

# Genomic surveillance of SARS-CoV-2 in Belgium

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

Situation update – 20<sup>th</sup> of April 2021  
(report 2021\_23)

## Executive summary

15.009 Belgian sequences of SARS-CoV-2 are publicly available on GISAID.

For baseline surveillance samples collected during the last two weeks,

- B.1.1.7 (20/501Y.V1) represented 85,9% (compared to 86,3% in the last report)
- B.1.351 (20H/501Y.V2) represented 3,7 (compared to 4,8% in the last report)
- P.1 (20J/501Y.V3, originally from Brazil) represented 4,9% (compared to 4,2% in the last report)
- B.1.617 (originally described in India) has been identified for the first time in Belgium during the last week

In this report, we focused our analysis on the first cases of B.1.617 found in Belgium and reviewed the recent scientific literature with regard to the impact of variants on vaccine efficacy.

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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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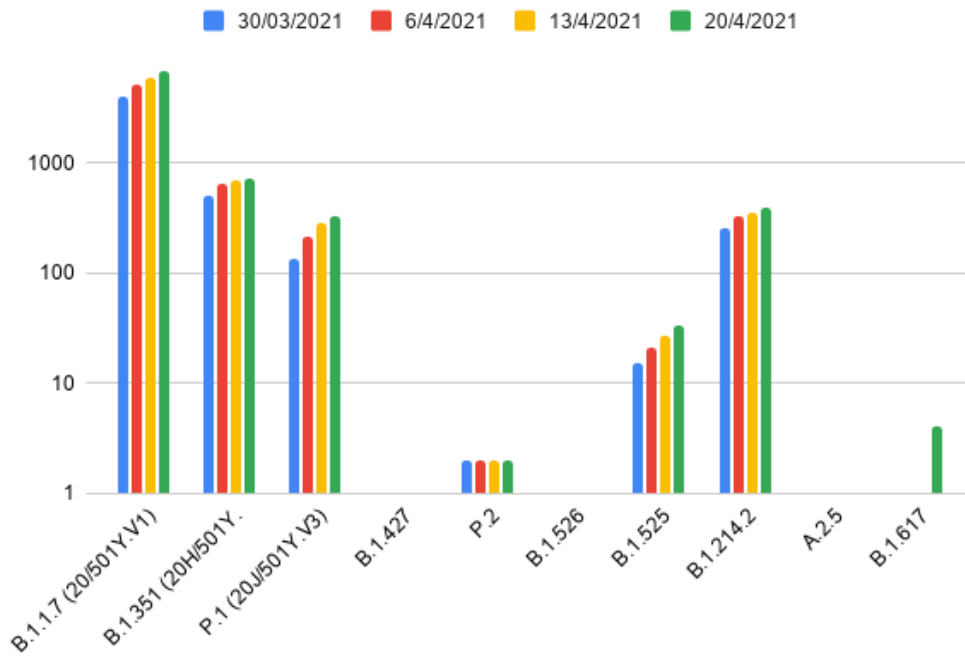
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## 1. Baseline surveillance

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.

	30/03/2021	6/4/2021	13/4/2021	20/4/2021	Epidemiological situation in Belgium	Regions with active circulation
B.1.1.7 (20/501Y.V1)	3909	5002	5890	6768	Dominant lineage	All regions
B.1.351 (20H/501Y.V2)	495	649	676	705	Emerging	Southern African region
P.1 (20J/501Y.V3)	131	212	279	326	Emerging	Latin America
B.1.427	1	1	1	1	Sporadic	Northern America
P.2	2	2	2	2	Sporadic	Latin America
B.1.526	0	0	0	0	Unreported	Northern and Latin America
B.1.525	15	21	27	33	Sporadic (increasing)	Western Africa
B.1.214.2	254	323	351	394	Emerging	Europe
A.2.5	0	0	0	0	Unreported	Central America
B.1.617	0	0	0	4	Sporadic (increasing)	India

