

Potential impact of intense travels during the summer season for the Belgian SARS-CoV-2 epidemic

National Reference Laboratory (UZ Leuven & KU Leuven)

Special report on the request of the Belgian Government Commissioner Covid-19
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In this report, we describe

1. How international travels have shaped the epidemic in Belgium during the last 15 months
2. What impact can be expected from the current vaccination rate as a risk reduction mechanism
3. Possible risk reduction strategies

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1. General considerations

The risk associated with travels is determined by a number of factors:

1. Intensity of travels

- a. EU countries : estimated high
- b. Outside EU : estimated moderate

2. Incidence, reproduction rate and emerging character of variants of concern in the visited countries

- a. UK: current negative trend
- b. EU: currently, overall positive trend, with a risk of evolution towards a negative trend during the summer
- c. Outside EU: variable, to be assessed regularly per country

3. Risk reduction interventions applied in the visited countries

- a. EU:
 - i. Screening travellers at entry (of the country of destination) does not imply the absence of viral circulation in that country. On the contrary, the virus is still actively circulating in all countries and the touristic season may play a role in amplification
 - ii. Interventions and rules aiming to reduce viral transmission may be less stringent during the summer season, as countries are willing to attract tourists
- b. Outside EU: variable, to be assessed per country

4. Testing and quarantine among returning travellers

- a. EU: Current assumptions at the EU commission level are that the EU as a whole has become a “safe zone” with regard to viral circulation. This is not the case, and the epidemiological situation may rapidly change during the summer.
- b. Outside EU: general precautions are generally well followed

5. Vaccination status

- a. EU:
 - i. Most countries now have a high coverage for elderly populations, which implies that the impact of a surge of viral circulation on the number of severe infections will be reduced (although not fully contained).
 - ii. A very high number of European citizens will be partially vaccinated during the summer season. This may play an important role in the selection of immune escape variants and a potential wrong impression of safety
 - iii. The majority of EU citizens are not yet vaccinated, which implies that viral circulation will not be contained by vaccination at this stage.
- b. Outside EU: variable, to be assessed per country

2. How international travels have shaped the epidemic in Belgium during the last 15 months

- February and March 2020

The initial sporadic travellers from China could be systematically identified, tested and set in quarantine. This prevented secondary cases in Belgium.

During the winter holidays (end of February 2020), an important number of Belgian travellers returned from a stay abroad, including from northern Italy, where the virus was already actively circulating along with a poorly documented exponential rise of infections and the testing & quarantine capacity in Belgium was limited. As a consequence, at least hundred of introduction events occurred, leading to the first epidemic wave. This situation was not specific to Belgium, and most EU countries experienced the same evolution (with different levels of intensity).

- Summer 2020

During the summer of 2020, most EU countries had a relatively low viral circulation, and this situation led to relaxations in terms of travels and general disease prevention interventions. Relaxed intervention measures and summer travel have been implicated as drivers of the second wave.

As described by [Hodcroft et al. \(2021\)](#), a rise of 20E (EU1) infections which occurred towards the end of the summer in Spain coincided with a peak of returning travels. As a result, several EU countries experienced a large number of simultaneous introductions, although 20E was not particularly more transmissible compared to other variants circulating at that time.

