KU LEUVEN

DEPARTMENT OF MICROBIOLOGY, IMMUNOLOGY AND TRANSPLANTATION

UZ LEUVEN | LABORATORIUMGENEESKUNDE

Genomic surveillance report

Update for Belgium, 17/05/2022

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Content

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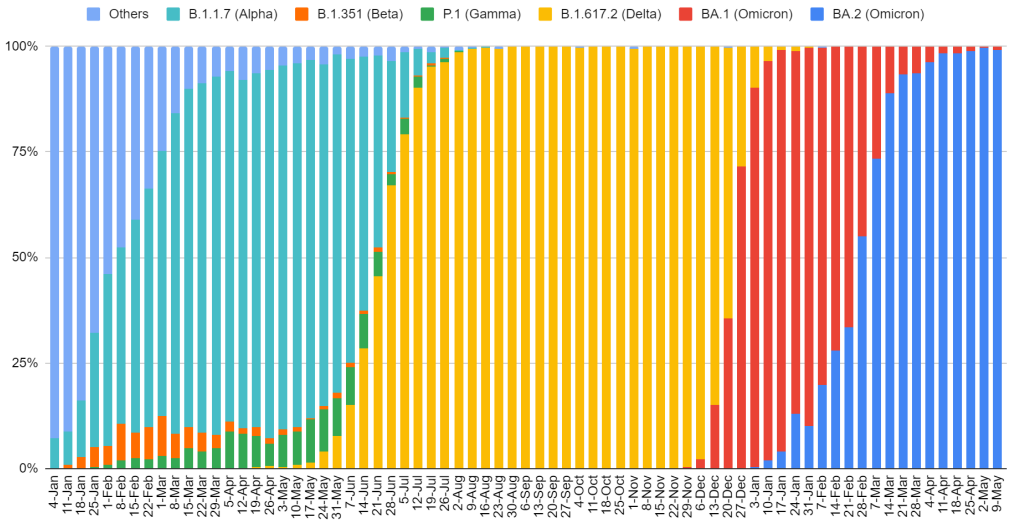
Executive summary

The Omicron BA.2 lineage currently represents 88-94% of new infections diagnosed in Belgium, and this situation is currently associated with a declining circulation of the virus (reported incidence during the last 14 days: 493 cases/100.000 habitants).



Worldwide, using the international database GISAID, the number of reported BA.4 (1633, including 40 from Belgium), BA.5 (1130, including 13 cases detected in Belgium) and BA.2.12.1 (25688, including 12 cases detected in Belgium) cases continue to increase. BA.4 and BA.5 have been recognized as variants of concern by the WHO.

At this stage, there is no indication that these emerging variants will lead to more severe disease compared to other Omicron sublineages but, as it has been the case with previous variants, the efficacy of monoclonal antibodies used for the treatment of high risk patients may be affected. The National Reference Center has been able to culture BA.4 and BA.5 isolates and will shortly initiate a series of studies that should allow better describing the eventual intrinsic resistance mechanisms and immune escape characteristics of these variants.

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 up to 88-94% of positive tests in the country. SGTF samples are presumed to be mainly Omicron BA.4 and BA.5, although Omicron BA.1 infections are still sporadically detected.

