

# Genomic surveillance of SARS-CoV-2 in Belgium

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

Situation update – 27 of July 2021  
(report 2021\_38)

## Executive summary

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

Among these, 763 sequences of positive SARS-CoV-2 samples collected between 12 and 25 July were reported in the context of baseline surveillance in the context of baseline surveillance,

- B.1.617.2 (*Delta*) represented 89% (compared to 75,5% in the last report) ↗
  - B.1.1.7 (*Alpha*) represented 8,4% (compared to 17,5% in the last report) ↘
  - P.1 (*Gamma*) represented 2,3% (compared to 5,3% in the last report) ↘
- Other variants represent altogether less than 1% of the circulating strains.

Other points of attention:

- The NRC performed 283 VOC PCRs on unselected positive samples analyzed during the week of July 19. B.1.617.1/.2 represented 95% (stable) of the results.

Authors (National Reference Laboratory – UZ Leuven and KU Leuven):

*Simon Dellicour, Lize Cuypers, Sunita Janssenswillen, Guy Baele, Piet Maes, Els Keyaerts, Tom Wenseleers, Barney Potter, Elke Wollants, Marc Van Ranst, Emmanuel André.*

With the collaboration of the laboratories of UCL, ULB, UMONS, UNAMUR, ULiège, UGent, UZA/UAntwerpen, JESSA ZH, AZ Delta, AZ Klina, IPG, AZ St Lucas Gent, OLVA 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>

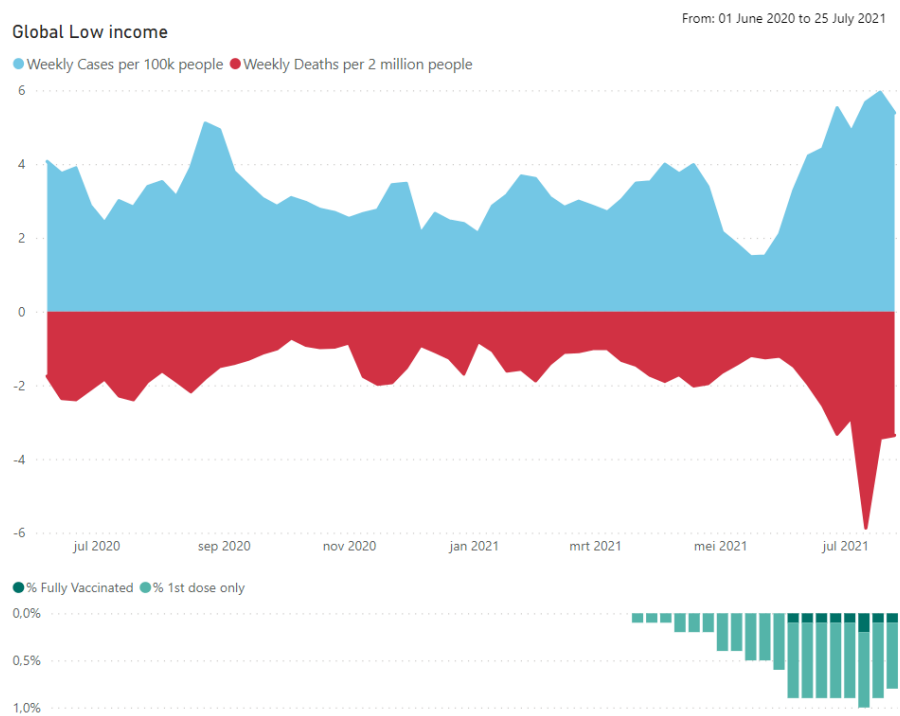
## Table of contents

1. International situation and observed impact of vaccination coverage
2. Combined impact of increasing vaccination coverage and disease-control measures on incidence and mortality in Belgium
3. Monitoring of VOCs
4. Testing of travellers
5. Update on re-infections: which variants do we observe?
6. Update on post-vaccination infections: which variants do we observe?

