KU LEUVEN

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Genomic surveillance report

Update for Belgium, 26/04/2022

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Content

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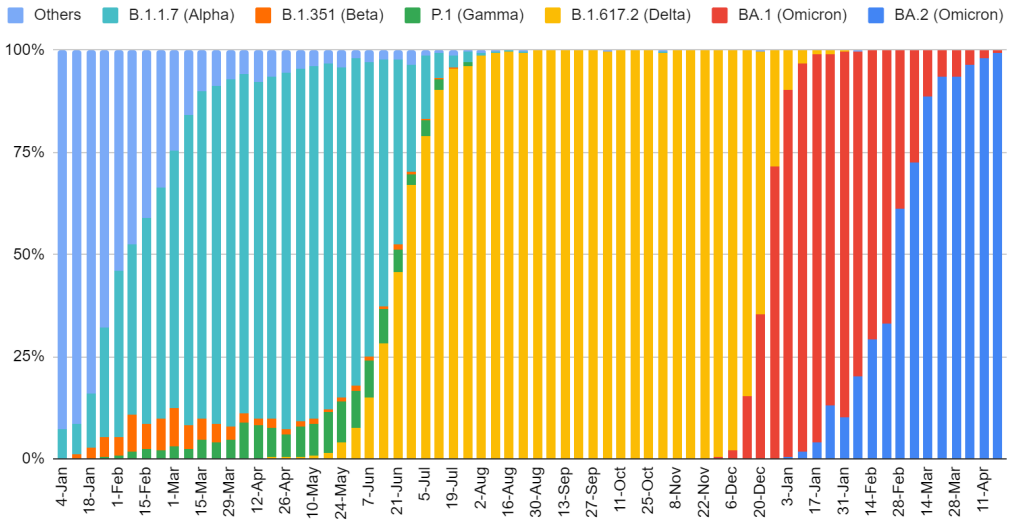
Executive summary

The share of BA.2 (including sublineages of BA.2) currently represents 98-99% of new infections diagnosed in Belgium, and this situation is currently associated with a high but stable circulation of the virus (reported incidence during the last 14 days: 816 cases/100.000 habitants).



In this report, we highlight the epidemiological situation in South-Africa, where the emergence of BA.4 and BA.5 is associated with a resurgence of infections. BA.4 has been identified regularly during the last weeks in Belgium and other European countries. These early cases may be considered as the early signs of a potential resurgence of infections in the coming weeks. Due to the recent changes in testing policies in Belgium, in particular a decrease in the utilization of the federal platform laboratories, it is challenging to estimate and monitor in real time the circulation of these new variants.

1 Epidemiological context and indicators related to diagnostic activities

Since the Alpha wave, the federal platform laboratories have been used for genomic surveillance purposes in addition to their diagnostic function to monitor in real life viral population replacement dynamics. We therefore used the share of positive samples (Cq <25) presenting or not an S gene target failure (SGTF) to reflect in real time rapidly evolving situations. This approach has been particularly efficient thanks to the very high number of samples referred to these laboratories and to the sequence of the different variants of concern which have emerged in Belgium: Alpha (SGTF), Delta (no SGTF), Omicron BA.1 & BA.1.1 (SGTF), Omicron BA.2 (no SGTG). The upcoming BA.4 and BA.5 present again the deletion 69/70 in the S gene and therefore are characterized by an SGFT.

Recently, the government decided to change the testing policies and decrease the activity of the federal platform laboratories. As a consequence, the precision of the genomic surveillance has been profoundly impacted and we insist on the fact that the numbers presented in Figure 1 have decreased in quality compared to previous months. Samples without SGTF (most likely to be BA.2 infections) currently represent up to 99% of positive samples tested in the federal platform laboratories.

