

# Genomic surveillance of SARS-CoV-2 in Belgium

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

Situation update – 6 of July 2021  
(report 2021\_35)

## Executive summary

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

Among these, 526 sequences of positive SARS-CoV-2 samples collected between 21 June and 4 July were reported,

- B.1.1.7 (*Alpha*) represented 42,6% (compared to 65,2% in the last report) ↘
- B.1.617.2 (*Delta*) represented 50,2% (compared to 23% in the last report) ↗
- P.1 (*Gamma*) represented 4,6% (compared to 8,6% in the last report) ↘
- B.1.351 (*Beta*) represented 1,1% (compared to 0,8% in the last report) =

Other points of attention:

- The NRC performed 142 VOC PCRs on unselected positive samples analyzed during the week of June 28. B.1.1.7 and B.1.617.1/.2 represented respectively 10,6% and 85,2% (↗) of the results.
- The total number of documented SARS-CoV-2 infections has started to rise again in Belgium after 3 months of decline. This increase is caused by B.1.617.2, and cannot be solely associated with increased testing.

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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, OLVZ 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

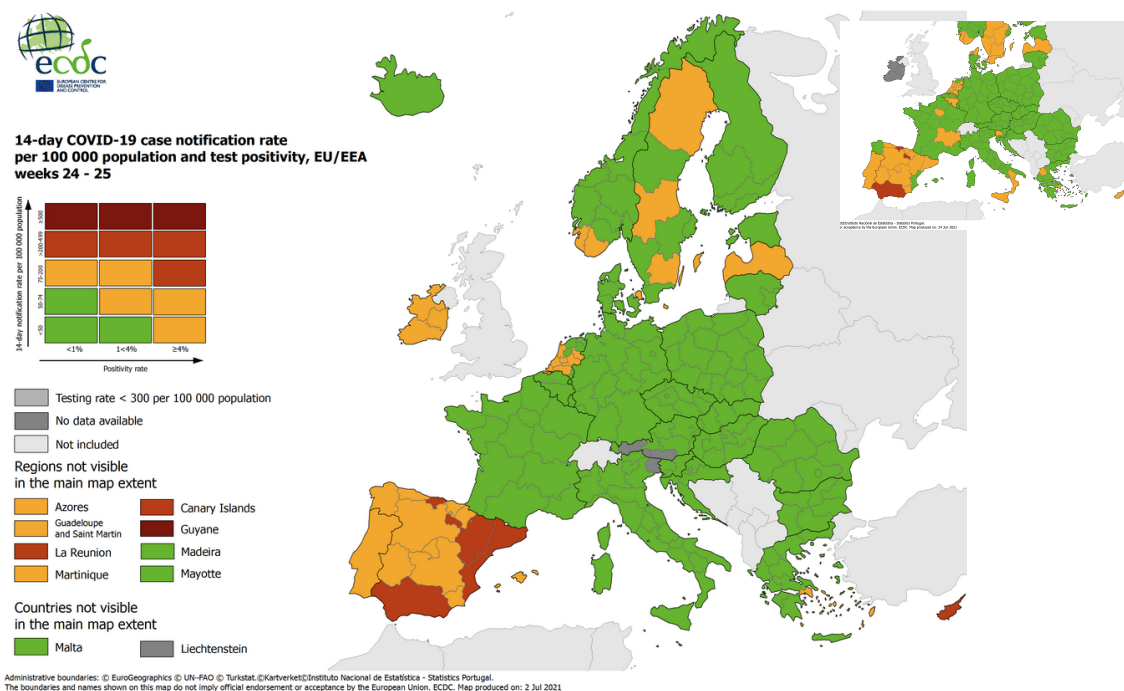
1. Monitoring of VOCs
2. First detection of Lambda (C.37) in Belgium
3. Testing of travellers
4. Summary of recently published study which focuses on the impact of international travels on the circulation of the virus during the last summer period (2020)