## 1. International situation and observed impact of vaccination coverage

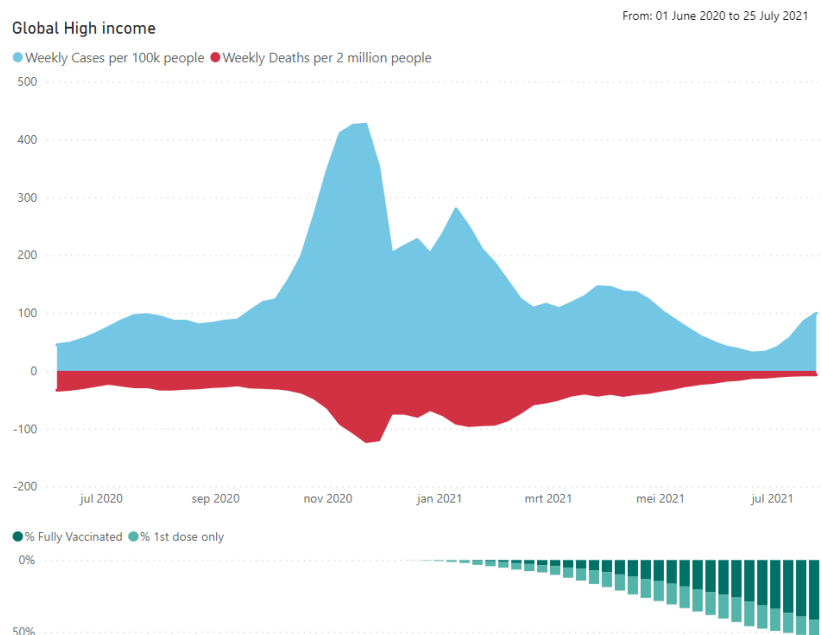
The Delta variant has become dominant in most parts of the world.

As illustrated in Figure 1, in low income countries with a very low vaccination coverage (<1%, mostly partially vaccinated), the emergence of the Delta variant results in both more cases and more fatalities compared to the previous waves of infections.



**Figure 1: Global, low income countries.** Evolution of weekly COVID-19 cases (per 100.000 people) and deaths (per 2.000.000 people) in parallel with the rollout of vaccination ([source](#)).

In high income countries with vaccination coverage reaching 50% (mostly fully vaccinated), there has been a clear disruption between the number of infections reported and the number of deaths. Although an uncontrolled rise of infections in high income countries inevitably translates into a rise of hospitalisations, the case fatality rate (CFR) has dropped by approximately 10 fold in the United Kingdom and Belgium since the rollout of vaccination (Figure 3).



**Figure 2: Global, high income countries.** Evolution of weekly COVID-19 cases (per 100.000 people) and deaths (per 2.000.000 people) in parallel with the rollout of vaccination ([source](#)).



**Figure 3: Belgium and the United Kingdom.** Evolution over time of the case fatality rate (CFR). In these countries, the large vaccination uptake among the most fragile groups has decreased importantly the proportion of confirmed deaths reported among confirmed cases (source: Our World in Data).