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



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

## 2. Monitoring of VOCs in Belgium

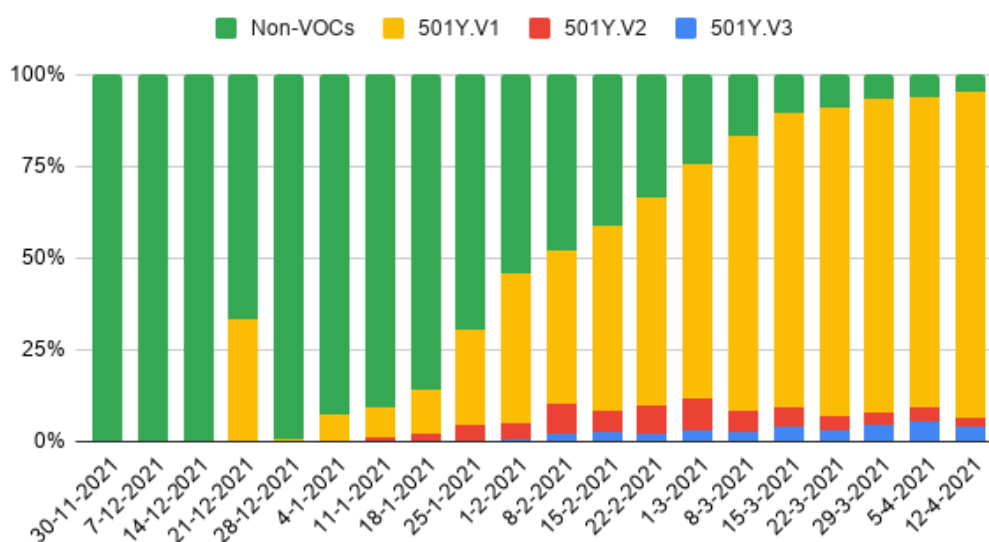
After a constant rise in proportion starting from January 2021, most new SARS-CoV-2 infections in Belgium are currently associated with a variant of concern (VOC), mostly B.1.1.7 (20I/501Y.V1). We recently experienced a notable increase in the number of infections and resulting hospitalisations, which can be related to the spread and dominance of 501Y.V1, a more transmissible and potentially more virulent variant compared to historical circulating strains.

- B.1.1.7 (20I/501Y.V1) represented 85,9% (compared to 86,3% in the last report)
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In the coming weeks and months, the combination of higher (but yet incomplete) vaccination coverage in the Belgian population, the continuous emergence of variants of the virus in all parts of the world, and the possible relaxation of social and travel policies will lead to an unprecedented situation with regard to genomic surveillance.

We will remain challenged in the risk assessment by incomplete and/or delayed characterization of emerging variants which emerge in countries with limited diagnostic and research capacities. In many circumstances, it is therefore not possible to promptly assess the risk related to emerging variants for the Belgian public health. In particular:

- 1) Competitive advantages of emerging variants in comparison with variants already circulating in Belgium
- 2) Effectiveness of vaccines widely used in Belgium against emerging variants, acknowledging that these variants may emerge in countries with low vaccination coverage or enrolling vaccines not used in Belgium



**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), 20I/501Y.V1 - B.1.17 (yellow), 20H/501Y.V2 - B.1.351 (red) and 20J/501Y.V3 - P.1 (blue).

