KU LEUVEN

DEPARTMENT OF MICROBIOLOGY, IMMUNOLOGY AND TRANSPLANTATION

UZ LEUVEN | LABORATORIUMGENEESKUNDE

Genomic surveillance report

Update for Belgium, 25/10/2022

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Content

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Cliniques Universitaires Saint-Luc, Centre Hospitalier CHU UCL Namur, 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, UZ Brussel, LHUB-ULB, UZ Leuven/KU Leuven and Sciensano HealthData.

Previous reports are available online using this link.

Executive summary

The first autumnal surge of SARS-CoV-2 infections (and probably also hospital admissions) seems to have peaked. This wave is mainly driven by behavioral and seasonal changes as well as waning immunity. It is caused by BA.5.2*-derived viruses, including BF.7 variants, which have dominated in Belgium since June 2022 and were already partly responsible for the last summer wave of infections with BA.5* variants.

Considering the current rise of BQ.1* and BQ.1.1*, we expect these variants will become dominant in the upcoming weeks, resulting in a second surge of infections. This projection is supported by a growth advantage currently estimated at 10% compared to the current dominant variants.

At the international level, BQ.1* is expected to become dominant in France in the coming days/weeks, with approximately 1-2 weeks advance in comparison to the evolution in Belgium. A close follow-up of the situation in France during the upcoming weeks should therefore be informative about the foreseen real-life impact of BQ.1* in Belgium, in particular with regard to disease severity.

Finally, the epidemiological evolution of the XBB* variant, including its eventual competitive advantage against BQ.1.1* will need to be followed up during the coming weeks.

1 International context

It is expected that BQ.1* variants will shortly dominate in most parts of the world including Europe. Data from India and Singapore suggest that XBB* is also able to outcompete BA.5*. In all cases, these rapid viral population replacements are expected to generate surges of infections driven by the ability of these variants to escape vaccine-induced immunity and immunity induced by previous variants.

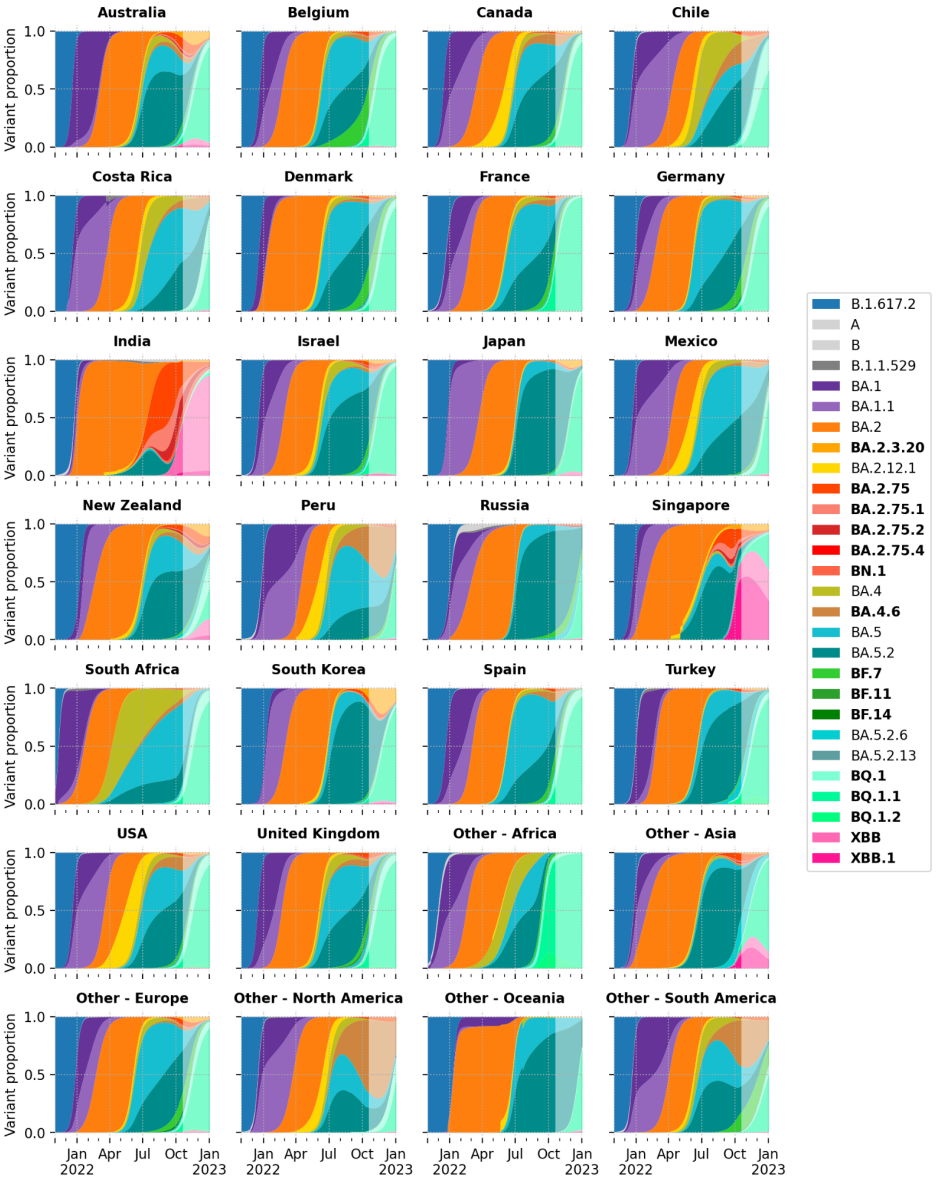

Figure 1: *Past and projected proportions of SARS-CoV-2 variants (Source: Moritz Gerstung available at https://github.com/gerstung-lab/SARS-CoV-2-International)*

In France, BQ.1* has now become dominant. The upcoming epidemiological evolution in our neighboring country will continue to be monitored in order to anticipate the impact of this emerging variant in the rest of Europe.