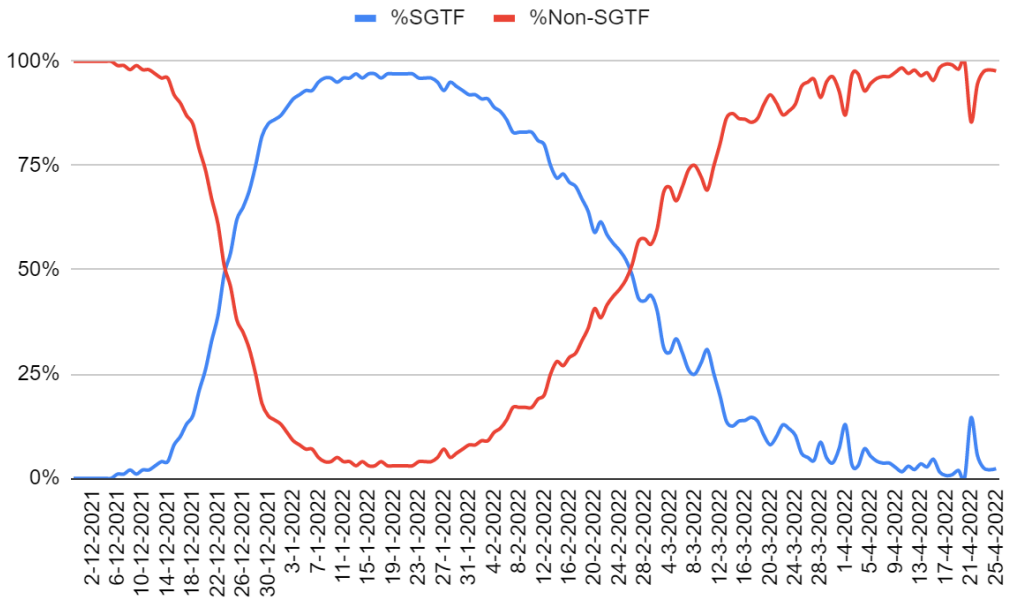


Figure 1: *S gene target failure (SGTF; blue: BA.1 & BA.1.1) and others (red: currently considered predominantly BA.2) among positive samples reported by the federal platform laboratories.*

Figure 2 highlights the total number of positive cases tested in the federal platform laboratories based on the presence or absence of SGTF. The low number of cases notified by these laboratories during the last weeks are due to the combination of lower viral circulation, lowered PCR testing intensity and lower referral of samples to federal platform laboratories. BA.4 has been identified in Belgium since 29/3/2022 and this lineage presents an SGTF.

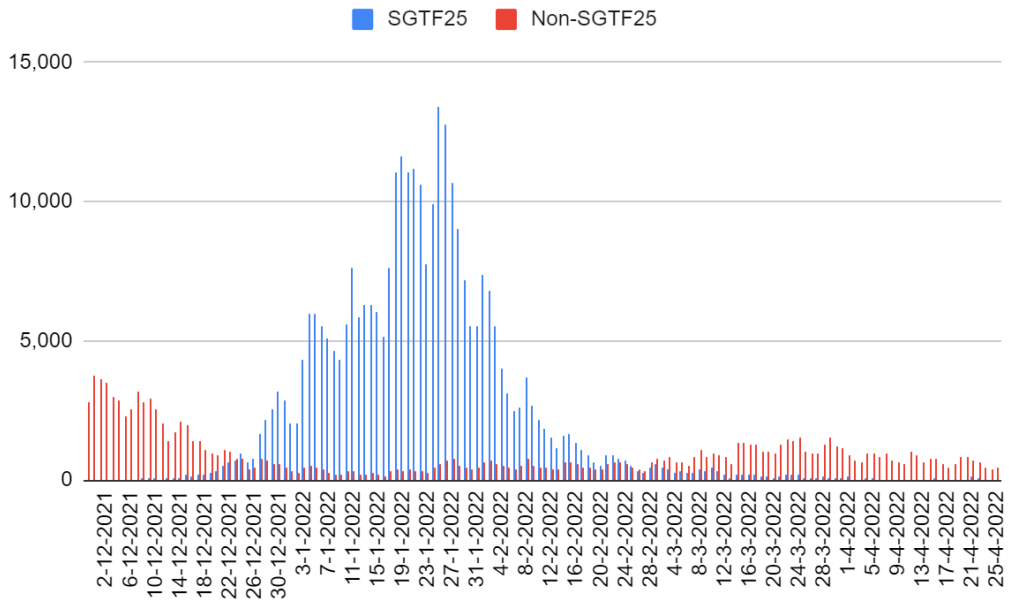


Figure 2: *Number of samples tested positive in the federal platform laboratories with S gene target failure (SGTF; blue) and without SGTF (non-SGTF; red). The absolute numbers are less representative of the actual epidemiology since a couple of weeks, as a result of a change in testing indications and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

2 Monitoring of Variants of Concern in Belgium

During the last two weeks of baseline surveillance - 11/4/2022 and 24/4/2022 - (714 sequences collected at this stage), BA.1 and BA.1.1 jointly represented 1.8% (↘) of the circulating strains, while BA.2 represented 98.2% (↗) of the strains. No Delta sequence was reported for the last five weeks (Figure 3).

