

Genomic surveillance of SARS-CoV-2 in Belgium

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

Situation update – 4th of February 2021
(report 2021_07)

Executive summary

Genomic surveillance in Belgium is based on whole genome sequencing (WGS) of a selection of representative samples, complemented with targeted active surveillance initiatives and molecular methods aiming to early detect and precisely monitor the presence of variants of concern (VOCs). Currently, 4.211 sequences of samples collected in Belgium since the start of the epidemic are available on GISAID in open access.

Since the 1st week of January 2021 (Week 1), 1.445 samples have been sequenced, among which 688 were 501Y.V1 and 90 501Y.V2. The evolution of the 501Y.V1 (B.1.1.7), is followed on a daily basis using the proportion of “S dropout” signals among positive PCR results from 8 distinct laboratories representing +/- 1/3 of all positive results reported in Belgium. Based on these numbers, we estimate the proportion of 501Y.V1 among newly diagnosed patients between 15% and 28%.

Belgium has experienced multiple introductions of VOCs during the first week of 2021 due to returning travellers. Since then, VOCs widely circulate in Belgium. The progressive shift in viral populations constitutes an objective epidemiological risk, although the impact of this phenomenon on overall COVID-19 incidence could be mitigated through a combination of interventions taking into account the higher infectiousness of emerging variants (infection control policies, broadened testing strategies, rapid outbreak management, vaccination).

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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 (501Y.V1), South Africa (501Y.V2) and Brazil (501Y.V3 and 20B/S.484K). These variants harbour a number of mutations and deletions associated with higher infectiousness and immune escape. All variants are spreading internationally, with 501Y.V1 and 501Y.V2 having been detected to date in Belgium.

2. Belgian genomic surveillance

The National Reference Centre has put in place genomic surveillance at the national level since the first introduction of the virus in February 2020. Along the way, other university centres have contributed to this surveillance effort, and the federal government has since 29/12/2020 supported a scale-up of this network, built upon the federal platform laboratories.

With the recent introduction of VOCs, genomic surveillance is to be composed in the future by 3 layers:

- Baseline surveillance (5% of positive samples from 24 sentinel laboratories) will be based on whole genome sequencing
- VOCs surveillance (reflex test to be performed on all positive samples from a restricted number of sentinel laboratories) will be based on the detection by PCR of a set of mutations and deletions of concern including but not limited to: S:del69 ; S:484K ; S:501Y). Different technical solutions are currently under evaluation.
- Active surveillance: combination of systematic test indications aiming to identify the presence of VOCs in specific groups (reflex VOC PCR among returning travellers, chronic infection, re-infection and infection after vaccination)

To date, 4.211 sequences originating from Belgian laboratories were uploaded on GISAID and are available in open access.

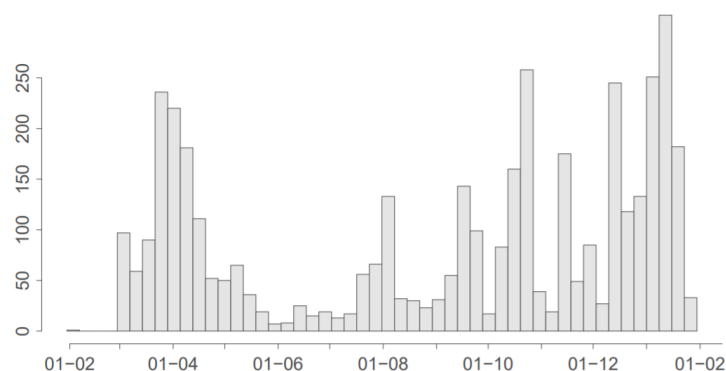


Figure 1: Number of Belgian sequences deposited on GISAID per week since the first case was diagnosed in the country. Federal support for scale-up started on 19/12/2020.

