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Genomic surveillance report

Update for Belgium, 14/06/2022

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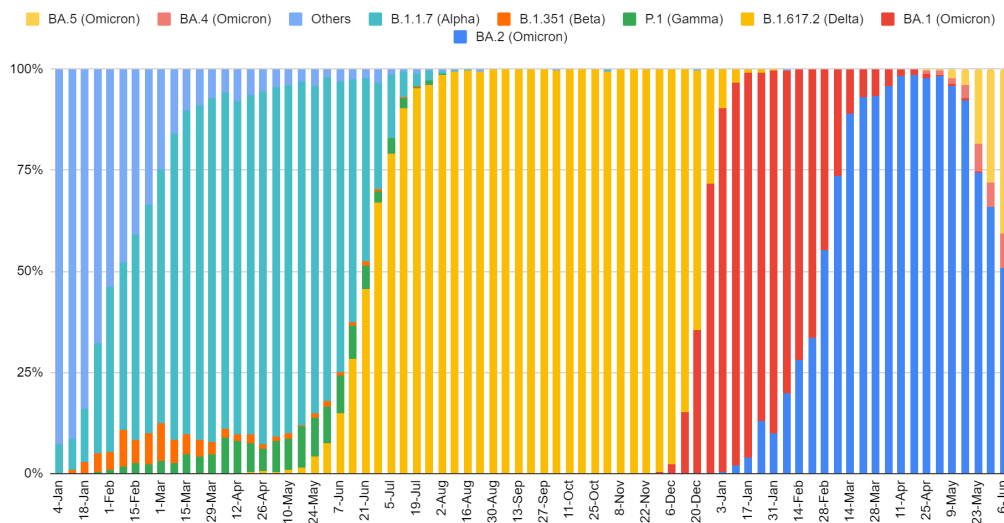
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Executive summary

From this week, Omicron BA.5 and BA.4 jointly represent the dominant lineages in Belgium. This shift is associated with an increase in the number of infections documented by the federal platform laboratories and a resurgence of the epidemic at national level ($R_t > 1$, increasing positivity rate).



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 SGTF.

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 34-49% 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 been rarely detected for the last month by the baseline surveillance effort conducted by the sequencing consortium.

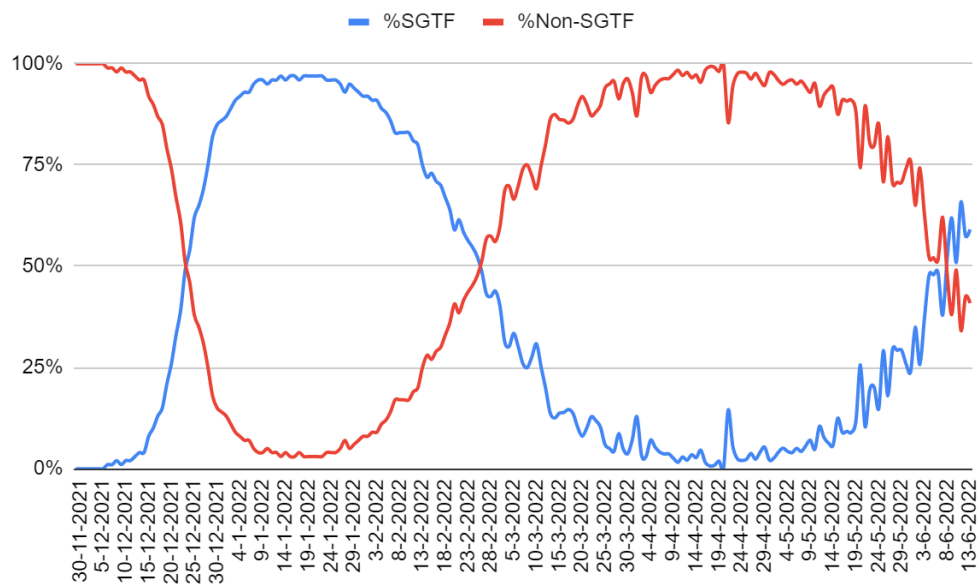


Figure 1: S gene target failure (SGTF, in blue: BA.1 & BA.1.1, BA.4 and BA.5, and potentially BA.2 with 69/70 deletion) and others (red: currently considered predominantly BA.2) among positive samples reported by the federal platform laboratories.