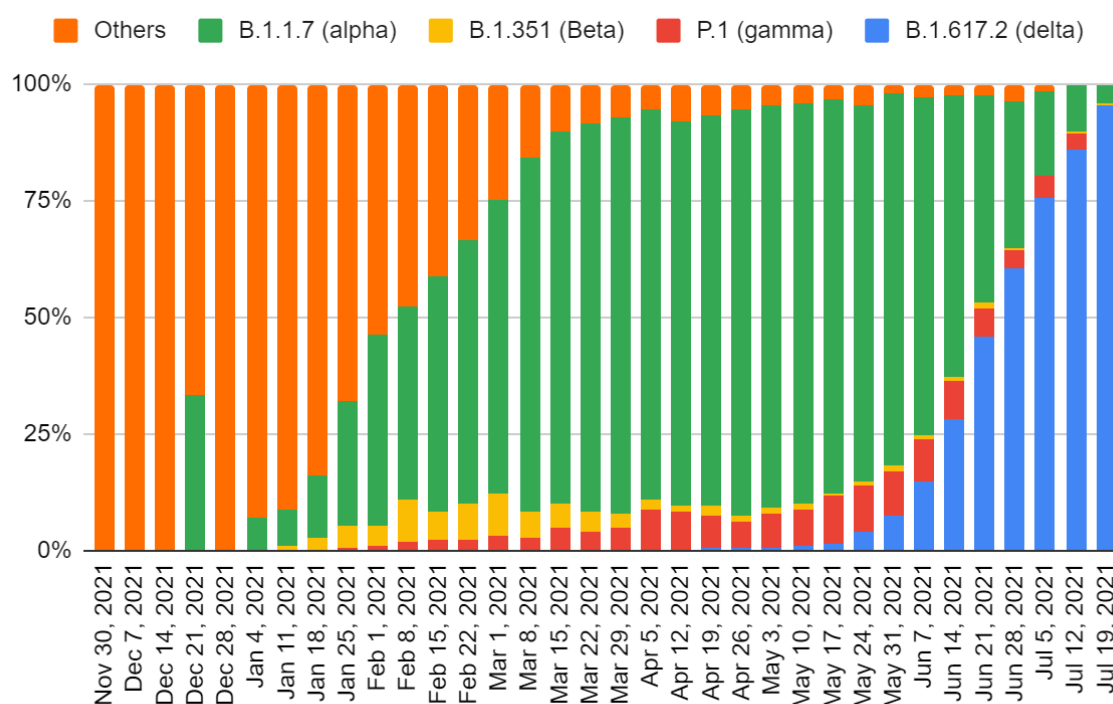
## 2. Comparison of the last three epidemic phases (or “waves”)

	nov-01 Peak wave 2	Mar 28 Peak wave 3	jul-11 Ongoing wave 4
<a href="#">Vaccination coverage (fully vaccinated)</a>	0%	4,65%	42,33%
<a href="#">Incidence per 100,000 hab (A)</a>	1913	291	62
<a href="#">Mortality per 2,000,000 two weeks later (B)</a>	468	52.46	1.9
Ratio mortality (B) / incidence (A)	0,245	0,18	0,031
<a href="#">Stringency index</a>	56,48	62,96	50,93

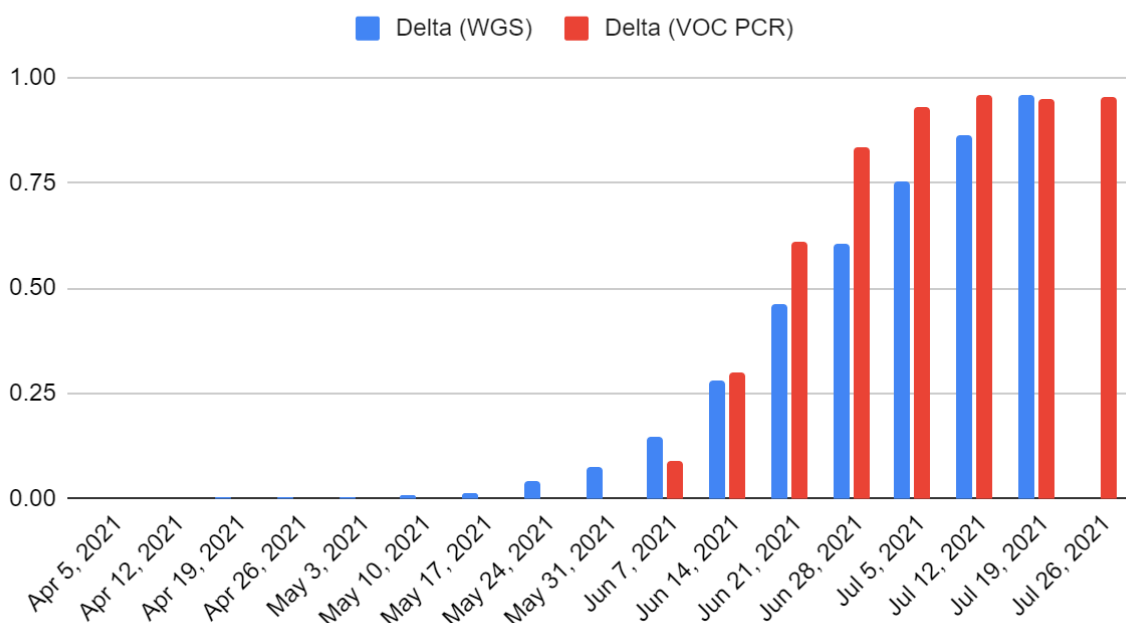
**Table 1: Comparison of the last three epidemic phases (or “waves”).** Between wave 2 and wave 3, the evolution of the vaccination coverage likely allowed a decrease in the proportion of people who died following COVID-19. This trend seems to be maintained during the current wave of infections, although definitive conclusions will only be possible after the peak of infections has been reached.

