Genomic surveillance of SARS-CoV-2 in Belgium

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

Situation update – 25th of May 2021
(report 2021_28)

Executive summary

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

For baseline surveillance samples collected during the last two weeks (1.510 sequences collected between 3 May and 16 May),
- B.1.1.7 (20/501Y.V1) represented 87,6% (compared to 90.3% in the last report).
- P.1 (20J/501Y.V3) represented 7,9% (compared to 5.8% in the last report).
- B.1.351 (20H/501Y.V2) represented 0,9% (compared to 0.5% in the last report).

Other points of attention:
- 58 sequences of B.1.617.2 were deposited to date on GISAID (increasing)
- 18 sequences of B.1.1.7 with the S:E484K mutation and 15 sequences of B.1.1.7 with the S:S477R mutation were deposited to date on GISAID (stable)

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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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1. Monitoring of VoCs in Belgium

Three variants of concern (VoCs) have been introduced in Belgium around the end of the year 2020. The B.1.1.7 variant, which has been introduced through numerous parallel introductions, has since then become the dominant lineage in the country and is considered to be responsible for the latest epidemic resurgence ("third wave").

Over the last month, during which a representative and stable genomic surveillance could be ensured, B.1.1.7 and P.1 represented respectively 84% and 8% of the sequences reported to GISAID from Belgium. All other variants currently represent less than 3% of the circulating strains. The evolution of the viral population is thus relatively stable for the moment, and the controlled increase of P.1 cases, ongoing since February 2021, does not seem to accelerate.

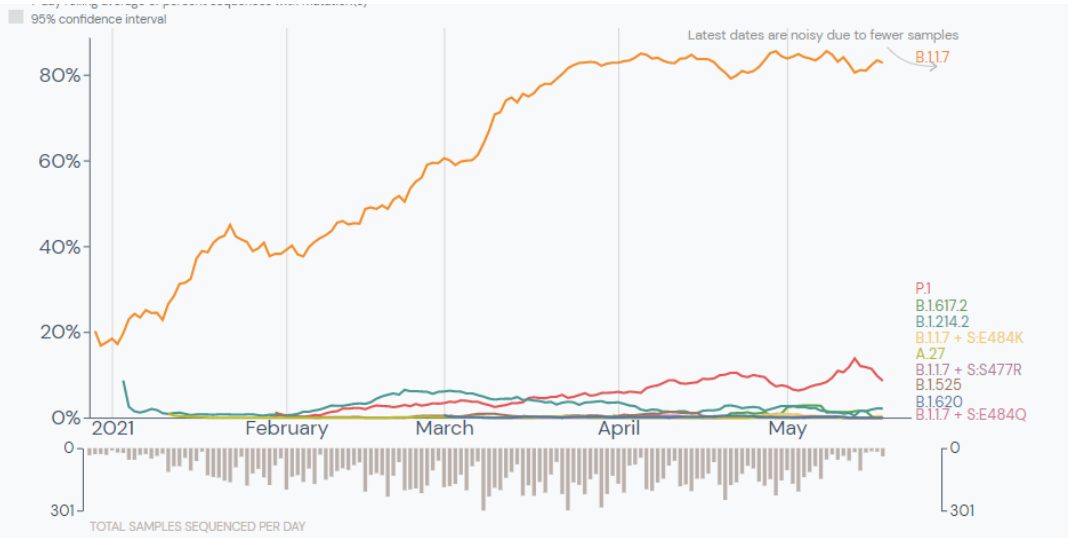

Figure 1: *Lineage prevalence over time in Belgium (combined active and baseline surveillance). B.1.1.7, P.1, B.1.351 and B.1.617.2 are currently classified as VoCs. B.1.617.1 and B.1.214.2 are among the variants of interest actively monitored in the country (source: outbreak.info & GISAID).*

<u>Particular attention to be given to B.1.617.2 (new VoC originally described in India)</u>

The increasing number of B.1.617.2 strains reported in Belgium is of concern, and this lineage is now the 3rd most frequent variant in Belgium among the strains deposited on GISAID during the last 3 weeks. Although targeted active case finding interventions tend to overrepresent the current incidence of this new VOC, its high transmissibility could potentially lead to a replacement phenomenon, as currently observed in the United Kingdom. However, it has still not been clearly established if the transmissibility of B.1.617.2 is similar or even higher than the one associated with B.1.1.7.

A rapid viral population replacement can have important consequences on national epidemiology. Targeted interventions such as active case finding and reinforced test/trace/isolation measures can help in reducing the speed of this phenomenon and therefore mitigating its impact. Further, continued rollout of vaccination is expected to have an important mitigation effect as it will reduce the proportion of infected people requiring medical care. Despite some first indications of reduced neutralization, the WHO (May 10, 2021) stated that current vaccines should continue to be effective against the B.1.617.2.

