

Genomic surveillance of SARS-CoV-2 in Belgium

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

Situation update – 29 of June 2021
(report 2021_34)

Executive summary

28.058 Belgian sequences of SARS-CoV-2 are now publicly available on GISAID.

Among these, 486 sequences of positive SARS-CoV-2 samples collected between 14 June and 27 June were reported,

- B.1.1.7 (*Alpha*) represented 65,2% (compared to 71,3% in the last report) ↘
- B.1.617.2 (*Delta*) represented 23% (compared to 15,7% in the last report) ↗
- P.1 (*Gamma*) represented 8,6% (compared to 9,7% in the last report) ↘
- B.1.351 (*Beta*) represented 0,8% (compared to 1,2% in the last report) ↘

Other points of attention:

- The NRC performed 63 VOC PCRs on unselected positive samples analyzed during the last 9 days. B.1.1.7 and B.1.617.1/.2 represented respectively 33,3% and 60,3% (↗) of the results.

- The decreasing epidemiological trend observed in Belgium is a very positive element as it will help mitigate the impact of the rapid viral population replacement currently taking place.

Currently, the absolute number of B.1.617.2 cases reported is not rising. This fragile equilibrium could be disrupted and lead to a deterioration of the epidemiological situation by a combination of (1) relaxation of measures, (2) an increasing number of travellers that will return from zones where the number of infections is rapidly increasing and (3) the foreseen limited coverage of testing offered to travellers coming back from red zones, resulting in a higher risk of secondary infections after importation of cases.

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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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International evolution

The Delta variant (B.1.617.2) has continued to spread globally. It has become the dominant lineage in several European countries, and other EU countries are expected to follow this evolution during the summer period.

- In the **European Region**, the number of infections is rising in Russia, the United Kingdom, Portugal and Moldavia. In other countries, the number of infections is stable or declining (Figures 1 and 2), but it should be noted that in these countries, B.1.617.2 is not yet dominant and that the situation will most likely evolve over the next few weeks.

