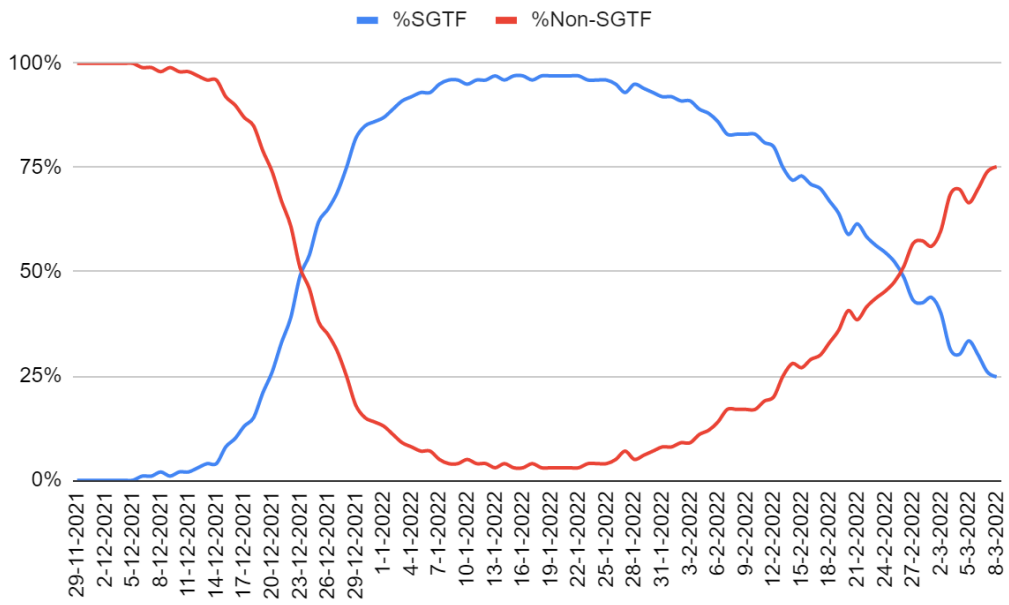


Figure 1: *S gene target failure (SGTF; blue: BA.1 & BA.1.1) and others (red: BA.2 and Delta) among positive samples reported by the federal platform laboratories.*

As shown in Figure 2, the increasing share of non-SGTF positive PCR results continues to appear to be due to a steep decrease in SGTF samples, rather than due to an increase of non-SGTF samples. This implies that there is currently no marked absolute increase of BA.2 infections. Nevertheless, BA.2 infections do not follow the decreasing pattern observed for BA.1, as they are currently stable. Therefore, the recent release of general disease control measures may lead to an increase of infections in the coming days and weeks. Nevertheless, accurately monitoring this situation will be difficult, as the general PCR testing indications have been reduced and no equivalent surveillance system has yet been put in place by the health authorities.

In this context, the National Reference Laboratory (NRL) has suggested maintaining sentinel PCR testing sites targeting a subset of university campuses and highly populated urban communities in order to allow a continued surveillance in populations that have previously been identified as being early affected during resurgence phases of the pandemic. Such surveillance systems would ensure early detection of negative trends despite reduced utilization of PCR testing during phases of low circulation of the virus.

