Genomic surveillance of SARS-CoV-2 in Belgium

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

Situation update – 27th of April 2021
(report 2021_24)

Executive summary

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

For baseline surveillance samples collected during the last two weeks,
- B.1.1.7 (20/501Y.V1) represented 81,4% (compared to 85,9% in the last report)
- P.1 (20J/501Y.V3, originally from Brazil) represented 8,0% (compared to 4,9% in the last report). This important increase should be considered as alarming, particularly if this increase consolidates in the near future.
- B.1.351 (20H/501Y.V2) represented 2,8 (compared to 3,7% in the last report)

- A cluster of students recently arriving from India and infected with B.1.617.2 has been identified during the last week. Their sequences have not yet been deposited on GISAID, and are therefore not integrated in this report.

In this report, we focused our analysis on the first cases of B.1.617 found in Belgium and reviewed the recent scientific literature with regard to the impact of variants on vaccine efficacy.

Authors (National Reference Laboratory – UZ Leuven and KU Leuven):
Guy Baele, Lize Cuypers, Piet Maes, Simon Dellicour, Els Keyaerts, Elke Wollants, Marc Van Ranst, Emmanuel André.

With the collaboration of the laboratories of UCL, ULB, UMons, UNamur, ULiège, UGent, UAntwerpen, Jessa ZH, AZ Delta, AZ Klina, IPG, AZ St Lucas Gent, OLV Aalst, Briant network, ZNA, AZ St Jan Brugge, and UZ Leuven/KU Leuven.

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. Baseline surveillance

Since the end of 2020, the list of variants of concern (VOCs) and variants under investigation has grown regularly, and we expect that this list will continue to increase as a consequence of both the upscaling of genomic surveillance around the world and the increased selective pressures exerted by the combination of partial herd immunity and stepwise vaccination rollout.

	30/03/2021	6/4/2021	13/4/2021	20/4/2021	27/4/2021		Epid. situation in Belgium	Regions with active circulation
B.1.1.7	3909	5002	5890	6768	7991		Dominant lineage	All regions
B.1.1.7 with E484K	0	0	0	1	2		Sporadic	UK
B.1.351	495	649	676	705	755		Emerging	Southern African region
P.1	131	212	279	326	427		Emerging	Latin America
B.1.427	1	1	1	1	1		Sporadic	Northern America
B.1.617.1	0	0	0	4	3		Sporadic	India
B.1.617.2	0	0	0	0	1		Sporadic	India

Table 1: *Updated list of internationally recognized variants of concern and number of sequenced strains in Belgium as reported in GISAID.*

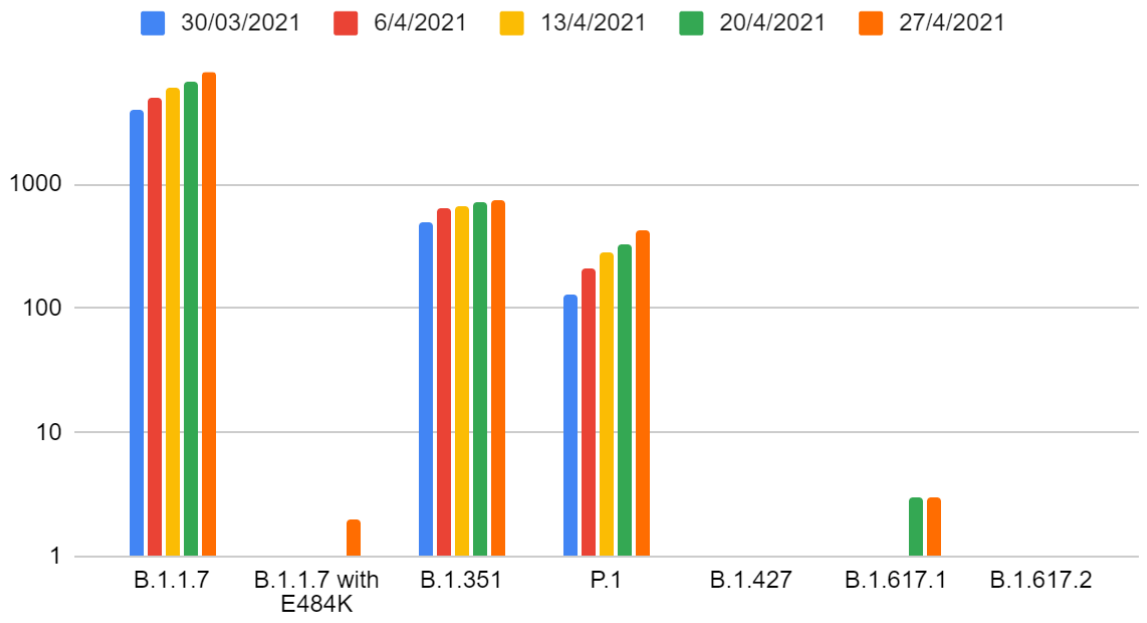

Figure 1: *Number (log scale) and evolution of Belgian sequences available on GISAID for variants of concern.*

