Genomic surveillance of SARS-CoV-2 in Belgium

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

Situation update – 25th of February 2021
(report 2021_14_corr)

Executive summary

Genomic surveillance in Belgium is organised around 3 different arms aiming to monitor the emergence and the further spread of specific viral populations (variants of concern or VOCs) which may impact disease control and/or vaccination strategies.

Through baseline surveillance, an unbiased selection of positive samples from 24 sentinel labs (selected based on geographical dispersion and diversity of clinical patterns) are analysed in designated sequencing platforms. Currently, 6.780 Belgian sequences are available on GISAID. During weeks 6,7 and the first days of week 8, 897 samples have been sequenced as part of the baseline surveillance, among which 413 were 20I/501Y.V1 (46%), 50 were 20H/501Y.V2 (5,6%) and 11 were 20J/501Y.V3 (1,2%).

The majority of new infections occurring in Belgium are now caused by a specific VOC. Collectively, these VOCs are now driving the epidemic in Belgium and could be the cause of an upcoming rise in daily infections.

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, UAntwerpen, Jessa ZH, AZ Delta, AZ Klina, IPG, AZ St Lucas Gent, OLV Aalst, Imelda, ZNA and UZ Leuven/KU Leuven.

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1. International context

Since the end of the year, 4 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 or P.1 and P.2). These variants harbour several mutations and deletions associated with higher infectiousness and immune escape. All variants are spreading internationally, with 4 VOCs having been detected to date in Belgium (2.009 for 20I/501Y.V1, 271 for 20H/501Y.V2, 24 for 20J/501Y.V3 – P.1 and 1 for P.2).

2. Baseline surveillance and proportion of VOCs among new infections in Belgium

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, 6.780 Belgian sequences are available on GISAID. During weeks 3 to 7, this scale-up effort allowed to cover **~5,8% of all positive samples** detected in the country. The genomic surveillance system in Belgium should focus at this stage on improving geographic coverage and meta-data collection (disease context, see below). It is not expected that baseline surveillance would improve significantly by increasing further the proportion of positive samples sequenced. For specific active surveillance activities beyond baseline surveillance, such as individual detection of well described VOCs, validated PCRs are considered as a faster and less expensive approach, and provide the information required by health inspectors.