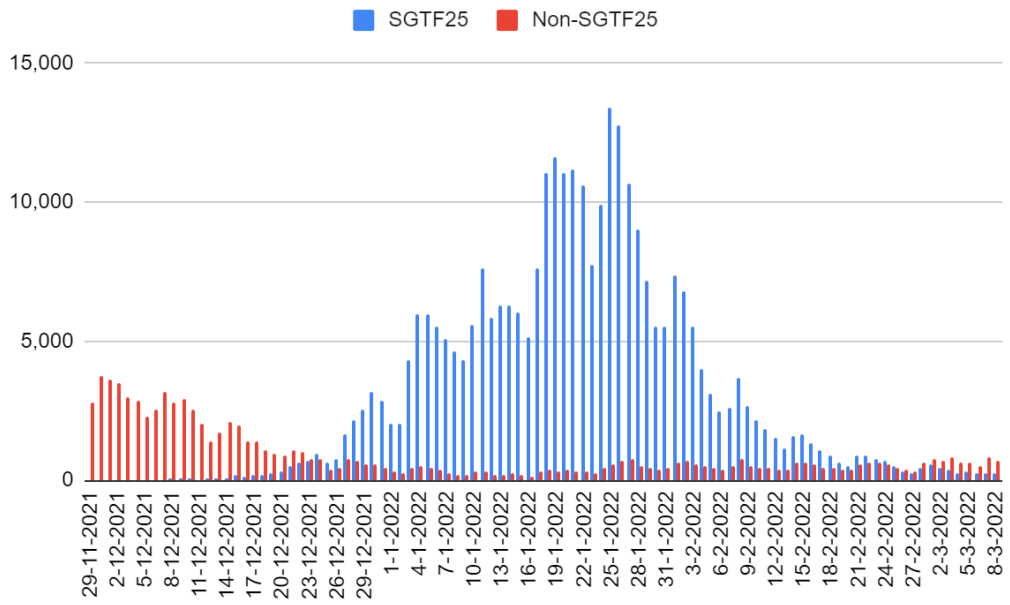


Figure 2: *Number of samples tested positive in the federal platform laboratories with S gene target failure (SGTF; blue) and without SGTF (non-SGTF; red).*

2 Monitoring of Variants of Concern in Belgium

During the last two weeks of baseline surveillance - 21/2/2022 and 7/3/2022 - (494 sequences collected at this stage), BA.1 and BA.1.1 jointly represented 57.9% (↘) of the circulating strains, while BA.2 represented 41.9% (↗) of the strains. Only one Delta sequence was reported for the last two weeks (Figure 3).

In the context of reduced viral circulation and political willingness to reduce the utilization of molecular diagnostic tests (PCR tests, a proportion of which are thereafter referred for sequencing), there is a significant risk that baseline surveillance in Belgium will be altered in the coming weeks, although continuity of surveillance remains critical including during phases of reduced viral circulation. To mitigate this risk, we suggest to refer positive samples for baseline genomic surveillance, with these samples originating from continued PCR screening offered to targeted populations identified above (selected university campuses and densely populated urban areas). These samples will complement the continued monitoring originating from hospitals, but they cannot be used as early indicators of emerging variants in the general population.

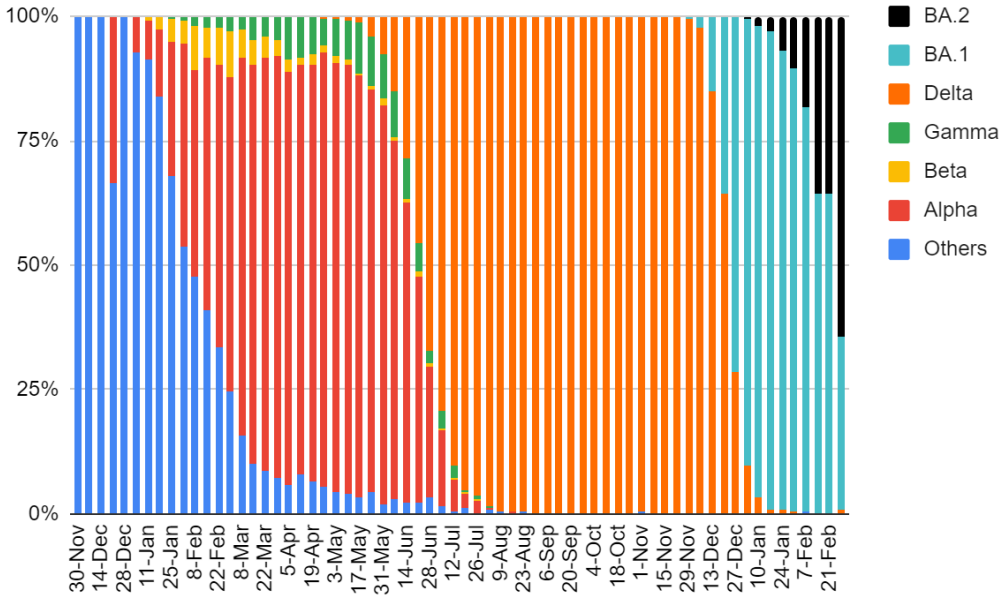


Figure 3: *Share of variants of concern per week in Belgium*