



# Genomic surveillance report

Update for Belgium, 08/11/2022

**Lize Cuypers, Lies Laenen, Guy Baele, Simon Dellicour, Piet Maes, Emmanuel André**

See page 2 for full list of authors and participating laboratories

November 2022

# Content

<b>Executive summary</b>	<b>3</b>
<b>International context</b>	<b>4</b>
<b>Monitoring of Variants of Concern in Belgium</b>	<b>6</b>

*This report was written in collaboration with:*

*Reile Janssen, Louis Nevejan, Tom Wenseleers, Bram Slechten, Johan Van Weyenbergh, Els Keyaerts, Joren Raymenants, Barney Potter, Elke Wollants, Marc Van Ranst and the Belgian Sequencing Consortium.*

*Corresponding author: lize.cuypers@uzleuven.be (National Reference Center for Coronaviruses, UZ Leuven)*

*Belgian Sequencing Consortium:*

*Cliniques Universitaires Saint-Luc, Centre Hospitalier CHU UCL Namur, ULB, UMon, UNamur, ULiège, UGent, UZA/UAntwerpen, Jessa ZH, AZ Delta, AZ Klin, 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) has peaked. This wave was 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.

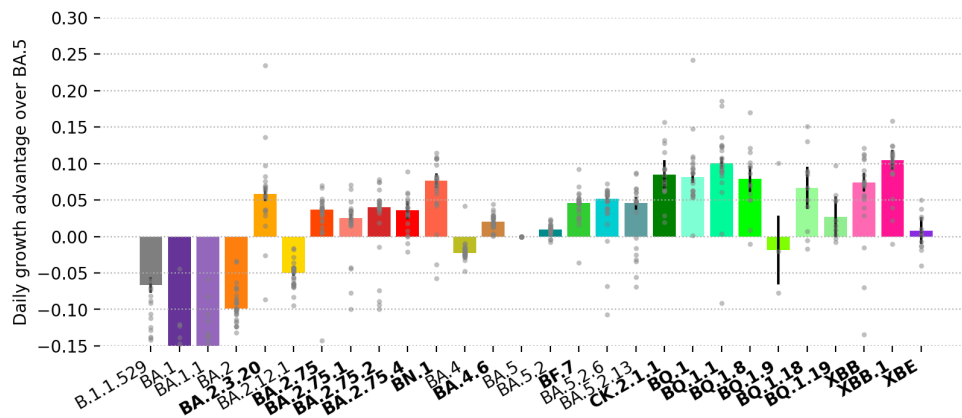
Omicron-derived BQ.1\* and XBB\* variants continue to show a growth advantage against BA.5 (and to a lesser extent against BF.7), and currently represent ~50% of the recent infections in Belgium. Although one would have expected that the dominance of more transmissible variants would have led to a concomitant surge of infections, this phenomenon has not yet been observed in Belgium or other countries, and the epidemiological evolution remains favorable at this stage.

In this report, we discuss the possible explanations of this (transient?) unpredicted evolution, including higher than expected cross-immunity and the possible impact of record-high temperatures during the last weeks of October 2022. If the latter hypothesis was to be validated, the expected surge of infections may be delayed, while the first hypothesis would tend towards a more sustained low circulation of the virus.

# 1 International context

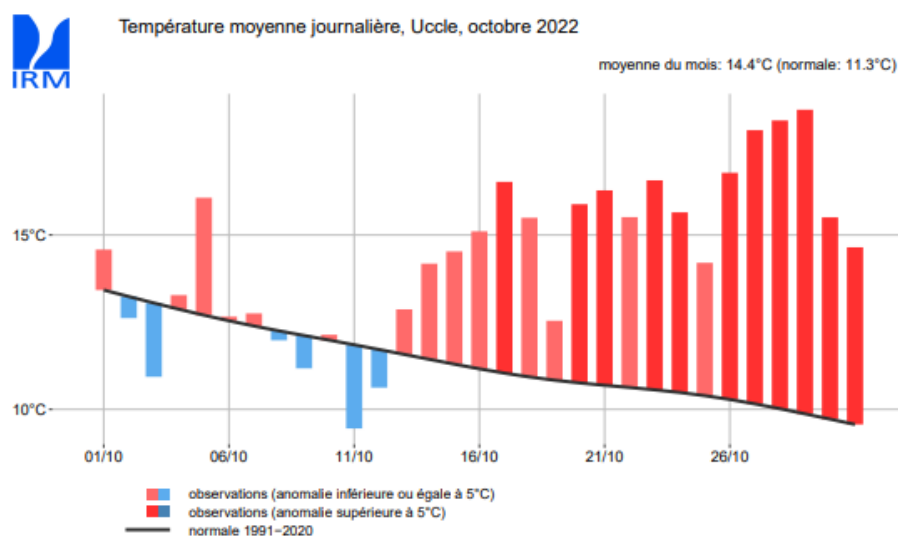
At the global level, the “Omicron” sub lineages emerge due to diversification, with an accumulation of variants which render genomic surveillance particularly challenging at present.