### 3. Monitoring of VOCs in Belgium

While first identified on 6 April 2021 in Belgium, the B.1.617.2 Variant of Concern (Delta) is now the dominant lineage in the country.

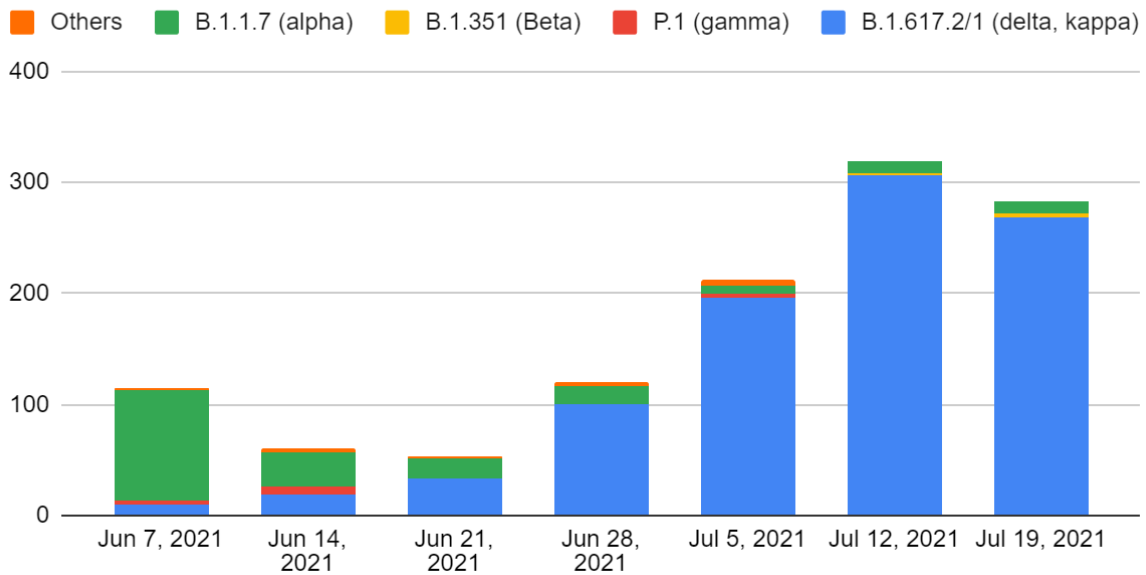


**Figure 4:** Weekly evolution of the frequency of variants of concern reported by the baseline surveillance network using a whole genome sequencing (WGS) approach.



**Figure 5:** Weekly evolution of the proportion of the Delta variant reported by the baseline national surveillance network using whole genome sequencing (blue), and rapid VOC PCRs performed among all positive cases received at the national reference laboratory in Leuven (red: mainly unbiased sampling, but limited geographical representativeness).