### 3. Current situation with regard to the circulation of B.1.617 in Belgium

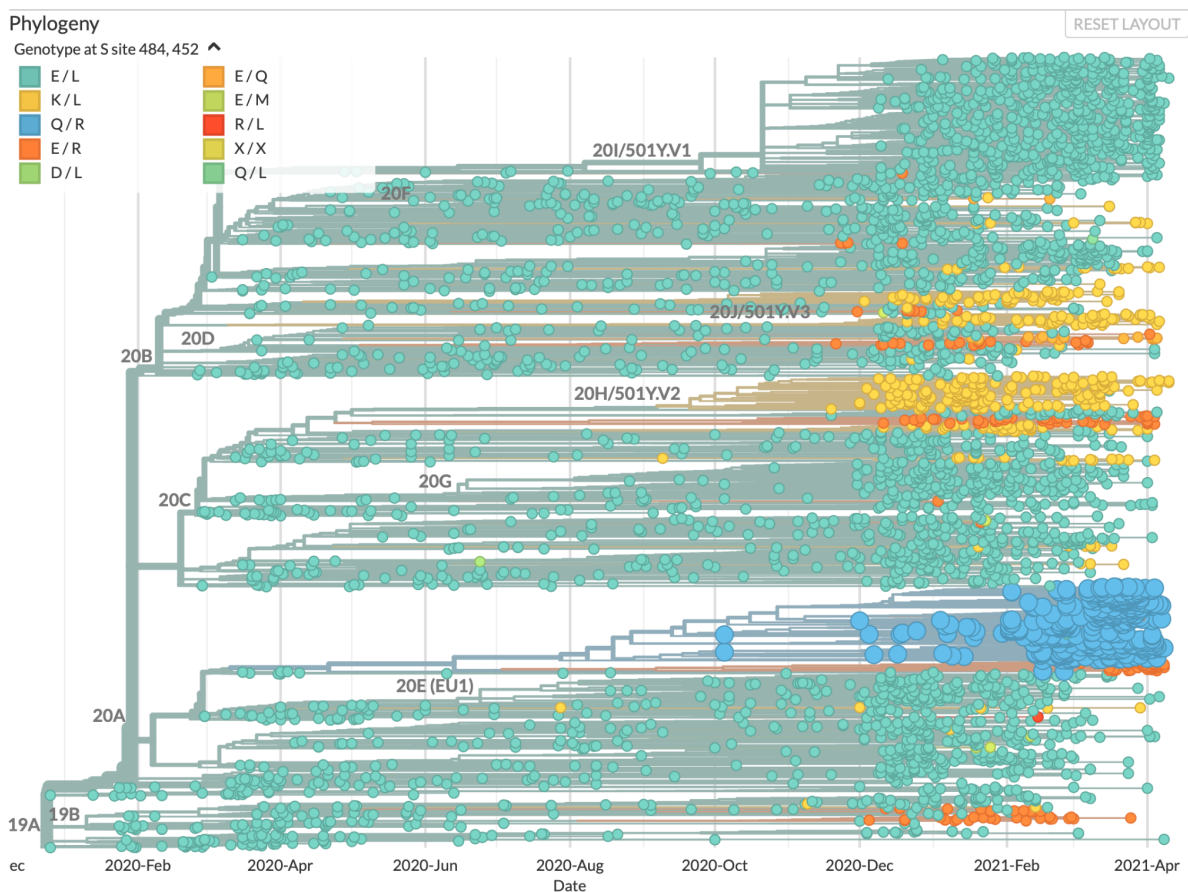
Lineage B.1.617 - which is characterized by mutations E484Q and L452R (see Figure 3) - has already been detected in several countries across the world, including Belgium, but mostly in India, the United Kingdom, and the United States of America. This variant has a couple of potentially concerning mutations but these are **probably** not as serious as some of the mutations present in the variants first described in the UK, South Africa and Brazil. For B.1.617, out of a total of 666 genome sequences on GISAID, 4 were found to date in Belgium, 71 in the USA, 179 in the UK and 298 from India. In the UK, this variant is hence now more prevalent than the P.1 variant that was first identified in Brazil, of which only 44 genomes have been made available to date. In the UK, the source of the exponential spread of B.1.617 is probably in part associated with its intense relations with India, a country now experiencing an unprecedented surge of infections.