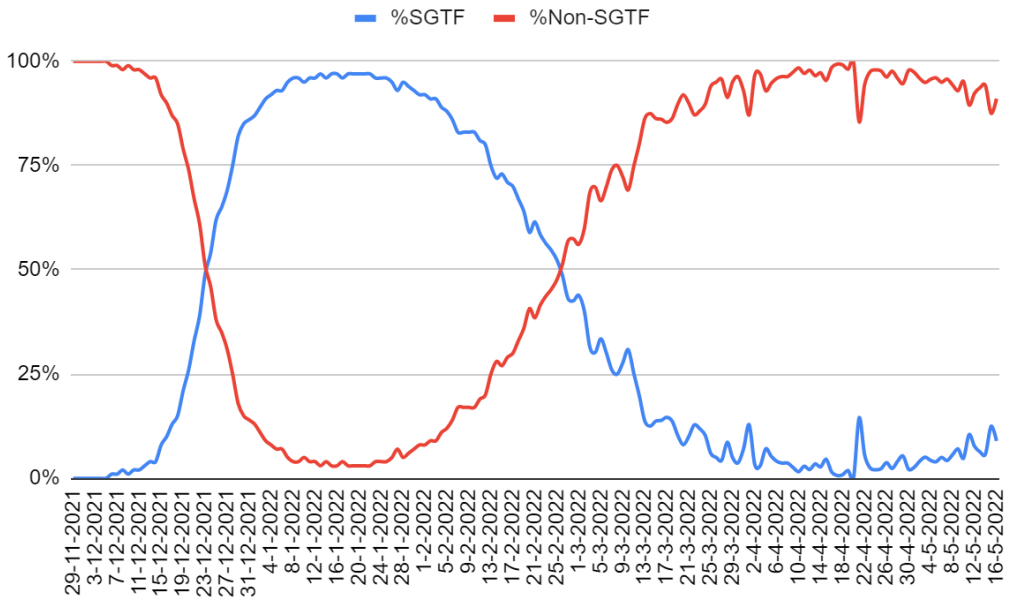


Figure 1: *S gene target failure (SGTF; blue: BA.1 & BA.1.1, BA.4 and BA.5, and potentially BA.2 with 69/70 deletion) and others (red: currently considered predominantly BA.2) among positive samples reported by the federal platform laboratories.*

2 Monitoring of Variants of Concern in Belgium

During the last two weeks of baseline surveillance - 02/05/2022 and 15/05/2022 - (1273 sequences collected at this stage), BA.1 and BA.1.1 jointly represented 0.4% (↘) of the circulating strains, while BA.2 represented 97.7% (↘) of the strains (Figure 3). Overall, 40 BA.4 and 13 BA.5 genomes have been detected in Belgium; a separate graph visualizes the progress of the cases over time (Figure 4).

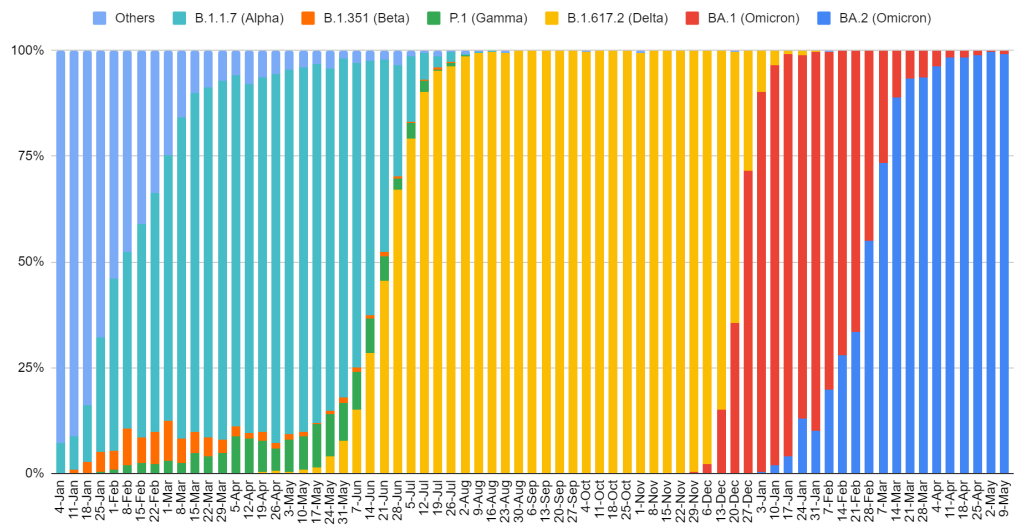


Figure 2: *Share of variants of concern per week in Belgium*

Figure 3 highlights the increasing share of BA.4, BA.5 and BA.2.12.1 Belgian genomes uploaded on GISAID during the last months. BA.4 has been identified in Belgium since 29/03/2022 (so far 40 genomes), and BA.5 since 24/04/2022 (so far 13 cases). Although numbers remain limited at this stage, this share of these new VOCs is increasing rapidly and these will probably become dominant in the coming weeks.