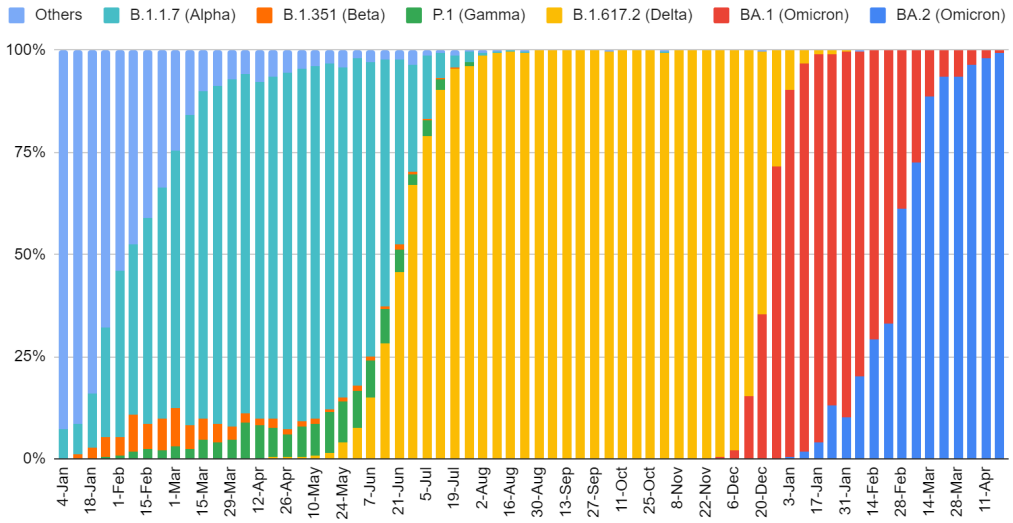


Figure 3: *Share of variants of concern per week in Belgium*

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, …). 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 - with mutation L452R so far being a signature mutation of the Delta variant). Although there is no scientific evidence at this stage that these new variants will give rise to increased transmissibility, post-vaccination immune escape or resistance to therapeutic monoclonal antibodies, these possibilities need to be actively and urgently investigated.

At this stage, the number of genomes published for both BA.4 and BA.5 remains limited (222 genomes reported worldwide, among which 184 from South Africa). The epidemiological situation in South Africa however raises concerns, as the emergence of these two variants is currently associated with a rise of infections (Figure 4).

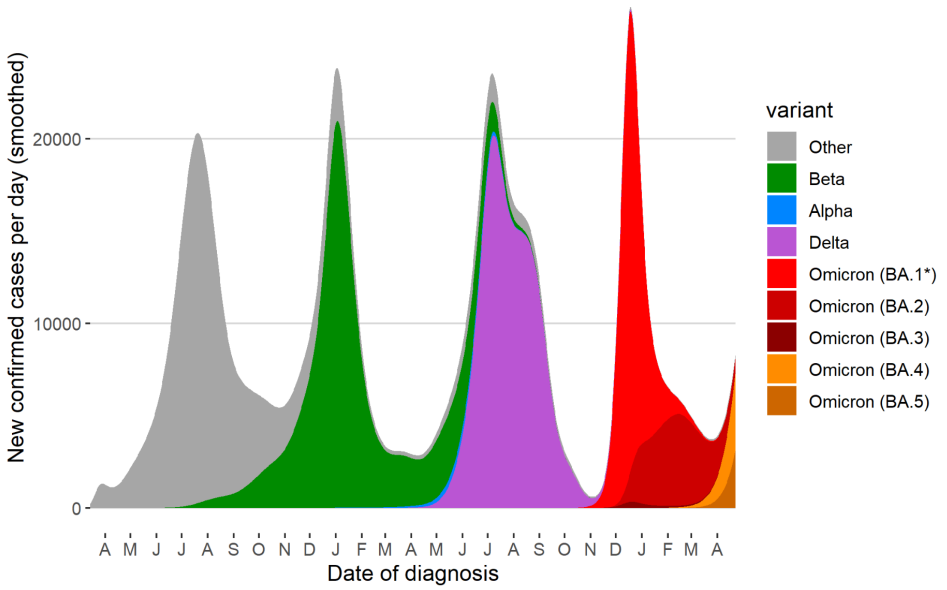


Figure 4: *New confirmed SARS-COV-2 cases per day by variant in South Africa (corrected for weekday effect and variable testing intensity). Source: Tom Wenseleers (KU Leuven)*

Considering these early signals in South Africa and the fact that these variants have already been reported by 10 countries in 4 continents (source: outbreak.info), we cannot exclude at this stage that a new global surge of infections will occur in the coming weeks.