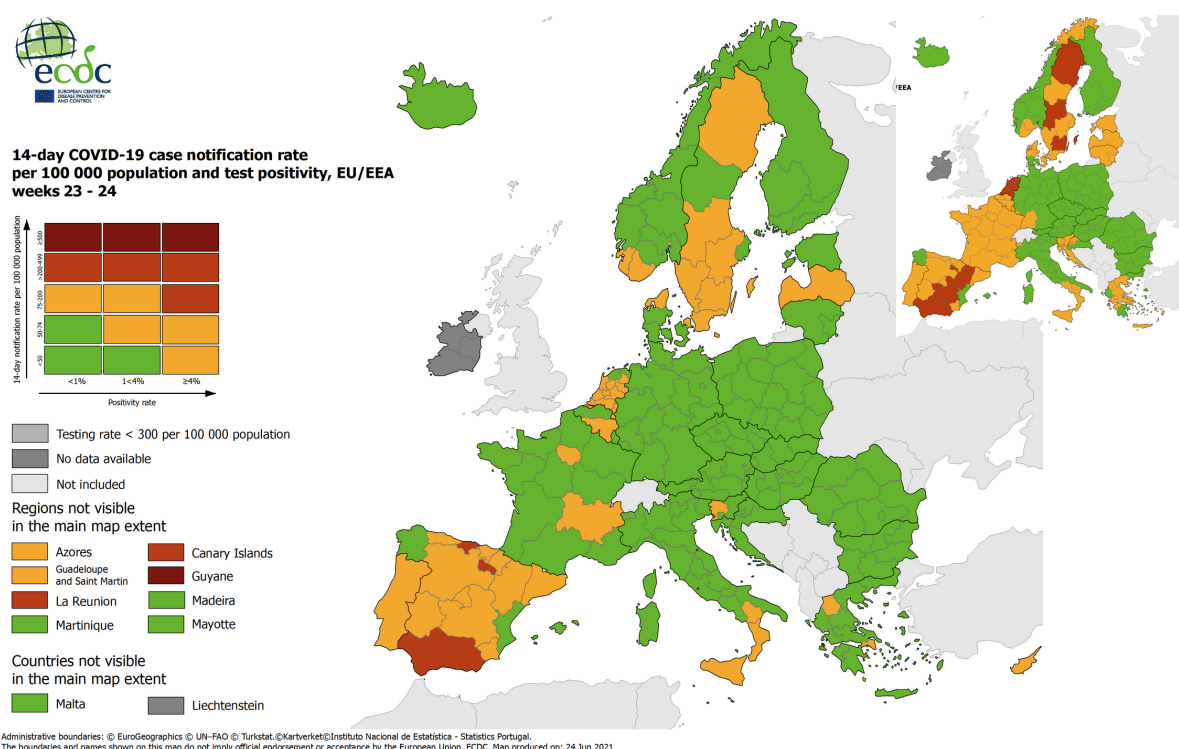


Figure 1. 14-day COVID-19 case notification rate per 100,000 inhabitants and test positivity rate (and comparison with the previous week). The situation in the EU region is globally positive.

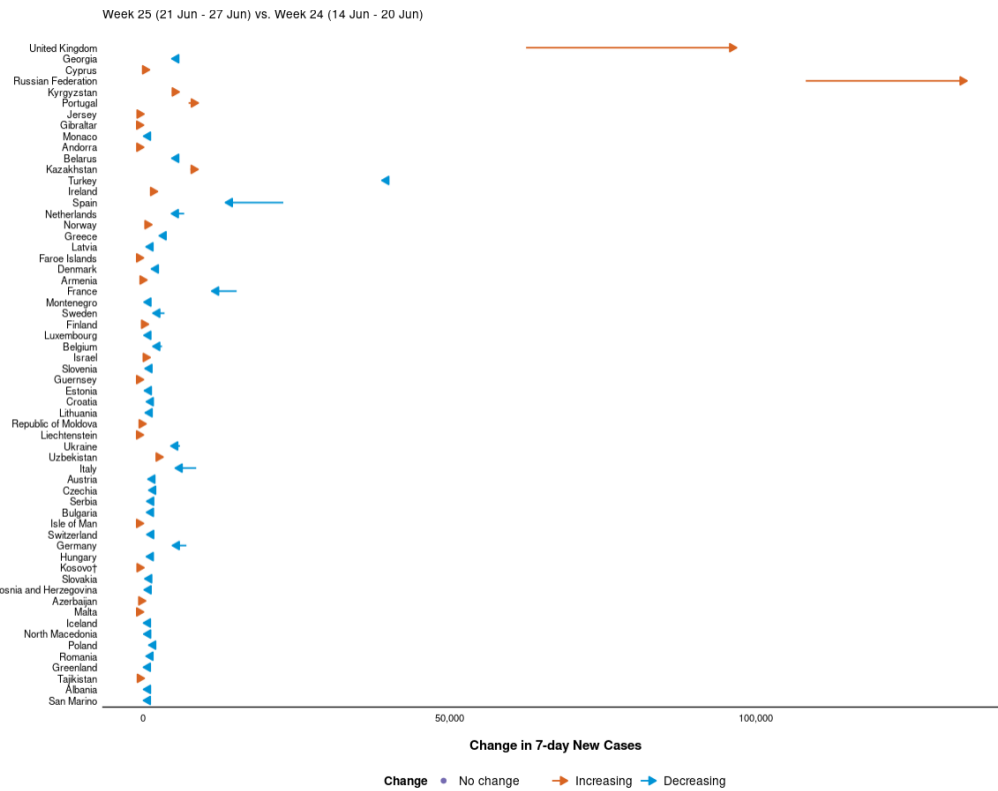


Figure 2. The United Kingdom and The Russian Federation are reporting a strong and sustained increase in new cases. Portugal shows an increase of infections which is currently more sustained than other EU countries. Belgium and its surrounding countries see a decrease in new cases (Source: WHO, <https://worldhealthorg.shinyapps.io/covid/>).

- In other regions of the world, the situation is still rapidly evolving in continents where vaccination coverage is very low (Africa, Latin America, Asia; Figure 3), a phenomenon which can be widely underestimated due to the limited diagnostic capacity in low-income countries. Several African cases are currently reporting a rapid rise of infections and deaths, including in countries with strong disease surveillance and control systems (Rwanda).