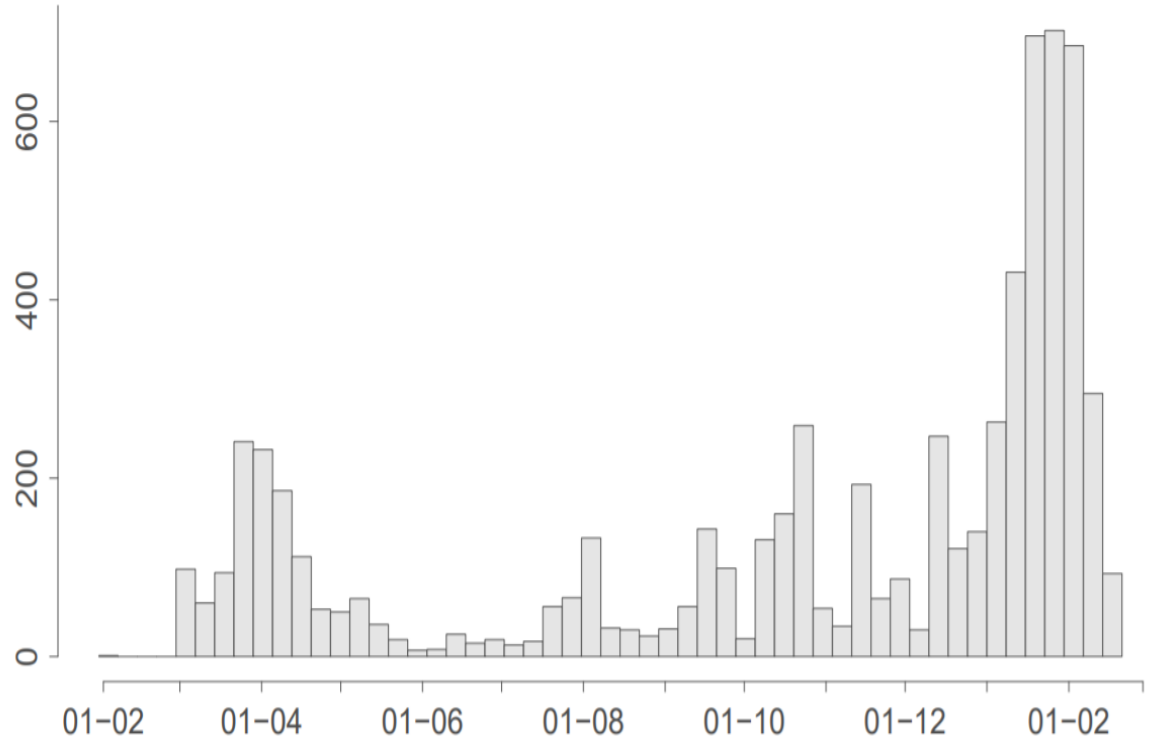

Figure 1: *Number of samples sequenced over time.*

Follow-up of 501Y.V1 (B.1.1.7) is performed using an additional indicator, which is the "S dropout" signal detected among positive COVID-19 PCRs reported by the 8 federal platform laboratories. In order to obtain the best view on the number of recent infections actively contributing to transmission, we consider for the daily follow-up only positive samples for which the N gene has a Cq value under 25. By excluding for this analysis, the samples with a Cq value between 25 and 30, we avoid including

possibly older infections and possible false positive S dropout signals that can occur when the signal is close to the limit of detection.

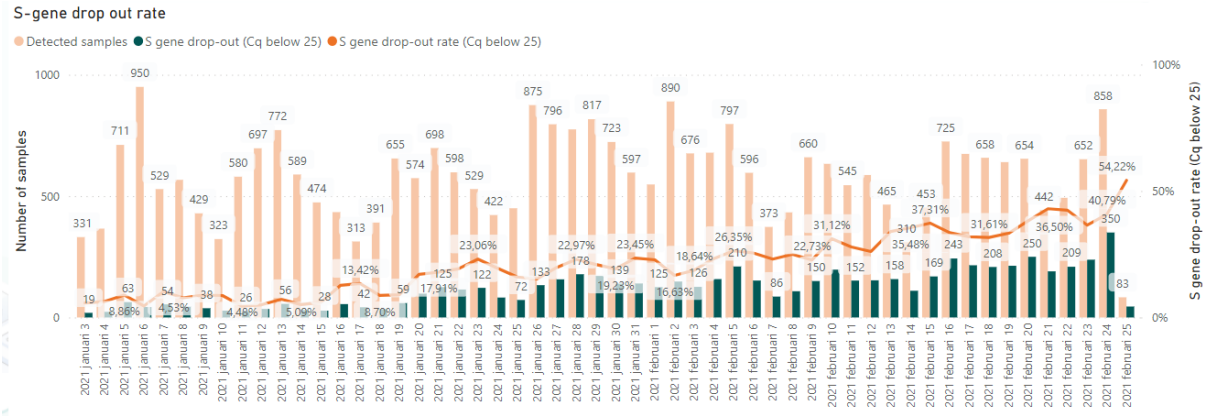

Figure 2: *Daily evolution of the proportion of infectious samples detected among all positive tests diagnosed in the federal platform laboratories (Presence of the S dropout signal and Cq <25).*

During weeks 6, 7 and the first days of week 8, 897 samples have been sequenced as part of the baseline surveillance, among which 413 were 20I/501Y.V1 (46%), 50 were 20H/501Y.V2 (5,6%) and 11 were 20J/501Y.V3 (1,2%).

3. Post-vaccination infections

With the rollout of the vaccination campaign, the number of post-vaccination infections will become more frequent. This can happen due to imperfect immune response (no vaccine is 100% effective) or to genetic particularities of the virus, a situation that would need to be rapidly identified. To date, the NRC did not identify mutations of concern among strains analysed in this context.

Until further notice or in case of specific arrangements, all clinical laboratories are asked to systematically refer these samples (regardless of the number of days post infection) to directly to the National Reference Laboratory using the dedicated laboratory form. The centralisation of the analysis of these samples will allow to maintain the required attention on the eventual genetic specificities of these strains.

4. Severity of cases

During the coming weeks, a particular attention will be given to the eventual increased prevalence of VOCs or mutations of concern among severely ill patients (ICU or hospitalized), in comparison with the proportions observed in general. The aim of this surveillance will be to eventually observe an impact on disease severity that would be caused by particular VOCs or mutations of concern. To date, the NRC did not make such observation.