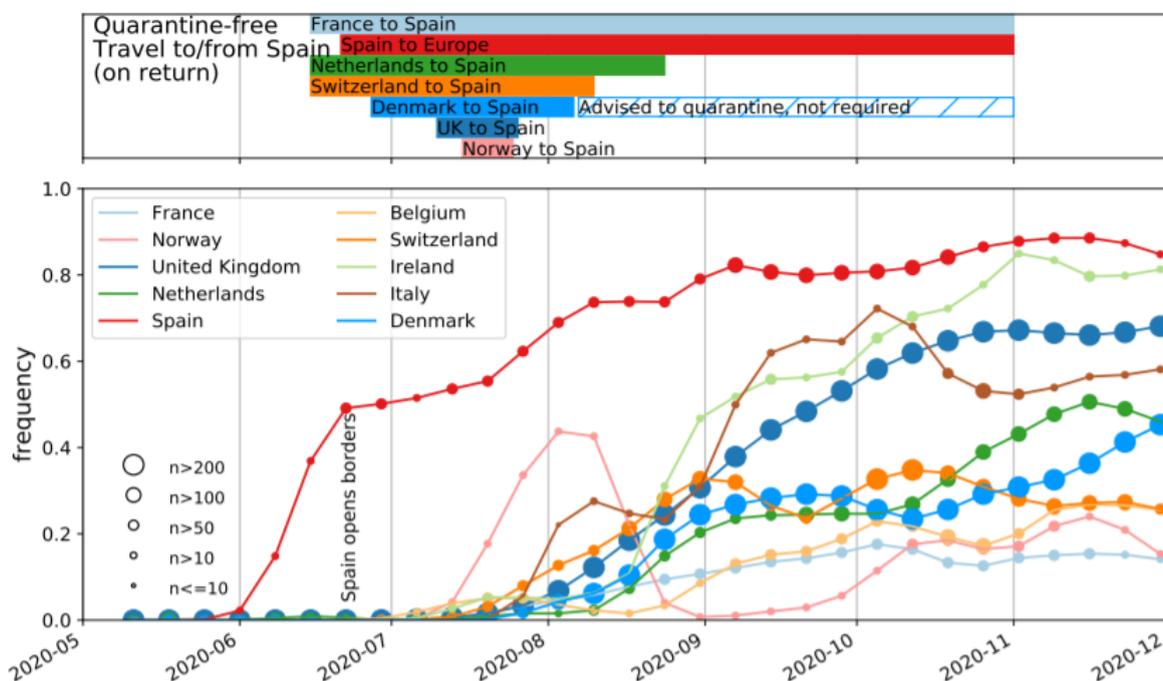


Figure 1 (from Hodcroft et al.): Frequency of submitted samples for 20E (EU1) in selected countries, with quarantine-free travel dates shown above. We include the eight countries which have at least 200 sequences for type 20E (EU1), as well as Norway and France. The symbol size indicates the number of available sequences by country and time point in a non-linear manner. Travel restrictions

from selected countries are shown to/from Spain, as this is the probable origin of the cluster. Most European countries allowed quarantine-free travel to other (non-Spanish) countries in Europe for a longer period. When the last data point included only very few sequences, it has been dropped for clarity. Frequencies are smoothing using a Gaussian with $\sigma = 1w$.

[In another study](#), Belgian researchers (KU Leuven and ULB) and their collaborators built a phylogeographic model to evaluate how newly introduced lineages, as opposed to the rekindling of persistent lineages, contributed to the COVID-19 resurgence in Europe. They inform this model using genomic, mobility and epidemiological data from 10 European countries and estimate that in many countries over half of the lineages circulating in late summer resulted from new introductions since June 15th.