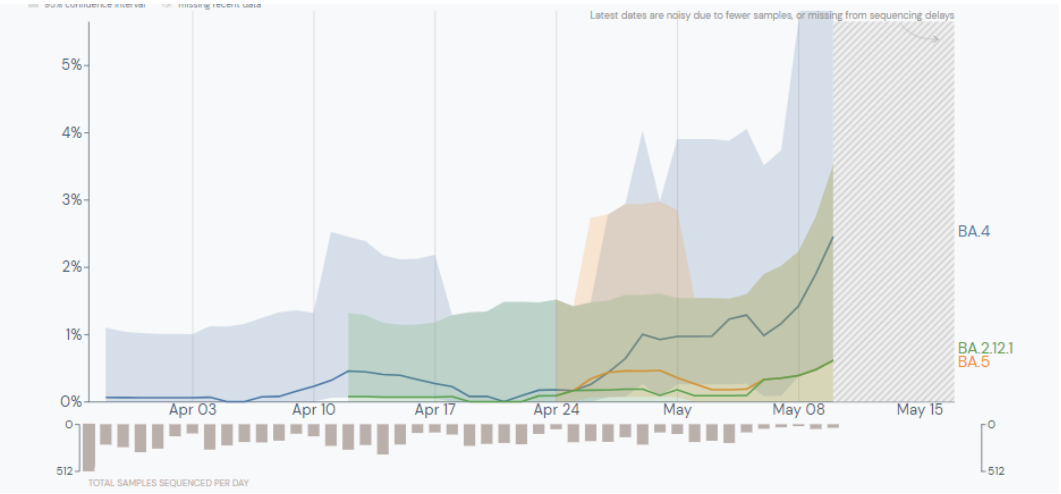


Figure 3: *Share of infections associated with BA.4, BA.5 and BA.2.12.1 during the last months in Belgium (outbreak.info)*