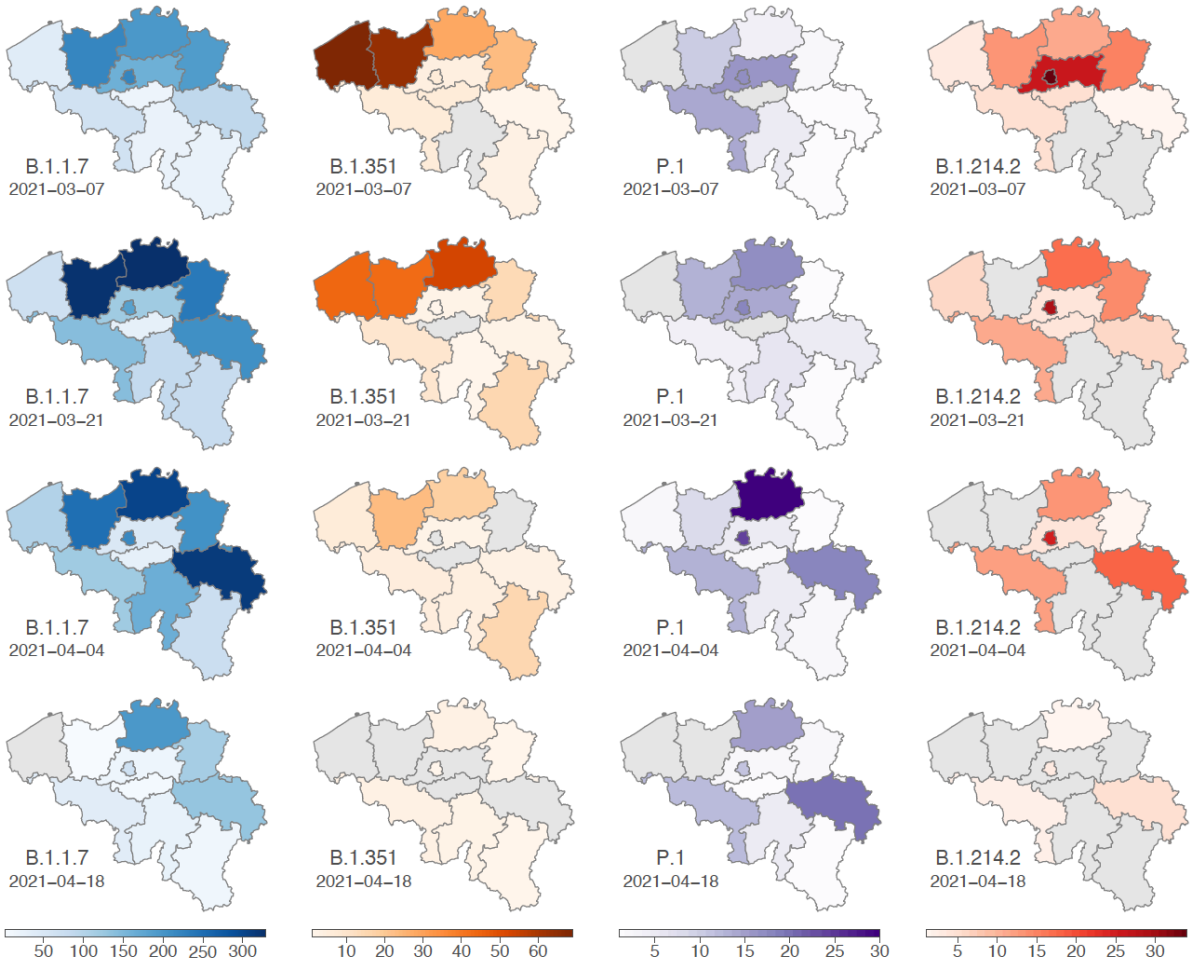

Figure 2: *Evolution of the number of cases associated with the 3 VOCs most frequently observed in Belgian provinces (B.1.1.7 ; B.351 and P.1). B.1.214.2 is not a VOC, but is currently closely followed-up as the majority of cases worldwide are reported from Belgium. For now, we here only report those numbers until April 18, 2021. Indeed, the number of sequences deposited in GISAID for the last few days is still too low to allow getting an overall overview of the heterogeneity among the different provinces. It will however be crucial to update this comparaison for the last two weeks in order to (i) confirm or not a recent increase in P.1 cases and (ii) figure out if this increase is more or less localised/attributed to a specific province.*

2. Monitoring of VOCs in Belgium

After a constant rise in proportion starting from January 2021, most new SARS-CoV-2 infections in Belgium are currently associated with a variant of concern (VOC), mostly B.1.1.7 (20I/501Y.V1). An important increase in the number of P.1 cases has been observed since the last report.

