Genomic surveillance of SARS-CoV-2 in Belgium

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

Situation update – 19 of October 2021
(report 2021_50)

Executive summary

52,226 Belgian sequences of SARS-CoV-2 are now publicly available on GISAID.

538 sequences of positive SARS-CoV-2 samples collected between 04/10/2021 and 17/10/2021 have at this stage been analysed in the context of baseline surveillance. Among these, B.1.617.2 and its sublineages (*Delta*) represented 100% of the circulating strains.

The genomic diversity of SARS-CoV-2 in Belgium is comparable with the situation described over the last 11 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

Table of contents

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 100% of the baseline surveillance samples sequenced.

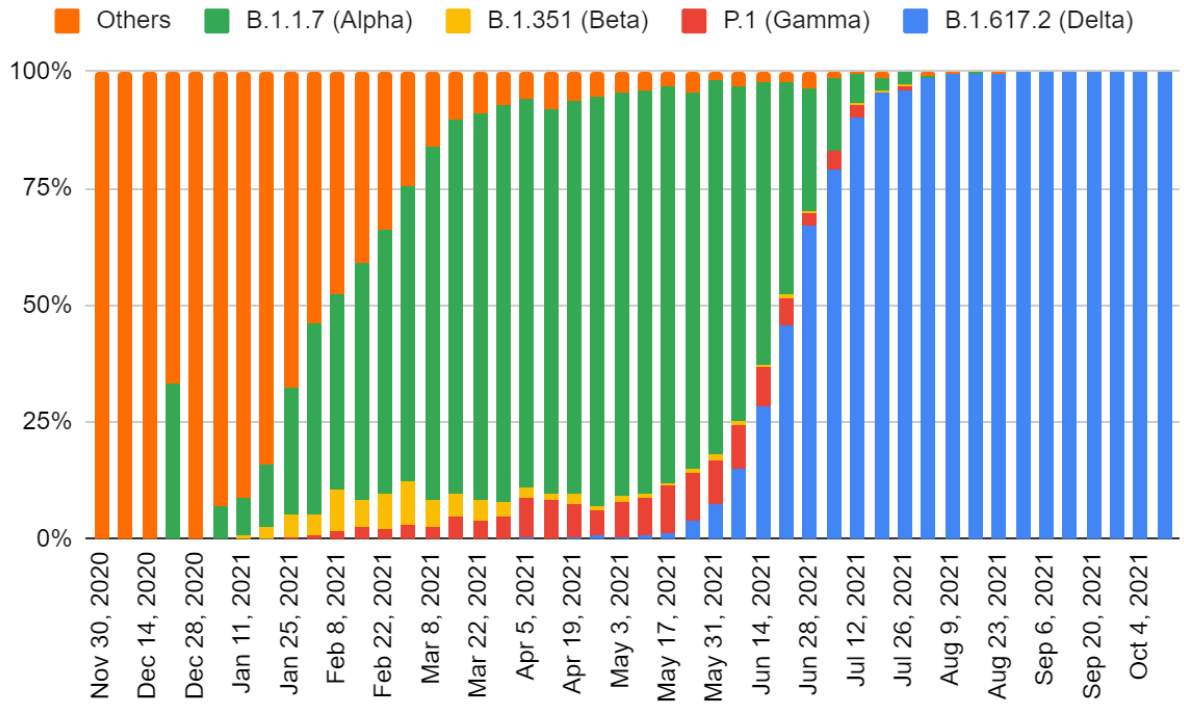

Figure 1: *Weekly evolution of the frequency of variants of concern reported by the baseline surveillance network using a whole genome sequencing (WGS) approach.*

2. Can the current rise in cases be associated with the emergence of a new variant in Belgium?

As previously described, different sublineages have been delineated within the large group of Delta B.1.617.2 genomes. Currently, AY.1 up to AY.41 sublineages have been defined (for all details please see https://cov-lineages.org/), with for some AY sublineages even additional subdivisions (e.g. AY.4.2). Over time, more and more sublineages have been defined due to the predominance of the Delta variant worldwide and the increased genomic surveillance on an international level.

Worldwide, two of these Delta sublineages seem to have a relative advantage compared to the other AY lineages, respectively AY.4 and AY.23. While **AY.4** is characterized by a high yet stable prevalence in the United Kingdom (UK), the number of infections related to Delta AY.4 in Belgium is much lower and the increase in infections assigned to AY.4 has been less steep compared to the UK (Figure 2). For the UK, this sublineage shows to be the dominant AY sublineage identified across the country.