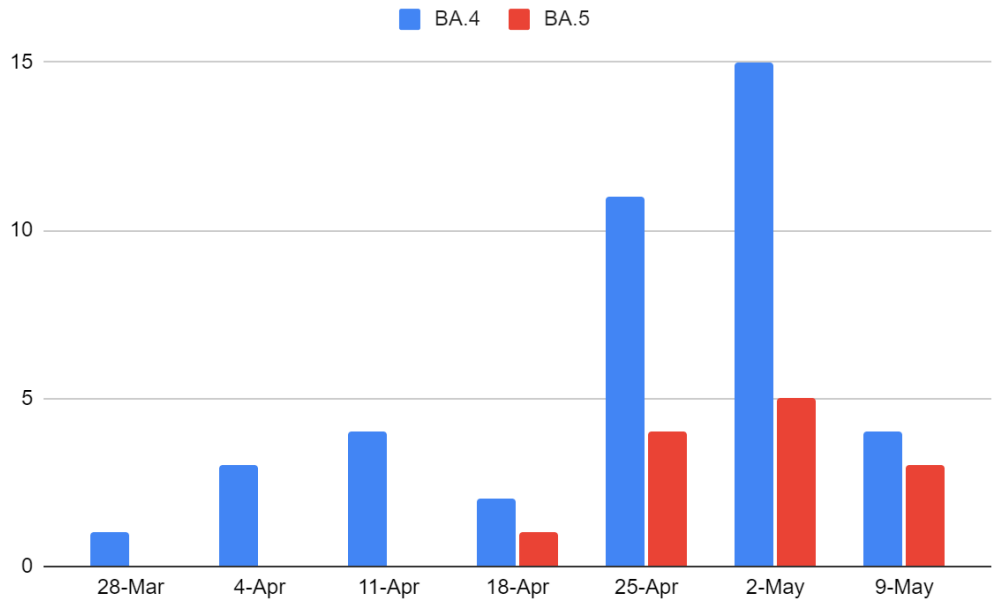


Figure 4: *Number of BA.4 and BA.5 cases reported on GISAID in Belgium per week. The first detection of BA.4 in Belgium dates from 29/03/2022 (in blue), while the first BA.5 case was sequenced on 24/04/2022 (in red). In total, 40 BA.4 and 13 BA.5 genomes from Belgium have been deposited to GISAID, with for both lineages the most recent infections dating from May 12th, stressing the close follow-up of infections and sequences by the national genomic surveillance consortium. For the last week (May 9 to May 15), the number of cases is lower due to the longer turn-around-time for sequencing compared to PCR, causing a delay of about one week. We expect to see the increasing trend of BA.4 and BA.5 lineages to continue during the next weeks.*

3 Relationship between and possible origins of the (initial) Belgian BA.4 and BA.5 cases

In Belgium, so far, 40 BA.4 genomes and 13 BA.5 genomes have been identified and published on GISAID by our genomic surveillance consortium. Through phylogenetic analysis on the currently available data, we were able to determine that the Belgian BA.4 genomes likely stem from multiple independent introductions into the country, directly or indirectly linked from (South) Africa, followed by local transmission in Belgium (Figure 5).

