KU LEUVEN

DEPARTMENT OF MICROBIOLOGY, IMMUNOLOGY AND TRANSPLANTATION

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Genomic surveillance report

Update for Belgium, 18/10/2022

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Content

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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 by the end of the month of October (or early November), resulting in a second surge of infections which is expected to be more pronounced than the first autumnal episode. This projection is supported by a growth advantage of 10-15% 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

The international genomic landscape is rapidly changing, and 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.

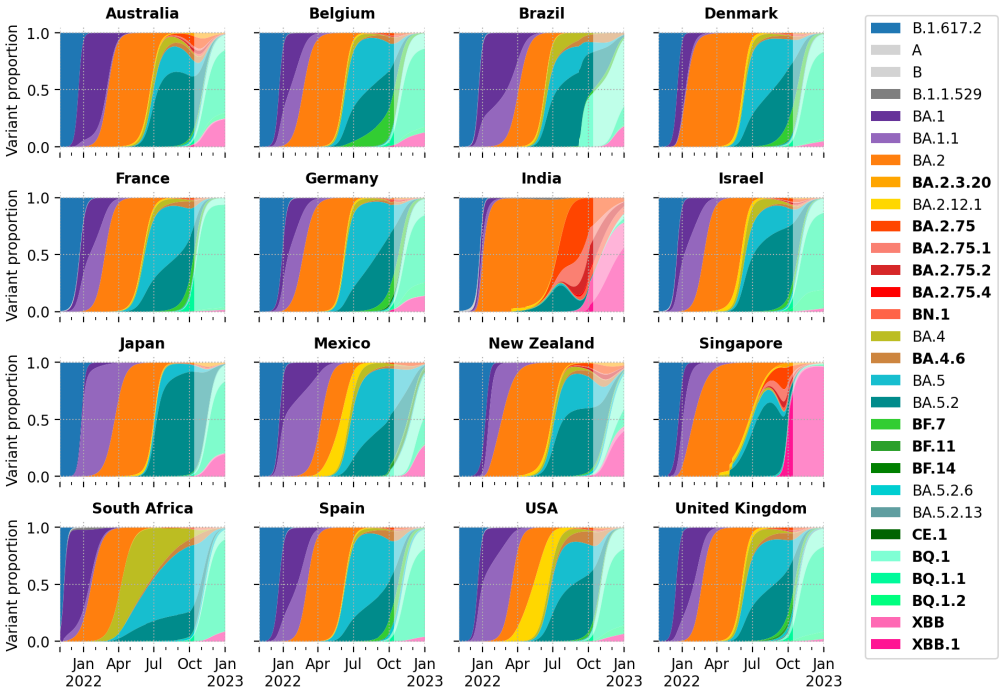

Figure 1: *Past and projected proportions of SARS-CoV-2 variants (Source: Moritz Gerstung available at https://github.com/gerstung-lab/SARS-CoV-2-International ; compatible with projections of Tom Wenseleers available at https://github.com/tomwenseleers/LineageExplorer/tree/main/plots/RBDmutations)*

The antibody evasion capability of BQ.1.1* and XBB* are related to an extensive antigenicity drift. Yunlong Cao *et al*. found that the antigenic distances of SARS-CoV-2 ancestral strain to XBB* and BQ.1.1* are already comparable to that of SARS-CoV-2 against SARS-CoV-1. The authors suggest in this preprint that these convergent variants could escape the binding of the majority of NAbs and cause inabilities to induce rapid increase of plasma neutralization. The authors suggest therefore to closely monitor disease severity caused by these new convergent variants.

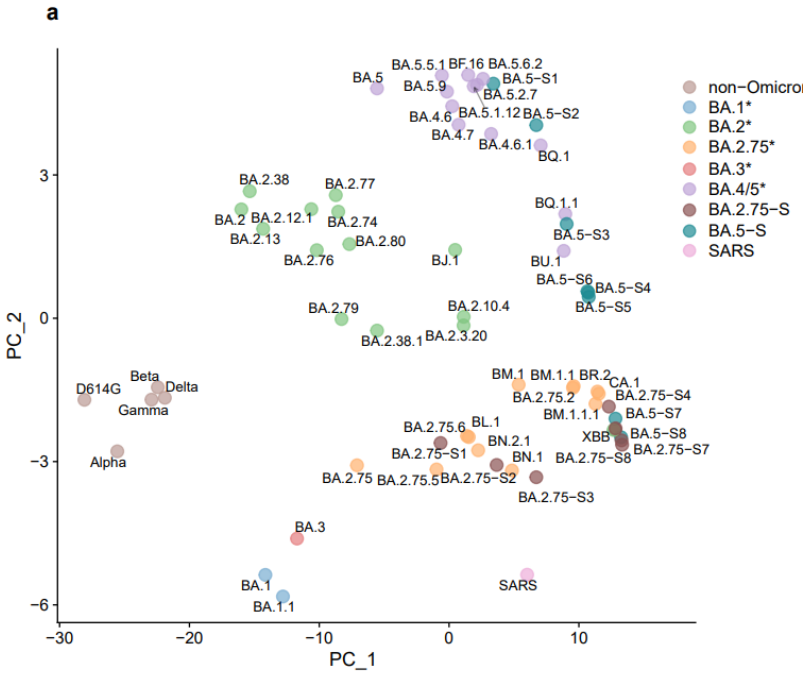

Figure 2: Antigenic map of SARS-CoV-2 variants constructed using plasma neutralization data by principal component analysis. (Source: Yunlong Cao et al. Preprint available at: https://www.biorxiv.org/content/10.1101/2022.09.15.507787v3).

