KU LEUVEN

DEPARTMENT OF MICROBIOLOGY, IMMUNOLOGY AND TRANSPLANTATION

UZ LEUVEN | LABORATORIUMGENEESKUNDE

Genomic surveillance report

Update for Belgium, 04/10/2022

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) represent the vast majority of the circulating strains and dominate in the current surge of infections.

In parallel, the genomic situation is rapidly evolving, with the recent emergence of variants potentially able to outpace current circulating viral strains and contribute to an epidemic resurgence in the upcoming weeks. Such rapid and simultaneous emergence of multiple variants with important growth advantages is unprecedented.

Variants under particular monitoring are:
- BQ.1*: high competitive advantage; recently identified in Belgium; steadily increasing both in proportion and total numbers
- BN.1 : high competitive advantage; the first two cases have recently been identified in Belgium
- XBB : high competitive advantage; the first two cases have recently been identified in Belgium
- BA.2.3.20: high competitive advantage; the first case has recently been identified in Belgium
- BA.2.75/BA.2.75.2: moderate competitive advantage; active low level circulation in Belgium with no current sign of acceleration

Considering the current and foreseen evolutions, we cannot exclude at this stage that BQ.1* or an alternative emerging variant would become dominant concomitantly or shortly after the peak of the current wave of infections, with as result a potentially prolonged duration of high viral circulation in the community.

At this stage, we do not have information on the severity of these emerging variants, but the foreseen high number of infections associated with a decreased activity of therapeutic antibodies will very probably lead to a consequent surge of hospital admissions. The efficacy of antiviral drugs is not expected to be affected.

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].

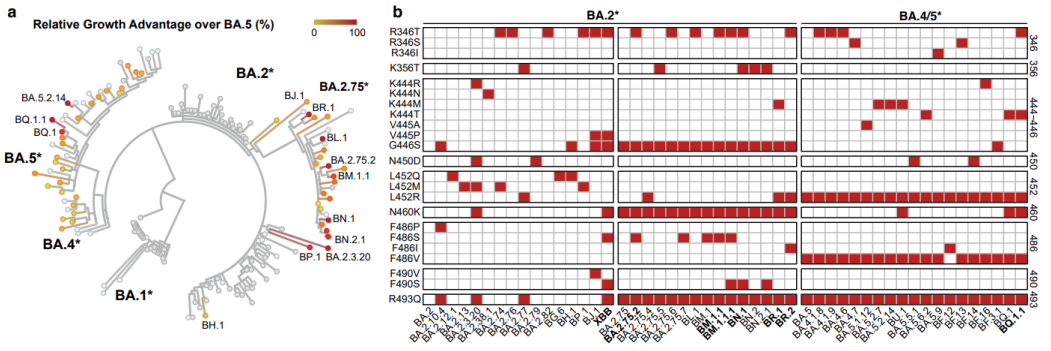

Figure 1: Convergent evolution of Omicron RBD with growth advantage over BA.5. a) Whole-genome maximum likelihood phylogenetic analysis of Omicron subvariants. Variants with a growth advantage over the original BA.5 are colored. Relative growth advantage values are calculated using CoV-Spectrum website. 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 (it represented 2,8% of the circulating strains around 19/09/2022).

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

2 Monitoring of Variants of Concern in Belgium

During the last two weeks of baseline surveillance - 19/09/2022 to 02/10/2022 - (686 sequences collected at this stage), BA.5 represented 91%, BA.4 represented 7%, and BA.2.75 represented 1% of the samples sequenced. Emerging variants mentioned above are not yet represented in Figure 2.