3 Relationship between the initial Belgian BA.4 cases

In Belgium, so far, 8 BA.4 genomes have been identified and have been published on GISAID, and no BA.5 have yet been reported by our genomic surveillance consortium. Note that the classification of some of these genomes has changed in recent days (see below). On Monday April 25th we performed a phylogenetic analysis of the - at the time - 4 publicly available BA.4 cases in Belgium (Figure 5).

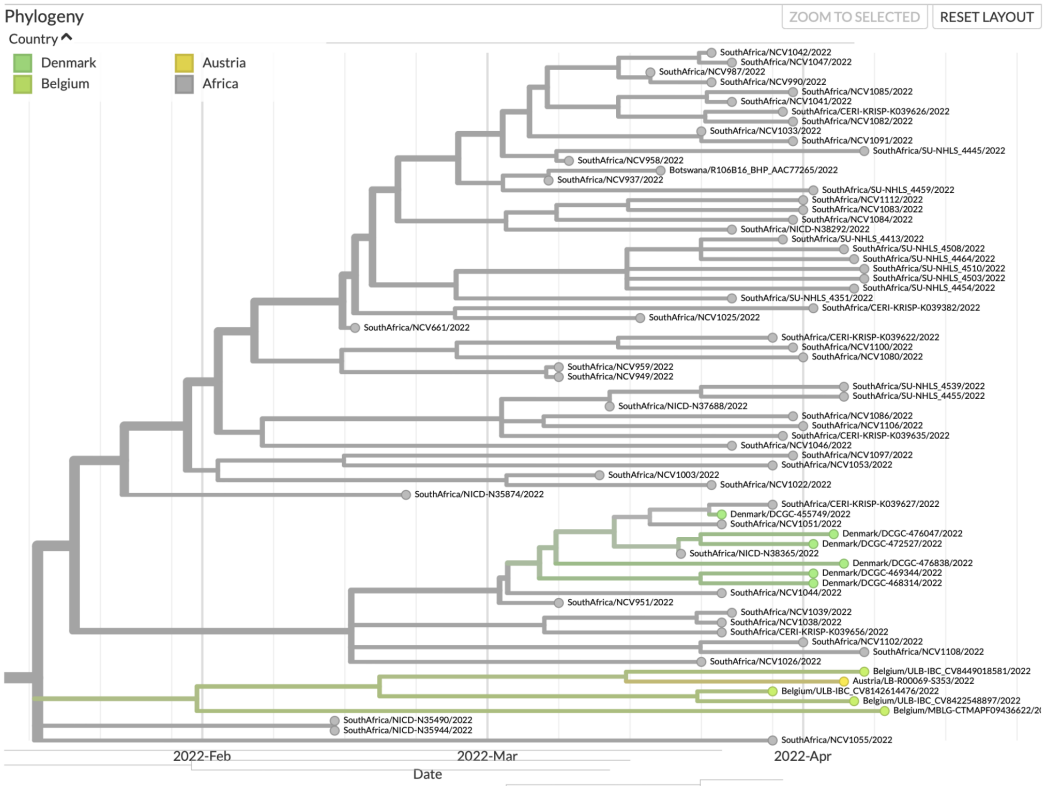


Figure 5: *The initial 4 Belgian BA.4 cases are shown to cluster together along with an Austrian BA.4 case. Note that 2 of these Belgian BA.4 have in the meantime been re-classified as BA.2.* lineages.*

Note that since this analysis was performed, the Belgium/ULB-IBC_CV8422548897/2022 (EPI_ISL_12086829) case has been re-classified as BA.2 whereas the Belgium/MBLG-CTMAPF09436622/2022 has been re-classified as BA.2.16. We are currently updating our analysis with the 8 Belgian BA.4 genomes listed on GISAID.

The multifurcation (left-hand side of Figure 5) from which these Belgian infection stem makes it difficult to determine where these infections have originated.

Of the 8 Belgian BA.4 cases currently on GISAID, 5 appeared in the Brussels Capital Region (2 from Vorst /Forest, 2 from Brussels and 1 from Schaarbeek), 1 from Limburg, 1 from Hainaut and 1 from Brabant Wallon. The sampling dates are the following: March 29, April 7, April 9, April 10, April 11, April 12 (2 genomes) and April 14, clearly showing an upsurge in BA.4 cases in the second week of April. Our follow-up phylogenetic analysis will hopefully shed more light on whether and how these BA.4 infections are related to one another.