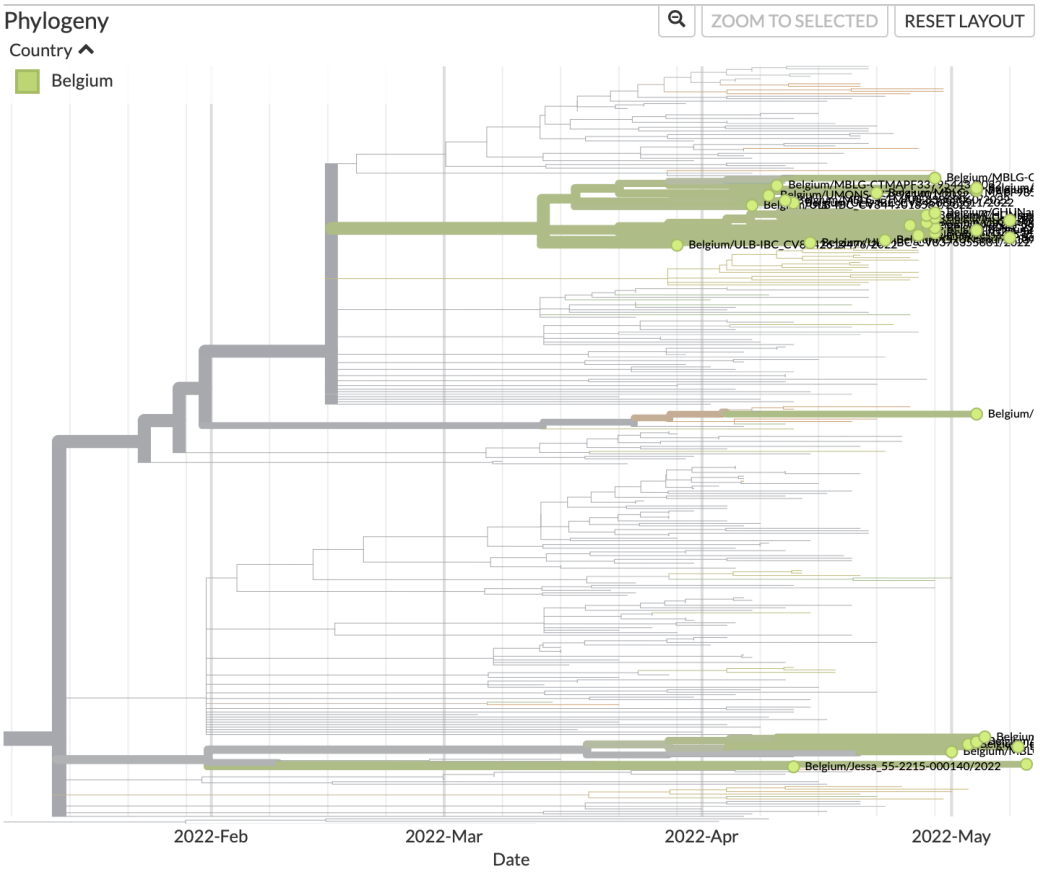


Figure 5: *The initial Belgian BA.4 cases are shown to stem from different introductions into the country, followed by - in most cases - local transmission within Belgium. Rapid phylogeographic analysis currently puts the backbone (i.e. the origin of the BA.4 introductions into Belgium) of the phylogeny in Africa (coloured in grey), likely South Africa (more detailed analysis would be needed to confirm the latter).*

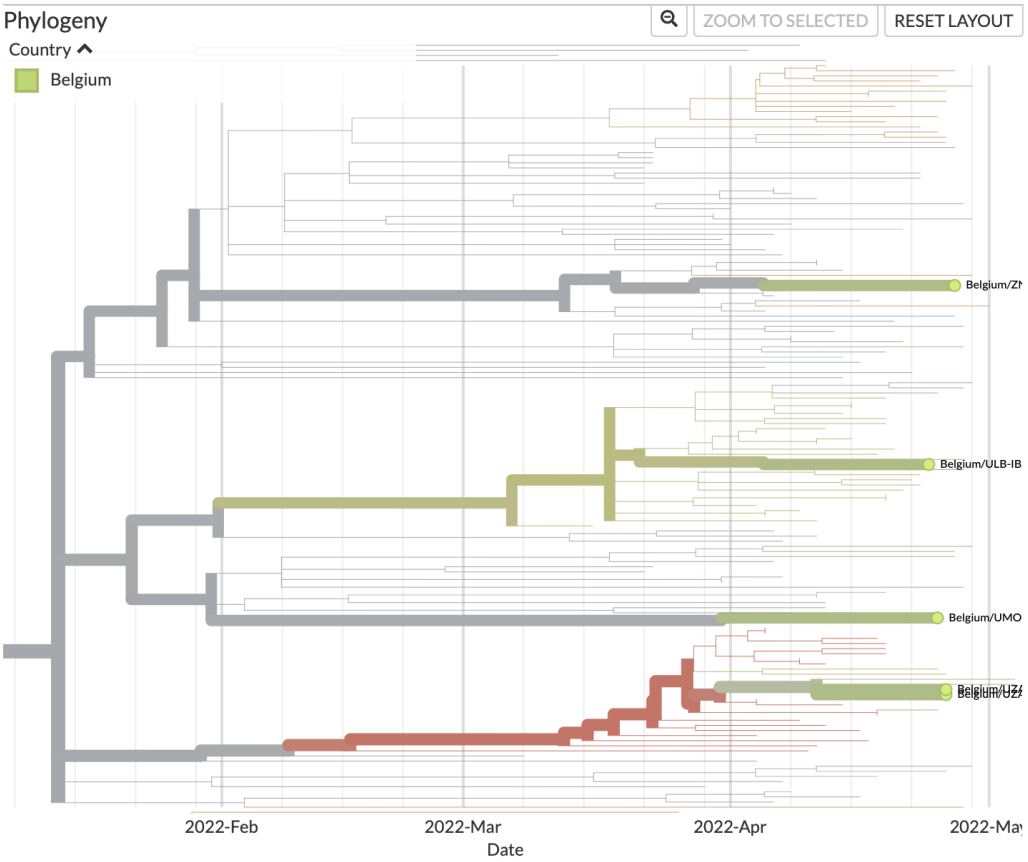


Figure 6: *The initial Belgian BA.5 cases stem from multiple introductions, with several likely originating on the African continent (possibly South Africa). Based on the currently available genomic data, two other introduction events are currently inferred to have occurred: one likely linked to a German cluster (second Belgian genome from the top; see Figure 7), and another likely from Portugal (bottom two Belgian genomes; see Figure 7).*

