KU LEUVEN

Department of MICROBIOLOGY, IMMUNOLOGY and TRANSPLANTATION

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Genomic surveillance report

Update for Belgium, 12/07/2022

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Content

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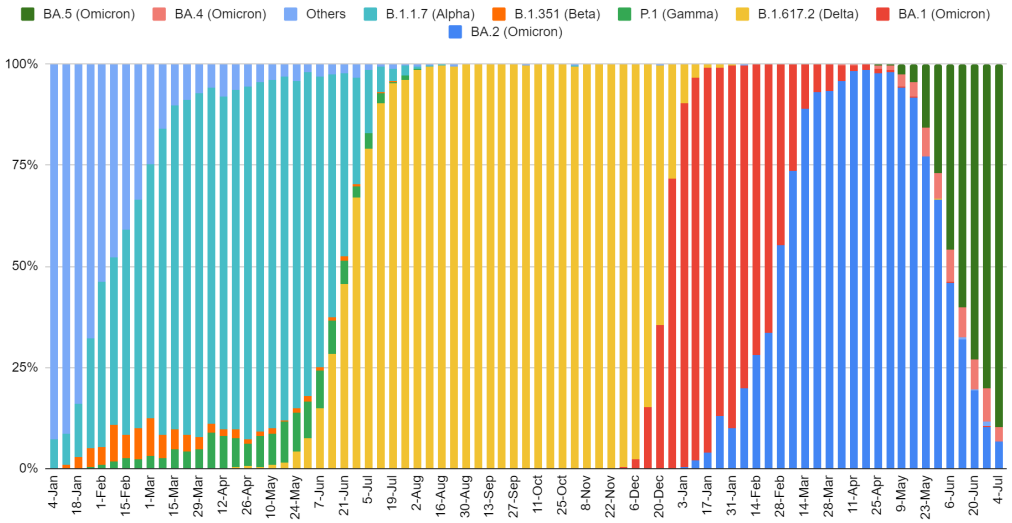
Previous reports are available online using this link.

Executive summary

Omicron BA.5 is now the dominant lineage in Belgium and now accounts for above 90% of the most recent infections. This recent shift is associated with an increase in the number of infections (Rt ~1.07), increasing positivity rate (36%) despite an increased testing intensity, and an increase in the number of hospital admissions, including ICU admissions.



In the meantime, international genomic surveillance highlighted the emergence of a new variant (BA.2.75) which seems to harbor the potential to outpace BA.5. These early observations mainly arise from India (where it is about to become the dominant lineage), but also from other continents including Europe. This emerging variant will be closely followed-up during the next weeks.

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 4-6% of positive tests in the country (declining share week by week). SGTF samples are presumed to be predominantly Omicron BA.5 and, to a lesser extent, BA.4. These samples represent 94-96% of the most recent samples analyzed (Figure 1).

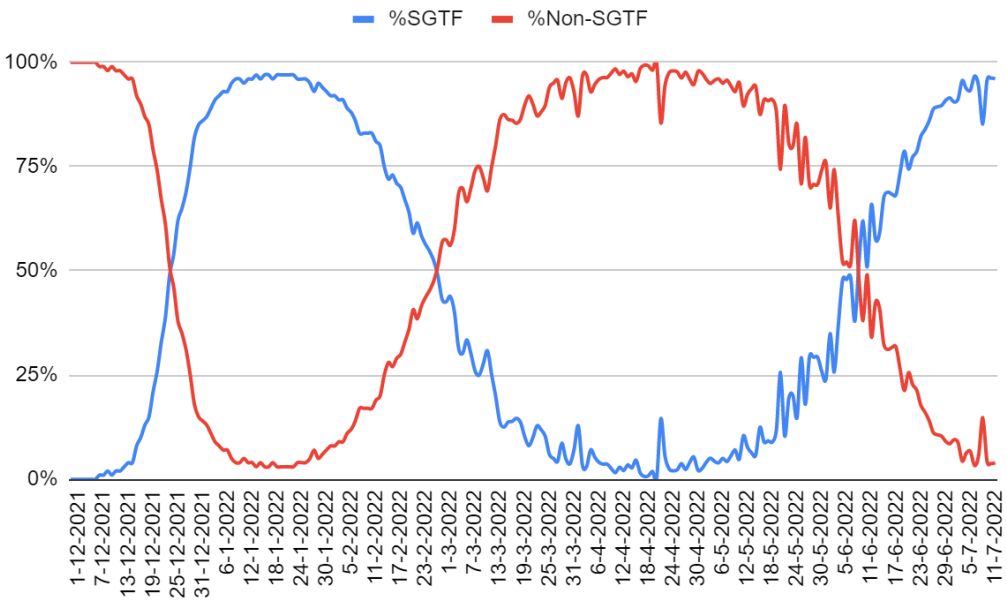


Figure 1: *S gene target failure (SGTF, in blue: BA.1 & BA.1.1, BA.4 and BA.5, and potentially BA.2 with 69/70 deletion) and others (red: currently considered predominantly BA.2) among positive samples reported by the federal platform laboratories.*