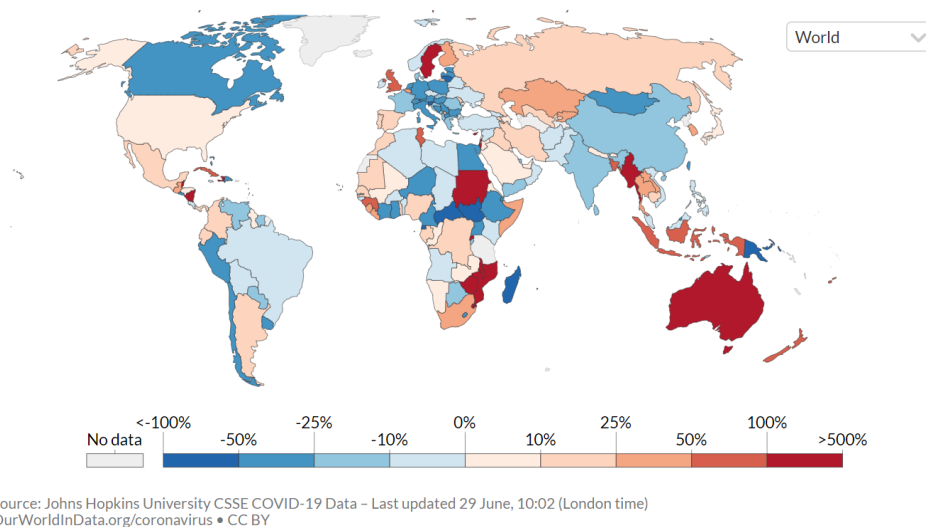


Figure 3 : Week by week change in confirmed COVID-19 cases (source : Oor World in Data)

Situation in Belgium

While it was first identified on 6 April 2021 in Belgium, the B.1.617.2 Variant of Concern (Delta) is on its path to become the dominant lineage in the country.

Between 14/6/2021 and 27/6/2021 (486 genomes available to date)

- B.1.1.7 (Alpha) represented 65,2%
- B.1.617.2 (Delta) represented 23%
- P.1 (Gamma) represented 8,6%
- B.1.351 (Beta) represented 0,8%

