Genomic surveillance of SARS-CoV-2 in Belgium

Report of the National Reference Laboratory (UZ Leuven & KU Leuven)

Situation update – 16 of November 2021
(report 2021_54)

Executive summary

63,708 Belgian sequences of SARS-CoV-2 are now publicly available on GISAID; compared to last week's report 2,248 sequences have been added.

683 sequences of positive SARS-CoV-2 samples collected between 01/11/2021 and 14/11/2021 have at this stage been analysed in the context of baseline surveillance. Among these, B.1.617.2 (*Delta*) and its sublineages represented 99.9% of the circulating strains. AY.43 currently represents 41% of the circulating strains.

The genomic diversity of SARS-CoV-2 in Belgium is comparable with the situation described over the last 15 weeks.

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With the collaboration of the laboratories of UCL, ULB, UMons, UNamur, ULiège, UGent, UZA/UAntwerpen, Jessa ZH, AZ Delta, AZ Klina, IPG, AZ St Lucas Gent, OLVZ Aalst, Briant network, ZNA, AZ St Jan Brugge, UZ Brussel, LHUB-ULB, and UZ Leuven/KU Leuven; and Sciensano HealthData.

Previous reports can be downloaded using the following link:
https://www.uzleuven.be/nl/laboratoriumgeneeskunde/genomic-surveillance-sars-cov-2-belgium

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1. Monitoring of VOCs in Belgium

While first identified on 6 April 2021 in Belgium, the B.1.617.2 Variant of Concern (Delta) is now the dominant lineage in the country, representing 99.9% of the baseline surveillance samples sequenced (see Figure 1). One Alpha infection was reported during the last two weeks.

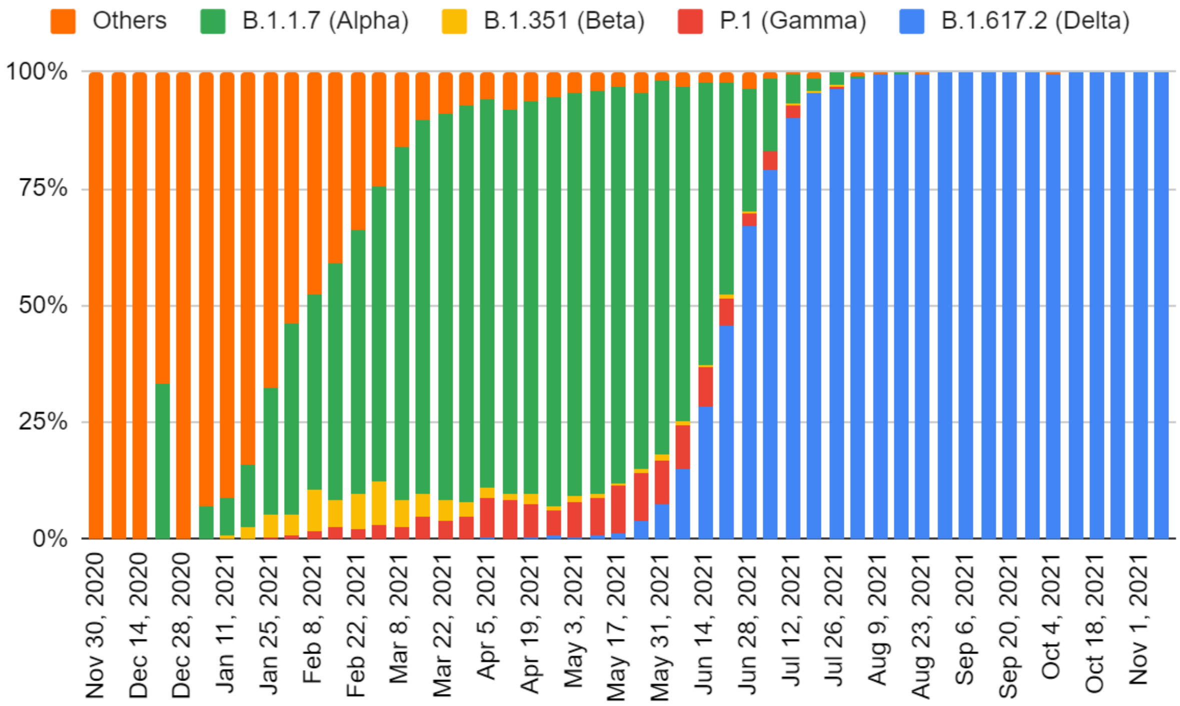

Figure 1: *Weekly evolution of the frequency of variants of concern reported by the baseline surveillance network using a whole genome sequencing (WGS) approach.*