- B.1.1.7 (20/501Y.V1) represented 81,4% (compared to 85,9% in the last report)
- B.1.351 (20H/501Y.V2) represented 2,8 (compared to 3,7% in the last report)
- P.1 (20J/501Y.V3, originally from Brazil) represented 8,0% (compared to 4,9% in the last report)
- B.1.617 (originally described in India) has been identified for the first time in Belgium during the last week

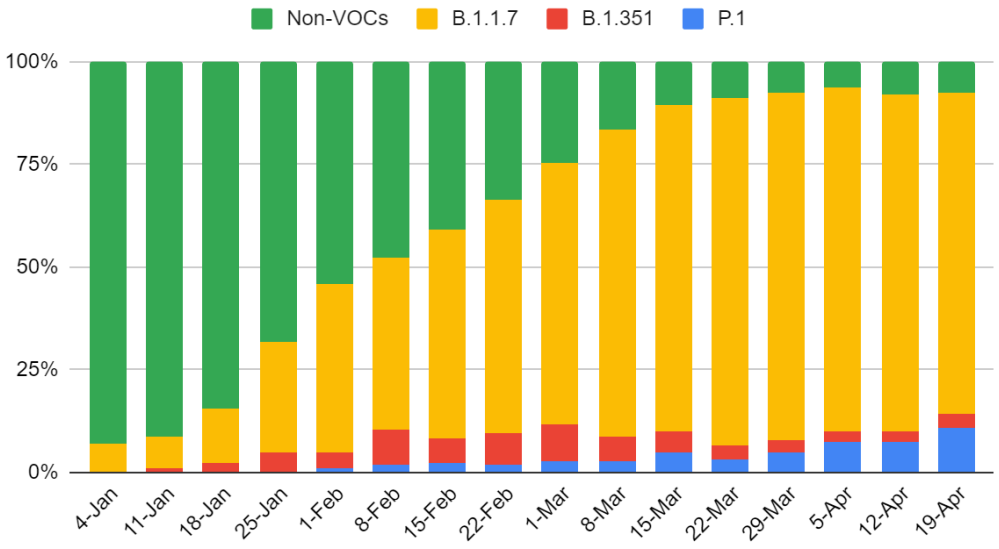

Figure 3: *Share of VOCs circulating in Belgium as measured through baseline WGS tests performed per sampling date since week 1 of 2021. Colour code: Non-VOCs and VOCs only observed sporadically (green), 20I/501Y.V1 - B.1.17 (yellow), 20H/501Y.V2 - B.1.351 (red) and 20J/501Y.V3 - P.1 (blue).*

Many laboratories in Belgium currently use the so-called “VOC PCR”, targeting specific molecular markers present among the most prevalent VOCs in the country, namely S:N501Y, S:E484K, S:K417T and S:K417N. To our knowledge, many clinical laboratories only use S:N501Y and S:E484K.

As the number of VOCs and Variants under Investigation is rising, we provide hereunder an updated interpretation table for the VOC PCR tests.