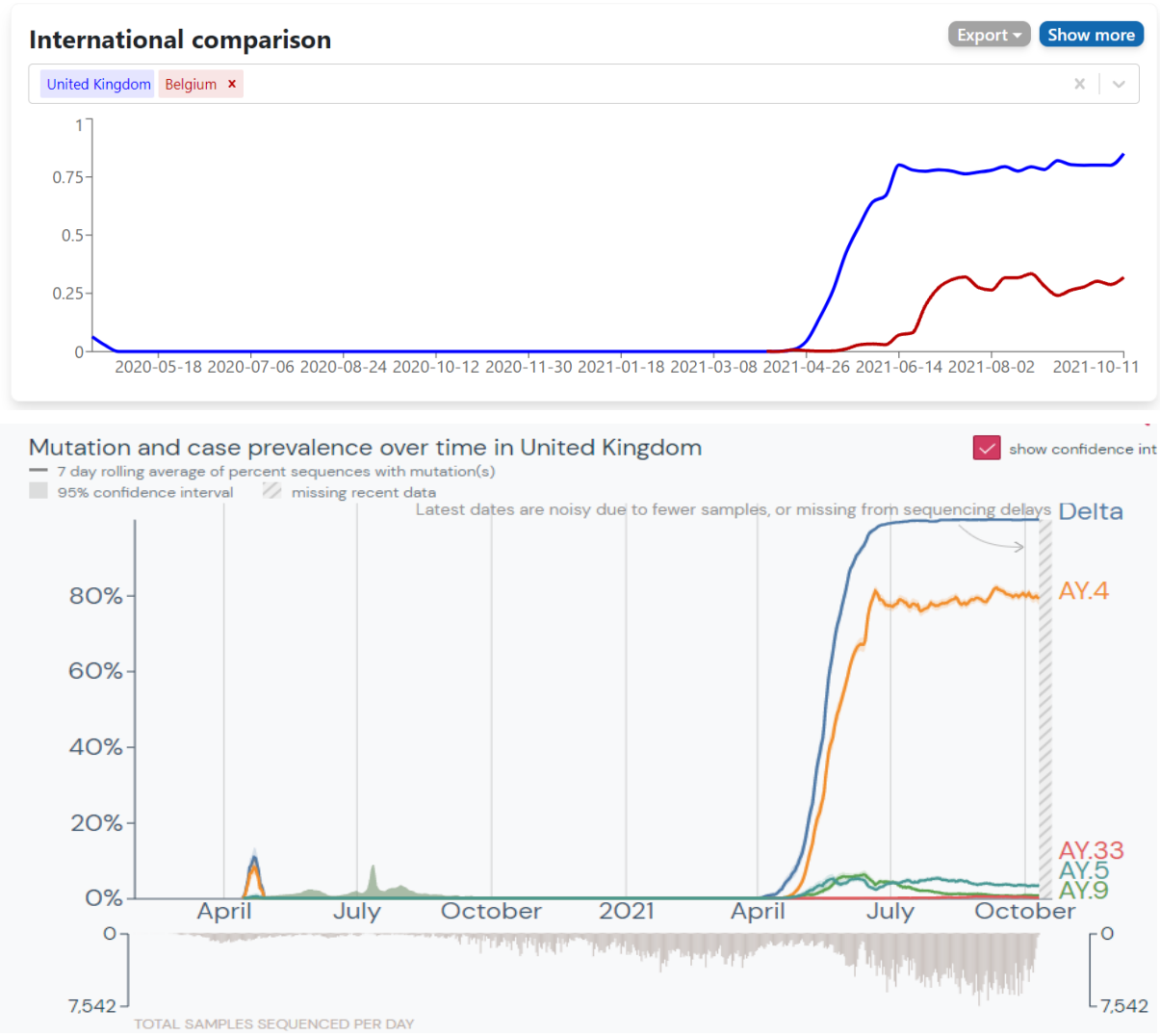

Figure 2: *Evolution of the prevalence of the Delta sublineage AY.4 over time in the UK and Belgium (upper panel). This lineage is dominant compared to other AY lineages identified in the UK (lower panel).*

Delta sublineage **AY.23** has been reported to be dominant in Singapore (Figure 3), while only a few cases have been identified in Belgium (<0.5% of the sequences assigned to the Delta variant).