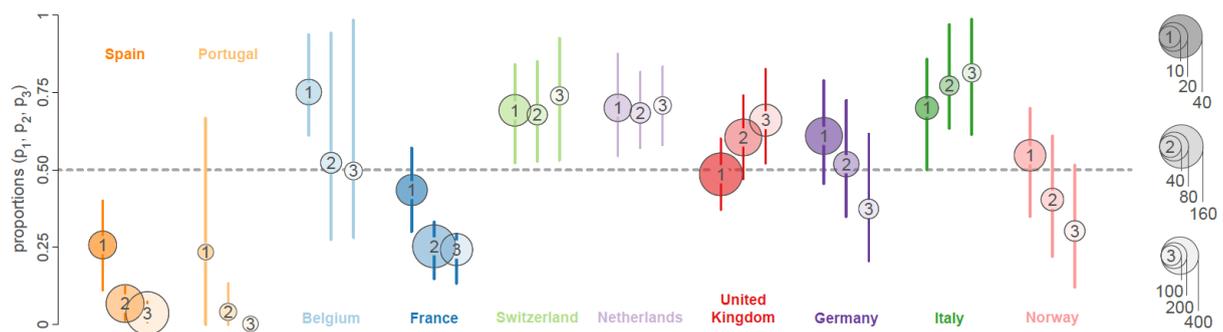


Figure 2 taken from the study: posterior estimates for the relative importance of lineage introduction events in 10 European countries and their association with incidence. We report three summaries (posterior mean and 95% HPD intervals) for each country: the ratio of unique introductions over the total number of unique persisting lineages and unique introductions between June 15 and August 15, 2020 (p_1), the ratio of descendant lineages from these unique introduction events over the total number of descendants circulating on August 15, 2020 (p_2), and the ratio of descendant taxa from these unique introductions over the total number of descendant taxa sampled after August 15, 2020 (p_3). The dot sizes are proportional to: (1) the total number of unique lineage introductions identified between June 15 and August 15, 2020, (2) the total number of lineages inferred on August 15, 2020, and (3) the total number of descendant sequences after August 15, 2020. The third ratio is not included for Portugal due to insufficient sequences sampled after August 15, 2020.

The results of this study show that the success in onward transmission of newly introduced lineages is negatively associated with local COVID-19 incidence during this period. The authors of this study conclude that the pervasive spread of variants in the summer of 2020 highlights the threat of viral dissemination when restrictions are lifted, and this needs to be carefully considered by strategies to control the current spread of variants that are more transmissible and/or evade immunity. Their findings indicate that more effective and coordinated measures are required to contain spread through cross-border travel even when vaccination begins to reduce disease burden.

- **December 2020 and January 2021 (Christmas holidays)**

The start of the Christmas holidays in Belgium coincided with a positive trend after an important second wave. This was once again considered as an opportunity to relax travel restrictions. Nevertheless, the UK, South-Africa and Brazil were at that time experiencing a surge of cases associated with new variants of concern (respectively B.1.1.7, B.1.351 and P.1).

Due to the geographical proximity with the UK and the intensity of travels, a large number of introductions of B.1.1.7 infections were documented. Despite wide testing of returning travellers from the UK and other countries, this situation led to multiple local clusters and a rapid shift with regard to circulating viral populations. This variant represented 70% of infections diagnosed in Belgium during the first 15 days of March 2021, was responsible for the “third wave” and still represents the majority of new infections occurring today.