Predicting upcoming epidemic surges relies on both the level of competitive advantages of emerging viral strains compared to circulating variants, and to seasonality patterns. Currently, BQ.1\* and XBB\* variants remain the most competitive variants in comparison with BA.5. Of note, in Belgium, baseline viral circulation includes a high proportion of BF.7 (~25%), a variant presenting an intermediate infectiousness potential between BA.5 and BQ.1\*.



**Figure 2:** Daily growth advantage of Omicron-derived SARS-CoV-2 variants against Omicron BA.5 (Source: Moritz Gerstung available at <https://github.com/gerstung-lab/SARS-CoV-2-International>, last update 7/11/2022)

Seasonality of viral circulation has further possibly been impacted during the recent weeks by record-high temperatures in Europe, including Belgium, as illustrated below<sup>1</sup>.

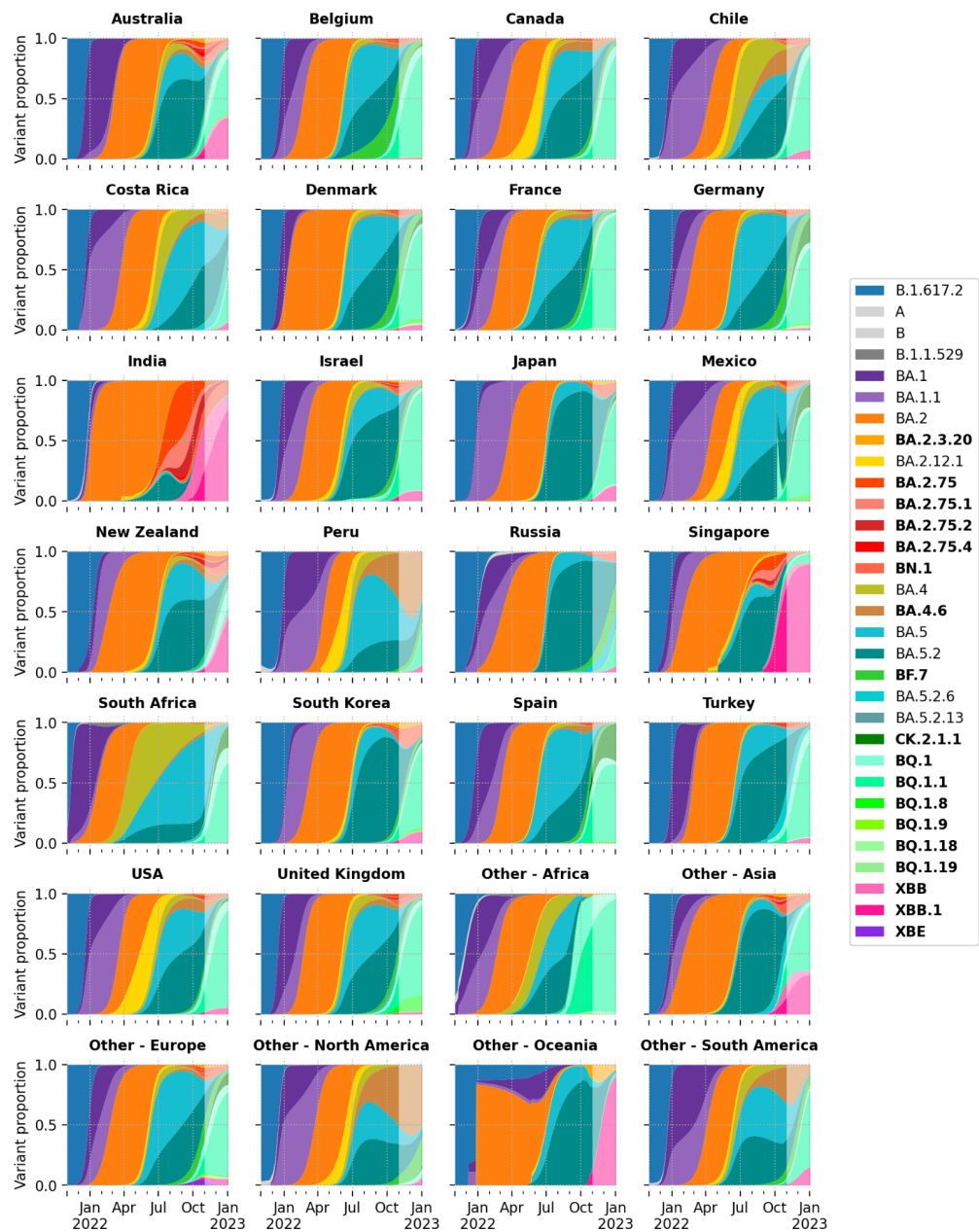


**Figure 3:** Mean daily temperature in Uccle, Belgium during the month of October 2022. The second part of the month has been marked by record-high temperatures which may have impacted (transiently) the epidemiological impact of BQ.1\* (Source: RMI)