2. Introductions of Delta sublineage A.Y.4.2 into Belgium

Lineage AY.4.2, a sublineage of Delta (B.1.617.2) was first detected in the United Kingdom (UK), is currently considered as variant of interest (VOI) and is characterized by spike mutations L452R, T478K, D614G, P681R, A222V and Y145H. This lineage has accounted for an increased proportion of Delta cases in the United Kingdom, Romania, Poland, and Denmark (among others). According to the latest report of Public Health England (November 12th, 2021), lineage AY.4.2. accounts for a slowly increasing proportion of cases in the UK. It accounts for **11.2%** of Delta cases in the most recent complete week of sequencing (17 to 23 October 2021). In more recent weeks, sequencing data is incomplete, however AY.4.2 accounts for **13.0%** of Delta cases in the week of 24 to 30 October 2021 and **14.7%** in the week of 31 October to 6 November 2021.

Currently, 43.667 genomes of Delta sublineage AY.4.2 are publicly available on GISAID, of which the majority (88.5%) originate from the United Kingdom. A total of **136 originate from Belgium**, most of which are included in the analyses in this document. In Figure 2, we show the outcome of our Nextstrain phylogenetic pipeline, indicating several independent introductions from abroad into Belgium.

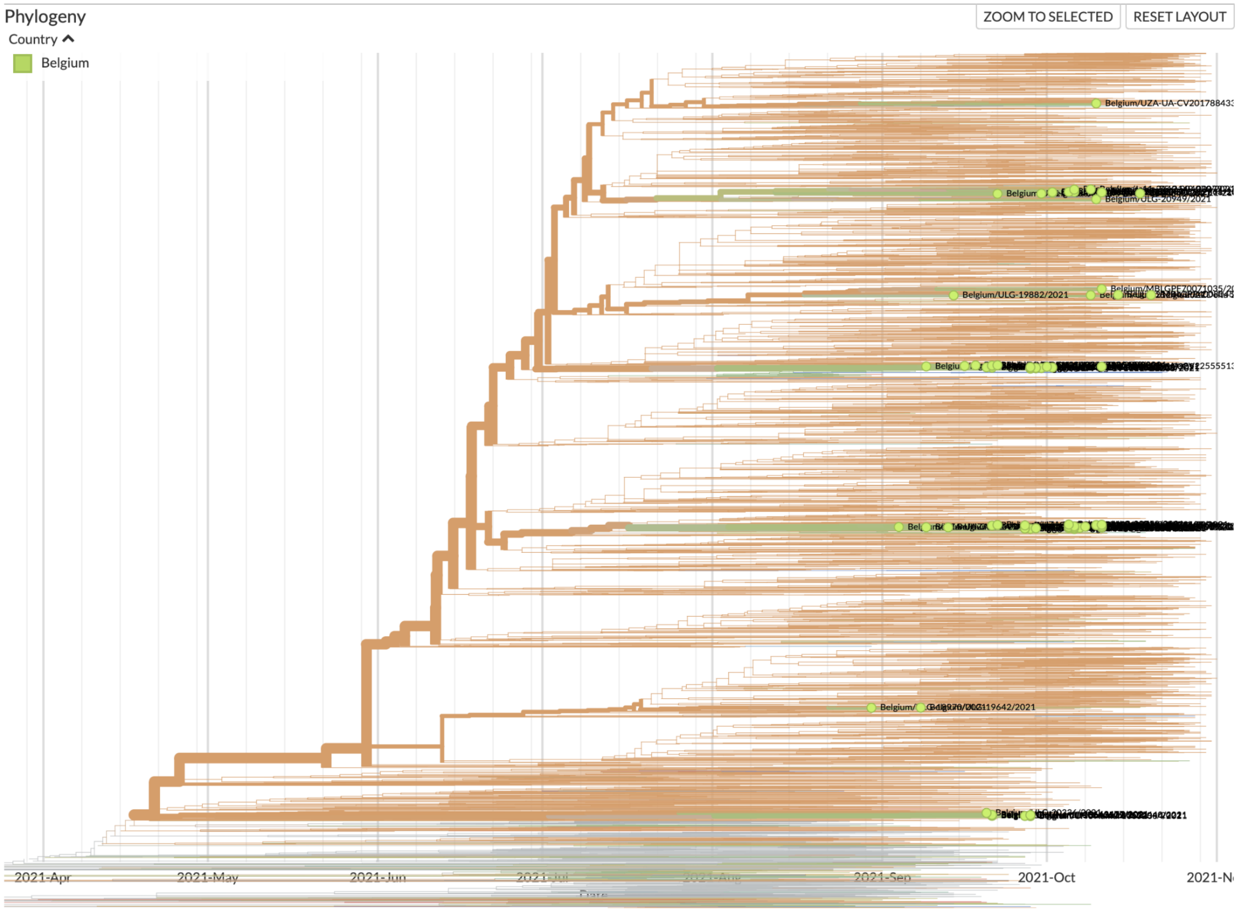

Figure 2: *Phylogenetic visualisation of Delta sublineage AY.4.2 with the Belgian sequences highlighted in green; several independent introductions of this lineage into Belgium can clearly be distinguished.*

The AY.4.2 sequences from Belgium are spread through the country, with cases having popped up in every province (Figure 3). We inspect specific “Belgian” clusters of AY.4.2 further in this document.