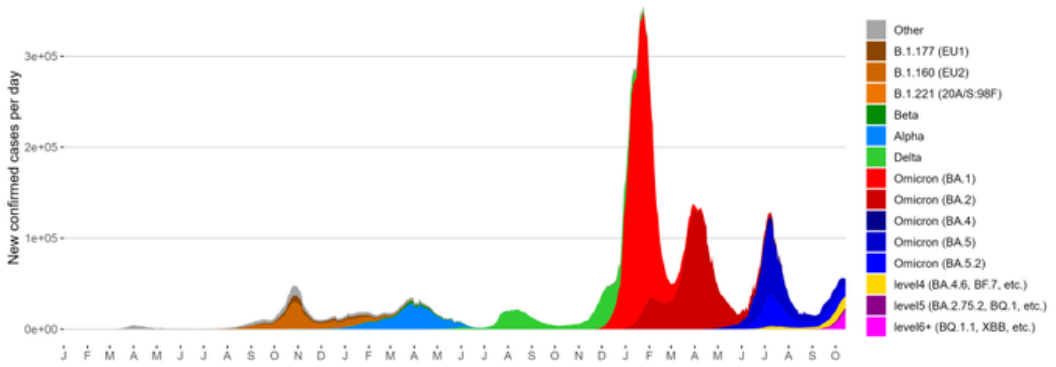

Figure 2: *New SARS-CoV-2 infections per variant in France. The impact of the increasing proportion of BQ.1* (in pink) on the total number of infections is yet to be observed (Source: Tom Wenseleers, KU Leuven*)

2 Monitoring of Variants of Concern in Belgium

Currently, it is estimated (24/10/2022) that BQ.1* samples represent 30-40% of the most recent infections in Belgium.

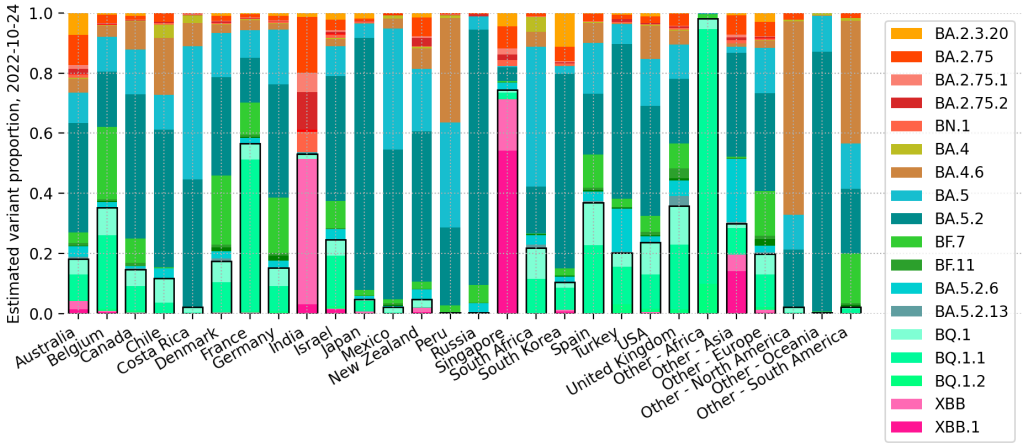

Figure 3: *Estimated variant proportions in different countries including Belgium (Source: Moritz Gerstung available at https://github.com/gerstung-lab/SARS-CoV-2-International)*

3 Changes in the genomic surveillance in Belgium

According to the latest RAG advice concerning the indications for genomic sequencing, dating from September 23, the genomic surveillance consortium was asked to limit the number of positive samples included in the baseline surveillance program to a maximum of 500 samples per week for the entire country. While previously a more variable number of sequences was generated on a weekly basis, according to the positivity rate and therefore the epidemiological situation, it was chosen to move towards a more stable number of samples for sequencing, therefore decreasing the overall cost of the surveillance program. While variants circulating at a low proportion are still key to be monitored and detected as early as possible, this lower number of samples included in the baseline surveillance is complemented with samples in the context of active surveillance, however no longer focusing on reinfections and infections post-vaccination. Mainly infections in populations with enhanced risk for mutations, as well as atypical PCR results, samples from travelers and a selection of samples from unusual outbreaks, will be key subjects for active surveillance purposes. Only samples with a clear indication for sequencing, accompanied with the associated metadata, will be considered for sequencing. This way a highly sensitive surveillance program can be maintained over the following months, providing guarantee that variants circulating at a proportion as low as 1% will be detected in time.

NB: Due to the national holiday of next week (1st of November - Ascension Day), our next report, n° 104, is exceptionally planned for the second week of November.