While the upcoming resurgence of infections related to a viral population replacement by BQ.1.1* is foreseen based on different sets of projections, we have until now limited data available to understand how BQ.1.1* and XBB* will enter in competition at a later stage. We will therefore need to monitor carefully the international situation, looking for countries concomitantly exposed to these two emerging variants.

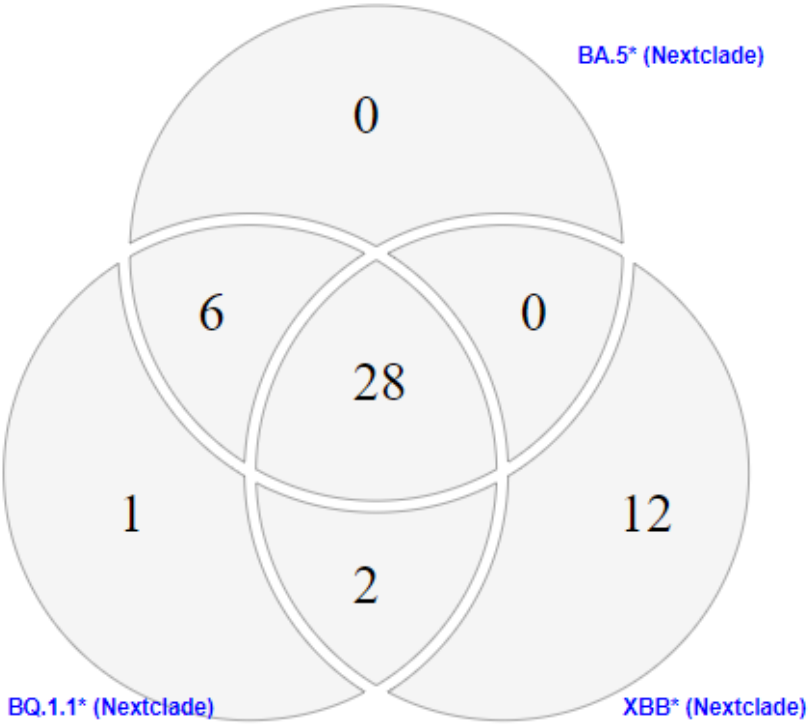

Figure 3: *Amino acid differences in the Spike proteins of (BA.5*, BQ.1.1* and XBB) variants. BQ.1.1 currently takes advantage of 3 mutations (S:R346T; S:K444T and S:N460K) to outcompete BA.5*. XBB is currently outcompeting BA.5* in Asia. It is not clear yet how these 2 emerging variants will co-evolve worldwide (Source: https://cov-spectrum.org/)*

2 Monitoring of Variants of Concern in Belgium

Emerging variants have been detected through the Belgian genomic surveillance system for several weeks, as highlighted in Table 1.

	Number of sequences on GISAID (numbers reported last week)	collection date first sample
BQ.1 (incl BQ.1.1)	201 (105)	20-08-2022
BQ.1.1	100 (52)	05-09-2022
BA.2.3.20	5 (4)	26-09-2022
BA.2.75 (incl BA.2.75.2, BN.1)	130 (98)	22-07-2022
BA.2.75.2	21 (20)	01-08-2022
BN.1	14 (6)	15-09-2022
XBB	6 (2)	21-09-2022

Table 1: *Number of emerging variants detected by the Belgian genomic surveillance system. BQ.1* and XBB* variants are widely discussed in the section above and highlighted in red (source: GISAID)*

Based on the collection date, it appears that BQ.1* shows a rapid and significant increase over the last weeks, with a doubling time of approximately one week since over one month (Figure 4). The proportion of XBB* strains remain limited at this stage, although an increase has been observed.

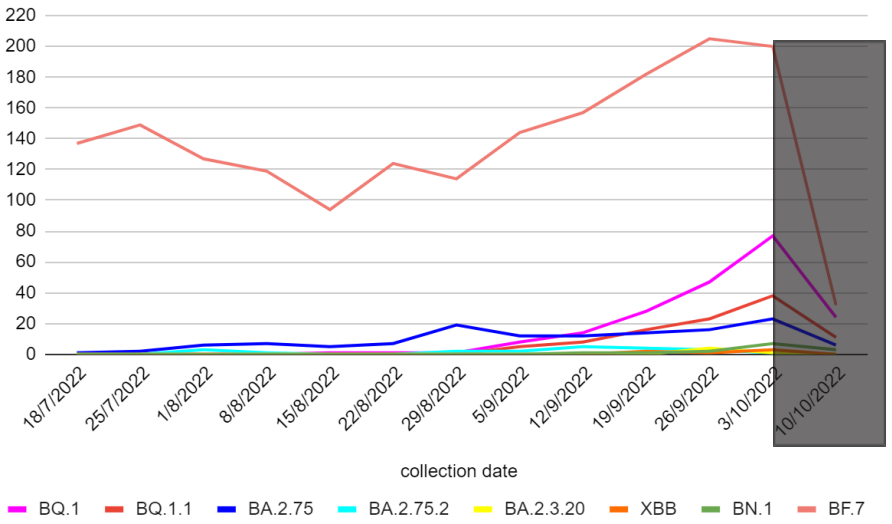

Figure 4: *Number of Belgian sequences reported on GISAID for emerging variants under monitoring. BF.7 has been added in this graph as it is among the currently dominant BA.5* related variants associated with the current surge of infections. We note that the number of BF.7 strains started to decrease +- concomitantly with the peak of the BA.5* autumnal wave, while BQ.1* variants continue to rise in proportion and absolute numbers. The total numbers for the last week (highlighted in gray) should be interpreted with caution as all sequences may not have been reported yet.*