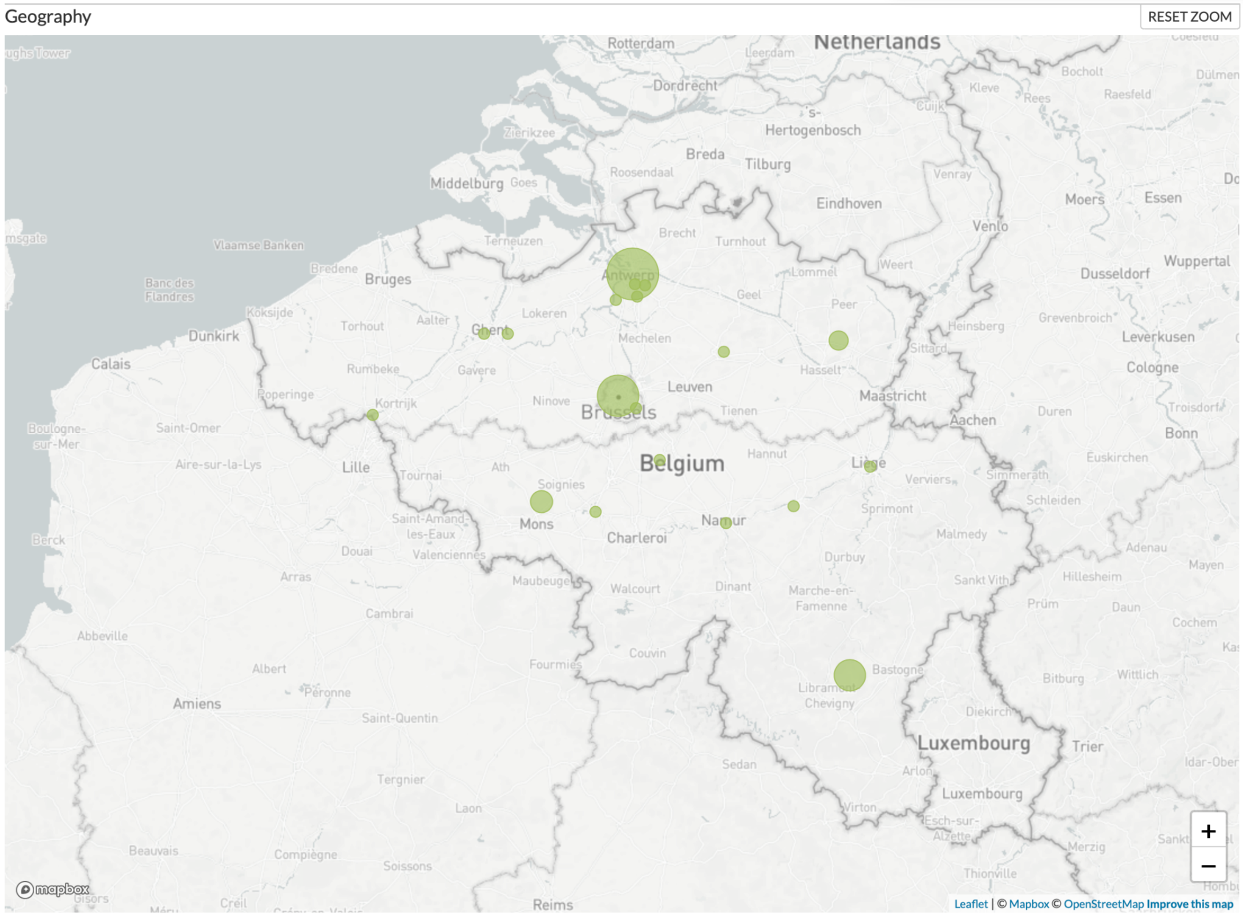

Figure 3: *Sampling locations of Delta sublineage AY.4.2 show the presence of cases in every province.*

Despite the presence of several independent introductions followed by local transmission in Belgium (Figure 2), such transmission cases are not local - i.e. restricted to a single city or province - however. We here inspect two local transmission clusters in more detail.

In Figure 4, we show a first case of “Belgian” local transmission of AY.4.2. Rather than remaining in a single location, infections spread to various major cities in Belgium (Ghent, Antwerp, Brussels, Mons and Namur).

A similar scenario can be seen in Figure 5, which actually shows multiple introductions into Belgium resulting in several small transmission chains, with the inferred origin most likely in Germany (more data will be needed to accurately resolve the ancestral origin, which currently favors Germany over the United Kingdom for this specific cluster).