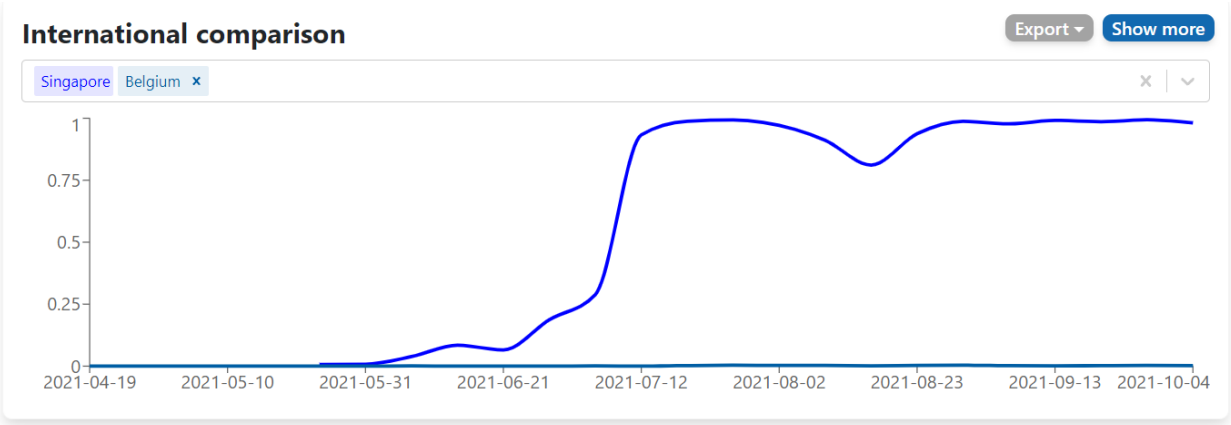

Figure 3: *Evolution of the prevalence of the Delta sublineage AY.23 over time in Singapore.*

Among the most prevalent Delta sublineages in Belgium (Figure 4), none seem to currently present a major advantage. While the evolution of the different AY lineages will be evaluated over time, and the dominant prevalence of both AY.4 and AY.23 in the UK and Singapore is worrisome, currently there is no indication that the recent rise in cases in Belgium is associated to the emergence of a new, more transmissible variant. In next week's report, detailed analyses on the growth advantage of the different AY sublineages will be presented.

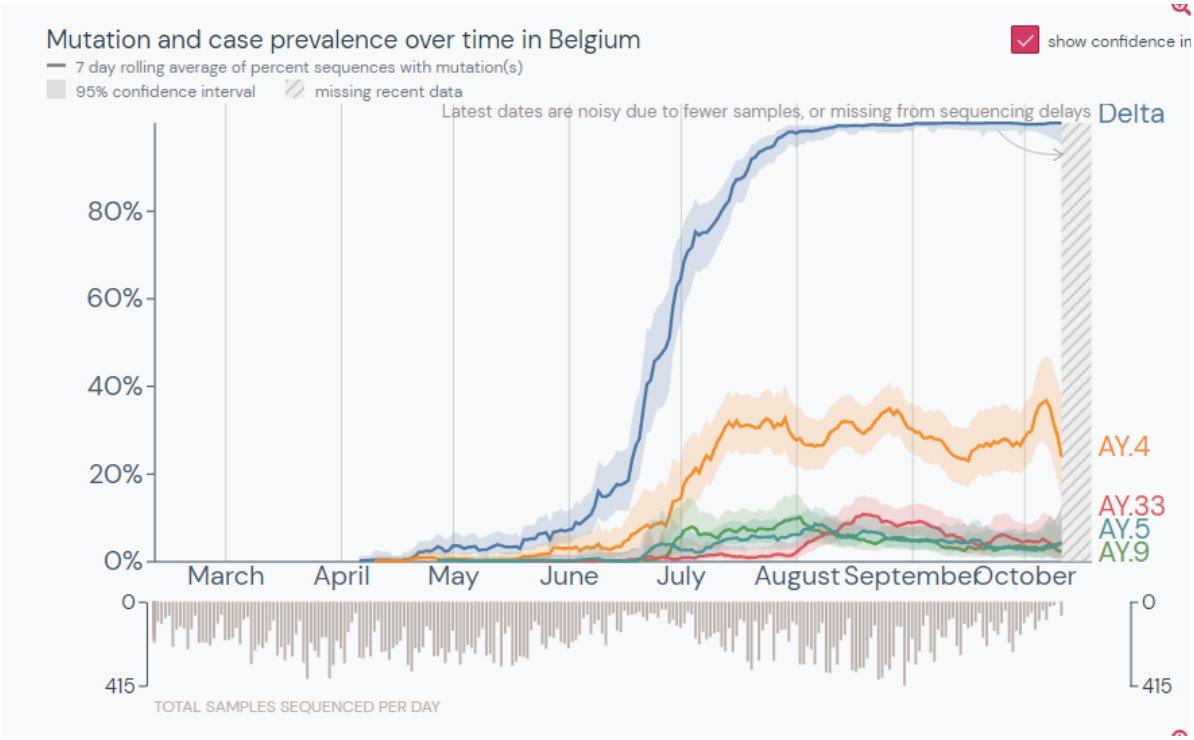

Figure 4: *Evolution of the prevalence of Delta and its sublineages in Belgium.*