## 1. Monitoring of VOCs

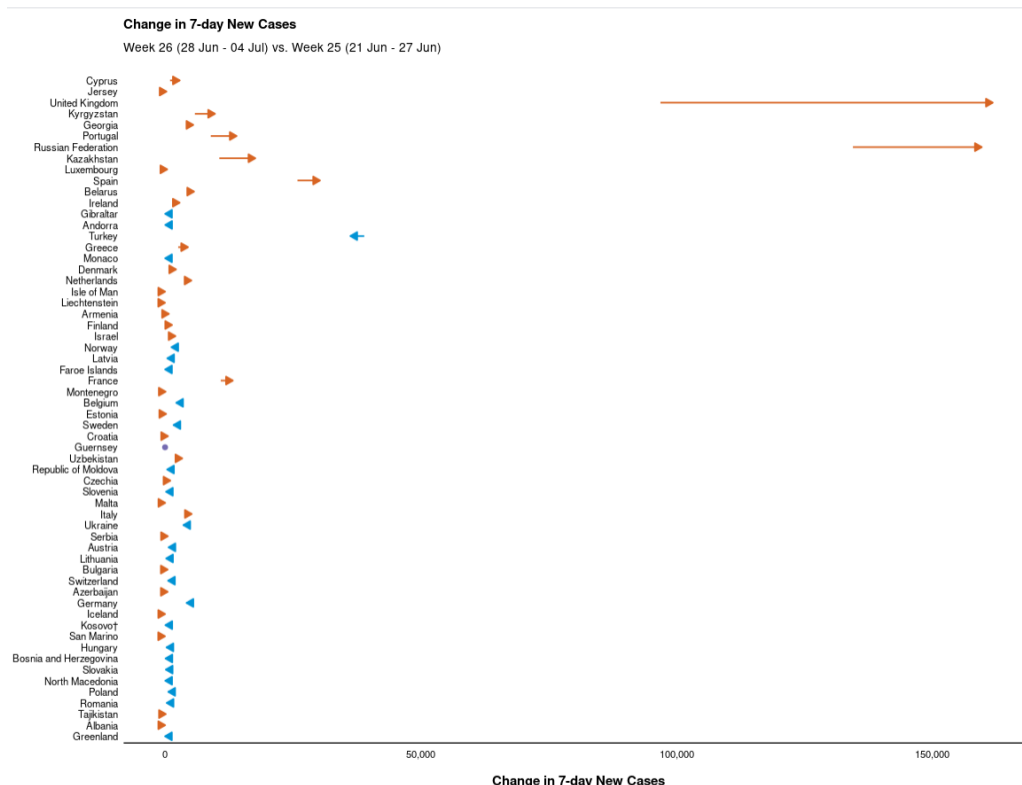
### International evolution

The Delta variant (B.1.617.2) has continued to spread globally. It has become the dominant lineage in several European countries, and other EU countries are expected to follow this evolution during the summer period.

- Infections in the **European Region are rising**. In particular, the number of infections is rising in Russia, the United Kingdom, Portugal, Spain, Ireland, Luxembourg, Finland, Malta, Feroe Island, Île de Mans and Moldavia. In other countries, the number of infections is stable or declining (Figures 1 and 2), but it should be noted that in these countries, B.1.617.2 is not yet dominant and that the situation will most likely evolve over the next few weeks.

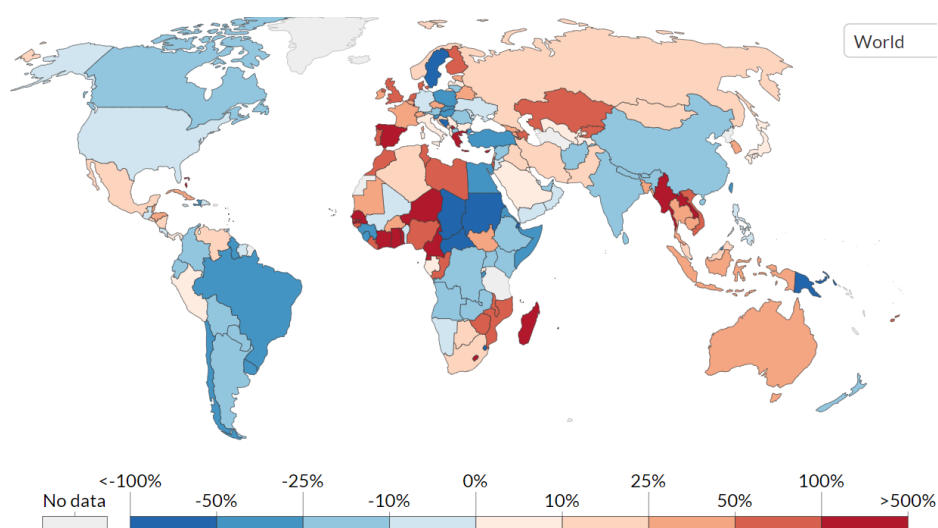


**Figure 1.** 14-day COVID-19 case notification rate per 100,000 inhabitants and test positivity rate (and comparison with the previous week).