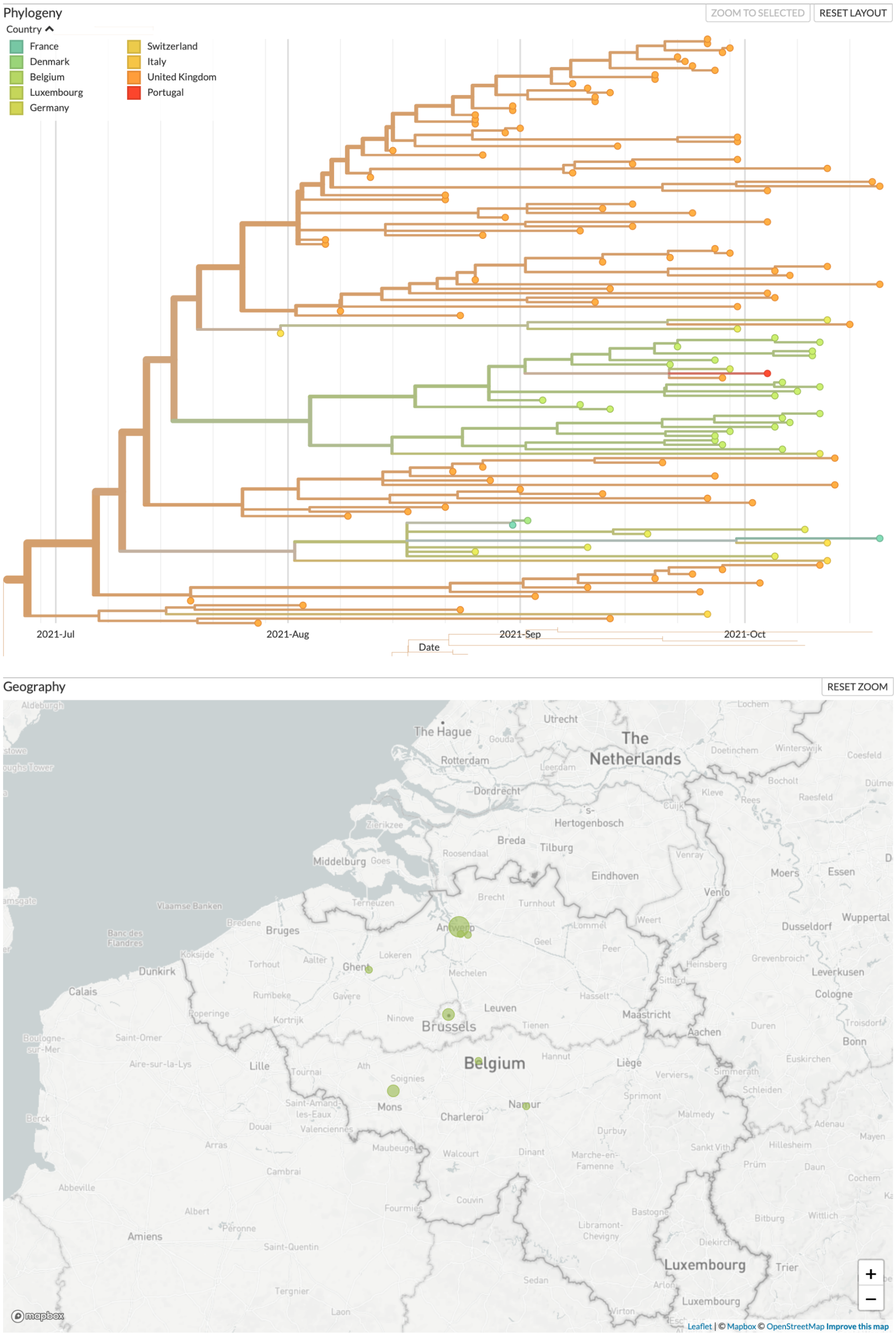

Figure 4: *Example of local transmission of AY.4.2 in Belgium. After an original introduction from the United Kingdom (orange), infections spread to major cities in Belgium (green): Ghent, Antwerp, Brussels, Mons, and Namur.*

