

# Genomic surveillance of SARS-CoV-2 in Belgium

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

Situation update – 13<sup>th</sup> of April 2021  
(report 2021\_22)

## Executive summary

13.932 Belgian sequences of SARS-CoV-2 are publicly available on GISAID. Since the 1st of January 2021, 11.205 unbiased positive samples were sequenced in the context of baseline surveillance.

For baseline surveillance samples collected during the last two weeks,

- B.1.1.7 (20/501Y.V1) represented 86,3%
- B.1.351 (20H/501Y.V2) represented 4,8%
- P.1 (20J/501Y.V3) represented 4,2%

The current epidemic surge is linked to a rapid increase in the total number of infections with B.1.1.7. Other variants of concern, in particular B.1.351 and P.1 actively circulate and tend to increase although this phenomenon is partly occulted by the recent and probably transient surge of B.1.1.7 infections.

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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, Briant network, ZNA, AZ St Jan Brugge, and UZ Leuven/KU Leuven.

Previous reports can be downloaded using the following link:

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

## Table of content

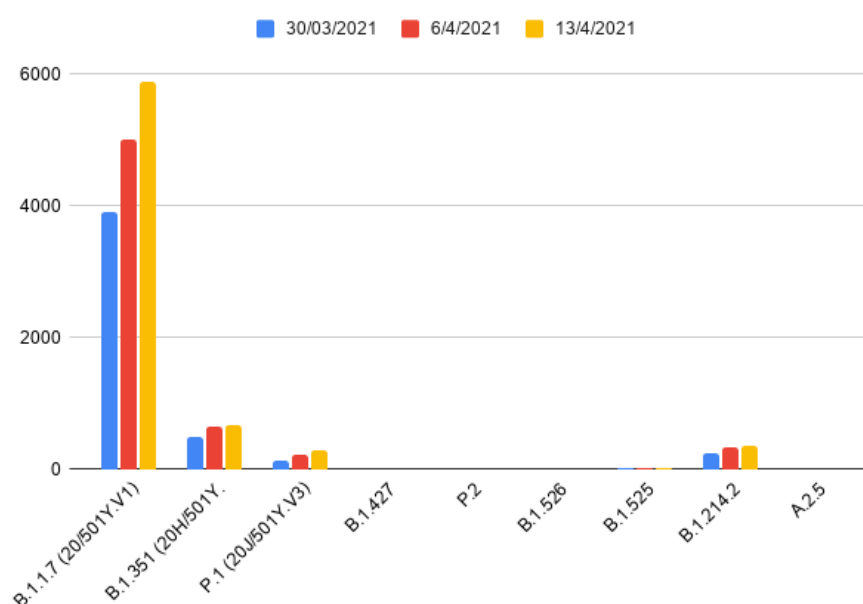
1. Baseline surveillance
2. Monitoring of VOCs in Belgium
3. Current situation with regard to the circulation of B.1.525 in Belgium
4. Under-utilisation of testing and positivity rate during the recent epidemic surge

## 1. Baseline surveillance

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 reported in Belgium (13/4/2021)	Epidemiological situation in Belgium (6/4/2021)	Regions with active circulation
B.1.1.7 (20/501Y.V1)	5890	Dominant lineage	All regions
B.1.351 (20H/501Y.V2)	676	Emerging	Southern African region
P.1 (20J/501Y.V3)	279	Emerging	Latin America
B.1.427	1	Sporadic	Northern America
P.2	2	Sporadic	Latin America
B.1.526	0	Unreported	Northern and Latin America
B.1.525	27	Sporadic (increasing)	Western Africa
B.1.214.2	351	Emerging	Europe
A.2.5	0	Unreported	Central America

**Table 1:** Updated list of internationally recognized variants of concern (red) and variants of interest (orange) and number of sequenced strains in Belgium as reported in GISAID.