3. Participating sentinel laboratories (baseline surveillance and VOCs monitoring)

Lab	Type of lab	Region/province	Baseline surveillance	Sequencing facility	Shipment of samples	VOCs surveillance
UZA	Federal platform (including clinical lab)	Antwerp	X	Antwerp	X	X
UZ Gent	Federal platform (including clinical lab)	East-Flanders	X	Ghent	X	X
UZ Leuven	Federal platform (including clinical lab)	Flemish Brabant	X	Leuven	X	X
Liège	Federal platform (including clinical lab)	Wallonia	X	Liège	X	X
Mons	Federal platform (including clinical lab)	Wallonia	X	Ghent => Mons		X
Namur	Federal platform (including clinical lab)	Wallonia	X	Liège => Namur	Expected this week	X
UCL	Federal platform (including clinical lab)	Brussels	X	Leuven => UCL	X	X
ULB	Federal platform (including clinical lab)	Brussels	X	Leuven => ULB	X	X
Medina	Private	West-Flanders	X	Ghent		
Synlab	Private	Wallonia	X	Liège	X	
CMA	Private	Antwerp	X	Leuven	X	
AML	Private	Antwerp	X	Antwerp	Expected this week	
Labo Luc Olivier	Private	Wallonia	X	Liège	X	
ASZ Aalst	Hospital	East-Flanders	X	Ghent		
Medisch labo Bruyland	Private	West-Flanders	X	Ghent		
ZOL Genk	Hospital	Limburg	X	Leuven	X	
LMO-LMC Sint-Truiden	Private	Limburg	X	Leuven	X	
AZ Turnhout	Hospital	Antwerp	X	Leuven	X	
IFAC Vivalia	Hospital	Wallonia	X	Liège	X	
LBS	Private	Brussels				
LHUB-ULB	Hospital	Brussels	X	Antwerp	X	
CRI	Private	East-Flanders	X	Ghent		
Eupen	Hospital	German-speaking part	X	Liège	X	
AZ Sint Jan Brugge	Hospital	West-Flanders	X	Leuven	Expected this week	

4. Activity per sequencing laboratory for recent samples

	Uploaded	%
KU Leuven	472	48,7
U Liège	256	26,4
AZ Delta Hospital	104	10,7
U Gent	77	7,9
U Antwerpen	31	3,2
Jessa Hospital	20	2,1
UCLouvain	7	0,7
ULB	1	0,1
	968	

Table 1 : Number of Belgian sequences uploaded on GISAID for samples collected between 1/1/2021 and 3/2/2021 by sequencing platform. Note that all sequences have not yet been uploaded.

5. Quality assurance

Under the coordination of the national reference centre, an increasing number of sequencing laboratories are actively involved in the genomic surveillance of SARS-CoV-2 in Belgium. These laboratories have agreed to develop shared quality assurance policies to ensure high quality standards for sequencing at all time.

Criteria and quality metrics are currently being discussed to align quality across the different partners, starting from sample to sequence, including both the wet- and dry-lab analyses, as well as the assignment of strains and interpretation of mutations across the SARS-CoV-2 whole genome. Along these parameters, key performance indicators such as turn-around-time (TAT) will be followed through time. To evaluate the workflow in place in each sequencing facility, labs have been asked to share their standard operating procedures and validation files with the NRC UZ/KU Leuven, and to participate in a first round of external quality control (EQA). A cross-validation panel of three samples will be compiled by the NRC UZ/KU Leuven, using samples from each participating sequencing lab, including samples for which a VOC was identified by the primary sequencing lab. Samples will be blinded and distributed to each sequencing facility by the NRC. Template result files will need to be completed and transferred to the NRC who will compare the results of the different sequencing labs. Based on the outcome of this first EQA, procedures will be adjusted when needed. Over the course of the following months, similar EQAs are planned, including labs that initiative SARS-CoV-2 whole genome sequencing. Quality assurance meetings to which all labs that actively participate in the genomic surveillance of SARS-CoV-2 will be invited, are scheduled on a regular basis.

6. Evolution of VOCs in Belgium

Since the 1st week of 2021 (week 1), 688 501Y.V1 and 90 501Y.V2 VOCs have been confirmed by WGS.