**Figure 2.** While the United Kingdom and The Russian Federation are reporting a strong and sustained increase in new cases. Portugal, Spain and France (popular touristic countries for Belgian citizens) show an increase of infections. (Source: WHO, <https://worldhealthorg.shinyapps.io/covid/>).

- In other regions of the world, the situation is still rapidly evolving in continents where vaccination coverage is very low (Africa, Latin America, Asia; Figure 3), a phenomenon which can be widely underestimated due to the limited diagnostic capacity in low-income countries. Several African cases are currently reporting a rapid rise of infections and deaths, including in countries with strong disease surveillance and control systems (Rwanda).



**Figure 3 :** Week by week change in confirmed COVID-19 cases (source : Our World in Data)

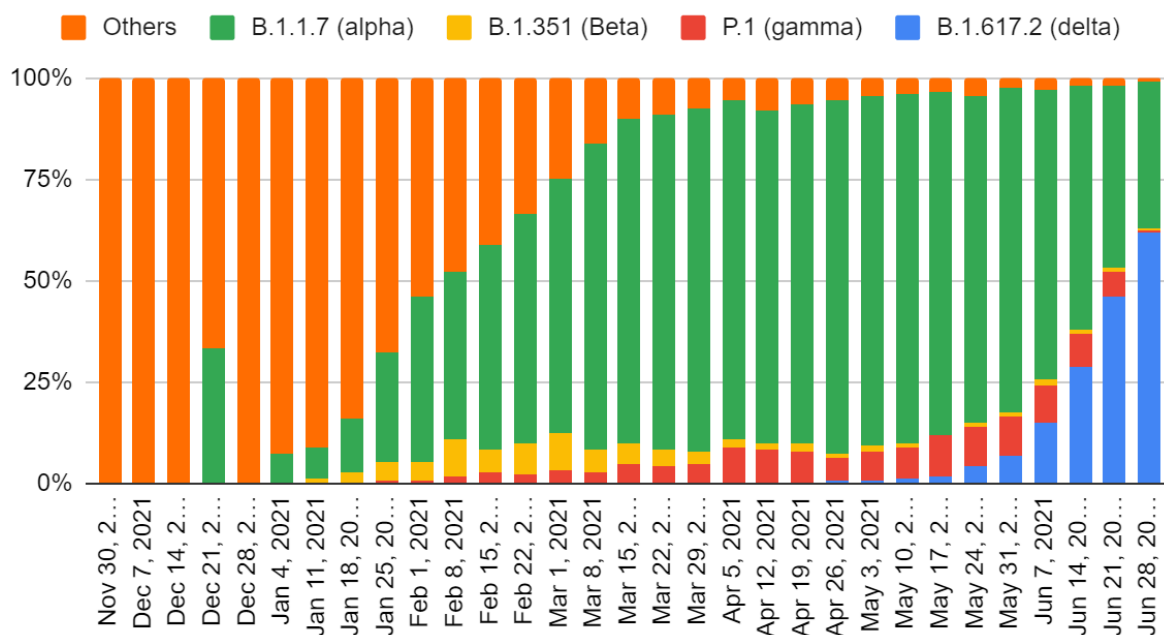
## Situation in Belgium

While it was first identified on 6 April 2021 in Belgium, the B.1.617.2 Variant of Concern (Delta) is on its path to become the dominant lineage in the country.