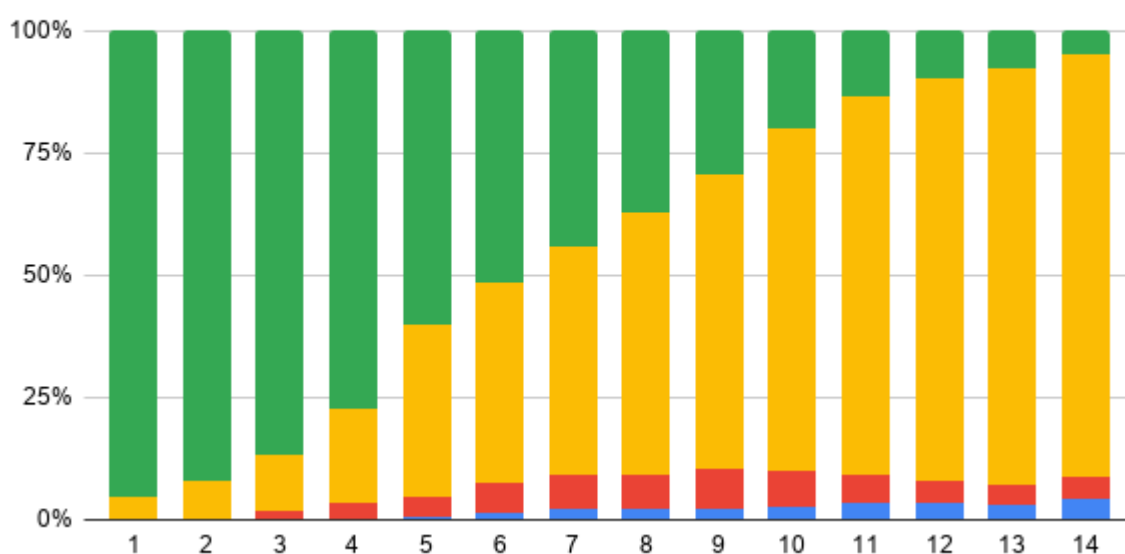
**Figure 1:** Number and evolution of Belgian sequences available on GISAID for variants of concern and variants of interest.

## 2. 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 variant of concern (VOC), principally B.1.1.7 (501Y.V1). This phenomenon had not translated into a significant rise of cases until recently. We recently experienced a notable increase in the number of infections and resulting hospitalisations, which can be related to the spread and dominance of 501Y.V1, a more transmissible and potentially more virulent variant compared to historical circulating strains.

For baseline surveillance samples collected during the last two weeks,

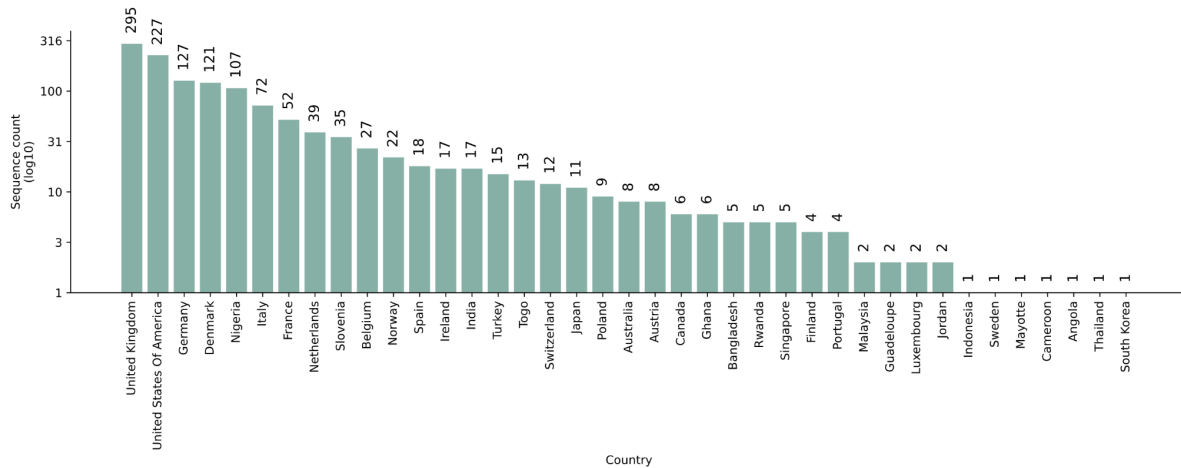
- B.1.1.7 (20/501Y.V1) represented 86,3%
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**Figure 2:** Share of VOCs circulating in Belgium as measured through baseline WGS tests performed per sampling date since week 1 of 2021. Colour code: Non-VOCs (green), 501Y.V1/B.1.17 (yellow), 501Y.V2/B.1.351 (red) and 501Y.V3/P.1 (blue).