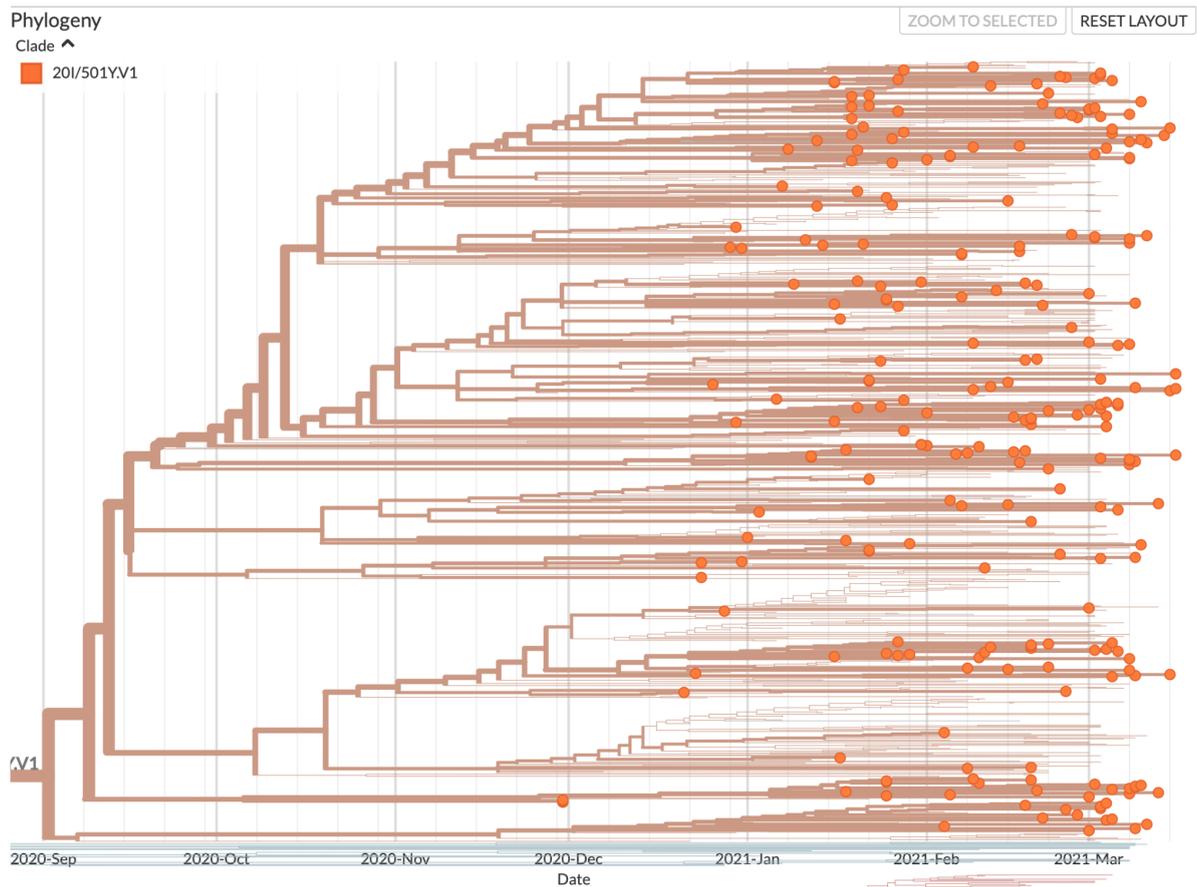


Figure 3: Multiple parallel introductions of B.1.1.7 leading to numerous secondary clusters and a rapid replacement (>75%) of circulating viral strains after 3,5 months.

A limited number of P.1 clusters which started during this same period are still active in Belgium, and represent today +/-10% of the new infections.