Considering that the viral population replacement is now reaching a plateau (>95% delta variants since 3 weeks), the utility of rapid VOC PCR tests for the purpose of early genomic surveillance has to be reconsidered based on the evolution of the epidemiology. Therefore, the NRC does not consider at this stage (and until indicators of a possible new viral population replacement phenomenon appears) VOC PCRs as a required complementary approach, also considering the structural WGS-based baseline genomic surveillance in place.



**Figure 6:** Weekly evolution of the number of variants of concern diagnosed at the national reference laboratory in Leuven (unbiased sampling, but limited geographical representativeness).

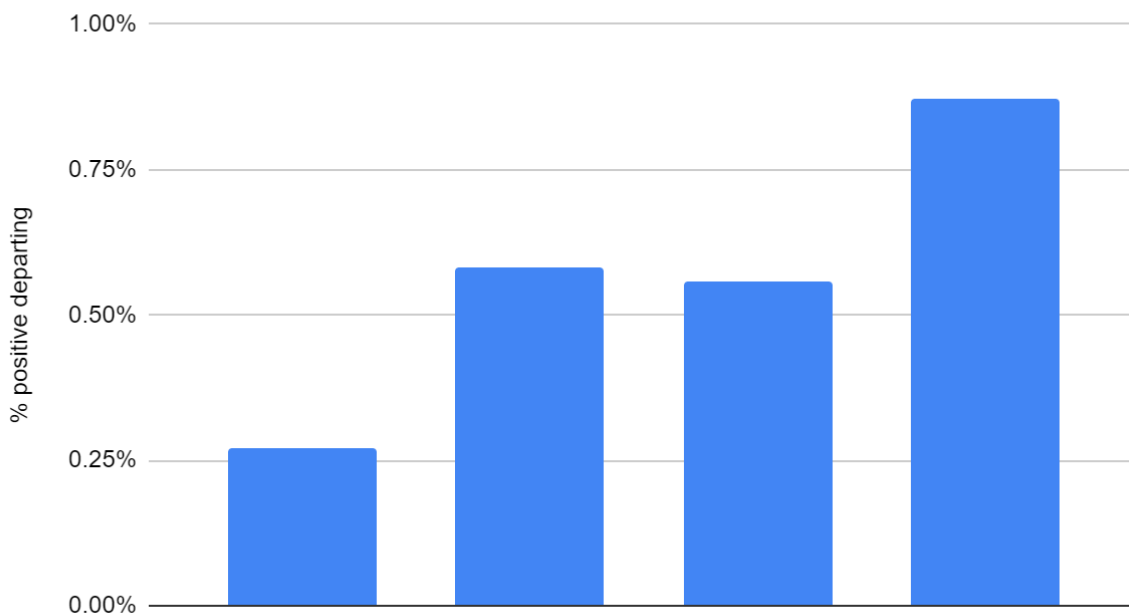
Lineage	Number of Belgian cases reported on GISAID	First reported
B.1.1.7 (Alpha)	20.744	30/11/2020
B.1.351 (Beta) and B.1.351.2	1.119	20/12/2020
P.1 (Gamma) and P.1.1	1.954	29/1/2021
B.1.617.2 (Delta)	2.461	6/4/2021
B.1.1.7 +S:E484K	49	31/3/2021
B.1.1.7 +S:S477R	36	15/3/2021
B.1.214.2	717	3/1/2021
A.27	20	11/1/2021
B.1.427 (Epsilon)	1	18/1/2021
B.1.525 (Eta)	83	30/1/2021
P.2 (Zeta)	2	9/2/2021
B.1.526 (Iota)	3	24/2/2021
B.1.1.318	61	3/3/2021
C.36.3	29	23/3/2021
B.1.617.1 (Kappa)	17	25/3/2021
B.1.619	123	
B.1.620	36	31/3/2021
C.37 (Lambda)	7	20/6/2021
P.3 (Theta)	3	27/6/2021
B.1.617.3	1	12/7/2021

**Table 2:** List of VOCs (red) and VOIs (orange) identified in Belgium to date and cumulative number of sequences available on GISAID (total of 34.508 sequences).