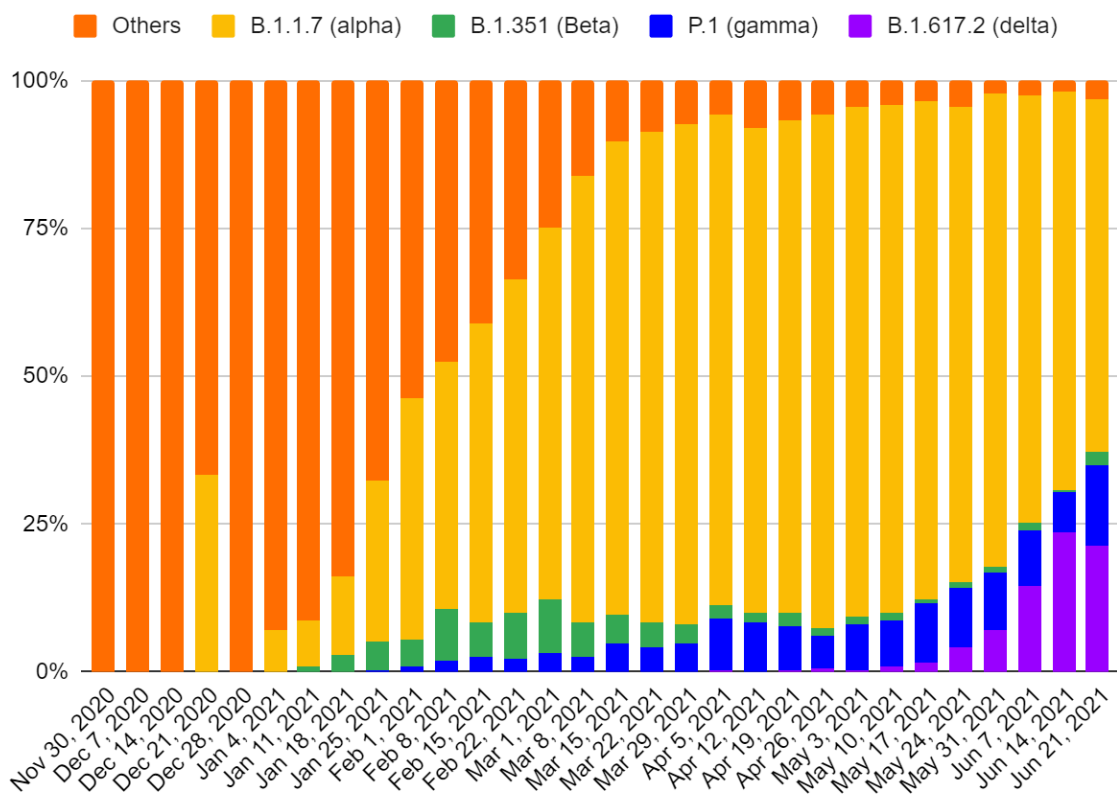


Figure 4: Weekly evolution of the frequency of variants of concern reported by the baseline surveillance network using a whole genome sequencing (WGS) approach.

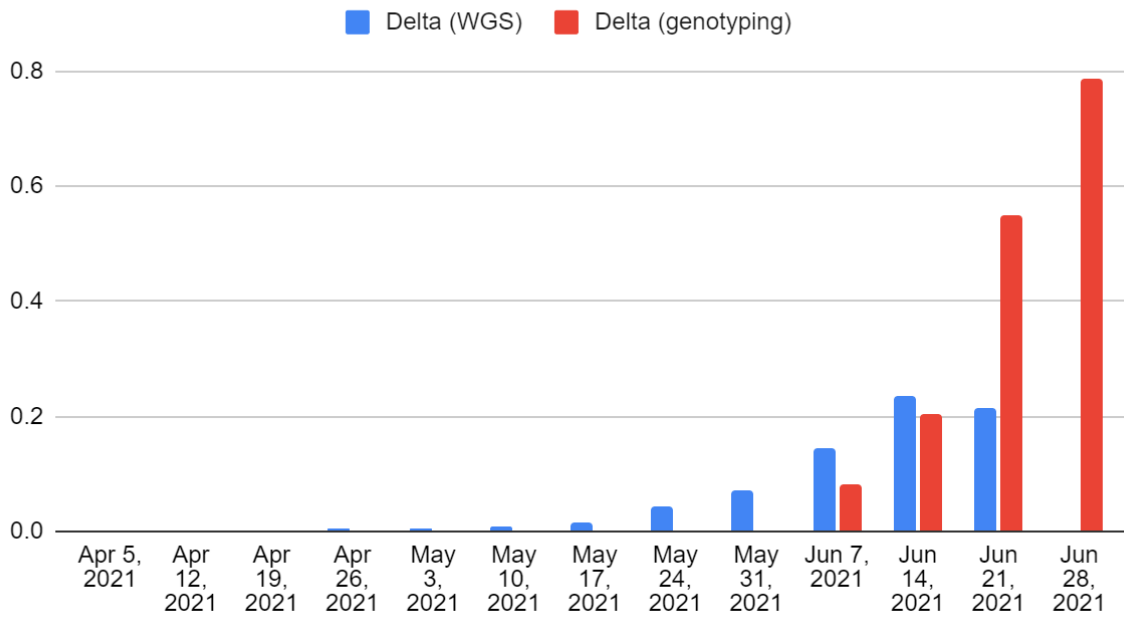


Figure 5: Weekly evolution of the frequency of variants of concern reported by the baseline national surveillance network using a whole genome sequencing (blue) and rapid VOC PCRs performed among all positive cases received at the national reference laboratory (red : mainly unbiased sampling, but limited geographical representativeness). Numbers for week 28 june are still limited (only 2 days reported for this week), and the final figure may thus be revised.

Lineage	Number of Belgian cases reported on GISAID	First reported
B.1.1.7 (Alpha)	17.138	30/11/2020
B.1.351 (Beta)	957	20/12/2020
P.1 (Gamma) and P.1.1	1.398	29/1/2021
B.1.617.2 (Delta)	394	6/4/2021
B.1.1.7 +S:E484K	26	31/3/2021
B.1.1.7 +S:S477R	33	15/3/2021
B.1.214.2	698	3/1/2021
B.1.525 (Eta)	71	30/1/2021
B.1.620	20	31/3/2021
B.1.1.318	53	3/3/2021
A.27	19	11/1/2021
B.1.617.1 (Kappa)	10	25/3/2021

Table 1: List of VOCs (red) and VOIs (orange) identified in Belgium to date and cumulative number of sequences available on GISAID (total of 28.058 sequences).