5. Positivity rate in federal platform laboratories

The proportion of positive samples detected among all samples tested is an indicator used to monitor throughout the different phases of the epidemic if the number of tests performed is sufficient to support disease-control interventions. Under 5%, we estimate that the situation is under control, while a positivity rate above 10% is usually the sign that testing should be leveraged to efficiently support disease-control interventions. A positivity rate above 15% is usually the sign that the situation is out of control and that a consistent proportion of infected patients are left untested.

This rate has increased from January to February (5,9% to 7,6%), and it was between 7,7% and 11% during the last week. Increasing testing and/or enlarging testing criteria should therefore be considered.

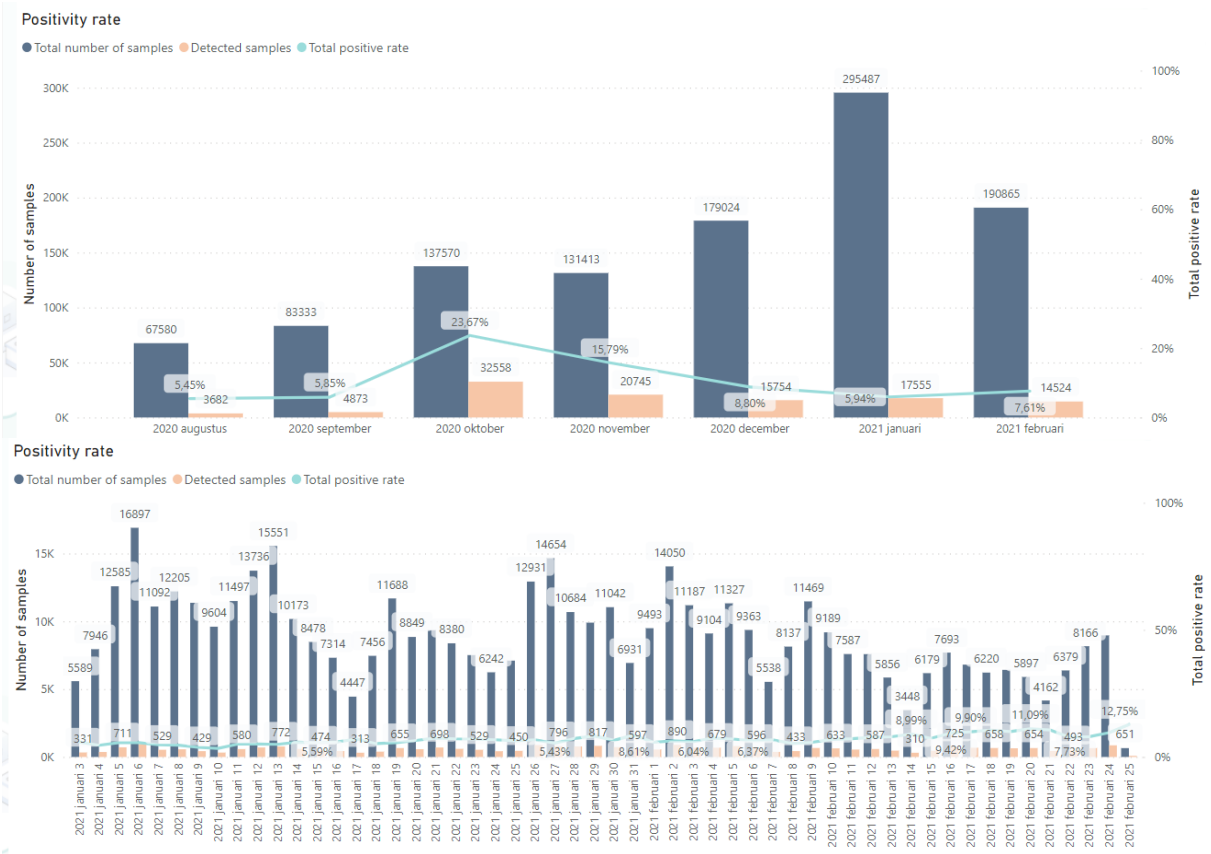

Figure 3: *Monthly (figure above) and daily (figure below) evolution of the proportion of infectious samples detected among all tests performed in the federal platform laboratories*

6. Proportion highly infectious samples among positive samples detected

The proportion of positive samples presenting a very high viral load (Cq < 15) can be seen as the number of patients diagnosed during the first days of infection, when they are highly infectious. This proportion tends to increase when the tracing is efficient in identifying recent transmissions but can also be observed in the early weeks of a resurgence.