#### 4. Testing of travellers

##### Departing travellers

During the last 4 full weeks (June 28 to July 25), the National Reference Center in Leuven has tested 32.210 departing travellers, among which 182 were tested positive. The positivity rate increased from 0,28% during the first week to 0,87% during the fourth week (Figure 7). The Delta variant represented 90% of the positive samples tested during the fourth week.



**Figure 7:** Positivity rate among departing travellers tested in the region of Leuven.



## Returning travellers

For the last 4 full weeks (June 28 to July 25),

- Among the travellers returning from abroad to the region of Leuven, 549 people were tested, among which 19 were tested positive (3,4%). The Delta variant represented 100% of the positive samples tested during the third and fourth weeks.

According to the data provided by Sciensano, at the Belgian level and during the last 8 weeks, 75% of the travellers who tested positive upon return were infected with the variant Delta. During this same period of time, 13,2% of the people tested positive for the variant Delta were returning travellers (Table 3).

	% of returning travelers among persons positive for the considered VOC*	% of persons positive for the considered VOC among all positive returning travelers**
Alpha	4,4 % (103/2355)	22,3 % (103/461)
Beta	14,3 % (5/35)	1,1 % (5/461)
Gamma	1,9 % (7/361)	1,5 % (7/461)
Delta	13,2 % (346/2622)	75,1 % (346/461)

**Table 3:** (\*) ratio between the number of returning travelers tested positive for a given VOC and the total number of persons tested positive for that VOC; (\*\*) ratio between the number of returning travelers tested positive for a given VOC and the total number of returning travelers tested positive for one of the four VOCs. N.B.: we only considered positive persons for which the travel history status is known (estimated for the last 8 weeks, i.e. weeks 22-29).

## 5. Update on re-infections: which variants do we observe?

### Surveillance methodology

A re-infection is defined as a distinct clinical episode of SARS-CoV-2 infection after a first positive SARS-CoV-2 test. Data is provided by Sciencano.

Table 4 highlights for the last two months the number of re-infection cases documented. Of the 4.383 infections reported, 71 re-infections were observed (1,6% of total). The proportion was the highest for people infected with the variant Delta (2,1%), which likely highlights the higher immune escape mechanism associated with this most recent SARS-CoV-2 variant.

	% of re-infections among persons positive for the considered VOC*
Alpha	1,2 % (22/1827)
Beta	0,0 % (0/23)
Gamma	0,7 % (2/267)
Delta	2,1 % (47/2266)

**Table 4:** Percentage of re-infections among persons tested positive for each VOC (only considering positive persons for which the pre-infection status is known) during the last 8 weeks (W22-29).