1

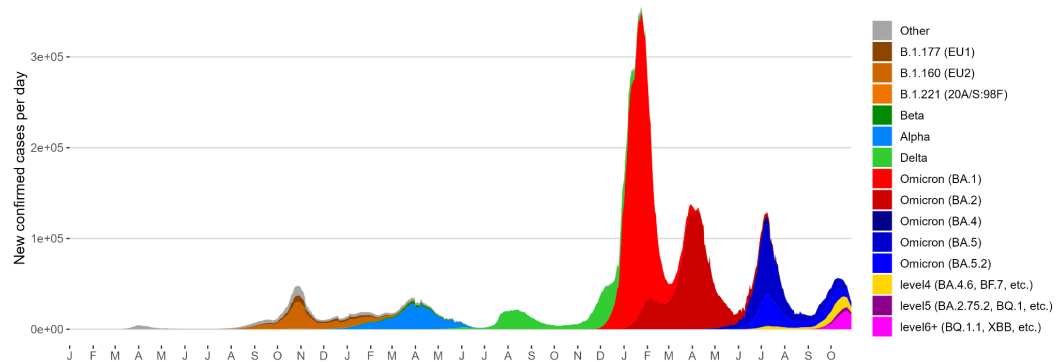
<https://www.meteo.be/uploads/media/6363746d7bf0f/bilan-climatique-mensuel-202210.pdf?token=/uploads/media/6363746d7bf0f/bilan-climatique-mensuel-202210.pdf>

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\*.



**Figure 4:** Past and projected proportions of SARS-CoV-2 variants (Source: Moritz Gerstung available at <https://github.com/gerstung-lab/SARS-CoV-2-International>, last update 7/11/2022)

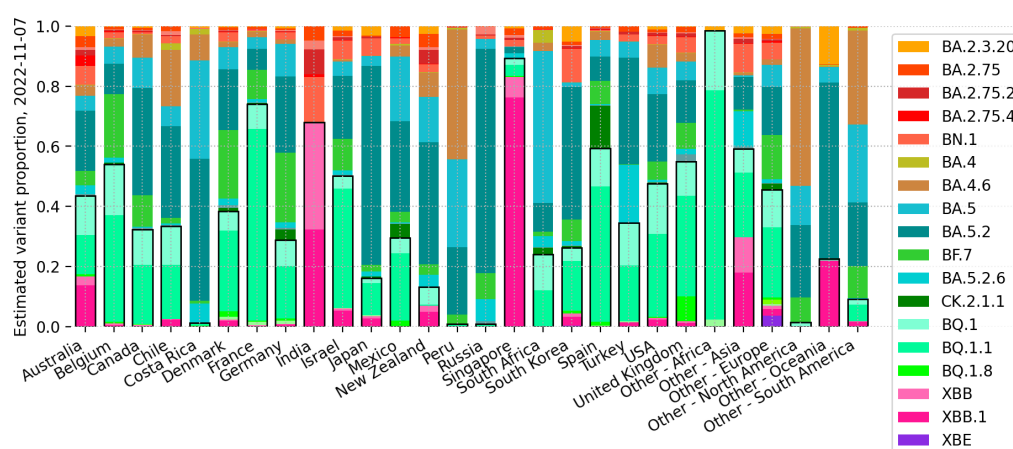
In France, BQ.1\* has been dominant for a couple of weeks. Considering past experiences with regard to rapid viral populations replacements, one would have expected a surge of infections concomitant with this evolution. Nevertheless, at this stage, the epidemiological evolution in our neighboring country remains favorable. This may be linked to a high level of cross-immunity between previous variants and BQ.1\* and/or the impact of record-high temperatures during this autumnal season.



**Figure 5:** 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 currently limited (Source: Tom Wenseleers, KU Leuven)

## 2 Monitoring of Variants of Concern in Belgium

Currently, it is estimated (7/11/2022) that BQ.1\* and XBB\* samples represent ~50% of the most recent infections in Belgium. The reported number of infections is still declining, suggesting that these new dominant variants do not have a reproduction number above 1 in the current situation, which has to be seen as a combination of immunity level, behaviors and seasonality.



**Figure 3:** Estimated variant proportions in different countries including Belgium (Source: Moritz Gerstung available at <https://github.com/gerstung-lab/SARS-CoV-2-International>, last update 7/11/2022)