## SARS-CoV-2 Sequences in Belgium

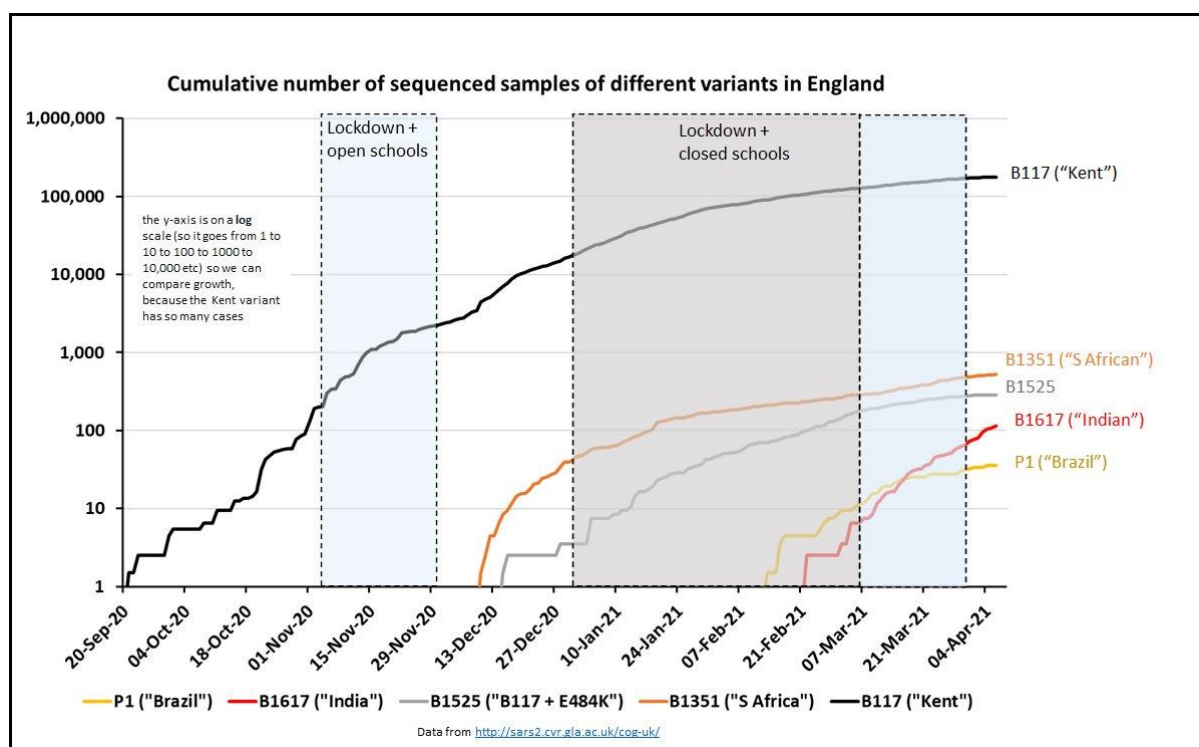


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Showing 4326 of 4326 genomes sampled between Dec 2019 and Apr 2021.



**Figure 3:** B.1.617 genomes (shown in blue; currently known in the media as the Indian variant or the 'double mutation' variant, which is a misnomer) are characterized by a specific combination of 13 mutations mutations including E484Q, L452R and P681R.



**Figure 4:** The fast growing B.1.617 variant in **England** (source: Christina Pagel, UK).

This variant has been around for some time. The first B.1.617 genome in the global database dates back to the 5th of October, 2020. Based on genomic information available on GISAID, B.1.617 was first detected in the UK on the 22<sup>nd</sup> of February 2021, and in the US on the 23<sup>rd</sup> of February 2021. In England, the new variant B.1.617 has already taken over the number of P.1 cases reported on GISAID. Of note, the number of P.1 cases in England has remained extremely limited. B.1.617 has been identified from genome data submitted by 21 countries as of 19 April 2021. The relative frequency of genomes from different countries is biased by the level of genomic surveillance in place in different countries; a country processing a high number of genomes may be more likely to detect variants.

Lineage B.1.617 has so far appeared in three Belgian locations: Schoten, Deurne and Sint-Joost-ten-Node. Overall, the detected number of infections is still quite low and does not seem to be increasing rapidly. India is currently witnessing a surge in marked surge in COVID-19 cases. The question is whether this is associated with the variant, with human behaviour (for example, the presence of large gatherings, and/or lack of preventive measures including hand washing, wearing masks and social distancing) or whether both are contributing. It is not clear at the present time whether B.1.617 is the main driver for the current wave in India, as there have only been less than 1000 sequences published from India out of about 4 million cases in this wave so far. An important caveat is also that these data can be influenced by selection of samples for sequencing that are uneven across locations.