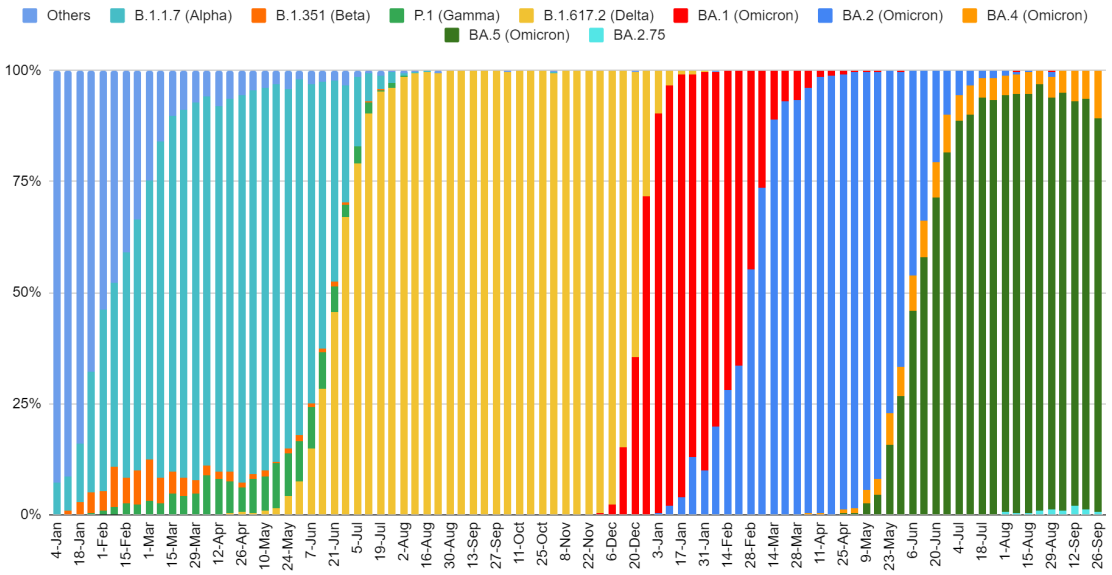

Figure 2: *Share of variants of concern per week in Belgium since January 2021.*

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

	Number of sequences on GISAID (compared to numbers reported last week)	Collection date of the first sample
BQ.1	51 (27)	20-8-2022
including BQ.1.1	*27 (13)*	5-9-2022
BA.2.3.20	1 (0)	*to be verified*
BA.2.75	80 (61)	22-7-2022
XBB	2	21-09-2022
NB.1	2	15-09-2022
including BA.2.75.2	*16 (9)*	1-8-2022

Table 1: *Number of emerging variants detected by the Belgian genomic surveillance system (source: GISAID, except for BA.2.3.20 which is not yet uploaded but confirmed)*

Based on the collection date, it appears that BQ.1* shows a rapid and significant increase over the last weeks, although the total numbers remain relatively low at this stage and are therefore still to be interpreted with caution. The initial rise of BA.2.75 sequences observed since end July 2022 seems to have been outpaced by BQ.1/BQ.1.1, and the number of BA.2.75.2 remains very limited at this stage (Figure 2).

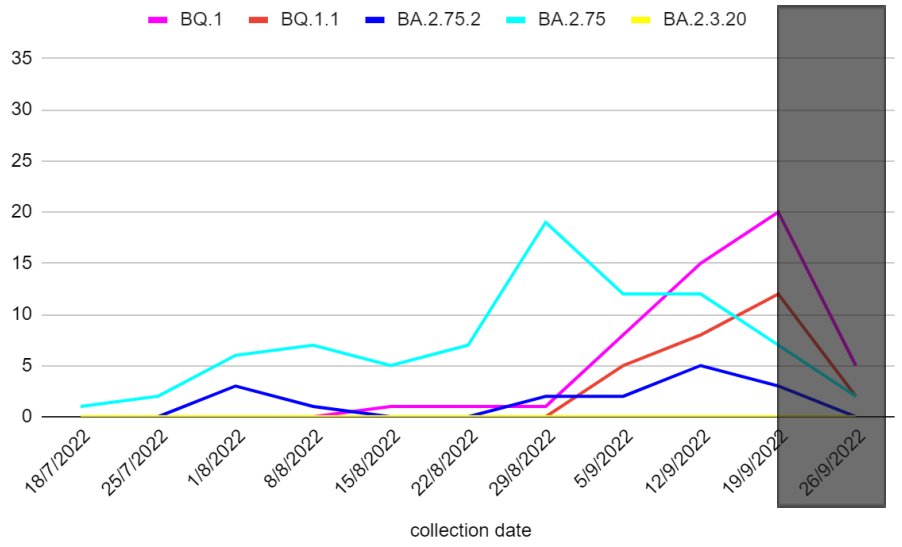

Figure 3: *Number of Belgian sequences reported on GISAID for emerging variants under monitoring. The total numbers for the last week (highlighted in gray) should be interpreted with caution as all sequences may not have been reported yet.*