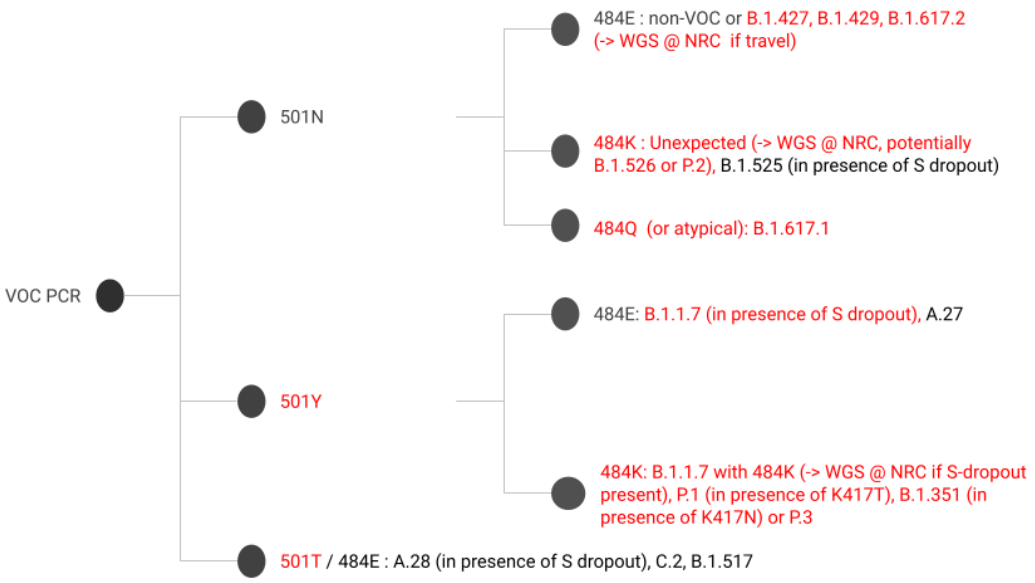

Figure 4: Updated interpretation algorithm of VOC PCR tests considering the increased number of VOCs and variants of interest.

3. Update regarding lineage B.1.617 and its sublineages

The vast majority of the infections currently reported from India and other countries are part of sublineages B.1.617.1 and B.1.617.2, while B.1.617.3 still remains relatively rare.

	World	Belgium
B.1.617.1	941	5
B.1.617.2	335	2
B.1.617.3	51	0

Table 2: Current distribution of the B.1.617 sub lineages as reported on GISAID

B.1.617.1 contains a number of spike mutations associated with antigenic escape or found in other variants of concern. Mutations at position 484 are well described as having a large impact on virus antigenicity and are associated with the B.1.351 and P.1 VOCs, however B.1.617.1 contains E484Q rather than the better described E484K, while B.1.617.2 does not present a mutation on site 484. The majority of antigenic escape studies (monoclonal antibody and/or polyclonal sera) that find changes at position 484 implicate E484K, and to a lesser extent E484G/D/A/Y, while E484Q is not observed. The studies where E484Q is routinely implicated, albeit at lower levels than E484K, are deep mutagenesis scanning studies which generally give a much larger variety of results. Unlike E484K, E484Q is not known to be associated with any change in receptor binding avidity. B.1.617.1 also contains the mutation L452R which is associated with antigenic escape from both monoclonal antibodies and convalescent antisera. L452R is also associated with enhanced receptor binding affinity. Additionally B.1.617.1 contains the furin cleavage site mutation P681R, similar to P681H. 681R/H are found in multiple variant lineages, such as B.1.1.7, B.1.1.318 and A.23.1. Both P681H and P681R have been shown to optimize spike cleavage by furin; it has been hypothesised that this optimisation may enhance virus transmissibility (Source: Public Health England, SARS-CoV-2 variants of concern and variants under investigation in England, Technical briefing 9, 22 April 2021).