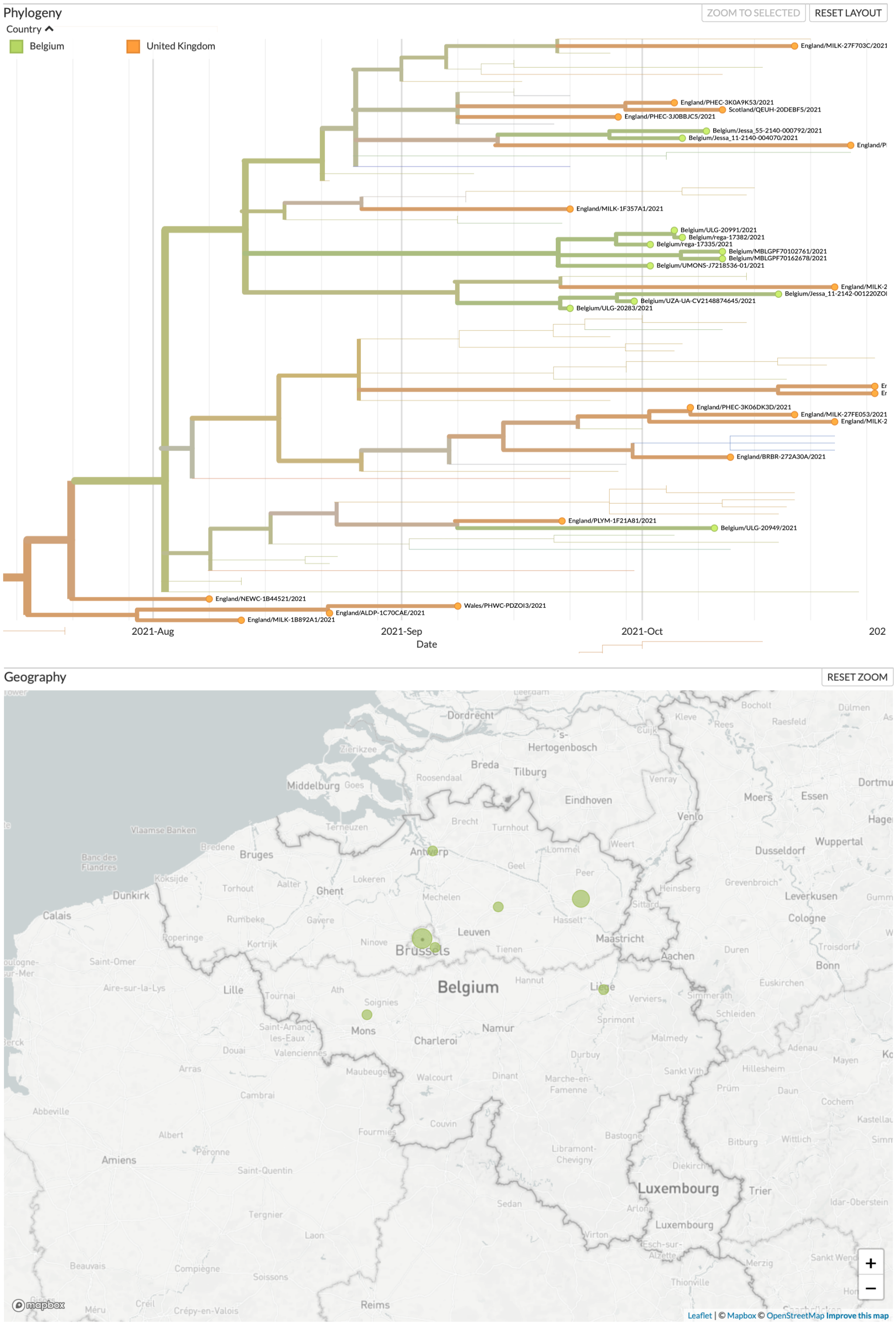

Figure 5: *Second example of local transmission of AY.4.2 in Belgium. After an original introduction from Germany (not explicitly shown), infections again spread to major cities in different provinces.*

3. A closer look at Delta sublineage AY.43

Among the different sublineagese in which the Delta variant is subdivided, only AY.43 represents more than 10% of the circulating strains. The previously mentioned AY.4.2 and AY.5.2 did not significantly evolve in proportion during the last weeks (see Figure 6).

The sublineage AY.43 is predominantly circulating in Europe, and prior to the designation of this new sublineage, half of the generated sequences were misclassified as AY.4. The first sequence was reported in week 