Genomic surveillance of SARS-CoV-2 in Belgium

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

Situation update – 23rd of March 2021
(report 2021_19)

Executive summary

9.469 Belgian sequences of SARS-CoV-2 are publicly available on GISAID. Since the 1st of January 2021, 7.601 unbiased positive samples were sequenced in the context of baseline surveillance.

For baseline surveillance samples collected during the weeks of 8/3/2021 and 15/3/2021, 20I/501Y.V1 represented 74%, 20H/501Y.V2 represented 6,2% and 20J/501Y.V3 represented 3,6% of all samples analysed.

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. Another variant of interest (VOI) named B.1.525 does not have the spike N501Y mutation found in 20I/501Y.V1, 20H/501Y.V2 and 20J/501Y.V3 (P.1 and P.2) but carries the same spike E484K mutation as the P.1, P.2 and 20H/501Y.V2 variants. It shares the same H69/V70 deletion as 20I/501Y.V1 and has a unique spike F888L mutation. This VOI was initially described in the UK and Nigeria in December 2020 but has since then been detected in 23 countries spread over four continents.

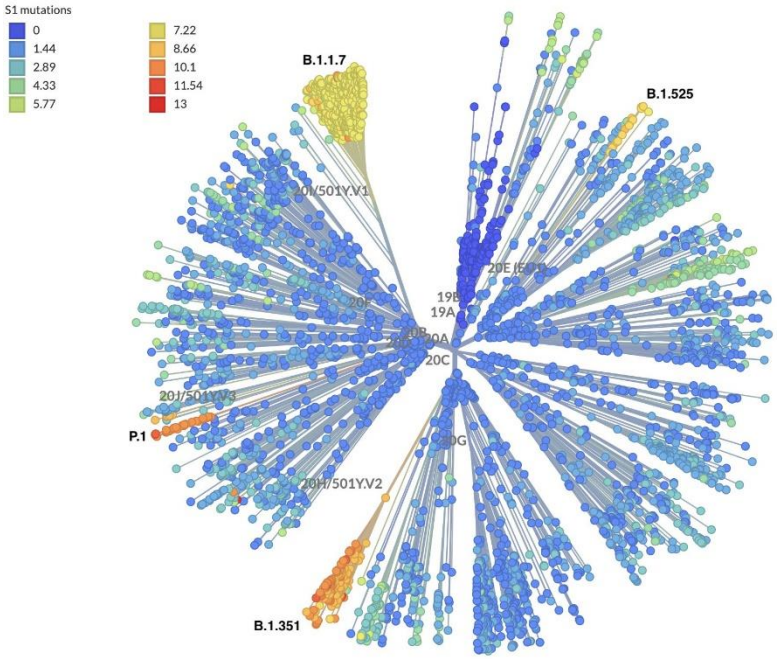

Figure 1: Mutations in the S1 region of the Spike protein may modify receptor binding and may contribute to antigenic drift. Variants of concern (VOCs) have shown excess S1 mutations as illustrated by the colour code.

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, 9.469 Belgian sequences are available on GISAID.

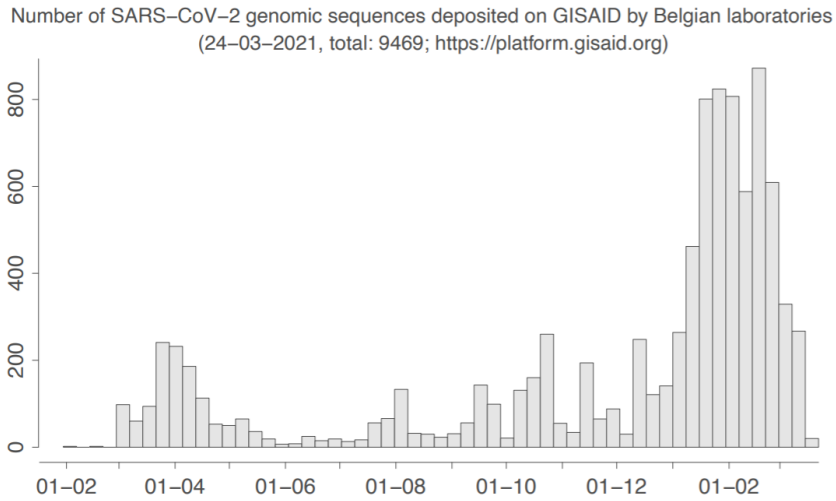

Figure 2: *Number of sequences of SARS-CoV-2 deposited on GISAID per sampling date (baseline surveillance and active surveillance)*