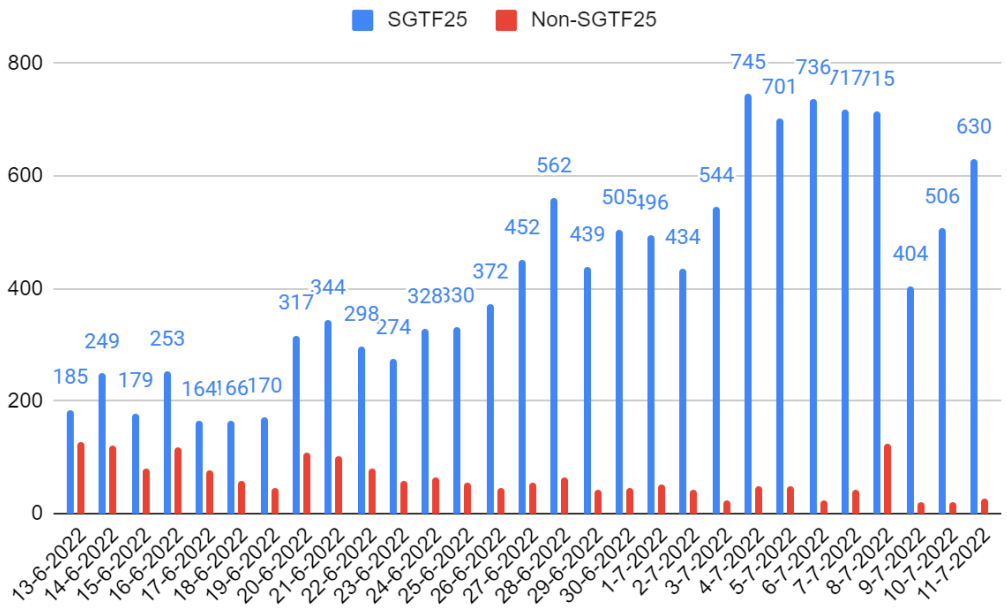


Figure 2: *S gene target failure (SGTF, in blue: BA.4 and BA.5, and potentially BA.2 with 69/70 deletion) and others (red: currently considered predominantly BA.2) among positive samples reported by the federal platform laboratories.*

2 Monitoring of Variants of Concern in Belgium

During the last two weeks of baseline surveillance - 27/06/2022 to 10/07/2022 - (768 sequences collected at this stage), BA.5 represented 81% (increasing trend), BA.2 represented 10% (decreasing trend) and BA.4 represented 8% (stable trend).

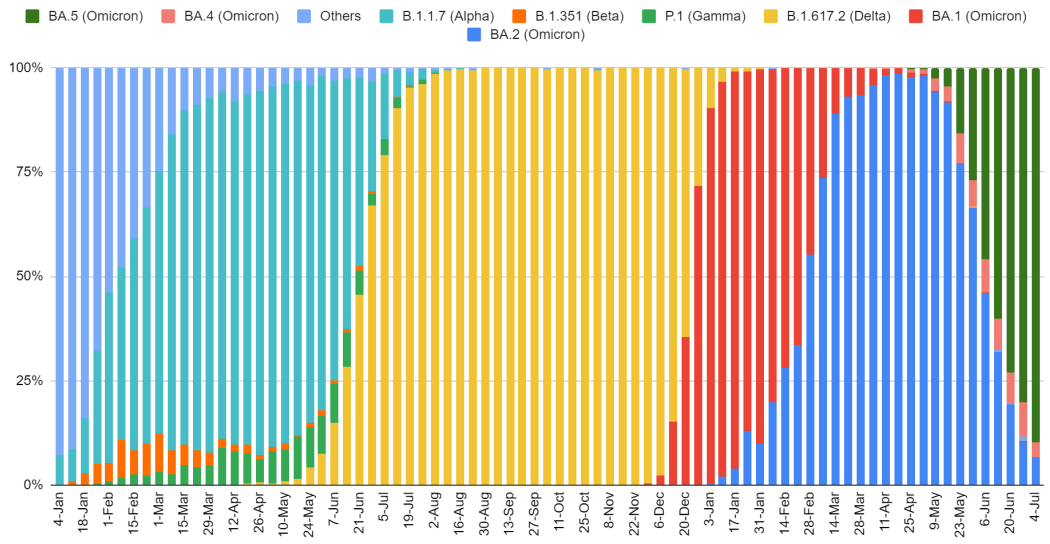


Figure 3: *Share of variants of concern per week in Belgium*

3 SARS-CoV-2 variant BA.2.75 ‘Centaurus’

A novel SARS-CoV-2 variant, BA.2.75, has been detected in India and has been reported to be rising quickly in prevalence. BA.2.75 is the latest in the line of Omicron variants and has a distinct set of spike mutations in addition to those found in BA.2, BA.4, BA.5, and other mutations outside the spike protein, indicating it was independently derived from the BA.2 clade.