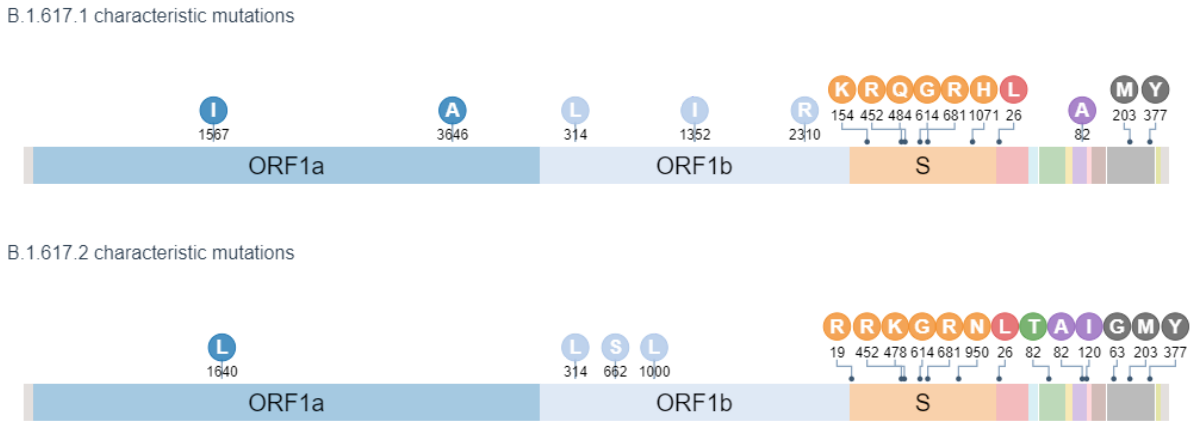

Figure 5: Characteristic mutations of B.1.617.1 and B.1.617.2 (source: outbreak.info)

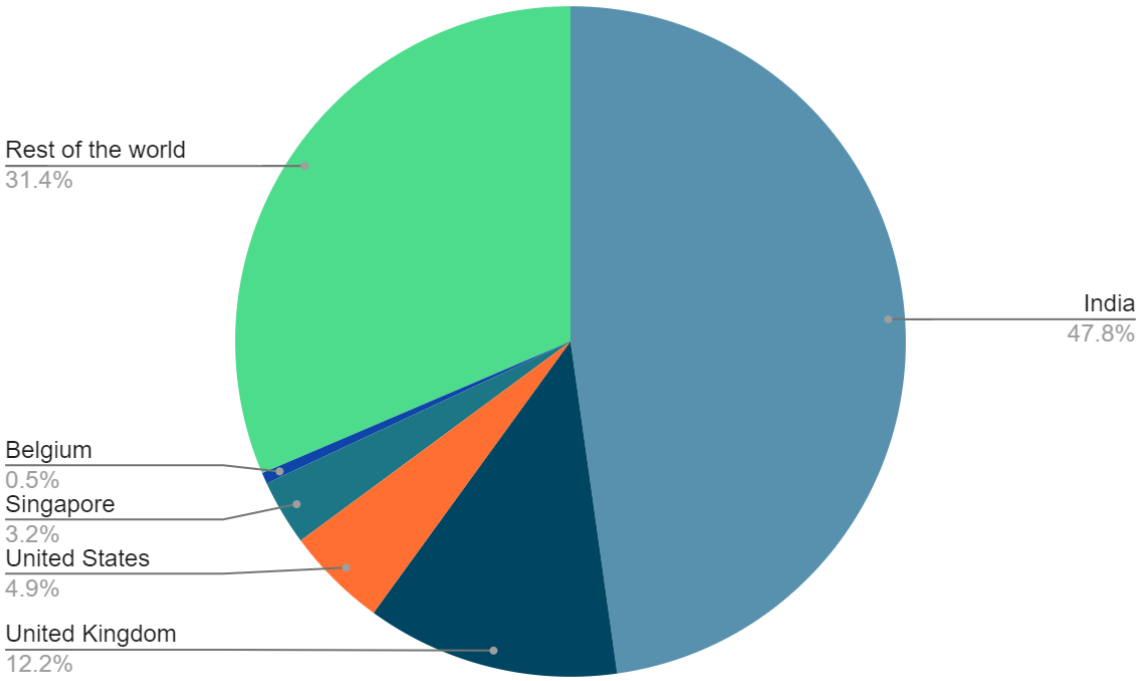

Figure 6: Origin of B.1.617 genomes available on GISAID

Update with regard to the circulation of B.1.617.2 in Belgium

In addition to the number of Belgian genomes mentioned in the previous section, an important cluster of foreign students who recently arrived in Leuven and Aalst, was recently identified. To date, 15 out of 21 of the students in Aalst, and 9 out of 22 of the students in Leuven were diagnosed with a positive PCR. Sequencing is ongoing, and all sequenced samples to date are of the B.1.617.2 lineage. All students - of Indian nationality and arriving from India via France - were subjected to the required pre-boarding testing (and tested negative) and quarantined themselves upon arrival in Belgium (and hence did not mingle with the rest of the population).

There was no direct travel from India to Belgium, with the students arriving in Paris (airport Charles de Gaulle, April 12th 2021) and then continuing their journey to Belgium via bus. As stated by Prof. Van Ranst, the students were most probably infected by a superspreader on this bus ride. Several of the infected students had already been vaccinated.