

Genomic surveillance of SARS-CoV-2 in Belgium

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

Situation update – 30th of March 2021

(report 2021_20)

Executive summary

12.122 Belgian sequences of SARS-CoV-2 are publicly available on GISAID. Since the 1st of January 2021, 8.161 unbiased positive samples were sequenced in the context of baseline surveillance.

For baseline surveillance samples collected during the last two weeks, 20I/501Y.V1 represented 77,4%, 20H/501Y.V2 represented 7,7% and 20J/501Y.V3 represented 3,7% of all samples analysed.

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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, the list of variants of concern (VOCs) and variants under investigation has grown regularly, and we expect that this list will continue to increase as a consequence of both the upscaling of genomic surveillance around the world and the increased selective pressures exerted by the combination of partial herd immunity and stepwise vaccination rollout.

	Cases detected in Belgium (GISAID 30/03/2021)	Regions with active circulation
B.1.1.7 (20/501Y.V1)	3909	All regions
B.1.351 (20H/501Y.V2)	495	Southern African region
P.1 (20J/501Y.V3)	131	Latin America
P.2	2	Latin America
B.1.427	1	Northern America
B.1.526	0	Northern and Latin America
B.1.525	15	Western Africa
B.214.2	254	Europe
A.2.5	0	Central America

Table 1: Updated list of internationally recognized variants of concern (Red) and variants currently monitored or under investigation in Belgium (Orange).

These variants are characterized by numerous mutations, deletions and insertions highlighted in Table 2. A number of these genetic variations typically interfere with key domains of the Spike protein, such as the receptor binding domain, or in regions considered as epitopes for human antibodies.

B.1.1.7 (20J/501Y/V1)	S:L18F																		Yes
B.1.351 (20H/501Y/V2)	S:H69 del	Yes																	Yes
P.1 (20J/501Y/V3)	S:L141 del																		Yes
P.2	S:Y144 del			Yes															
B.1.427	S:ins 214																		
B.1.526	S:ins 215																		
B.1.525	S:D215G								Yes										Yes
B.214.2	S:Q414K									Yes									Yes
A.2.5	S:N450K										Yes								Yes
	S:L452R											Yes							Yes
	S:K417N								Yes										
	S:K417T								Yes										
	S:E484K								Yes	Yes									Yes
	S:N501Y								Yes	Yes	Yes								Yes
	S:D614G								Yes	Yes	Yes								Yes
	S:A701V									Yes									
	S:V1176F										Yes								
	OffA:120 del																	Yes	
	N:D3L																		Yes

Table 2: Non-exhaustive list of mutations S protein of the VOCs and variants under investigation.

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, 12.122 Belgian sequences are available on GISAID.

Number of SARS-CoV-2 genomic sequences deposited on GISAID by Belgian laboratories (30-03-2021, total: 12122; <https://platform.gisaid.org>)