Update on introductions and local transmission of B.1.617.2 in Belgium

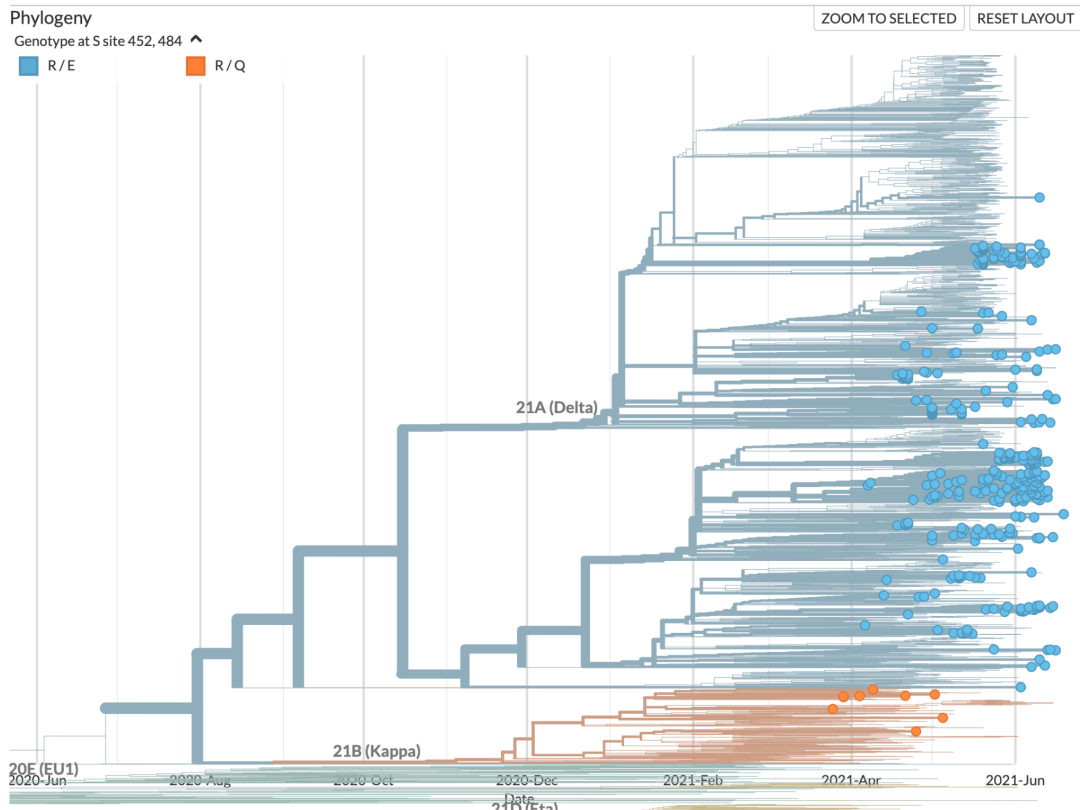


Figure 6: 381 Belgian genomes in the latest available Nextstrain build show both small and large local transmission clusters within Belgium for B.1.617.2.