Lineage	Number of Belgian cases reported on GISAID	First reported
B.1.1.7	12.032	30/11/2020
B.1.351	895	20/12/2020
P.1	839	29/1/2021
B.1.617.2	58	6/4/2021
B.1.1.7 +S:E484K B.1.1.7 +S:S477R	18 15	31/3/2021 15/3/2021
B.1.525	55	30/1/2021
B.1.620	16	31/3/2021
A.27	9	11/1/2021
B.1.617.1	8	25/3/2021

Table 1: List of VoCs (red) and VoIs (orange) actively in Belgium to date on number of sequences on GISAID

2. Evolution of variants of concern in India and the United Kingdom

India

The epidemiological situation in India is improving. In this country where a very important surge of infections was observed recently, B.1.617.2 has outpaced other lineages, including B.1.1.7 and B.1.617.1.

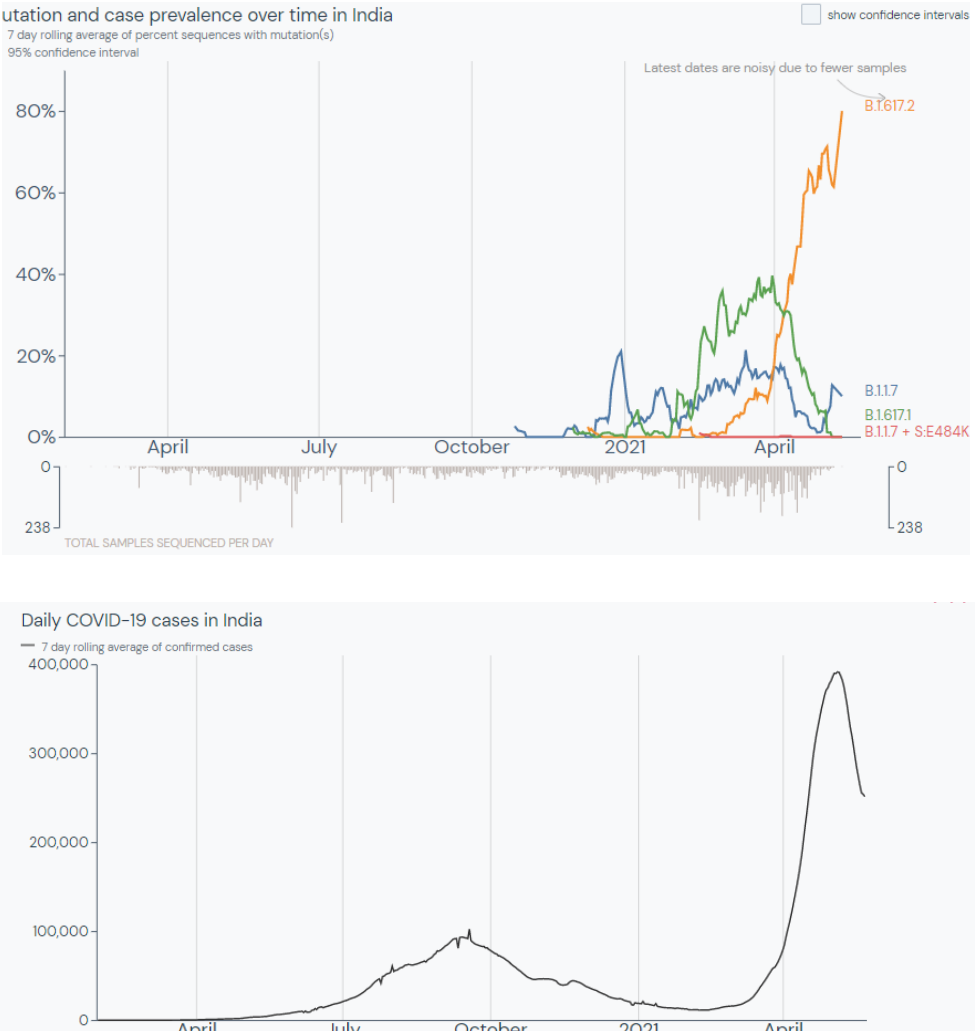

Figure 2: *Evolution of the share of viral populations and epidemiological situation in India (source: outbreak.info & GISAID).*

The United Kingdom

The situation in the United Kingdom is closely monitored as this country has the most extended and strongest genomic surveillance program, and has a more advanced vaccination coverage compared to Belgium. The UK had also, until recently, B.1.1.7 as dominant lineage, therefore observations from this country are relevant for the Belgian context.

In the context of a stable and low-level circulation of the virus, the UK observes a rapidly increasing number of B.1.617.2 infections. A rapid viral population shift has started, and reports from the UK suggest that B.1.617.2 represents today more than 50% of new infections.

This viral population replacement happens at a rapid pace, which increases the risk for an epidemic resurgence associated with such a phenomenon. Signs of an eventual rise in the total number of infections will be followed during the next weeks.