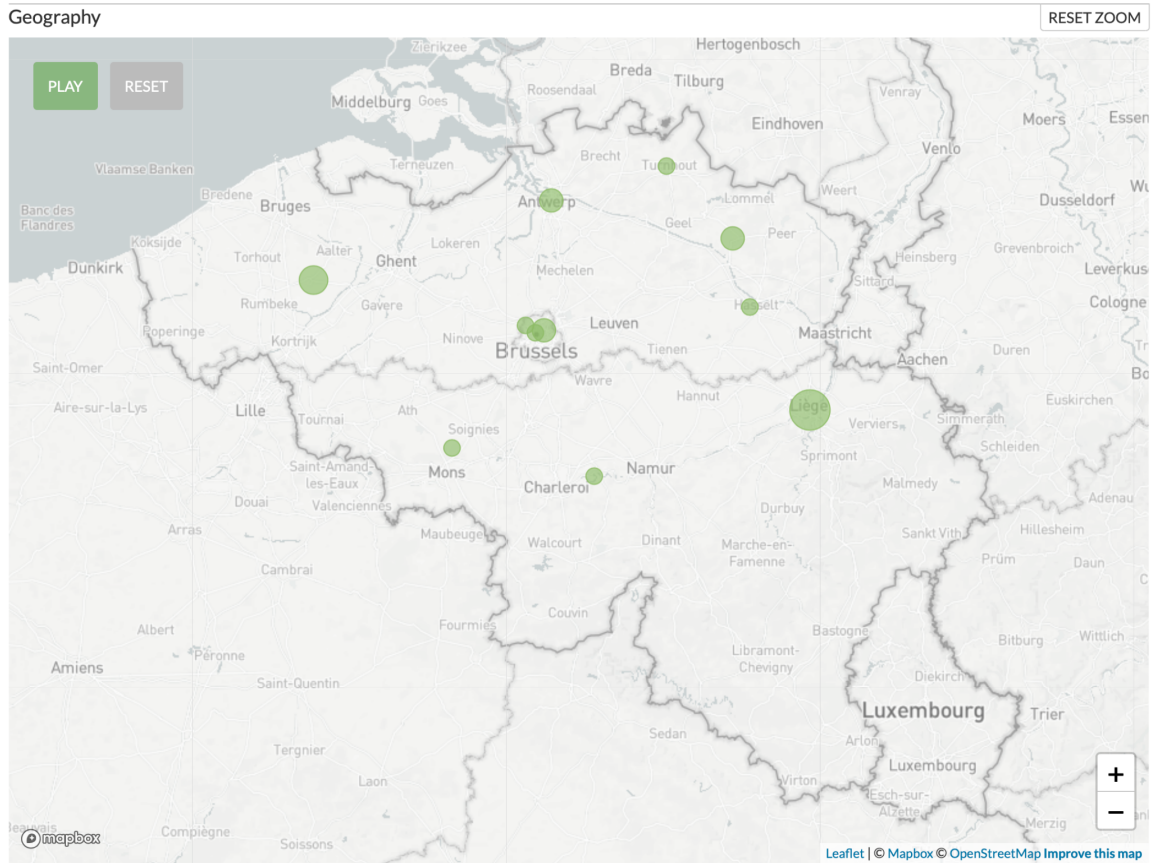
### 3. Current situation with regard to the circulation of B.1.525 in Belgium

Lineage B.1.525 - which is characterized by a series of mutations including E484K - appears in many countries across the world, including Belgium, as shown in Figure 3. Out of a total of 1,511 genome sequences, 27 were found to date in Belgium.



**Figure 3:** Sequence count per country for genome sequences of lineage B.1.525. The height of the bar is the logged number and the numbers above the bar are the raw counts. Source: [https://cov-lineages.org/global\\_report\\_B.1.525.html](https://cov-lineages.org/global_report_B.1.525.html)

Lineage B.1.525 has so far appeared in most Belgian provinces, except for East Flanders and Luxemburg (see Figure 4). Overall, the detected number of infections is still quite low and does not seem to be increasing rapidly, although new cases are still being detected regularly. Figure 5 shows that Belgian B.1.525 genomes cluster mostly with genomes from Germany and England. B.1.525 was first detected by genome sequence in mid-December in Nigeria but was also quickly found in cases in the United Kingdom, France, and elsewhere. After only two months, B.1.525 represented over 20% of genomes sequenced in Nigeria. An early genome sequence from Angola predates the earliest Nigerian genomes, and it's unclear from available records whether travel between these countries offers an explanation for these findings. Due to the rather limited number of sequences available from Western African countries, we cannot definitively state at this stage if the Belgian infections originate from European travels or beyond (in particular Western Africa).