25 (end of June 2021). So far, no additional mutations of biological relevance have been noted compared to the other Delta sublineages. Worldwide, its prevalence is currently 5%, while in several European countries it exceeds rates of 20%. For Belgium, the percentage of AY.43 sequences attributed to Flanders is somewhat higher (46%) compared to Wallonia (37%) and Brussels (33%), overall representing 41% of all circulating strains. The highest prevalence rates of sublineage AY.43 in Europe are reported for the countries France, Finland, Turkey, and Bosnia and Herzegovina.

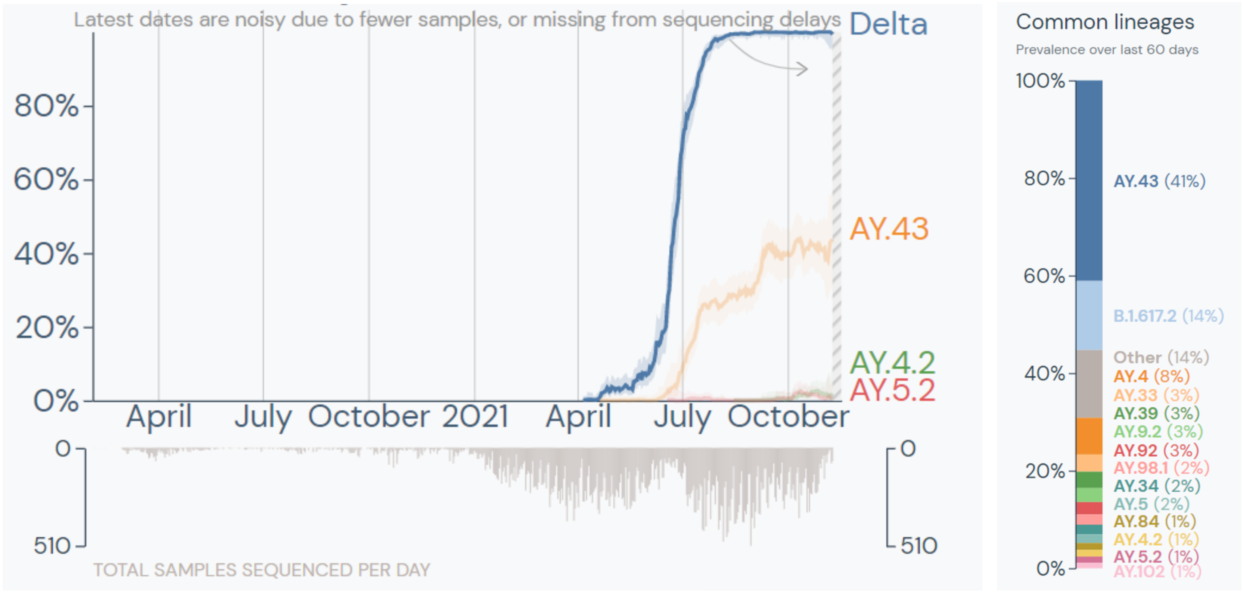

Figure 6: *Evolution of the proportion of selected Delta lineages and sublineages (AY.43, AY.4.2 and AY.5.2) during the last months in Belgium.*