Genomic surveillance of SARS-CoV-2 in Belgium

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

Situation update - 28 of January 2021
(5th report for 2021)

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 aiming to early detect and precisely monitor the presence of variants of concern (VOCs). Currently, 3.368 sequences of samples collected in Belgium since the start of the epidemic are available on GISAID in open access.

Since the 1st of December 2020, a total of 1.977 sequences have been produced by the sequencing platforms participating to the federal genomic surveillance initiative. 601 501Y.V1 and 91 501Y.V2 VOCs have been identified (increasing trend; numbers are an under-estimation of the current situation). As 87% of "S dropout" PCR results are now confirmed by sequencing, it is not anymore mandatory that these strains are systematically sequenced to confirm the presence of 501Y.V1. The proportion of presumptive 501Y.V1 remains estimated between 15% and 25% of all positive strains.

Belgium has recently experienced multiple introductions of variants of VOCs, particularly since the last days of 2020. The consolidated genomic and epidemiological data are consistent with a rapidly increasing number of events of local transmission, including in schools and nursery homes. Circulation of VOCs is steadily increasing in all age groups.

Content of this document

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1. International context

Since the end of the year, 3 variants of concern (VOCs) have arisen independently of one another in the United Kingdom (501Y.V1), South Africa (501Y.V2) and Brazil (501Y.V3). These variants harbour a number of mutations and deletions associated with higher infectiousness and immune escape. All 3 variants are spreading internationally, with 501Y.V1 and 501Y.V2 having been detected in Belgium.

2. Belgian genomic surveillance

The National Reference Centre hosted at UZ Leuven – KU Leuven 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 through complementary initiatives, and the federal government has recently supported a scale-up of this network, built upon the federal platform laboratories. During the last week, a few clinical laboratories have independently started submitting a limited number of sequences on GISAID. To date, 3.368 sequences originating from Belgian laboratories were uploaded on GISAID and are available in open access. The map hereunder represents the current availability of sequences per province in Belgium.

Baseline Surveillance. A representative sampling of the positive cases in Belgium organised with the collaboration of a sentinel network of laboratories, allows to follow over the time the trends in the genetic diversity of circulating strains of SARS-CoV-2. 24 pre-selected labs were contacted by the National Reference lab and agreed to refer 5% of their positive samples for the baseline surveillance system. The first shipments of samples have been organised and the sentinel network should be fully set up in the coming weeks. The selection of participating labs was made to ensure an optimal geographical coverage and a diversity of clinical severity patterns (university hospitals, regional hospitals, GPs and community-based testing centres). The aim is to cover at all times a minimum of 2% of all positive cases in Belgium, with the possibility to increase this coverage if asked or required for public health reasons.

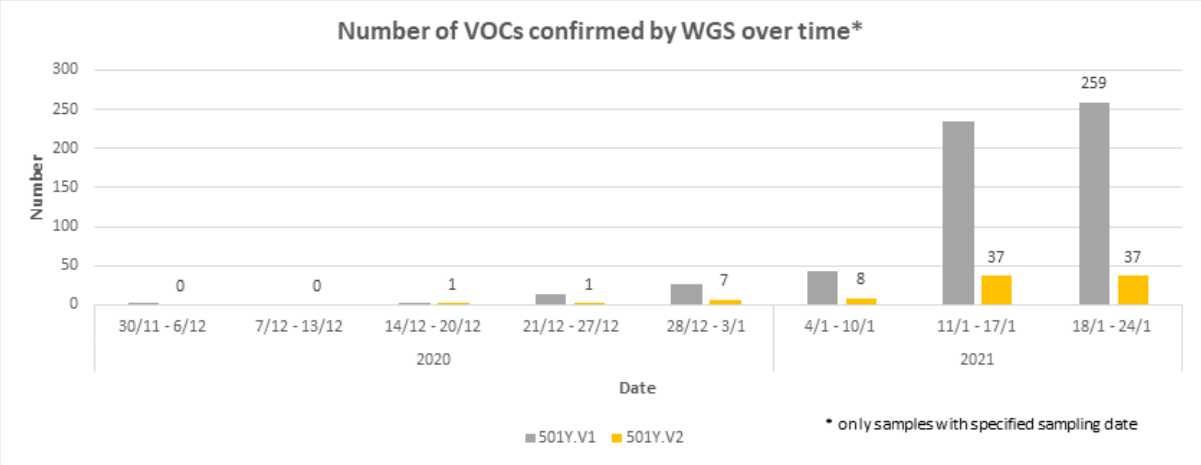
Active surveillance aims to promptly identify the introduction of emergence of (possible) variants of concern (VOCs). This surveillance is available for all clinical laboratories and does not systematically require WGS testing. Currently, active surveillance in Belgium focuses on:

- Systematic screening of VOCs among returning travellers
- Systematic screening of VOCs among atypical PCR or antigen diagnostic test results (including “S dropouts”)
- Genetic characterization of a subset of strains in the situation of outbreaks
- Genetic characterization among patients experiencing re-infection or infection after vaccination
- Genetic characterization among patients presenting a higher risk of chronic infection and mutant selection (e.g. immunocompromised, antiviral therapy)