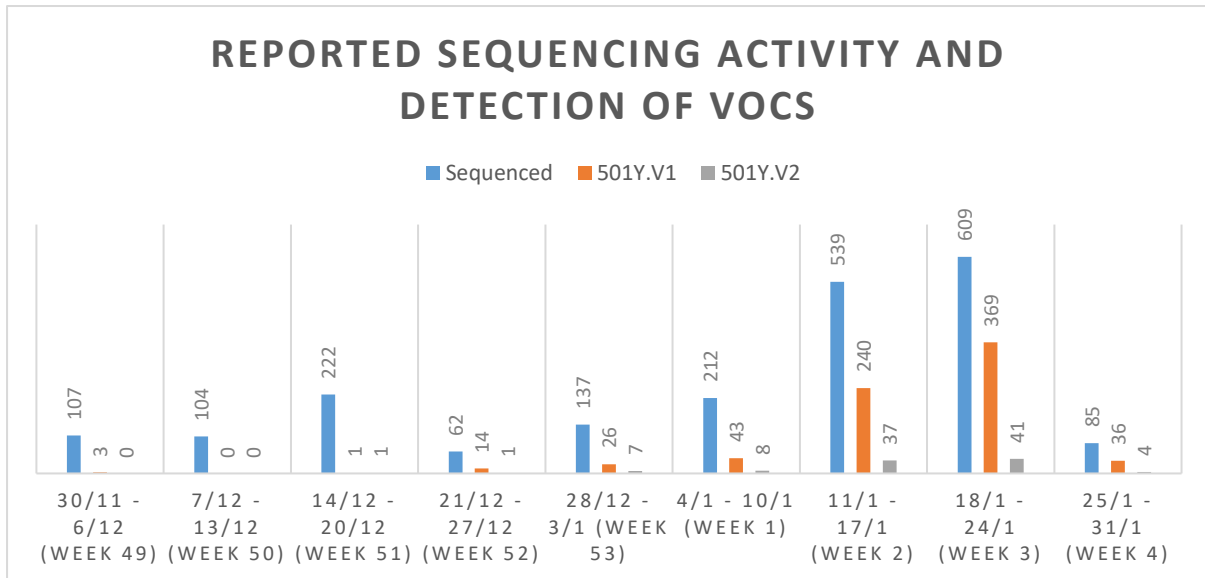


Figure 2: Reported sequencing activity and detection of VOCs since week 49 of 2020 as reported by KU Leuven, U Liège, U Gent and U Antwerpen.

1.445 sequences from samples collected since the start of the year were performed by KU Leuven, U Liège, U Gent and U Antwerpen, and 968 Belgian sequences from 2021 have currently been uploaded on GISAID, including sequences uploaded from other laboratories.