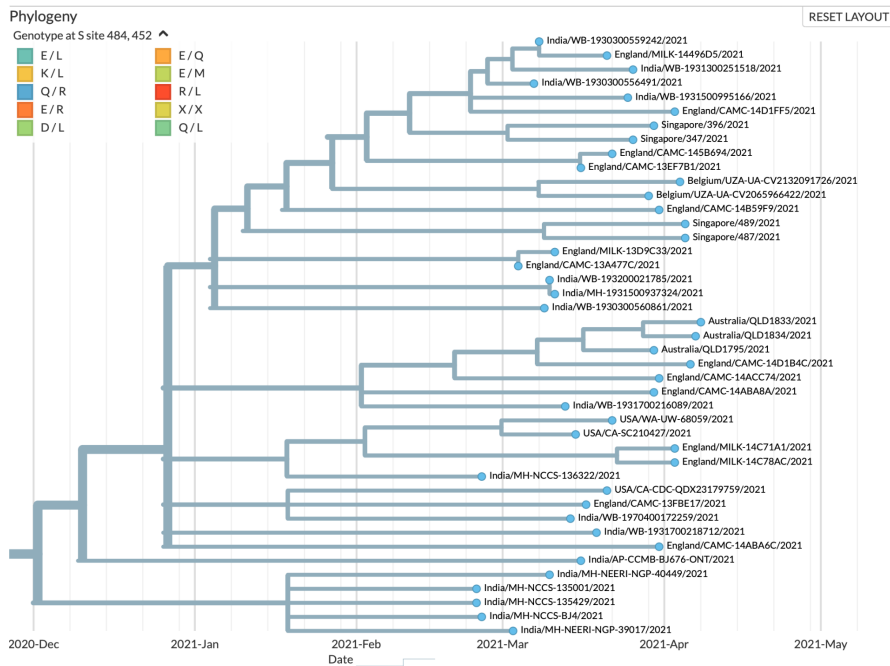
#### Important observations regarding the situation in **Belgium**:

- For the very few patients identified with the B.1.617 variant, only mild symptoms were reported and none of them needed to be hospitalized, even in the case of underlying health problems. Based on these very limited numbers, at this stage we cannot estimate the severity of disease associated with this variant, and we will therefore need to rely on observations by other countries, in particular the UK.
- No travel history is currently known, pointing to local transmission within Belgium. Phylogenetic analysis clusters the cases from Schoten together in a global analysis (Figure 6)

## SARS-CoV-2 Sequences in Belgium

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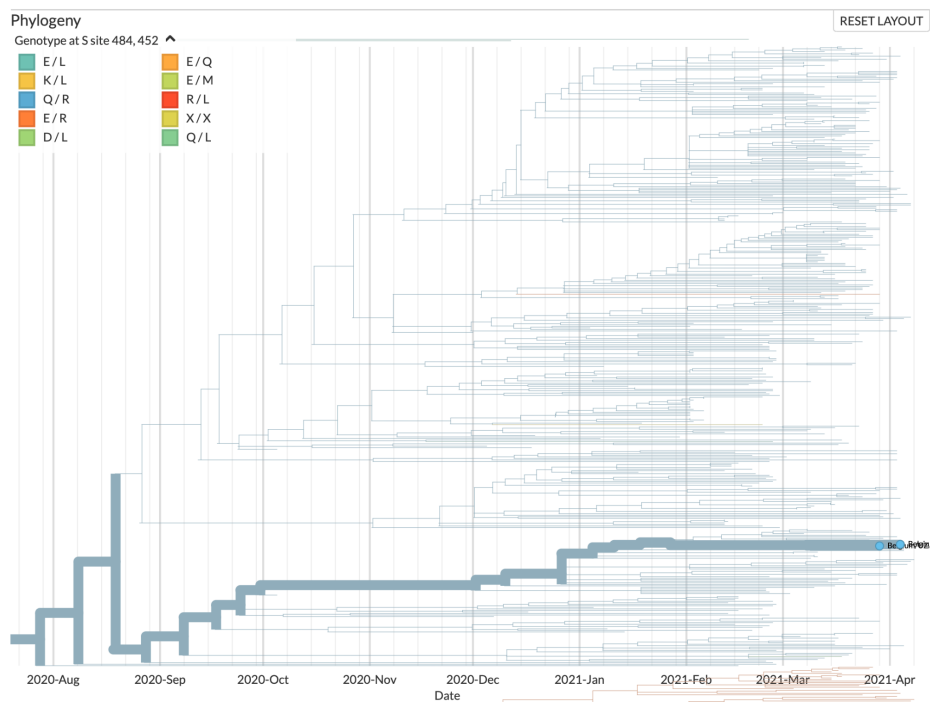
Showing 43 of 4326 genomes sampled between Feb 2021 and Apr 2021.