3. Monitoring of variants of concern (VOCs)

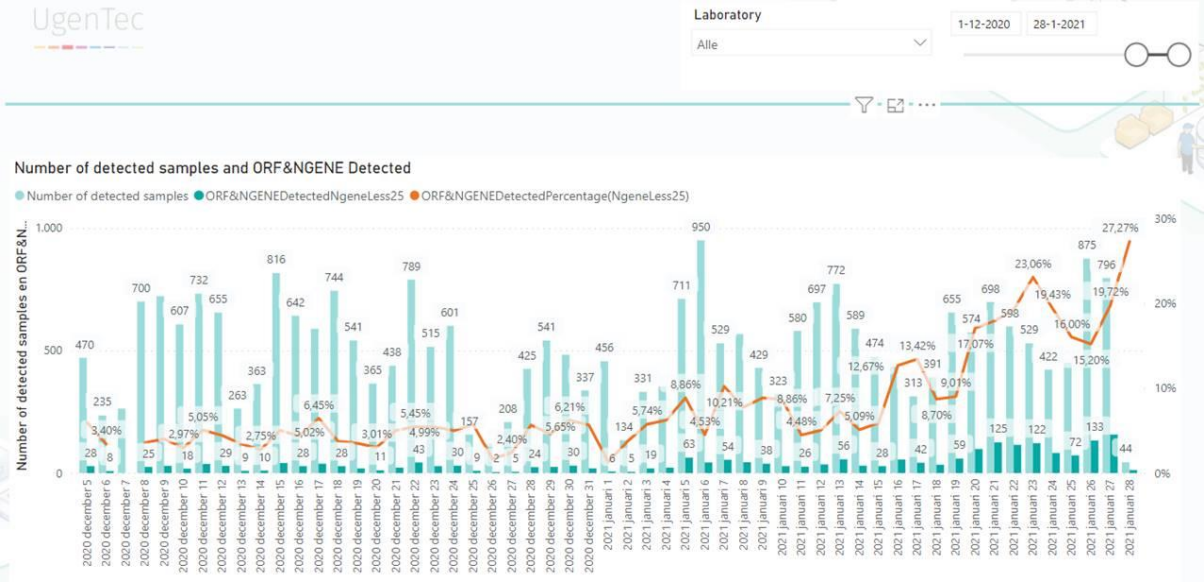
Since the 1st of December, 1.977 sequences have been produced by the participating sequencing laboratories. During the week of 18/1/2021, 7 out of 39 WGS analysis performed in the context of baseline surveillance were confirmed 501Y.V1 (20%).

The graph below highlights the increasing number of VOCs detected by WGS per week (based on sampling date) since the first VOC was detected in Belgium. Of note, due to the important number of samples, all platform bis laboratories do not systematically confirm anymore by WGS the 501Y.V1 VOC when del69 and 501Y are observed, nor confirm 501Y.V2 when 501Y is present. The figure below therefore underestimates the actual detection of VOCs.



4. Relative importance of VOCs compared to other circulating strains in Belgium

Across the 8 laboratories composing the federal testing platform (over 484.000 PCR tests performed since 1/12/2020), the proportion of “S dropouts” among positive SARS-CoV-2 PCR is between 15% and 25% (last 8 days).



In parallel, the proportion of WGS-confirmed 501Y.V1 among “S dropouts” has increased over the last 4 weeks, and was 87% during the last 2 weeks (441 confirmed among 507 sequenced for “S dropout”). Therefore, although non-501Y.V1 strains harbouring del69 (causing the S dropout) still circulate in Belgium, the amount and the evolution of “S dropout” PCR results can currently be considered as a very good marker of the evolution of the 501Y.V1 in Belgium.

We received the distribution by age and week for “S dropouts” and “non S dropouts” positive PCR results from 7 out of 8 platform bis laboratories for the last 4 weeks. This data supports the introduction of 501Y.V1 in the first week of the year (returning travellers), mainly detected in the adult population. More recently, a higher number of these strains have been detected in younger and older groups, possibly resulting of a combination of factors: higher transmissibility including in nursing homes and the educational sector, and an intensified testing strategy offered in these groups.

Week	Namur	# S-gene dropouts					# non S-gene dropouts				
		0 – 19 years	20 - 39 years	40 - 59 years	60 – 79 years	80 – 99 years	0 – 19 years	20 - 39 years	40 - 59 years	60 – 79 years	80 – 99 years
28-12 – 3/1		0	1	0	0	0	29	74	49	22	1
4/1 – 10/1		1	6	5	1	4	47	167	105	42	6
11/1 – 17/1		0	3	0	4	8	55	97	87	35	1
18/1 – 24/1		3	4	4	4	15	48	69	91	45	9

Week	Leuven	# S-gene dropouts					# non S-gene dropouts				
		0 – 19 years	20 - 39 years	40 - 59 years	60 – 79 years	80 – 99 years	0 – 19 years	20 - 39 years	40 - 59 years	60 – 79 years	80 – 99 years
28-12 – 3/1		1	2	2	1	0	31	60	48	29	9
4/1 – 10/1		3	1	0	1	0	40	77	60	30	20
11/1 – 17/1		1	10	3	5	2	53	98	62	26	18
18/1 – 24/1		28	9	11	7	7	35	92	58	23	40

