Genomic surveillance of SARS-CoV-2 in Belgium

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

Situation update – 9th of March 2021
(report 2021_17)

Executive summary

8.277 Belgian sequences of SARS-CoV-2 are currently available in open access on GISAID, among which 4.545 are unbiased samples collected after the 1st of January 2021 in the context of baseline surveillance.

For baseline surveillance samples collected during the weeks starting on the 22nd of February and the 1st of March 2021, 20I/501Y.V1 represented 57,55% and 47,71%, 20H/501Y.V2 represented 5,4% and 15,6% and 20J/501Y.V3 represented 1,84% and 2,75% of all samples analysed.

The proportion of 501Y.V1 seems to stabilize at country level (not in every province, as discussed later in this report), the proportion of VOCs harbouring immune escape mechanisms (501Y.V2 and 501Y.V3) continues to increase. This phenomenon will be followed, in particular as vaccination is currently being rolled out in the country.

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. International context

Since the end of 2020, 3 variants of concern (VOCs) have arisen independently of one another in the United Kingdom (20I/501Y.V1), South Africa (20H/501Y.V2) and Brazil (20J/501Y.V3). These variants harbour several mutations and deletions associated with (or investigated for) higher infectiousness and immune escape. All variants are spreading internationally and have been detected in Belgium.

2. Baseline surveillance

Since support was offered by the federal government at the end of December 2020, both the temporal coverage (number of sequencing analyses performed per week) and geographical coverage (residence of the patients sampled) have improved significantly. Currently, 8.277 Belgian sequences are available on GISAID.

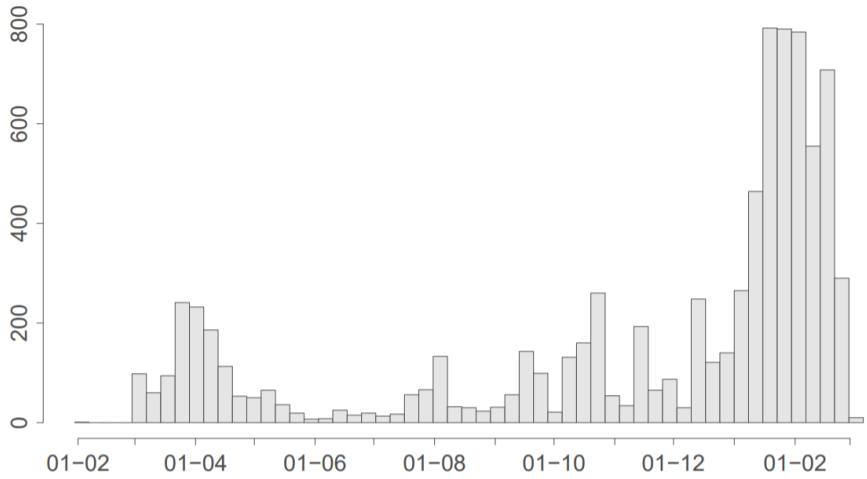

Figure 1: *Number of sequences of SARS-CoV-2 deposited on GISAID per sampling date (baseline surveillance and active surveillance)*

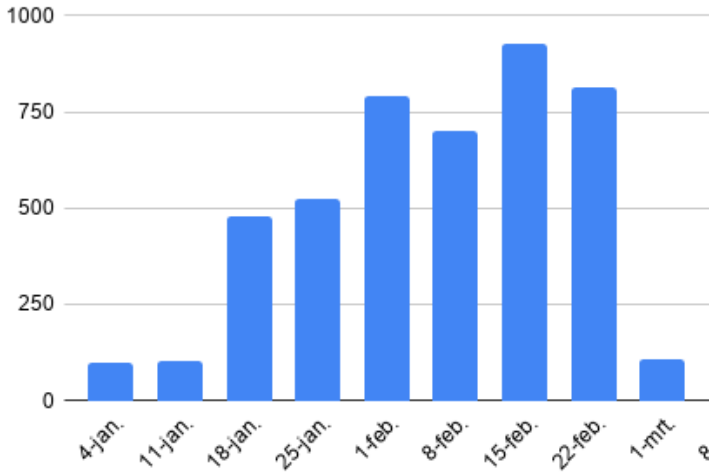

Figure 2: Number of baseline WGS tests performed per sampling date since week 1 of 2021

3. Monitoring of VOCs in Belgium

The majority of new SARS-CoV-2 infections in Belgium are currently due to VOCs. This phenomenon has not translated until now in a significant rise of cases, while this phenomenon has been observed in other European countries, including the UK, the Netherlands, France or Spain.