## 6. Update on post-vaccination infections: which variants do we observe?

### Surveillance methodology

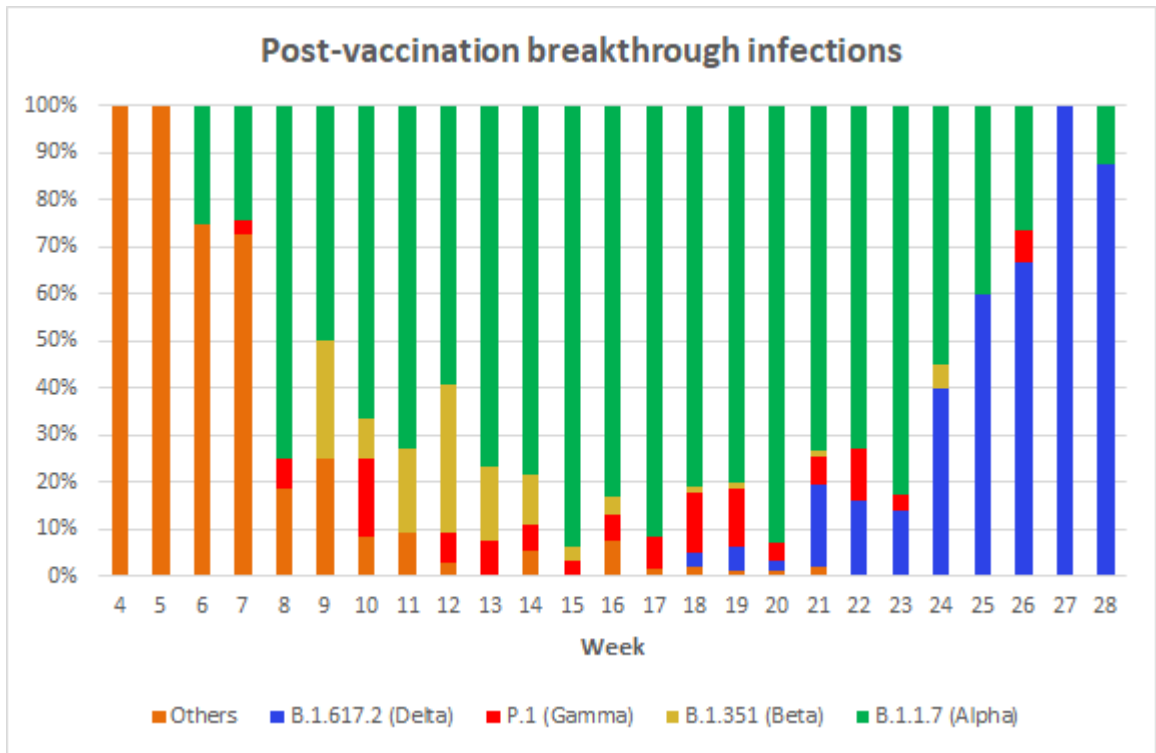
A breakthrough infection is defined as a positive SARS-CoV-2 test at least 7 days after the full completion of a vaccination scheme. To facilitate the transfer of samples that meet the definition to the sequencing lab in Leuven, laboratories that submit RT-PCR test results to HealthData, will receive an automatic message from HealthData notifying them that a particular sample meets the criteria of a post-vaccination breakthrough case. It remains the responsibility of each lab to verify whether the sample meets the criteria for sequencing (viral load is sufficiently high) and if so, to send the sample accompanied with the completed application form to the NRC UZ/KU Leuven.

### Intermediate results

The NRC is actively collecting information on post-vaccination infections, of which to date, 946 samples could be typed. All 946 samples were sampled between January 28 and July 15, 2021. Of the 946 samples, detailed vaccination information is currently available for 362 samples of which 20 infections do not meet the criteria of a post-vaccination breakthrough case (<7 days after full completion of the vaccination scheme). For the more than 500 records with incomplete vaccination details, the NRC hopes to still collect the large majority.

For the 926 samples for which - as of today - there is no evidence (e.g. number and dates of doses that proof the vaccination scheme is not complete) that they do not meet the criteria of a post-vaccination breakthrough infection, the brand of the vaccine is available for 35,9% (332/926). Of those 332 cases, 82,5% has been vaccinated with two doses of COMIRNATY (Biontech/Pfizer), followed by Moderna (5,1%), VAXZEVRIA (AstraZeneca) (4,8%) and one dose of Janssen (7,5%).

In parallel to baseline surveillance, the evolution of the four main VOCs (Alpha, Beta, Gamma and Delta) are currently being followed over time, and visualized in Figure 8 for the 926 cases which are currently presumed to be post-vaccination breakthrough infections. Since the number of typed cases varies per week and is rather limited (<60 infections on a weekly basis prior the month of May), the variability in percentages of VOCs is higher compared to the more stable baseline surveillance effort and is considered for some weeks to be highly influenced by the occurrence of post-vaccination infections in the context of outbreaks in nursing homes.



**Figure 8:** Share of the different variants of concern among post-vaccination breakthrough infections over time.