This rate has increased significantly from January to February (14% to 23%), and the proportion was above 30% during the last week, a proportion comparable with the month of October 2020, at the start of the second wave. The risk of super-spreading events is currently important, and we therefore discourage large events, in particular when transmission cannot be prevented efficiently.

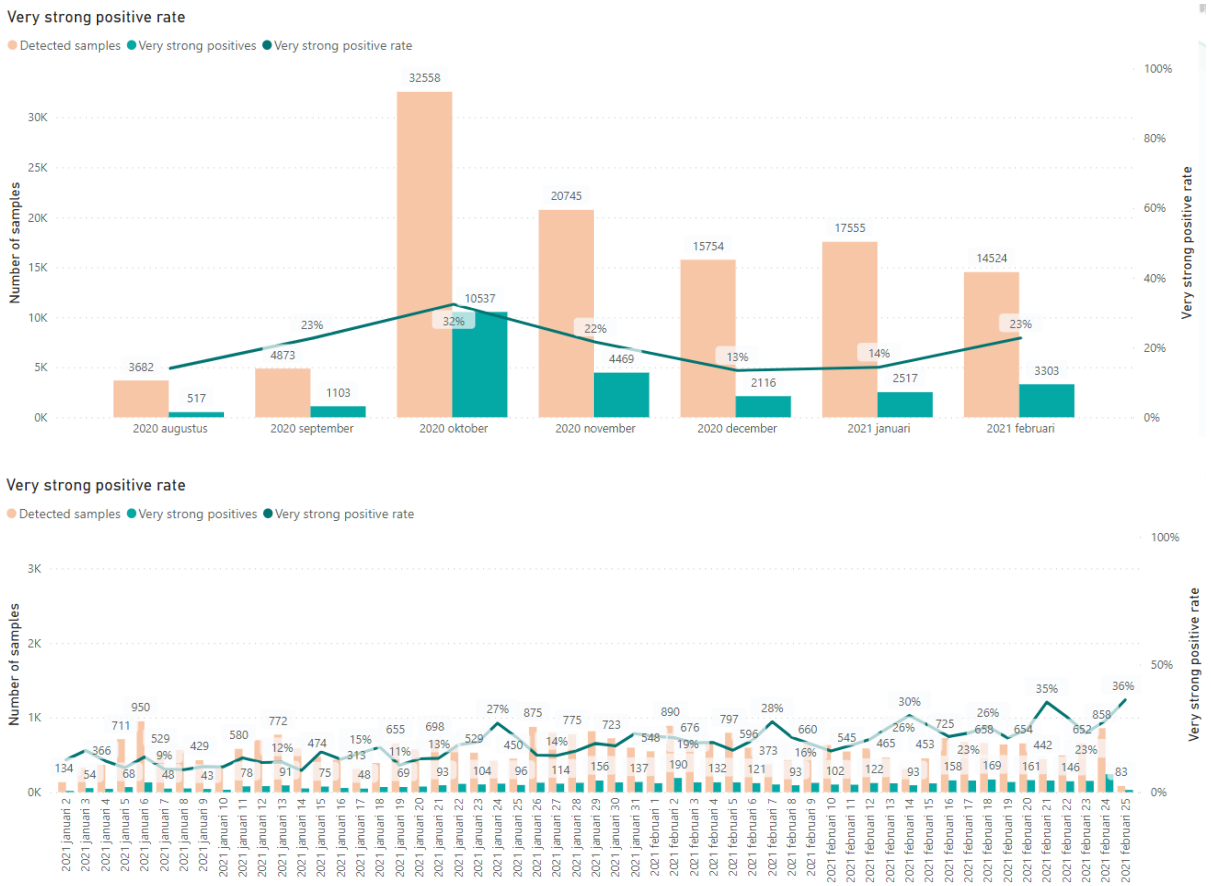

Figure 4: *Monthly (figure above) and daily (figure below) evolution of the proportion of highly infectious samples detected among all positive tests diagnosed in the federal platform laboratories (Cq <15).*