Between 21/6/2021 and 4/7/2021 (526 genomes available to date)

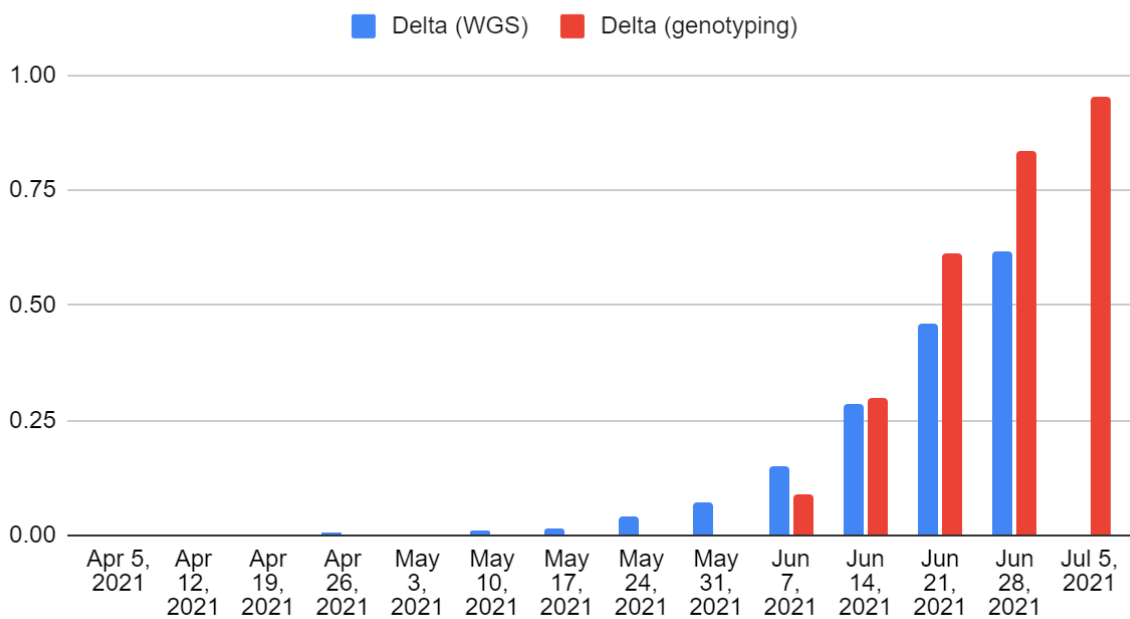
- B.1.1.7 (Alpha) represented 42,6%
- B.1.617.2 (Delta) represented 50,2%
- P.1 (Gamma) represented 4,6%
- B.1.351 (Beta) represented 1,1%

## Non-VOCs, 501Y.V1, 501Y.V2, 501Y.V3 and B.1.617.2



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

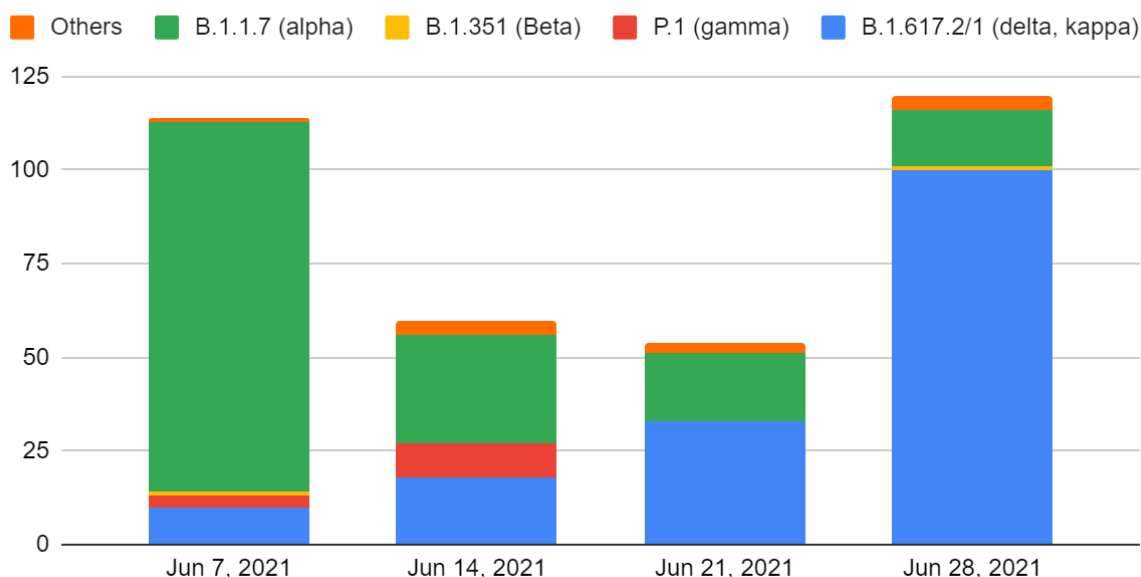
## Delta (WGS) and Delta (genotyping)