## SARS-CoV-2 Sequences in Belgium

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Showing 2 of 4326 genomes sampled between Mar 2021 and Apr 2021. Filtered to [Belgium \(22\)](#).



**Figure 6:** Two Belgian B.1.617 genomes (from Schoten) currently resemble most closely those found in England (upper) and are found to be clustering together within the overall clade of B.1.617.

#### 4. Impact of variants of concern on vaccine efficiency: what do we know so far?

**Lineage B.1.1.7 (20I/501Y.V1):** Available data are reassuring on the efficacy of both Oxford-AstraZeneca (ChAdOx1, hereafter referred as the “AZ” vaccine) and Pfizer-BioNTech (BNT162b2 mRNA, hereafter referred as the “Pfizer” vaccine) vaccines against this variant. A study performed in Scotland (Vasileiou *et al.* 2021, preprint) revealed that a single dose of those vaccines resulted in substantial reductions in the risk of hospitalisation. 28 to 34 days post-vaccination, the first doses of the AZ and Pfizer vaccines were associated with a vaccine effect for hospitalisation of 94% (95% CI [73-99]) and 85% (95% CI [76-91]), respectively.

**Lineage B.1.351 (20J/501Y.V2):** A first study performed in South Africa indicated that two doses of the AZ vaccine do not show protection against mild-to-moderate COVID-19 due to this variant (Madhi *et al.* 2021, *NEJM*). This study is, however, based on a restricted number of positive SARS-CoV-2 patients ( $n = 42$ ). Moreover, we still lack results from large clinical studies aiming to determine the efficacy of the AZ vaccine to prevent severe SARS-CoV-2 infections and related hospitalisations. Of note, a recent study performed on Syrian hamsters shows that the AZ vaccine allows preventing lower respiratory infections caused by the B.1.351 and B.1.1.7 lineages (Fischer *et al.* 2021, preprint). While performed on animals, those results are encouraging as they do not discard the possibility that the AZ vaccine would still be efficient to prevent severe cases caused by the B.1.351 lineage. However, the efficacy of the AZ vaccine against a variant like B.1.351 remains a current source of concern.

According to a press release (<https://www.nih.gov/news-events/news-releases/>), the single dose Johnson & Johnson vaccine (Ad.26.COV2.S or JNJ-78436725, hereafter referred as the “J&J” vaccine), which is a vector vaccine similar to the AZ one, still shows a 57% effectiveness in South Africa (compared to 72% in the US) where the B.1.351 lineage is massively circulating, and would be 85% effective in preventing severe/critical COVID-19 across all geographical regions. According to a press release from the company (<https://www.pfizer.com/news/press-release>, 01/04/2021), the Pfizer vaccine would be “100% effective in preventing COVID-19 cases in South Africa, where the B.1.351 lineage is prevalent” (but the results of this study are not published yet). A recent study demonstrated, however, an increased breakthrough rate: vaccinees infected at least a week after the second dose were disproportionately infected with B.1.351 (odds ratio of 8:1; Kustin *et al.* 2021, preprint).

**Lineage P.1 (20J/501Y.V3):** To our knowledge, there is still no large study on the efficacy of the AZ vaccine when confronted with the P.1 lineage. A recent study by Dejnirattisai *et al.* (2021, preprint) shows that antibody neutralization against P.1 was still efficient but reduced 2.6-fold for the Pfizer vaccine serum and 2.9-fold for the AZ vaccine serum. Other preliminary results based on the analyses of neutralising activities are encouraging for the Pfizer vaccine (Liu *et al.* 2021, *NEJM*). Regarding the J&J vaccine, 69% of the circulating variants were P.1 or P.2 in Brazil at the time the trial was conducted. Since this trial reported a 85% efficacy in preventing severe/critical COVID-19 across all geographical regions (South Africa, Latin America, US), this would indicate that the J&J vaccine indeed allows a protection against severe infections due to the P.1 variant.