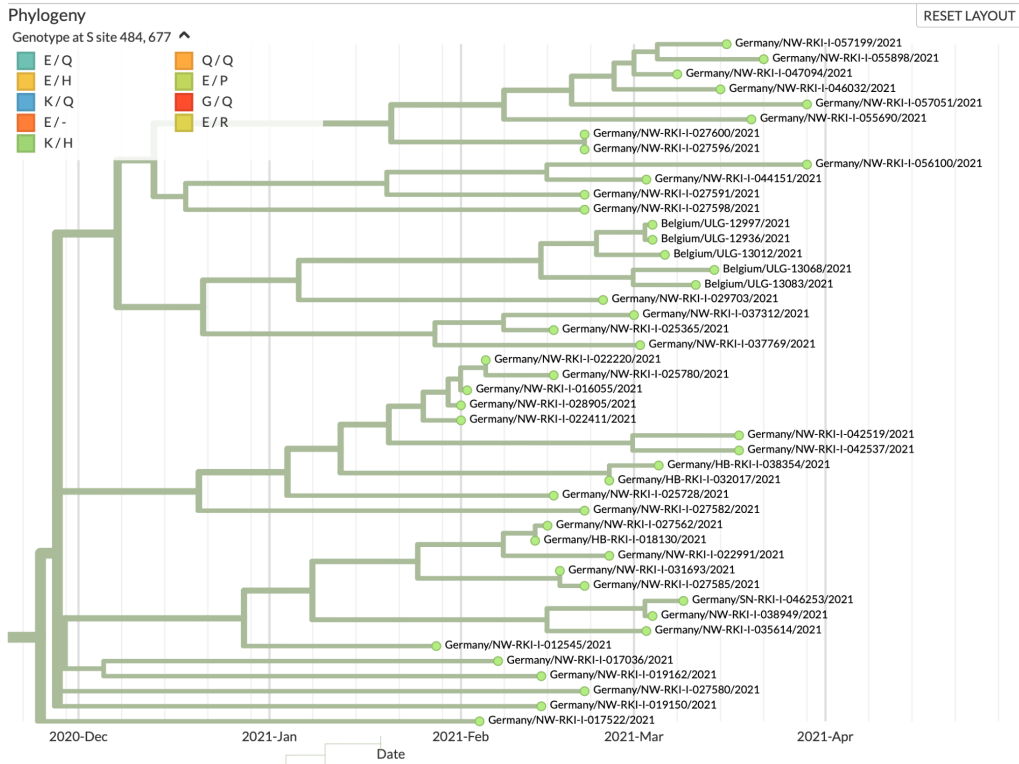


**Figure 4:** Geographic spread in Belgium of B.1.525 genomes that are available on GISAID.

## SARS-CoV-2 Sequences in Belgium

Built with [GuyBaele/sars-cov-2-belgium](#). Maintained by [Barney Isaksen Potter](#).