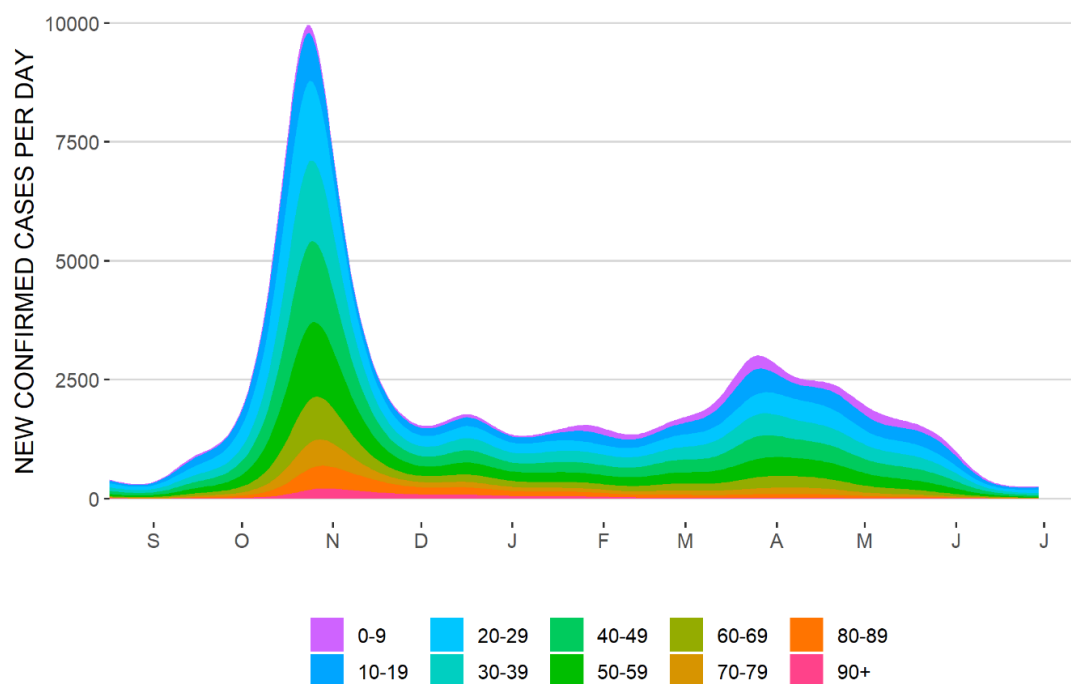
**Figure 5:** Weekly evolution of the frequency of variants of concern reported by the baseline national surveillance network using whole genome sequencing (blue), and rapid VOC PCRs performed among all positive cases received at the national reference laboratory in Leuven (red: mainly unbiased sampling, but limited geographical representativeness). Numbers for week 5th of July are still limited, and the final figure may thus be revised.

The situation in Belgium is currently characterized by:

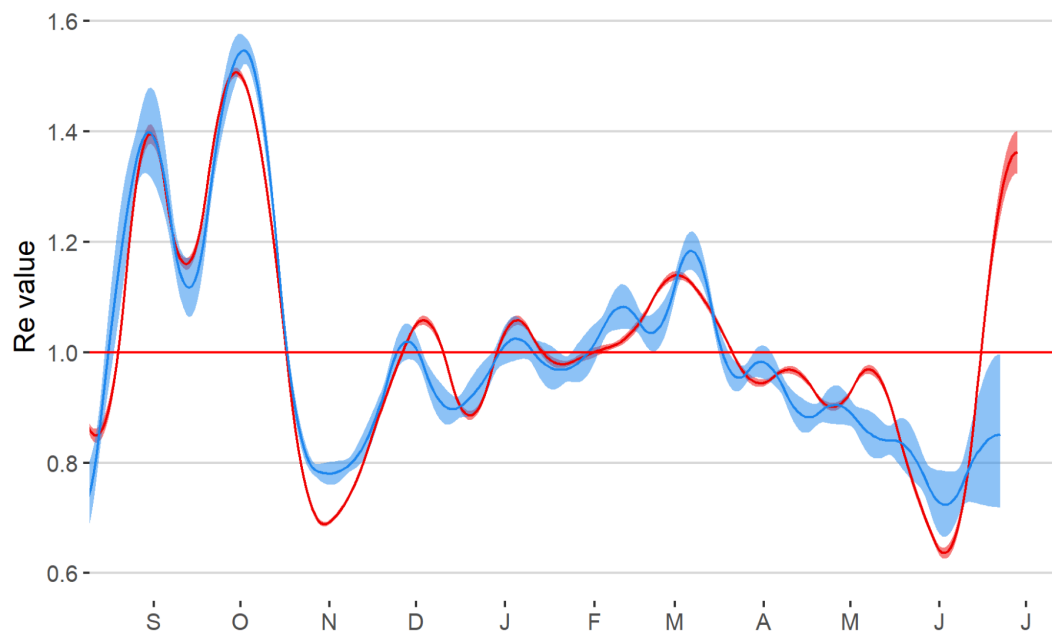
- A recent rise in the number of infections, a phenomenon directly associated with the variant Delta which has recently become the dominant lineage in Belgium (Figure 6)
- This recent rise of infections is mainly present at this stage in younger age groups, which are not yet widely vaccinated (Figure 7)
- The rise in the number of infections has not translated at this moment in an increase of infections requiring hospitalisation (Figure 8)



**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).



**Figure 7:** New confirmed COVID cases per day in Belgium corrected for testing intensity (Source : Tom Wenseleers, KU Leuven)



**Figure 8:**  $R_e$  value at moment of infection in Belgium calculated from case (Red) and hospitalisation data (blue). Corrected for variable testing intensity (Source : Tom Wenseleers, KU Leuven)

Lineage	Number of Belgian cases reported on GISAID	First reported
B.1.1.7 (Alpha)	18.245	30/11/2020
B.1.351 (Beta) and B.1.351.2	1.044	20/12/2020
P.1 (Gamma) and P.1.1	1.666	29/1/2021
B.1.617.2 (Delta)	589	6/4/2021
B.1.1.7 +S:E484K	45	31/3/2021
B.1.1.7 +S:S477R	33	15/3/2021
B.1.214.2	712	3/1/2021
B.1.427 (Epsilon)	1	18/1/2021
B.1.525 (Eta)	74	30/1/2021
B.1.526 (Iota)	8	9/2/2021
P.2 (Zeta)	2	9/2/2021
C.36.3	22	23/3/2021
B.1.620	22	31/3/2021
B.1.1.318	55	3/3/2021
A.27	19	11/1/2021
B.1.617.1 (Kappa)	12	25/3/2021
C.37 (Lambda)	1	20/6/2021

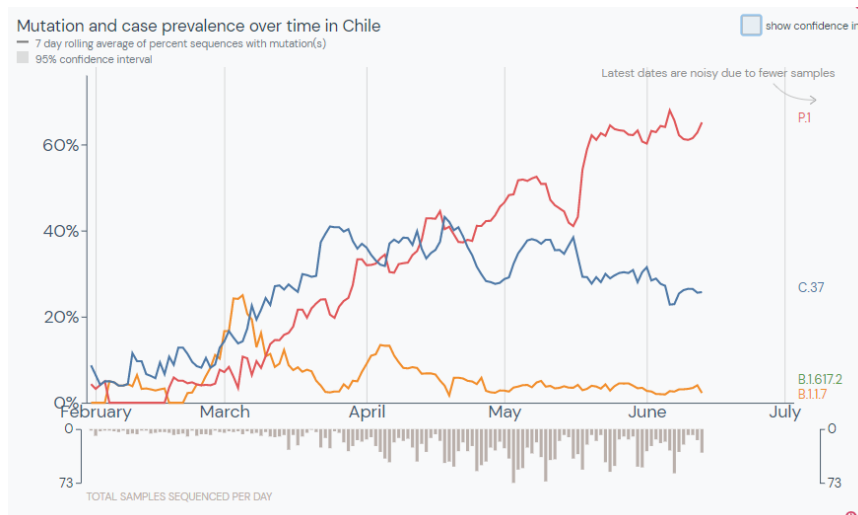
**Table 1:** List of VOCs (red) and VOIs (orange) identified in Belgium to date and cumulative number of sequences available on GISAID (total of 29.658 sequences).