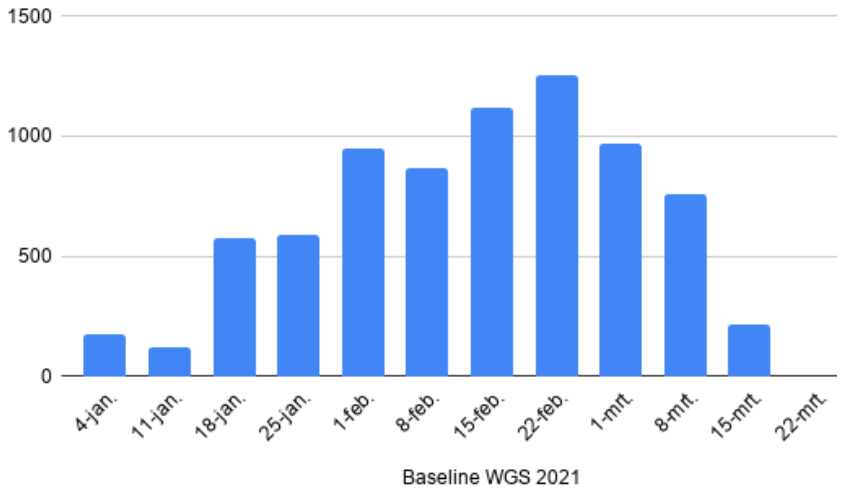

Figure 3: Number of baseline WGS tests performed per sampling date since week 1 of 2021

3. 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 VOC, principally 501Y.V1. This phenomenon had not translated into a significant rise of cases until recently. We are currently observing an increase in the number of infections and hospitalisations, which can be directly related to the spread and dominance of 501Y.V1, a more transmissible and more virulent variant compared to historical circulating strains.

For baseline surveillance samples collected during the weeks of 8/3/2021 and 15/3/2021, 20I/501Y.V1 represented 74% (increasing trend), 20H/501Y.V2 represented 6,2% (stabilizing trend to be confirmed in upcoming reports) and 20J/501Y.V3 represented 3,6% (increasing trend) of all samples analysed.

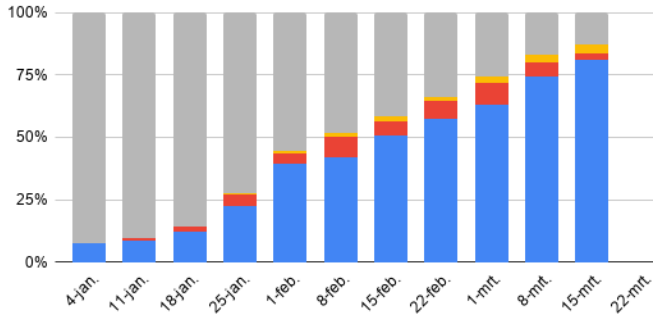

Figure 4: Share of VOCs circulating in Belgium as measured through baseline WGS tests performed per sampling date since week 1 of 2021. Colour code: Non-VOCs (grey), 501Y.V1 (blue), 501Y.V2 (red) and 501Y.V3 (yellow).

The evolution of 501Y.V1 is further followed daily using the rate of S gene target failure (SGTF) among positive cases from the 8 federal platform laboratories.

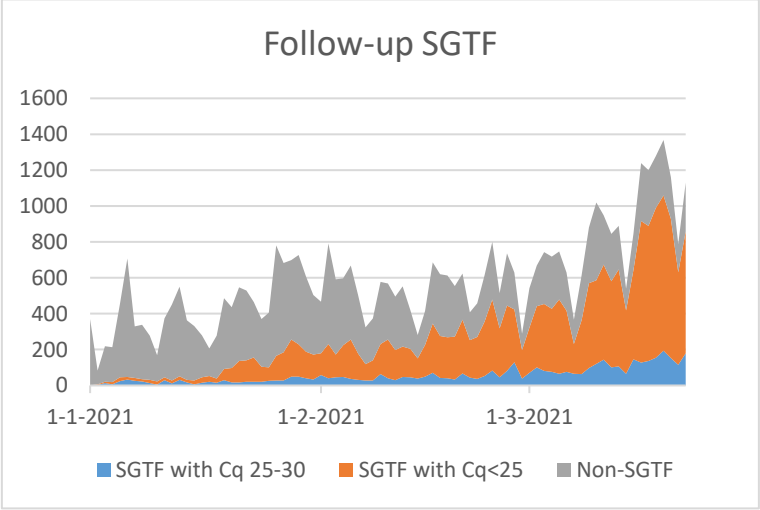

Figure 5: Evolution of the number of positive samples detected in federal platform laboratories. SGTF is caused by a deletion in position 69-70 of the spike gene and is highly presumptive of 501Y.V1 (B.1.1.7). Blue: SGTF with low viral load (Cq25-30); orange SGTF with a high viral load, consistent with infectiousness and recent infection (Cq<25); Grey: other circulating strains, including non-VOCs, 501Y.V2 and 501Y.V3.

