



Genomic surveillance report

Update for Belgium, 27/09/2022

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Executive summary

Omicron BA.5 remains the dominant lineage in Belgium and accounts for around 90% of the most recent infections.

Nevertheless, the genomic situation is rapidly evolving, with the recent emergence of variants potentially able to outpace current circulating viral strains and provoke an epidemic resurgence in the upcoming weeks. Variants under particular monitoring are:

- BQ.1/BQ.1.1: high competitive advantage; recently identified in Belgium
- BA.2.3.20: high competitive advantage; no evidence of introduction in Belgium
- BA.2.75/BA.2.75.2: moderate competitive advantage; active low level circulation in Belgium

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, 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 to consider these sets of mutations as a convergent evolutionary process driven by the selective advantages they provide in the current epidemiological situation (figure 1).

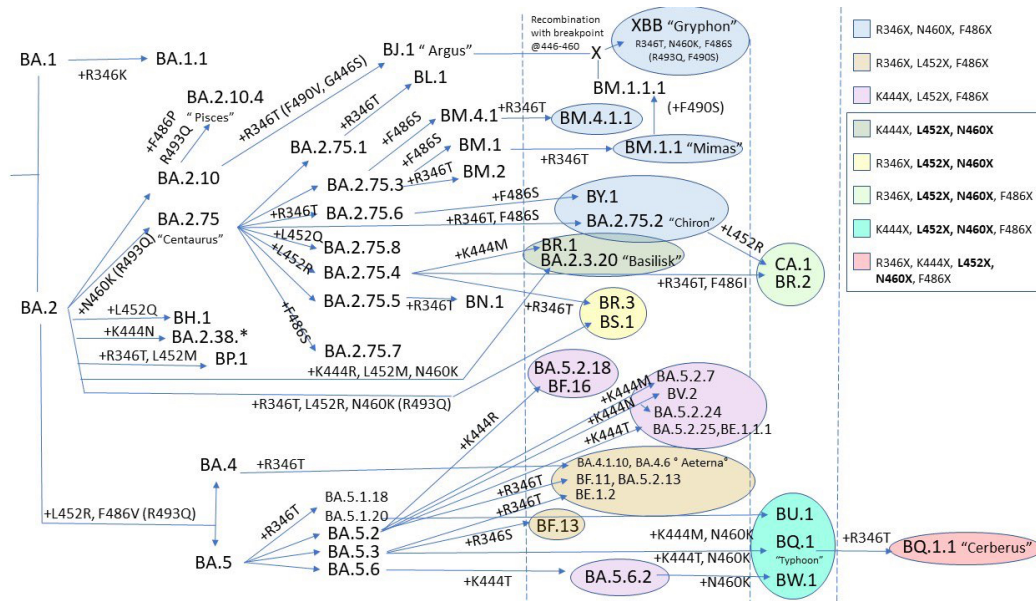


Figure 1: Schematic representation of Omicron sublineages and their respective sets of acquired mutations.

More recently, early signals tend to suggest a potential rapid spread of BQ.1.1 in Europe and of BA.2.30 in North America (Figure 2). The growth rate advantage of the latter two emerging variants compared to the circulating strains is currently estimated around 10-15% per day, meaning that these could generate a rapid viral population replacement and drive a subsequent wave of infections (Figure 3).