## 2. First detection of Lambda (C.37) in Belgium

The first case of C.37 has been recently reported in Belgium (uploaded on GISAID on 2 July).

C.37 (variant under investigation; Lambda) has been one of the dominant strains in Latin America (mainly Peru and Chile) since the start of the year. This variant will probably not become a variant of concern, as it does not compete efficiently with P.1 (see example of Chile below), and will therefore probably not be successful in countries where Delta is dominant.



**Figure 9:** Co-evolution of P. 1 (Gamma) and C.37 (Lambda) in Chile. So far, there is no sign that Lambda would be more infectious than Gamma (Source: outbreak.info)

## 3. Testing of travellers

During the last 5 days, the National Reference Center in Leuven has tested 5.636 departing travellers, among which 19 were tested positive (0,34%). The Delta variant represented 56% of the positive samples tested.

During the last 5 days, the National Reference Center has tested 59 returning travellers, among which 1 was tested positive (1,69%), again with the Delta variant.

## 4. Summary of a recent study published last week and focusing on the impact of international travels on the circulation of the virus during the last summer period (2020)

On the eve of summer holidays, a study conducted by researchers of the KU Leuven and ULB and published in the journal Nature, assesses how newly introduced viral lineages contributed to COVID-19 resurgence after last summer in Europe. The researchers show that in the majority of European countries under investigation, more than half of the lineages circulating at the end of summer 2020 resulted from new introductions since June 15. Despite the progress of vaccination campaigns, the authors conclude that conditions similar to those demonstrated in their study could provide fertile ground for the spread and resurgence of the virus, and in particular variants of the

virus that are associated with a higher transmissibility and/or evade immune responses triggered by vaccines and previous infections.

Link to read the whole study: <https://www.nature.com/articles/s41586-021-03754-2>

Following the first wave of SARS-CoV-2 infections in spring 2020, Europe experienced a resurgence of the virus starting late summer. Although it appears clear that travel had a significant impact on the circulation of the virus, it remains challenging to assess how it may have restructured and reignited the epidemic in the different European countries.

In this study published last week, the researchers built a phylogeographic model to assess how newly introduced viral lineages, as opposed to persisting ones, contributed to the resurgence of COVID-19 in Europe. Their model was informed using epidemiological, mobility, and viral genomic data from ten European countries (Belgium, France, Germany, Italy, Netherlands, Norway, Portugal, Spain, United Kingdom, Switzerland). Their analyses show that in the majority of the countries under investigation, more than half of the lineages circulating at the end of the summer resulted from new introductions since June 15. The researchers also show that the success of transmission of the newly introduced lineages was predicted by the local incidence of COVID-19: in countries that experienced a relatively higher summer incidence (e.g. Spain, Portugal, Belgium and France), the introduction events led to proportionately fewer active transmission chains after August 15.

These results illustrate the threat of viral spread via international travel, a threat that must be carefully considered by strategies to control the current spread of variants that are more transmissible and/or evade immunity.

The pandemic exit strategy offered by vaccination programs is a source of optimism that also sparked proposals by EU member states to issue vaccine passports in a bid to revive travel and rekindle the economy. In addition to implementation challenges and issues of fairness, there are risks associated with such strategies when immunization is incomplete, as likely will be the case for the European population this summer.

The authors of the study conclude that conditions similar to those demonstrated in their study could provide fertile ground for viral dissemination and resurgence, which may now also involve the spread of variants that evade immune responses triggered by vaccines and previous infections. They hope that a well-coordinated, unified implementation of European strategies to mitigate the spread of SARS-CoV-2 will reduce the chances of future waves of infection.