Week	Liège	# S-gene dropouts					# non S-gene dropouts				
		0 – 19 years	20 - 39 years	40 - 59 years	60 – 79 years	80 – 99 years	0 – 19 years	20 - 39 years	40 - 59 years	60 – 79 years	80 – 99 years
28-12 – 3/1		0	0	0	0	0	2	5	9	6	3
4/1 – 10/1		0	0	0	0	0	9	28	40	26	42
11/1 – 17/1		0	3	0	0	0	11	20	38	15	28
18/1 – 24/1		2	2	1	0	0	12	12	7	12	24

Week	ULB	# S-gene dropouts					# non S-gene dropouts				
		0 – 19 years	20 - 39 years	40 - 59 years	60 – 79 years	80 – 99 years	0 – 19 years	20 - 39 years	40 - 59 years	60 – 79 years	80 – 99 years
28-12 – 3/1											
4/1 – 10/1											
11/1 – 17/1		28	58	56	14	12	53	195	143	42	18
18/1 – 24/1		19	50	57	18	28	53	139	108	32	30

Week	Mons	# S-gene dropouts					# non S-gene dropouts				
		0 – 19 years	20 - 39 years	40 - 59 years	60 – 79 years	80 – 99 years	0 – 19 years	20 - 39 years	40 - 59 years	60 – 79 years	80 – 99 years
28-12 – 3/1		0	1	3	1	0	49	154	124	62	16
4/1 – 10/1		0	2	2	1	0	46	189	172	85	22
11/1 – 17/1		0	3	4	2	1	80	179	138	91	24
18/1 – 24/1		2	5	4	2	1	101	141	176	78	34

Week	UCL	# S-gene dropouts					# non S-gene dropouts				
		0 – 19 years	20 - 39 years	40 - 59 years	60 – 79 years	80 – 99 years	0 – 19 years	20 - 39 years	40 - 59 years	60 – 79 years	80 – 99 years
28-12 – 3/1		1	1	3	1	0	52	141	113	27	6
4/1 – 10/1		0	0	0	0	0	80	281	175	55	9
11/1 – 17/1		0	23	5	6	0	96	396	239	61	14
18/1 – 24/1		14	30	20	5	0	69	174	128	52	31

Week	Antwerp	# S-gene dropouts					# non S-gene dropouts				
		0 – 19 years	20 - 39 years	40 - 59 years	60 – 79 years	80 – 99 years	0 – 19 years	20 - 39 years	40 - 59 years	60 – 79 years	80 – 99 years
28-12 – 3/1		5	4	4	0	1	58	127	122	54	66
4/1 – 10/1		9	10	5	1	0	73	177	186	59	61
11/1 – 17/1		11	26	22	1	0	85	171	142	65	67
18/1 – 24/1		63	32	35	5	1	137	143	124	41	40

Week	Total	# S-gene dropouts					# non S-gene dropouts				
		0 – 19 years	20 - 39 years	40 - 59 years	60 – 79 years	80 – 99 years	0 – 19 years	20 - 39 years	40 - 59 years	60 – 79 years	80 – 99 years
28-12 – 3/1		7	9	12	3	1	221	561	465	200	101
4/1 – 10/1		13	19	12	4	4	295	919	738	297	162
11/1 – 17/1		40	126	90	32	23	433	1156	849	335	168
18/1 – 24/1		131	132	132	41	52	455	770	690	283	207

Since 11/1/2021, we observe among all age groups a higher increase rate from one week to the other in the “S gene dropout” group compared to the “non S gene dropout” group. This is consistent with the observations previously made of a higher infectiousness of the 501Y.V1 variant.

% increase from one week to the other	Total	# S-gene dropouts						# non S-gene dropouts				
		0 – 19 years	20 - 39 years	40 - 59 years	60 – 79 years	80 – 99 years		0 – 19 years	20 - 39 years	40 - 59 years	60 – 79 years	80 – 99 years
28-12 – 3/1												
4/1 – 10/1		186%	211%	100%	133%	400%		133%	164%	159%	149%	160%
11/1 – 17/1		308%	663%	750%	800%	575%		147%	126%	115%	113%	104%
18/1 – 24/1		328%	105%	147%	128%	226%		105%	67%	81%	84%	123%

5. Strengthened surveillance of VOCs

- Technical validation of rapid targeted multi-target PCRs aiming to detect and presumptively characterize VOCs is ongoing in two laboratories
- A meeting with all clinical laboratories (>100 participants) has been organised on 28/1/2021 to explain the genomic surveillance plan and the current epidemiological situation
- A meeting with all provincial governors has been organised on 28/1/2021 to explain the current epidemiological situation and the implications
- Several media communications have been made to explain the current situation (FR and NL media)
- Discussions with RIZIV-INAMI are ongoing to consolidate the genomic surveillance initiative