4. Post-vaccination outbreaks in Belgium

Thanks to collaborations with the different sequencing platforms as well as the health inspectors, CRAs of nursing homes and AZG (collaborations with Cocom and Aviq are still to be consolidated in that regard), the National Reference Laboratory has been informed to date of six post-vaccination outbreaks (starting more than 7 days after complete vaccination) in nursing homes for which sequencing information is available. While we are currently investigating these outbreaks, the key information we have today are the following:

- No severe infections were reported
- Outbreaks have been caused by different variants, including VOCs and non-VOCs. We do not observe at this stage a particular VOC systematically associated with these events
- At least part of these outbreaks seems to be associated with an incomplete immune response by some residents of the nursing homes

5. Genomic surveillance of severe COVID-19 infections

As discussed in our last report, there is now evidence that each variant of the virus is not equally virulent, and this must be better investigated and monitored. Better understanding the virulence (increased or eventually decreased) of each variant should help in the future to anticipate the public health consequences of resurgence phenomena, and eventually guide vaccination strategies in the long run.

This evaluation is complex to realize due to the constantly evolving incidence and relative incidence of each variant in the general population. This information is nevertheless well captured by the current baseline surveillance system.

On top of this genomic surveillance program, we decided to add an additional arm, in order to have a better view on the frequency of each variant among severe infections. In a first phase, we will ask all sequencing platforms to systematically sequence all the positive samples of their patients entering in ICU, on top of the baseline surveillance efforts. These cases will be reported separately from the baseline surveillance. In a further stage, we might suggest extending this indication to all SARS-CoV-2 infections requiring intensive care.

6. Update on the B.1.214.2 variant of interest

As discussed in our report of 18/2/2021, we have been following the circulation of an emerging variant of interest (VOI), named B.1.214.2. While most non-VOC variants have massively decreased in frequency since the start of the year, this variant of interest with a spike insertion (VOI-SI) has been observed in most provinces of the country and seems to experience a sustained transmission (Figure 6), although represents a minority of currently circulating strains (0-15%).

The National Reference Laboratory, in collaboration with the university of Liège and several other laboratories of the SARS-CoV-2 WGS consortium and which have reported this VOI, is currently preparing an extensive report on this situation. This VOI cannot, at this stage, be considered as the cause of the current surge of cases in Belgium.

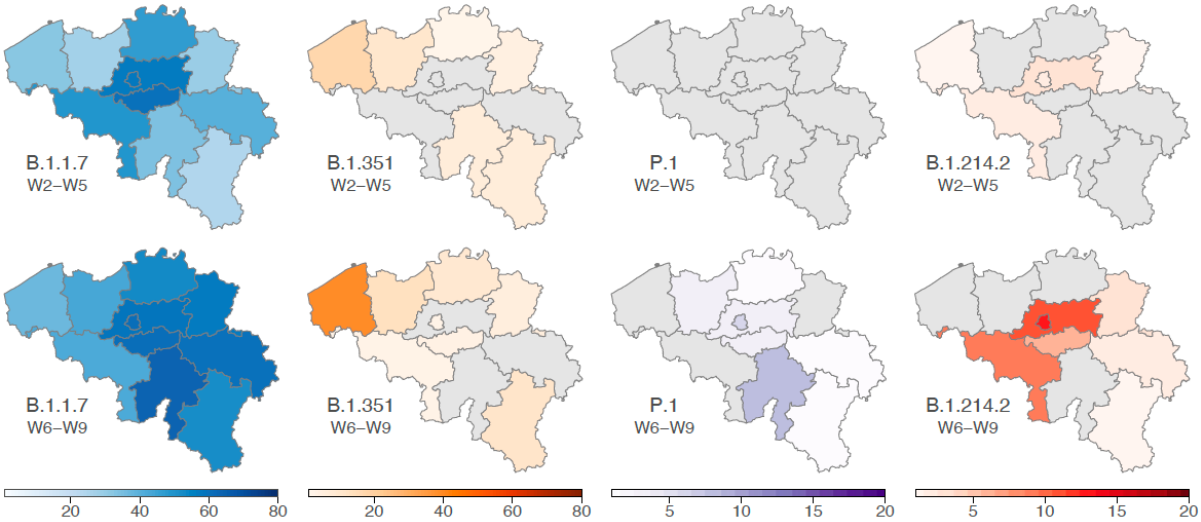

Figure 6: Relative percentage of detection of each VOC in Belgian provinces, during two successive time periods: weeks 2-5 and weeks 6-9, 2021. For the Walloon Brabant, the number of SARS-CoV-2 genomic sequences is however relatively low ($n < 50$) for both time periods under consideration, which might affect our estimates.