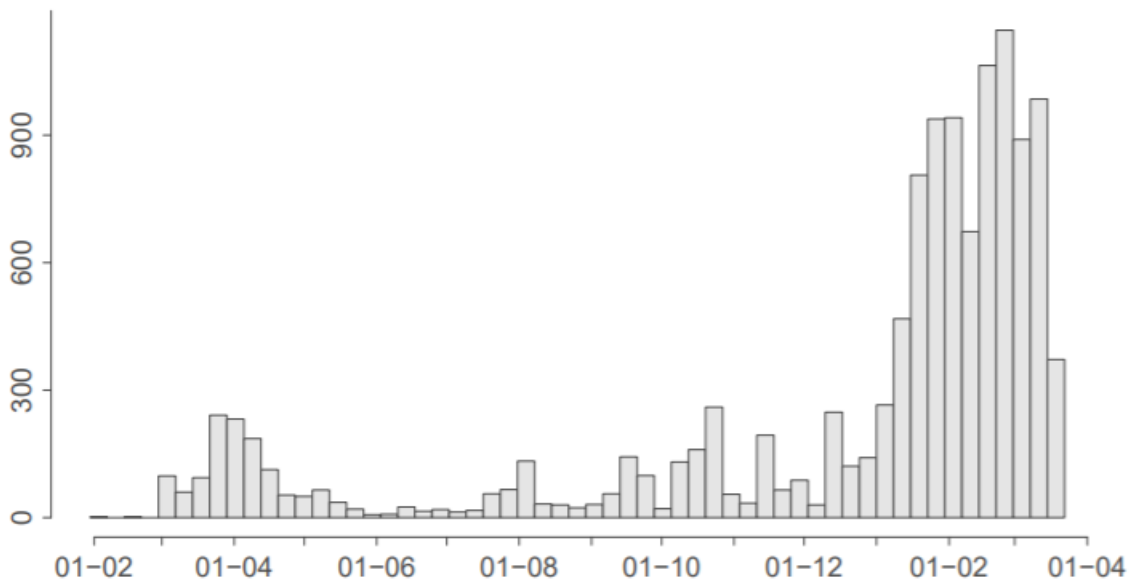


Figure 1: Number of sequences of SARS-CoV-2 deposited on GISAID per sampling date (baseline surveillance and active surveillance)

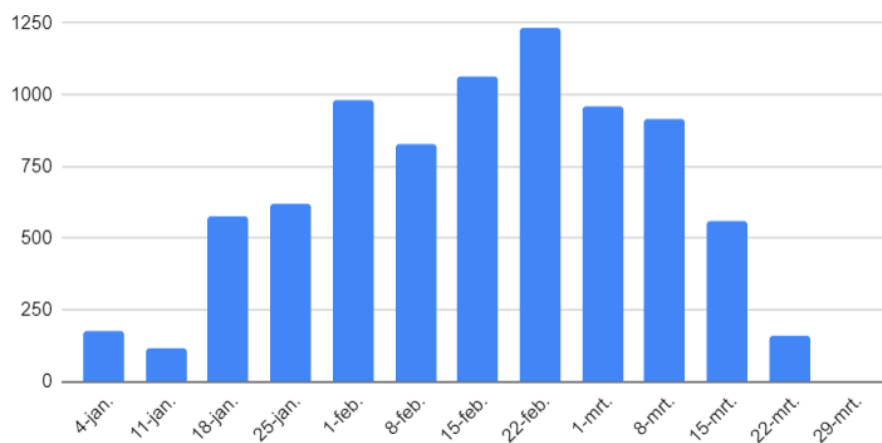


Figure 2: Number of baseline WGS tests performed per sampling date since week 1 of 2021

3. Monitoring of VOCs in Belgium

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.

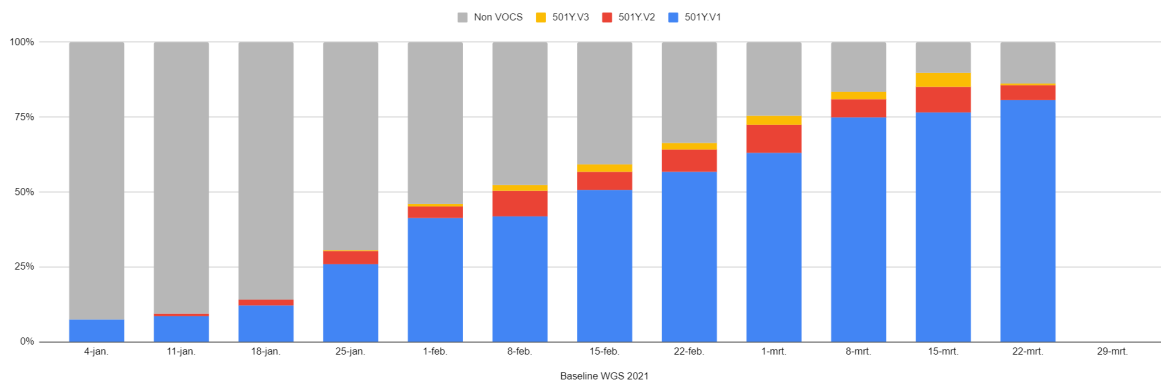


Figure 3: Share of VOCs circulating in Belgium as measured through baseline WGS tests performed per sampling date since week 1 of 2021. Colour code: Non-VOCs (grey), 501Y.V1 (blue), 501Y.V2 (red) and 501Y.V3 (yellow).