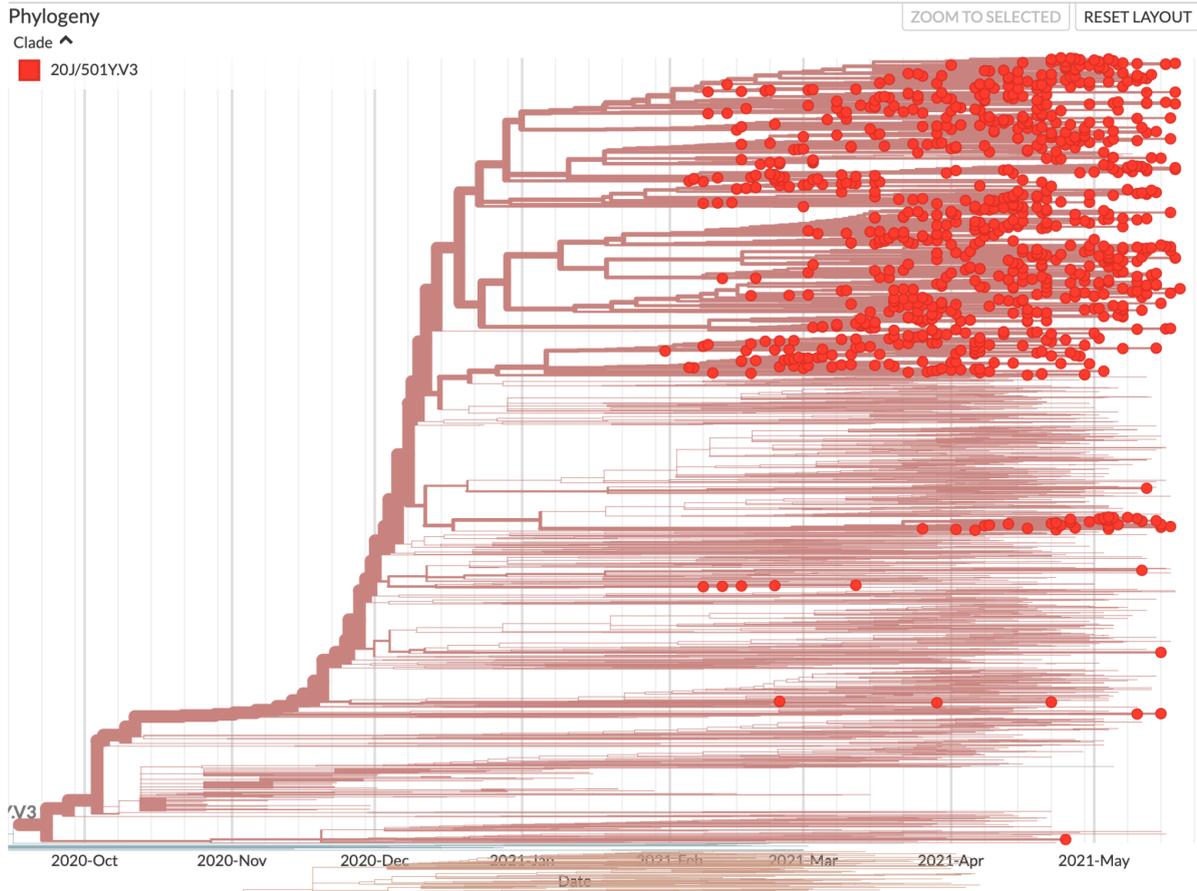


Figure 4: Overview of the global P.1 phylogeny including all currently available Belgian genomes which are indicated as dots in the tree. All Belgian genomes were included while for other countries a representative set is part of the tree.

- March and April 2021

More recently, the epidemiological situation in India (characterized by a high circulation of the lineage B.1.617.2), has been associated with multiple introductions of this variant of concern in Belgium. This situation coincides today with further planned relaxations and release of travel restrictions within the EU.

In the absence of very active disease control measures, and considering the current situation in Belgium and the EU, we expect that the further relaxations will lead to a rise of infections during the coming weeks, as it is now observed in the UK.

