

# Genomic surveillance of SARS-CoV-2 in Belgium

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

Situation update – 9<sup>th</sup> of March 2021  
(report 2021\_17\_corr)

## 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 22<sup>nd</sup> of February and the 1<sup>st</sup> 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.

Previous reports can be downloaded using the following link:

<https://www.uzleuven.be/nl/laboratoriumgeneeskunde/genomic-surveillance-sars-cov-2-belgium>

Authors (National Reference Laboratory – UZ Leuven and KU Leuven):

*Piet Maes, Lize Cuypers, Guy Baele, Els Keyaerts, Elke Wollants, Marc Van Ranst, Emmanuel André.*

With the collaboration of the laboratories of UCL, ULB, UMons, UNamur, ULiège, Ugent, UAAntwerpen, 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.

## Table of content

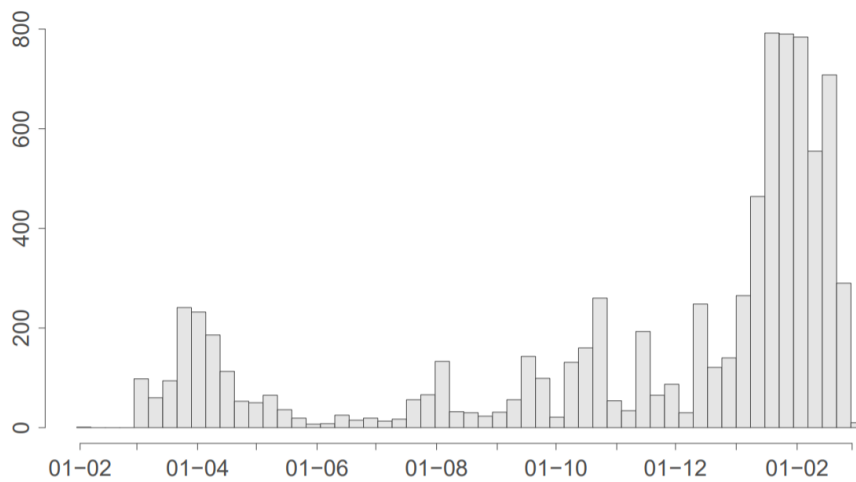
1. International context and genomic surveillance outside Belgium
2. Baseline surveillance
3. Monitoring of VOCs in Belgium

## 1. International context

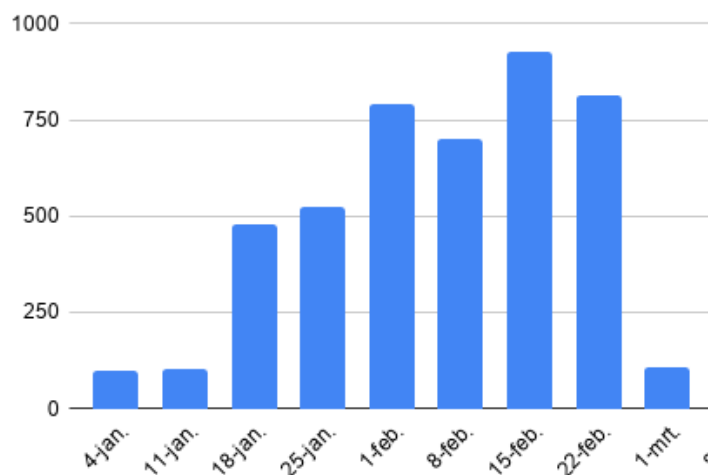
Since the end of 2020, 3 variants of concern (VOCs) have arisen independently of one another in the United Kingdom (20I/501Y.V1), South Africa (20H/501Y.V2) and Brazil (20J/501Y.V3). These variants harbour several mutations and deletions associated with (or investigated for) higher infectiousness and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



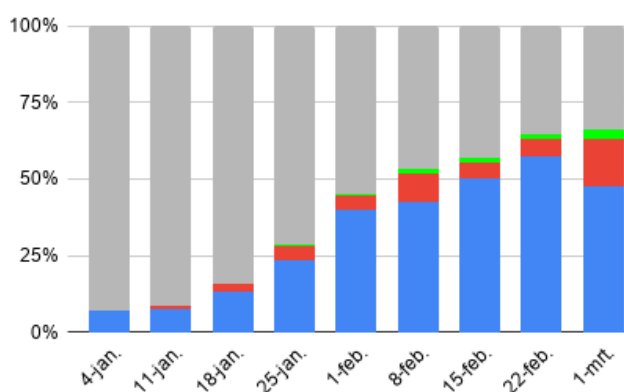
**Figure 2:** Number of baseline WGS tests performed per sampling date since week 1 of 2021

### 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 1<sup>st</sup> 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 1<sup>st</sup> 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)