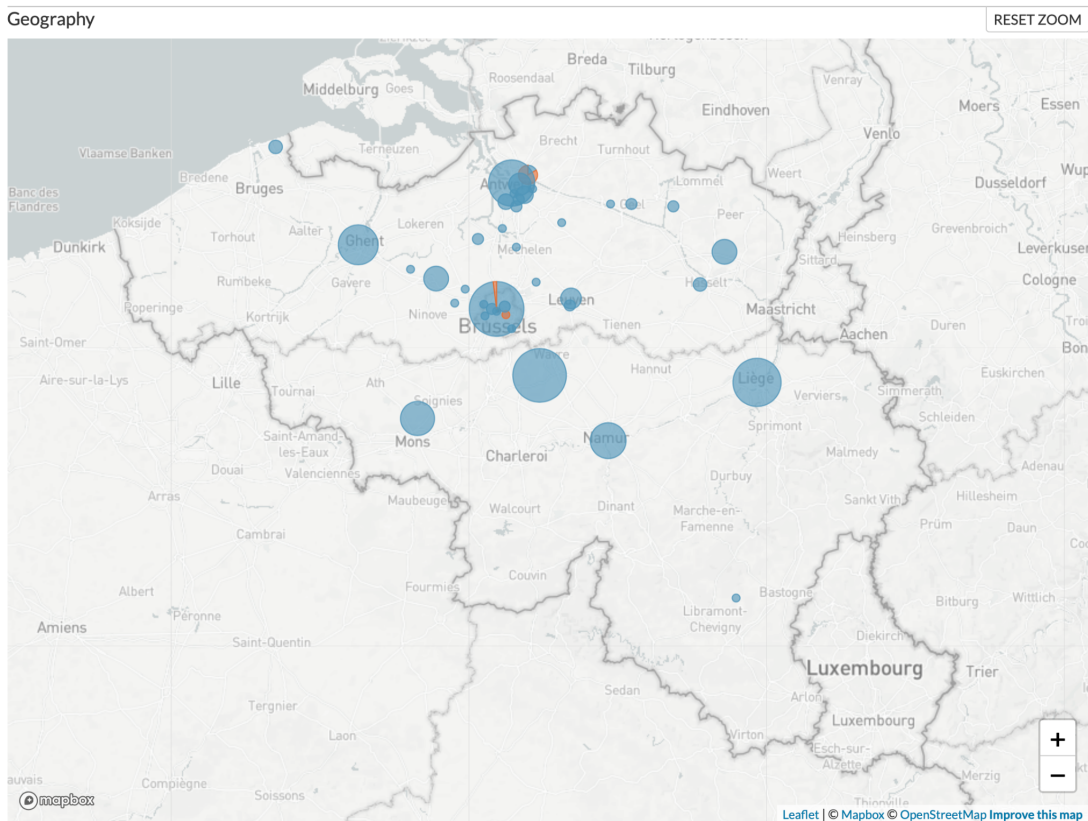


Figure 7: B.1.617.2 is present in all Belgian provinces but mostly in and around major cities.

Two large clades of B.1.617.2 can be seen in Figure 6. In Figures 8 and 9, we look into each of those clades in more detail, focusing on the possible relationship between the situation in Belgium and the United Kingdom.

Whereas Figure 8, showing less than half of the Belgian B.1.617.2 genomes (the upper blue part in Figure 6), indicates the importance of our connection to/with the United Kingdom, Figures 9 and 10 (showing the majority of Belgian infections; the lower blue part in Figure 6) paint a somewhat different picture. While some infections and local transmission clusters in Belgium can still be linked to the United Kingdom (see Figure 9), Figure 10 shows the impact of Asian countries (India, Singapore, ...) on the increase of B.1.617.2 infections in Belgium.