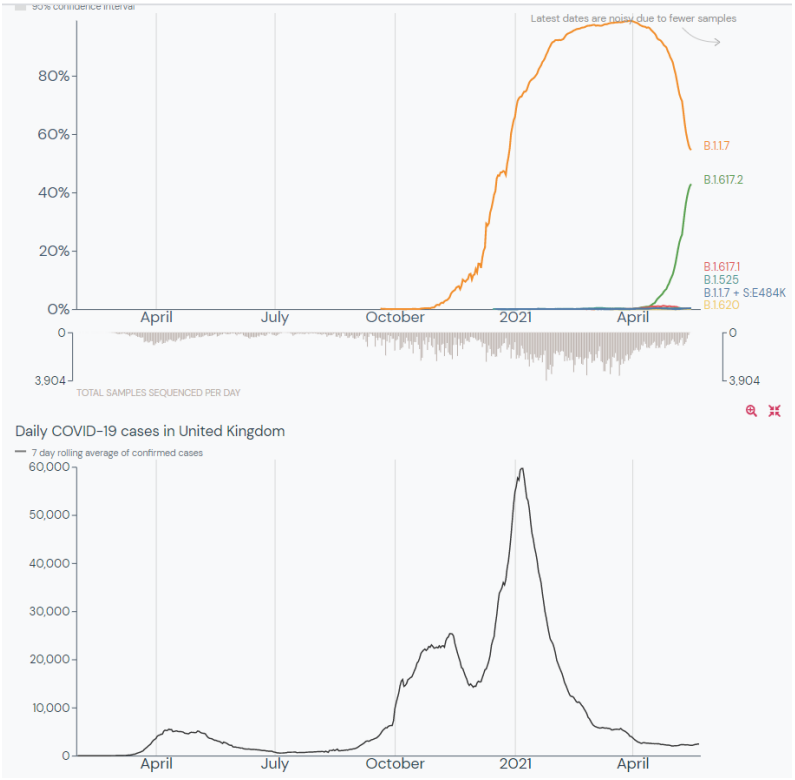

Figure 3: *Evolution of the share of viral populations and epidemiological situation in the United Kingdom (source: outbreak.info & GISAID).*

3. Description of a new lineage detected in Belgium (B.1.1.1 with 69/70del, L452R and S477N)

A new lineage has recently been observed in Belgium (19 sequences reported to date, among which 18 analysed in the same laboratory), Germany (17 sequences reported to date), the United States (14 sequences reported to date) and the United Kingdom (1 sequence reported to date). The Belgian cases associated with this new variant are currently considered as part of one unique and geographically contained cluster.

According to the current data available, this strain was first highlighted in New York on April 20th, and was first described in Belgium on May 17th.

This lineage has not yet been given a formal identification number (process ongoing), and is characterized by a number of Spike protein mutations, including:

- 69/70del (also present in B.1.1.7). This mutation is responsible for the "S gene target failure" in the PCR kit used by the federal platform laboratories
- R346S
- L452R (also present in B.1.617, B.1.427/B.1.429, B.1.526.1)
- S477N (also present in B.1.526.2)

The latter 3 mutations could be associated with a modification of epitopes typically targeted by anti-S antibodies. This could lead to an immune escape mechanism, and this new variant will therefore be closely monitored in the future. This lineage does not harbor the N501Y and E484K spike mutations.

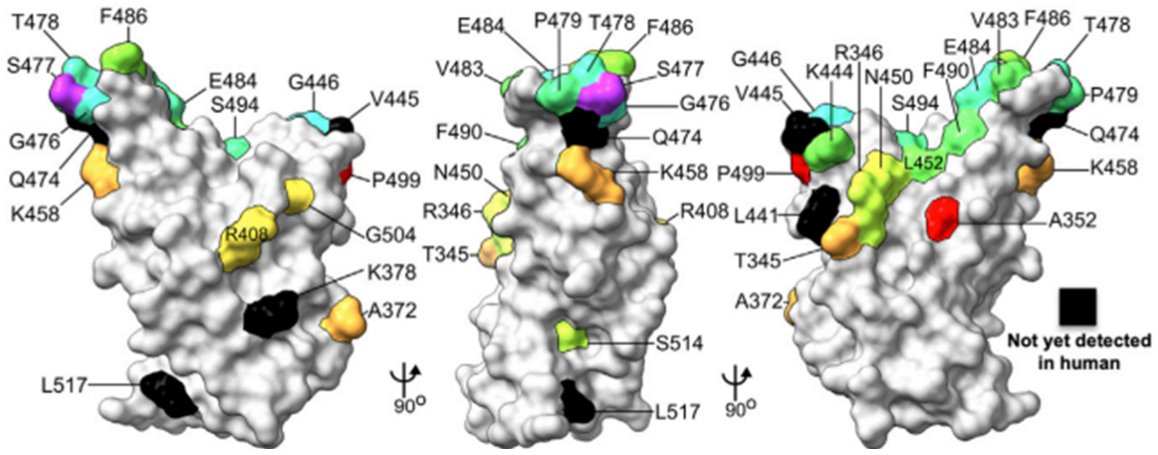

Figure 4: Sites of the spike mutations presumptively associated with immune escape (Liu et al., 2021, Cell Host & Microbe 29, 477–488)