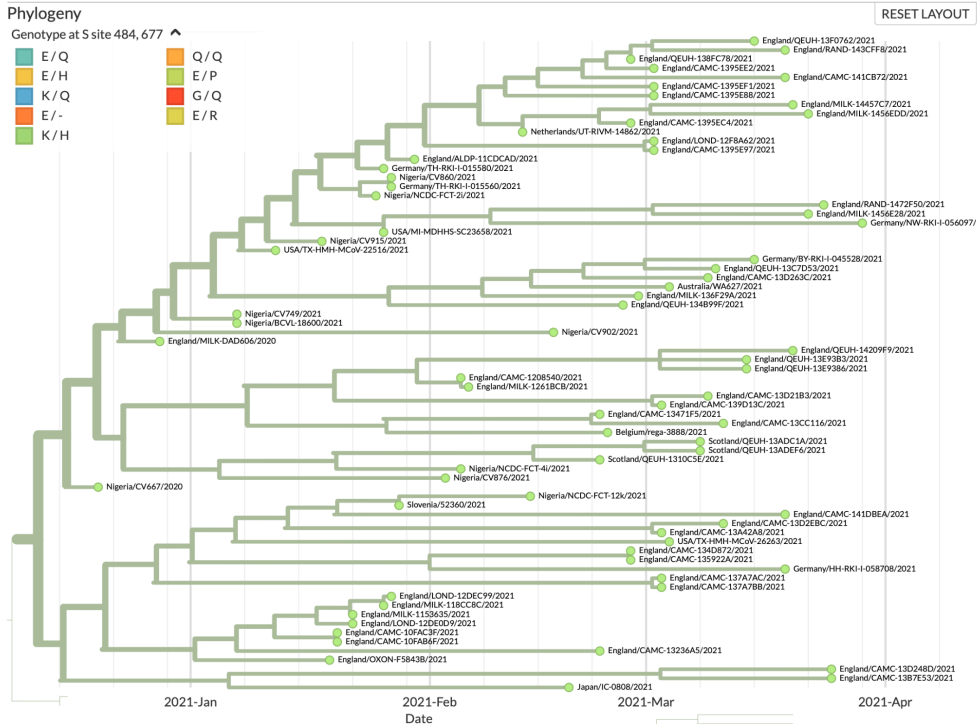
Showing 46 of 4903 genomes sampled between Jan 2021 and Mar 2021. Filtered to {Belgium (49) , Germany (157) }.



## SARS-CoV-2 Sequences in Belgium

Built with [GuyBaele/sars-cov-2-belgium](#). Maintained by [Barney Isaksen Potter](#).

Showing 72 of 4903 genomes sampled between Dec 2020 and Mar 2021.

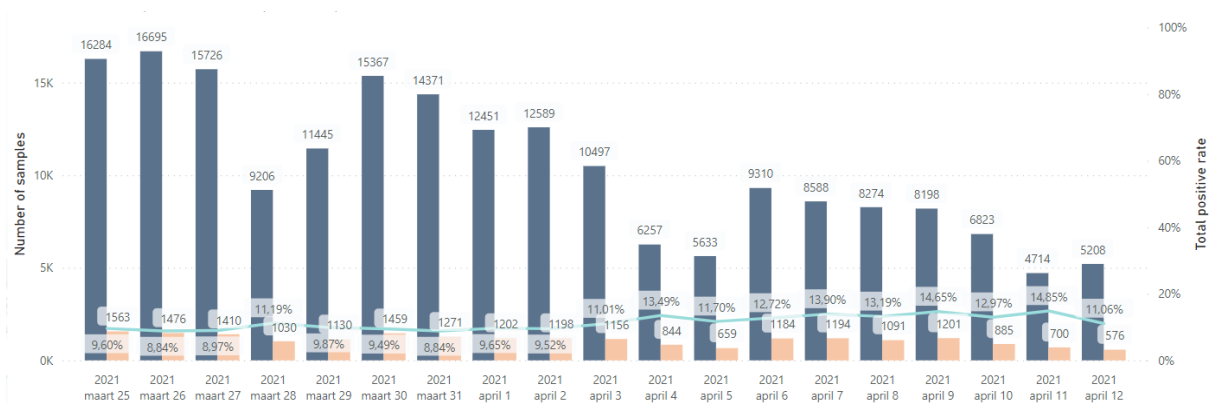


**Figure 5:** Belgian B.1.525 genomes resemble most closely those found in Germany (upper) and England (lower), suggesting that the spread to Belgium occurred via those countries.

#### 4. Under-utilisation of testing and positivity rate during the recent epidemic surge

Since 25/3/2021, when a new lockdown was decided in Belgium, over 200.000 tests were performed by the federal platform laboratories. During this period of time, the positivity rate remained high, and ranged between 8,8% to 14,8% (11/4/2021, see Figure 6). In parallel, the number of tests performed per day decreased significantly, with less than 5.000 tests performed on 11/4/2021, while the capacity of this platform was over 17.000 tests on 23/3/2021.

This paradoxical under-utilisation of testing capacity during the recent surge of cases is sub-optimal: a high positivity rate generally signs that a consistent number of cases and clusters remain undetected, and therefore hampers the possibility to rapidly control the surge of infections. The current positivity rate is the highest since the start of the year (6,1% in January, 7,8% in February, 9,5% in March and 12% in April, see Figure 7).



**Figure 6:** Number of samples processed at the federal platform laboratories between March 25 and April 12, together with the number of positive samples and positivity rate.