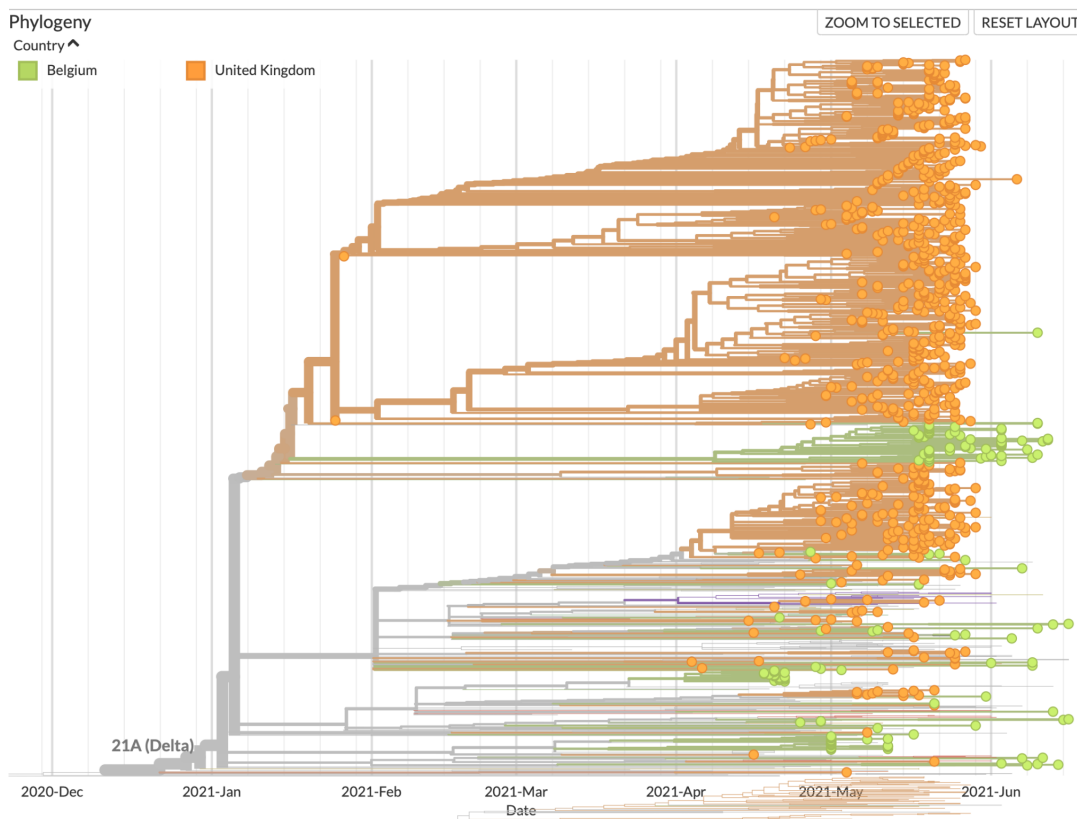


Figure 8: Top clade in Figure 7 analysed in more detail (orange: United Kingdom; green: Belgium). The largest (transmission) cluster of infections is nested within an otherwise entirely UK clade, suggesting the role of the UK in seeding a proportion of B.1.617.2 introductions into Belgium, in a similar manner as to what was observed at the time of B.1.1.7. Single-case introductions and smaller transmission clusters in Belgium can be seen to have both a UK and a non-UK origin.