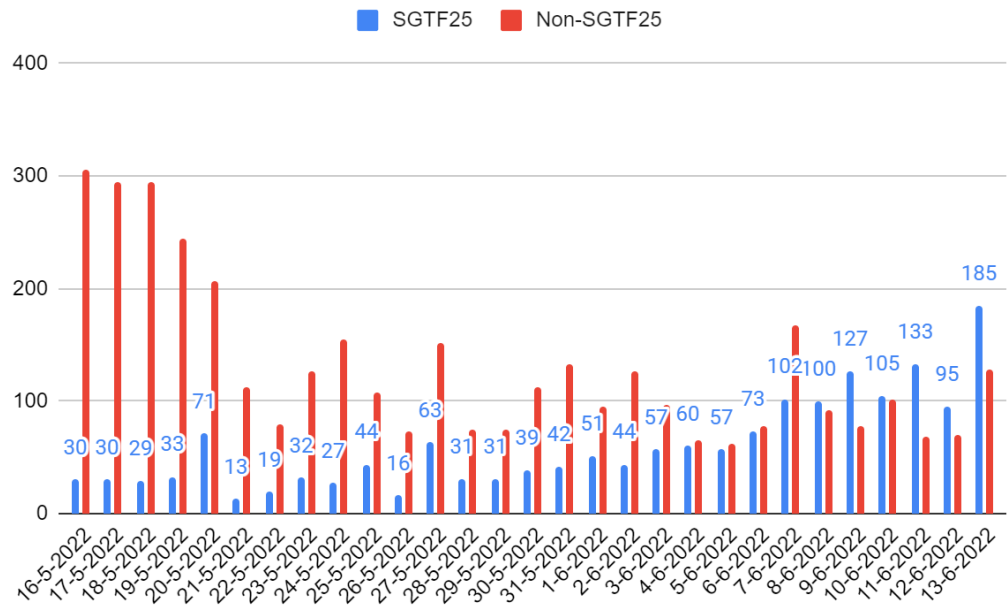


Figure 2: S gene target failure (SGTF, in blue: BA.4 and BA.5, and potentially BA.2 with 69/70 deletion) and others (red: currently considered predominantly BA.2) among positive samples reported by the federal platform laboratories.

2 Monitoring of Variants of Concern in Belgium

During the last two weeks of baseline surveillance - 30/05/2022 to 12/06/2022 - (546 sequences collected at this stage), one BA.1 strain was reported, while BA.2 represented 62.5% (significantly decreasing over the two weeks considered) of the circulating strains (Figure 3). Overall, 198 BA.4 and 387 BA.5 genomes have so far been detected in our country, respectively representing 6.4% (=) and 30.8% (↗) of the genomes for the last two weeks. Based on the latter, it seems that BA.5 has an advantage over BA.4 and will most likely become the dominant lineage in the upcoming weeks in Belgium.

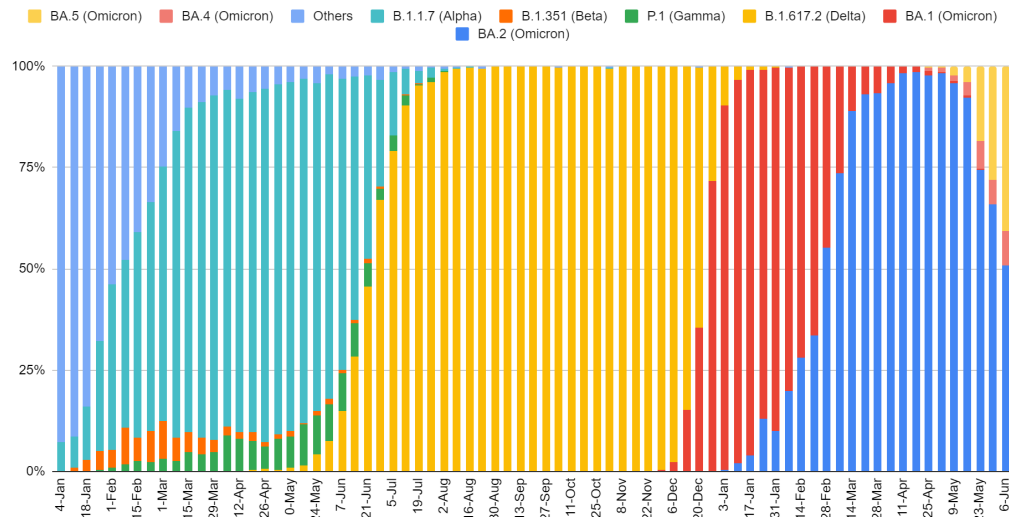


Figure 3: Share of variants of concern per week in Belgium