Phylogenetic and rapid phylogeographic analysis of the currently available BA.5 data point to a quite different story compared to the BA.4 analysis shown in Figure 5. Rather than (relatively speaking) a limited number of introductions followed by local transmission in Belgium, the initial Belgian BA.5 genomes seem to stem from multiple independent introductions, based on the currently available data. Further, at this stage the origins of these initial introductions appear to be mixed, with at least several introductions linked to (South) Africa but also to Germany and Portugal. In Figure 7, we show that some of the Belgian BA.5 genomes can be found within predominantly German and Portuguese BA. 5 clades. Additional data are needed to determine whether these introductions have led to onward transmission in Belgium (as we are currently seeing for BA.4; see Figure 5).

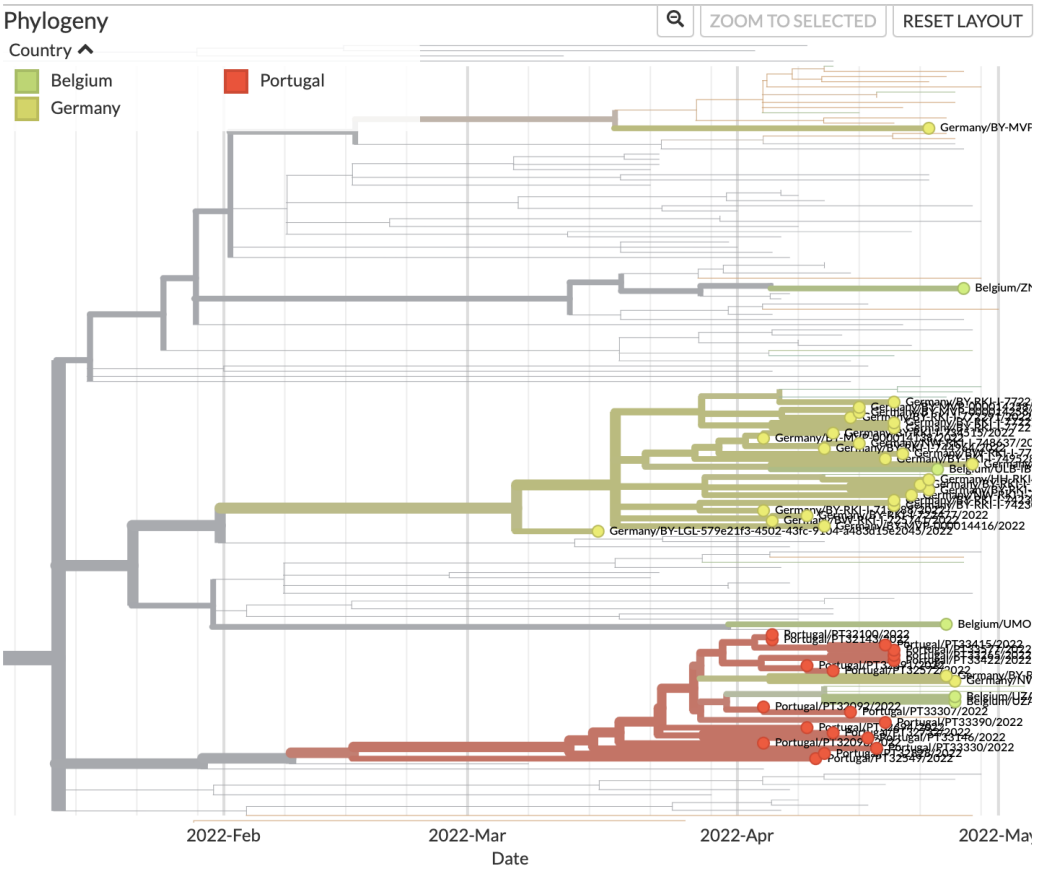


Figure 7: *At least 1 of the initial Belgian BA.5 cases can be found within a predominantly German cluster (top cluster), whereas at least 2 of the initial Belgian BA.5 cases can be found within a predominantly Portuguese cluster (bottom cluster).*