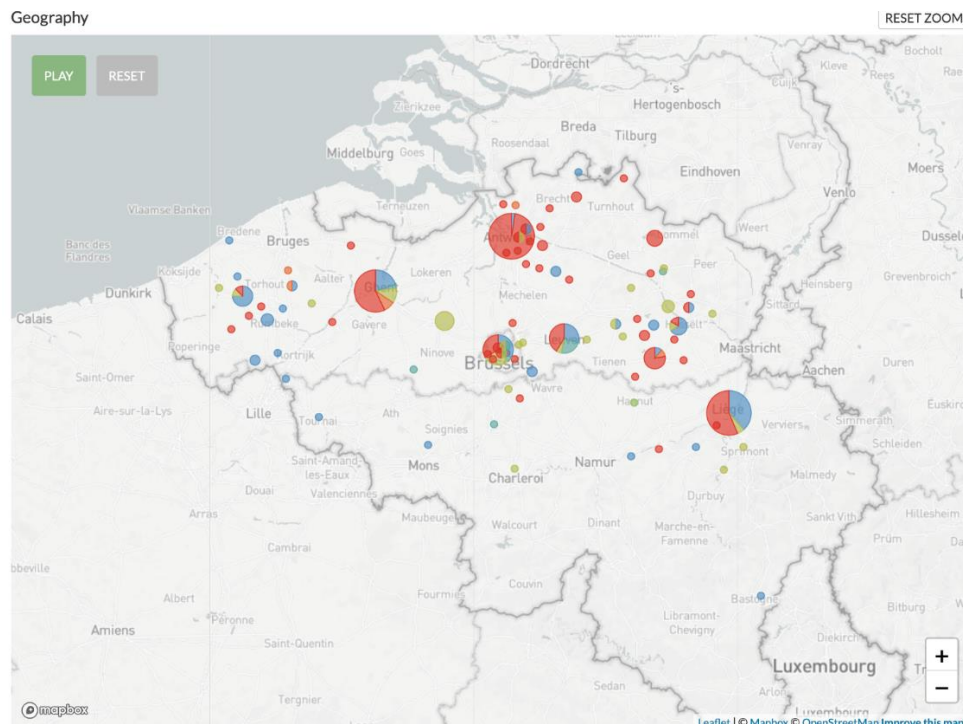


Figure 3. Origin and characterization of sequences uploaded on GISAID since 01/01/2021. 501Y.V1 is coloured in red and 501Y.V2 is coloured in orange.

Evolution over time in share of S-dropout among positive PCR results

Across the 8 laboratories composing the federal testing platform (over 559.000 PCR tests performed since 1/12/2020), the proportion of “S dropouts” among positive SARS-CoV-2 PCR remained between 15% and 25% over the last 14 days, and the overall positivity rate remained stable during the same period of time.

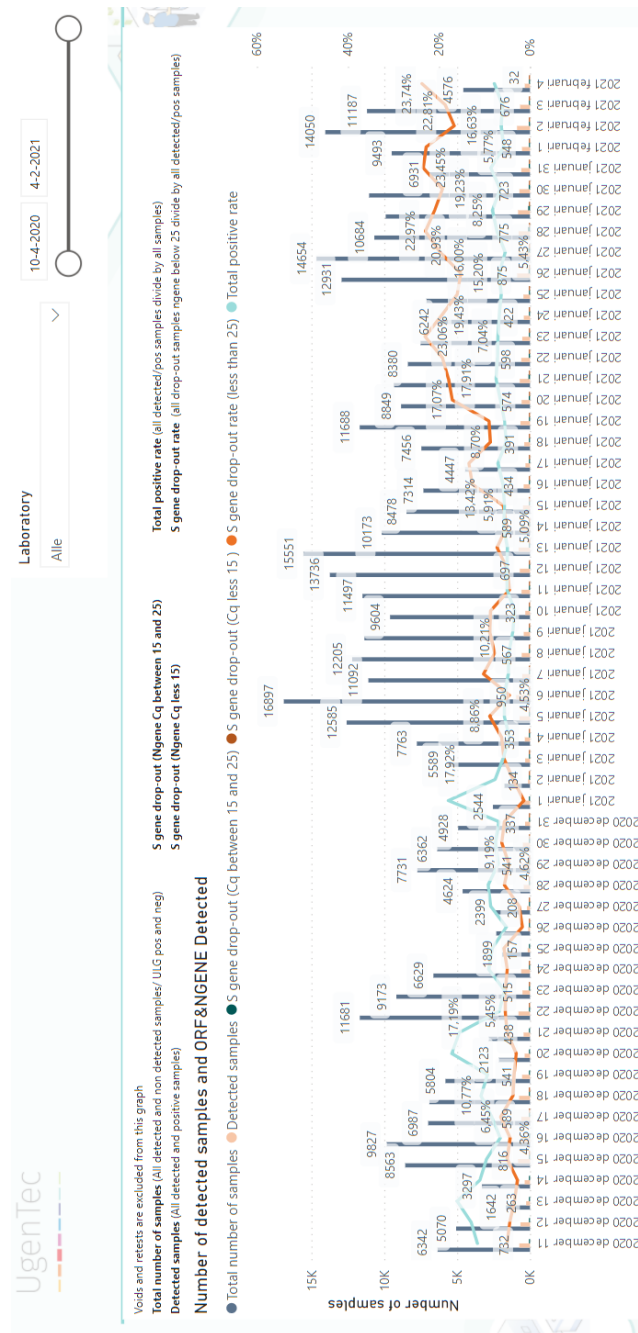


Figure 4 : Evolution of the share of S dropout (orange line) and positivity rate (light blue line) over time in the federal platform laboratories.