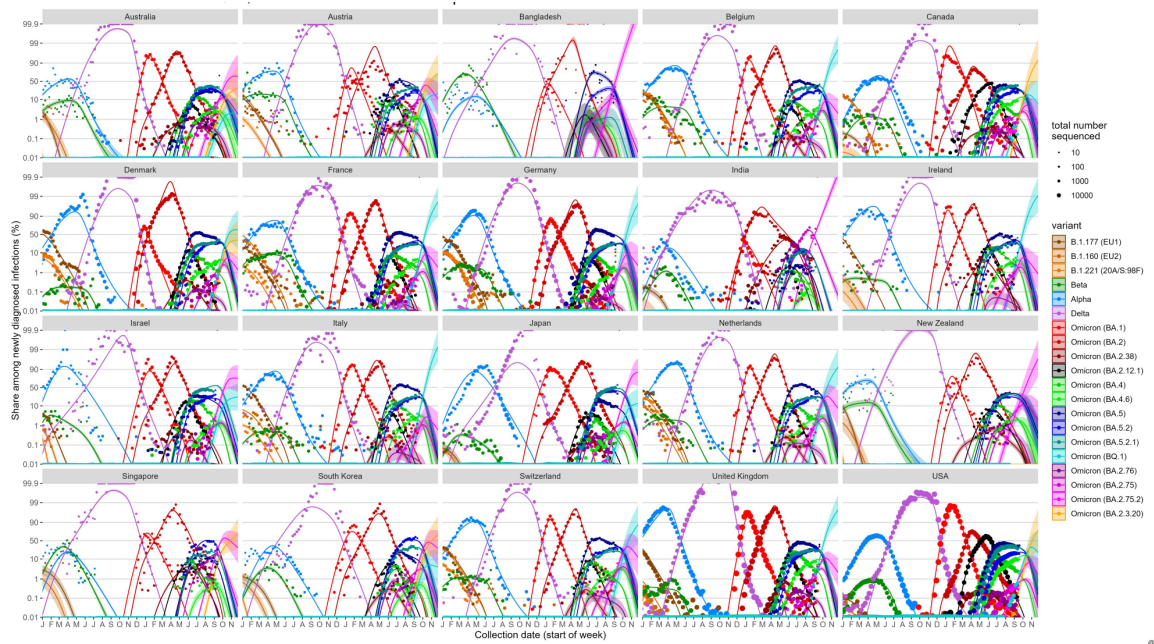


Figure 2: Projections of SARS-COV-2 lineage frequencies based on GISAID and COG-UK data (Tom Wenseleers, KU Leuven)

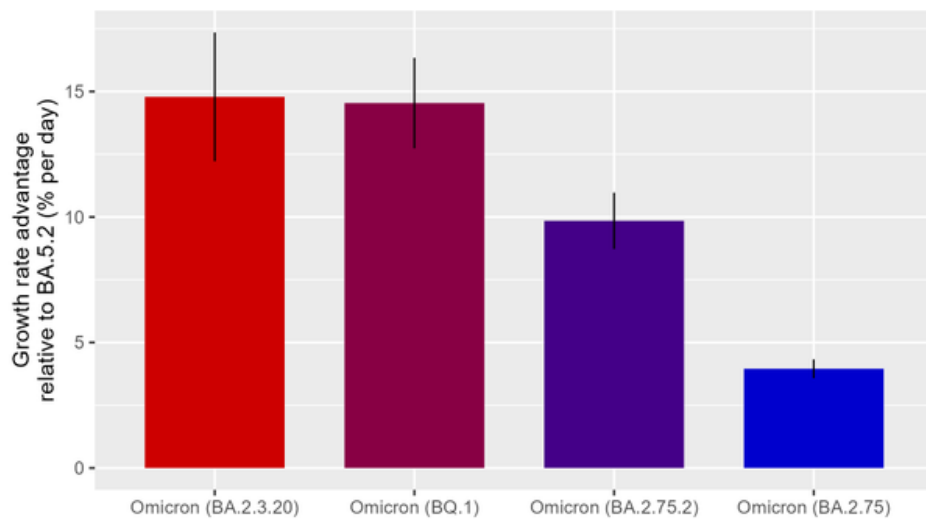


Figure 3: Growth rate advantage of emerging SARS-CoV-2 Omicron subvariants (Tom Wenseleers, KU Leuven)

2 Monitoring of Variants of Concern in Belgium

During the last two weeks of baseline surveillance - 12/09/2022 to 25/09/2022 - (482 sequences collected at this stage), BA.5 represented 90%, BA.4 represented 7.5% and BA.2.75 represented 2% of the samples sequenced. Emerging variants mentioned above are not yet visible in figure 4.