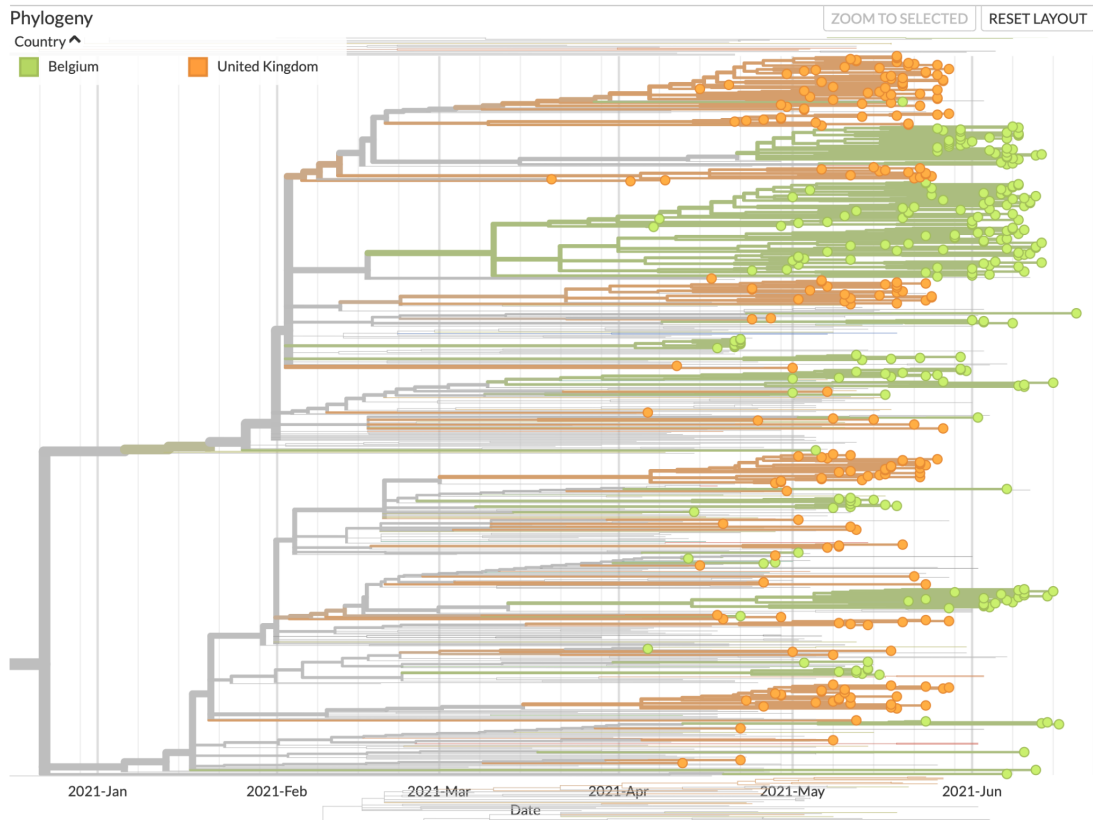


Figure 9: Bottom clade in Figure 7 analysed in more detail (orange: United Kingdom; green: Belgium), showing - to a lesser extent as in Figure 8 - the importance of the situation in the UK for Belgium.

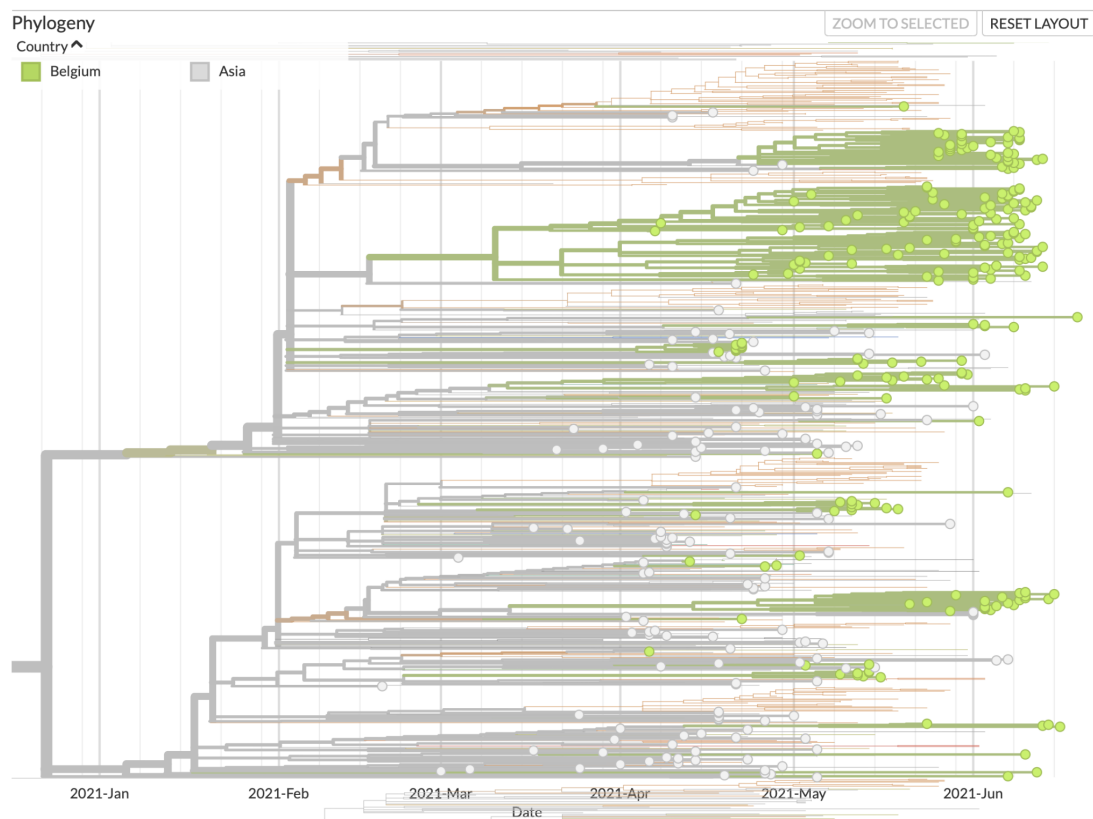


Figure 10: Alternative representation of Figure 9 to assess the relationship between Asian countries and Belgium, showing the importance of introductions from those countries into Belgium.