4. Update on B.1.214.2 variant of interest

There has recently been attention in the media about a new “Belgian Variant”, and several points reported are incorrect or imprecise.

First, with regard to the place where this variant originated, there is currently no evidence that the genetic markers of the B.1.214.2 lineage emerged in the Republic of the Congo. The B.1.214 lineage (now renamed B.1.214.1) was described in April 2020 in Central Africa, but none of the African sequences harbour the additional spike mutations, insertion and deletions which are typical of the B.1.214.2.

Second, although the B.1.214.2 lineage now actively circulates in Belgium, such strains have been reported in Switzerland (22/11/2020), the United Kingdom (5/12/2020) and France (28/12/2020) before the first case was described in Belgium (3/1/2021). This situation may change as retrospective sequencing efforts are ongoing in Belgium and several other European countries.

Finally, the Figure hereunder highlights that the strains currently circulating in Belgium do not belong to the same cluster, suggesting that the current situation in Belgium is consequent to multiple parallel introduction events during the End-of-the-year holidays (week 53 of 2020 and week 1 of 2021).

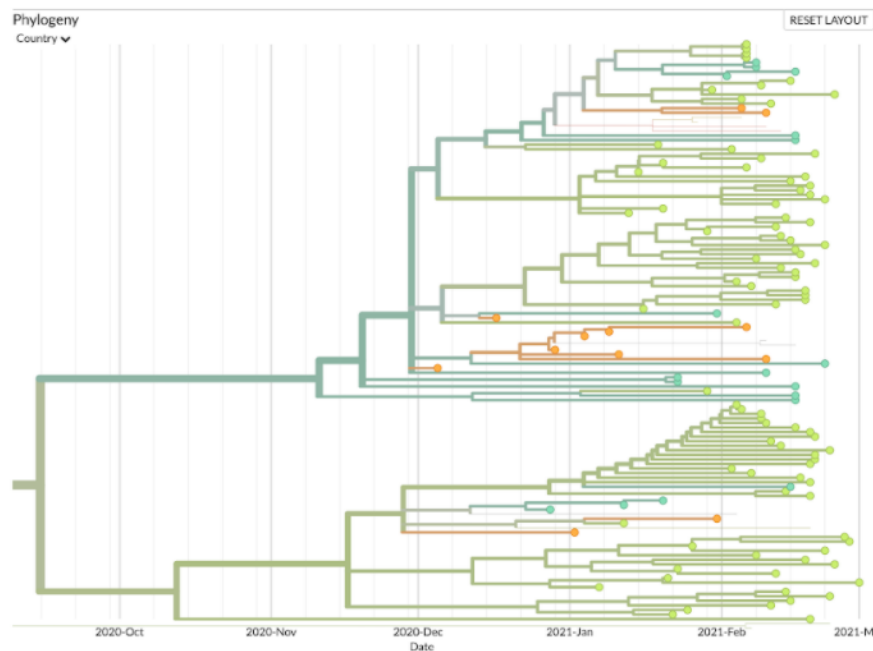


Figure 4: Clustering of sequences of B.1.214.2 originating from Belgium (light green), France (orange) and the United Kingdom (darker green)

As a conclusion, at the current state of our knowledge, we estimate that there is a significant probability that this variant of interest emerged in the European continent somewhere around October 2020. It is still unclear to us why B.1.214.2 seems to circulate well in Belgium, and several studies are ongoing to better understand the virulence and the eventual immune escape mechanisms of this variant.