For samples collected during the weeks of 22nd of February and 1st of March 2021, 20I/501Y.V1 represented 57,55% and 47,71%, 20H/501Y.V2 represented 5,4% and 15,6% and 20J/501Y.V3 represented 1,84% and 2,75% of all samples analysed. The data from the week starting on 1st of March are still incomplete (121 sequences reported to date), and the changes in proportions reported in Figure 3 may therefore evolve when more data become available.
While the increase in the proportion of 501Y.V1 seems to slow down at the country level (not in every province, as discussed below), the proportion of VOCs harbouring immune escape mechanisms (501Y.V2 and 501Y.V3) continues to increase. This phenomenon will be followed, in particular as vaccination is currently being rolled out in the country.

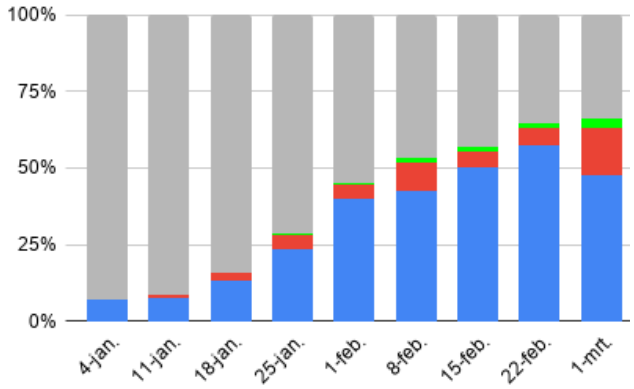

Figure 3: Share of VOCs circulating in Belgium as measured through baseline WGS tests performed per sampling date since week 1 of 2021. Colour code: Non-VOCs (grey), 501Y.V1 (blue), 501Y.V2 (red) and 501Y.V3 (green)

We currently observe different dynamics in the progression of the 501Y.V1 among the different Belgian provinces, as illustrated by the "S dropout" rate among positive PCR samples reported by federal platform laboratories. The progression is sustained in the provinces of Namur, Mons and Antwerpen, while we observe a slowdown in the progression in Gent and Brussels, and even a regression in Liège and Leuven.

	January 2021	February 2021	March 2021
Namur	10%	40%	66%
Mons	3%	31%	62%
Antwerpen	15%	39%	61%
Gent	23%	38%	43%
Brussels (ULB)	10%	38%	44%
Brussels (UCL Saint-Luc)	11%	29%	35%
Liège	7%	30%	24%
Leuven	11%	31%	19%

Table 1: Share of positive PCR results presenting a genetic marker of 501Y.V1 (S:del69)

The factors underlying these different dynamics are currently being investigated. This may be due to province-specific differences in testing & tracing strategies or the competition of 501Y.V1 with other strains more infectious or more resistant to immunity, including VOCs (501Y.V2 and 501Y.V3) and eventually other variants consistently reported in different parts of the country. In this context, a wider utilization and reporting of reflex VOC PCRs in the federal platform laboratories would allow to better understand the dynamic underlying the co-evolution of the different variants. As discussed in previous reports, we recommend to use a combination of genetic markers including S:N501Y, S:E484K, S:K417T and S:K417N to discriminate the different VOCs. Such test has been validated by the National Reference Laboratory UZ/KU Leuven and could be rapidly implemented in the other laboratories, in particular federal platform laboratories which have the advantage to be spread in different provinces and share a common IT platform facilitating further analysis.