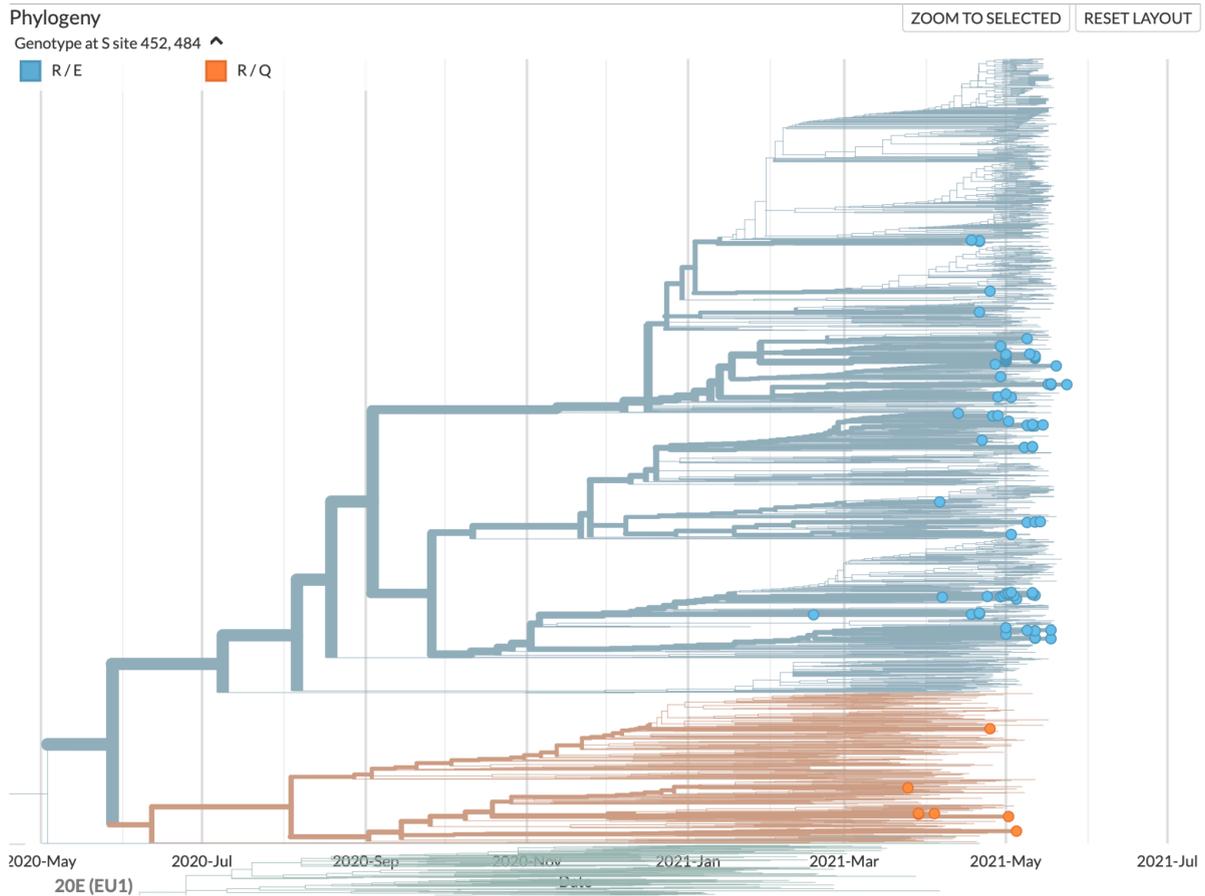


Figure 5: The currently available Belgian B.1.617.1 (orange) and B.1.617.2 (blue) genomes on GISAID are highlighted in the tree, showing many introductions into Belgium (Belgian genomes indicated as dots in the tree) and are definitely not the result of a single source of origin. This illustrates the importance of screening incoming travelers and performing contact tracing.

3. What impact can be expected from the current vaccination rate as a risk reduction mechanism

1. Most countries now have a high coverage for elderly populations, which implies that the impact of a surge of viral circulation on the number of severe infections will be reduced (although not fully contained).
2. A very high number of European citizens will be partially vaccinated during the summer season. This may play an important role in the selection of immune escape variants and an inappropriate sense of safety.
3. The majority of EU citizens are not yet fully vaccinated, which implies that viral circulation will not be contained by vaccination at this stage.

A recent modelling study for the United Kingdom suggests that vaccination in adults alone is unlikely to completely halt the spread of COVID-19 cases and that lifting containment measures early and suddenly can lead to a large wave of infections ([Moore et al. 2021](#)).

Considering the reduced effectiveness of vaccines to prevent infections caused by B.1.617.2, including severe infections, a surge of hospitalisations cannot be excluded in the coming months in Belgium if the combination of the four elements below is present

- (1) emerging VOCs in countries massively visited by,
- (2) intense travels and
- (3) limited testing & quarantine policies remains present
- (4) rapid relaxation of measures in Belgium

4. Possible risk reduction strategies

- Reinforce the awareness in the general population with regard to “safe travel abroad” rather than only maintaining the focus on “negative test at entry & corona pass”. This perception could lead to a multiplication of high risk contacts during travels
- Reduce the barriers for testing (and eventually quarantine) upon return, including from EU countries (EU is not a “safe zone”)
- Maintain and reinforce genomic surveillance in the EU and at the international level