KU LEUVEN

DEPARTMENT OF MICROBIOLOGY, IMMUNOLOGY AND TRANSPLANTATION

UZ LEUVEN | LABORATORIUMGENEESKUNDE

Genomic surveillance report

Update for Belgium, 11/10/2022

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

See page 2 for full list of authors and participating laboratories

October 2022

Content

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: lies.laenen@uzleuven.be (National Reference Center for Coronaviruses, UZ Leuven)

Belgian Sequencing Consortium:

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

SARS-CoV-2 BA.5* viruses harboring an R346 spike mutation and BF.7 (corresponding to BA.5.2.1 with a spike mutation R346T) continues to represent the vast majority of the circulating strains and dominate in the current surge of infections, which may now have peaked.

In parallel, a number of emerging variants have been detected in Belgium through the genomic surveillance network. Among these variants under close monitoring, genomic surveillance highlights a proportion of BQ.1* and BQ.1.1* doubling every week. Considering that the latter variant currently represents around 10% of the circulating strains, a new surge of infections driven by a new viral population replacement could therefore be expected by the end of the month.

1 International context

Following the major waves of infections provoked by the variants Delta, Omicron BA.1 and Omicron BA.2, a number of Omicron-related variants have emerged around the world. Among these, BA.5 and BA.4 became dominant in most western countries, while BA.2.75 became dominant in several Asian countries.

Most of the latest emerging variants have emerged around the world from the successful BA.2 and BA.5 Omicron variants, acquiring sets of additional mutations diversely associated with increased immune escape and/or infectiousness. Many of these sublineages have acquired similar mutations despite not originating from the same clone, allowing the scientific community to consider these sets of mutations as a convergent evolutionary process driven by the selective advantages they provide in the current epidemiological situation. Preliminary studies suggest that these convergent mutations can cause striking evasion of convalescent plasma, including those from BA.5 breakthrough infection, and existing antibody drugs[1].

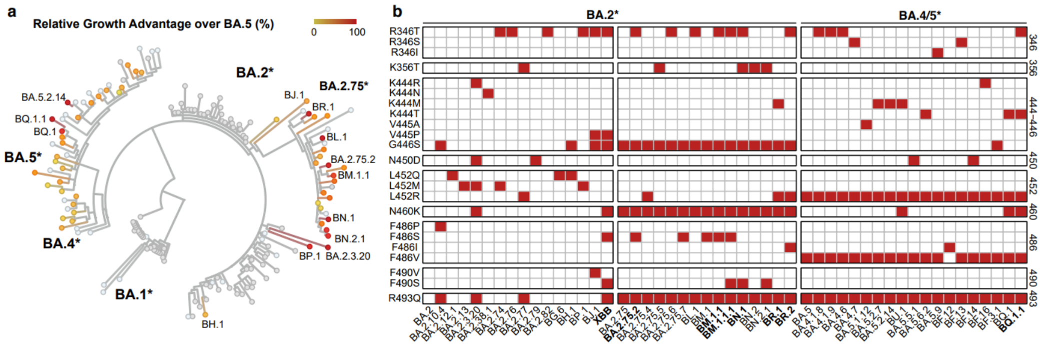

Figure 1: Convergent evolution of Omicron RBD with growth advantage over BA.5. a) Whole-genome maximum likelihood phylogenetic analysis of Omicron subvariants. Variants with a growth advantage over the original BA.5 are colored. Relative growth advantage values are calculated using CoV-Spectrum website. b) Key RBD mutations in emerging SARS-CoV-2 BA.5 and BA.2.75 subvariants (source: preprint https://www.biorxiv.org/content/10.1101/2022.09.15.507787v3.full.pdf)

While BQ.1* became dominant in Nigeria (and probably in other neighboring countries with lower levels of genomic surveillance, too) approximately one month ago, its emergence in Europe is more recent. In Belgium, this variant doubles in proportion every week, representing around 10% of the circulating strains today.

---

[1] https://www.biorxiv.org/content/10.1101/2022.09.15.507787v3

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)	105 (51)	20-08-2022
BQ.1.1	52 (27)	05-09-2022
BA.2.3.20	4 (1)	26-09-2022
BA.2.75 (incl BA.2.75.2, BN.1)	98 (80)	22-07-2022
BA.2.75.2	20 (16)	01-08-2022
BN.1	6 (2)	15-09-2022
XBB	2 (2)	21-09-2022

***Table 1:** Number of emerging variants detected by the Belgian genomic surveillance system (source: GISAID)*

Based on the collection date, it appears that BQ.1* shows a rapid and significant increase over the last weeks (Figure 2). Such increase is currently not observed with other variants under monitoring, and we therefore currently estimate that BQ.1* will become dominant by the end of the month of October.

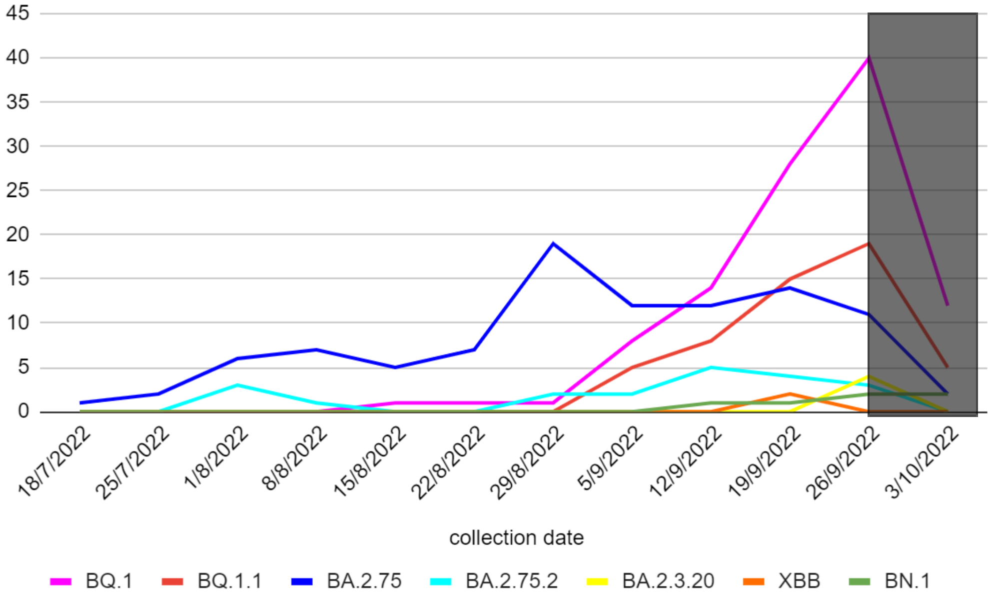

***Figure 3:** Number of Belgian sequences reported on GISAID for emerging variants under monitoring. The total numbers for the last week (highlighted in gray) should be interpreted with caution as all sequences may not have been reported yet.*