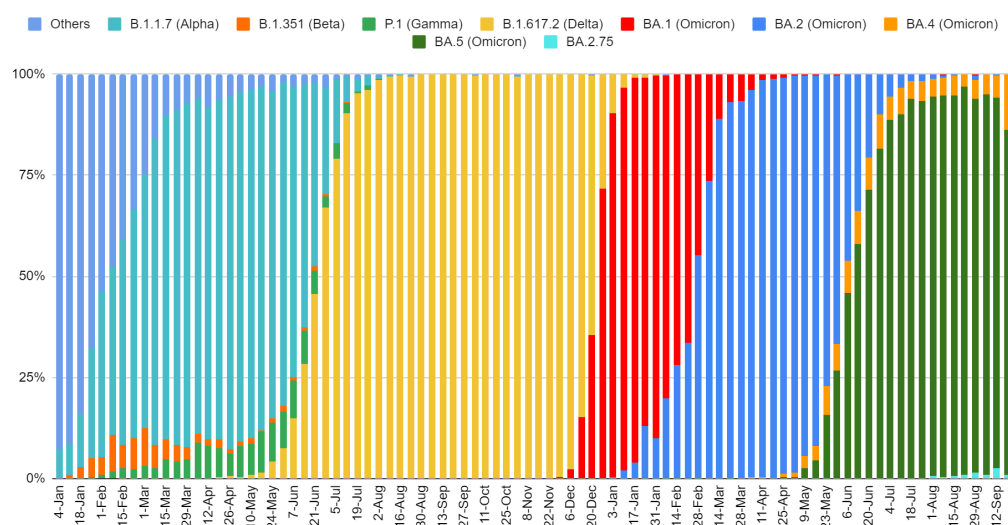


Figure 4: Share of variants of concern per week in Belgium since January 2021.

Emerging variants BQ.1 (including BQ.1.1), and BA.2.75.2 have been detected through the Belgian genomic surveillance system since several weeks, as highlighted in Table 1.

	number of sequences on GISAID	collection date of the first sample
BQ.1	27	20-8-2022
<i>including BQ.1.1</i>	13	5-9-2022
BA.2.3.20	0	
BA.2.75	61	22-7-2022
<i>including BA.2.75.2</i>	9	1-8-2022

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, and particularly BA.1.1 show 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 since two weeks, and the number of BA.2.75.2 remains very limited at this stage. No BA.2.3.20 samples have been reported yet (Figure 4).

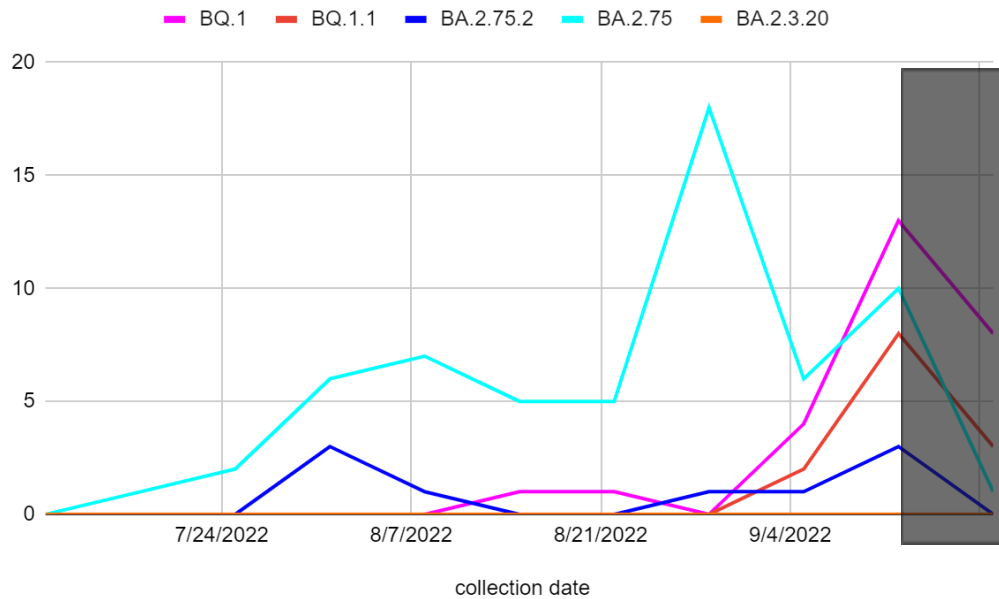


Figure 4: Number of Belgian sequences reported on GISAID for emerging variants under monitoring. The total numbers for the last week should be interpreted with caution as all sequences may not have been reported yet.