The World Health Organization has already warned about BA.2.75 (https://www.who.int/activities/tracking-SARS-CoV-2-variants) and continues to monitor the variant as it spreads to more regions of the globe. While confirmed cases due to BA.2.75 are for now relatively low, numbers are expected to increase in the coming weeks. In India, BA.2.75 appears to have a very high growth advantage of 16% per day over all other BA.2 sub-lineages (https://science.thewire.in/the-sciences/ba-2-75-sub-variant-new-covid-19-wave/).

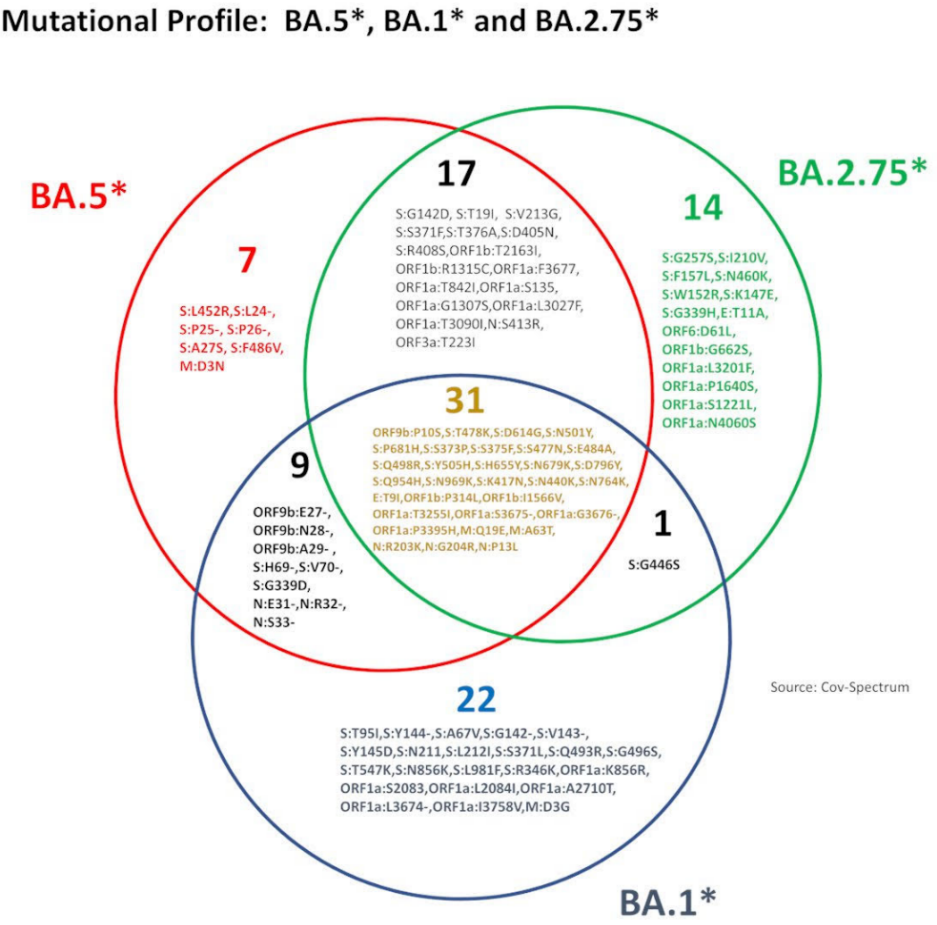


Figure 4. Mutation profiles of the BA.1, BA.5 and BA.2.75 sub-variants (https://science.thewire.in/the-sciences/ba-2-75-sub-variant-new-covid-19-wave/).

The BA.2.75 sub-variant has some notable mutations in the key spike protein: four in the N-terminal domain and four in the receptor-binding domain (see Figure 4). The lineage-defining signature mutations are spike K147E, W152R, G446S, and R493Q. The last two – G446S and R493Q – are more cause for concern. The G446S mutation can influence both immune escape and ACE2 binding. Given the data at hand, it is very likely that while this mutation could decrease the sub-variant's binding efficiency, it could contribute to significant immune escape. This in turn implies reinfections and breakthrough infections could drive the spread of BA.2.75 (https://science.thewire.in/the-sciences/ba-2-75-sub-variant-new-covid-19-wave/).

GISAID currently holds 157 BA.2.75 genomes. At the time of writing, BA.2.75 was not yet detected in Belgium, and only a single genome from The Netherlands was uploaded to GISAID. Of the 157 available genomes, 120 are from India, 14 from the United Kingdom, 6 from the USA and 4 from Canada. Other countries with fewer genomes are Indonesia, Japan, Nepal, Turkey, Australia, New Zealand and Martinique.