KU LEUVEN

DEPARTMENT OF MICROBIOLOGY, IMMUNOLOGY AND TRANSPLANTATION

UZ LEUVEN | LABORATORIUMGENEESKUNDE

Genomic surveillance report

Update for Belgium, 22/03/2022

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Content

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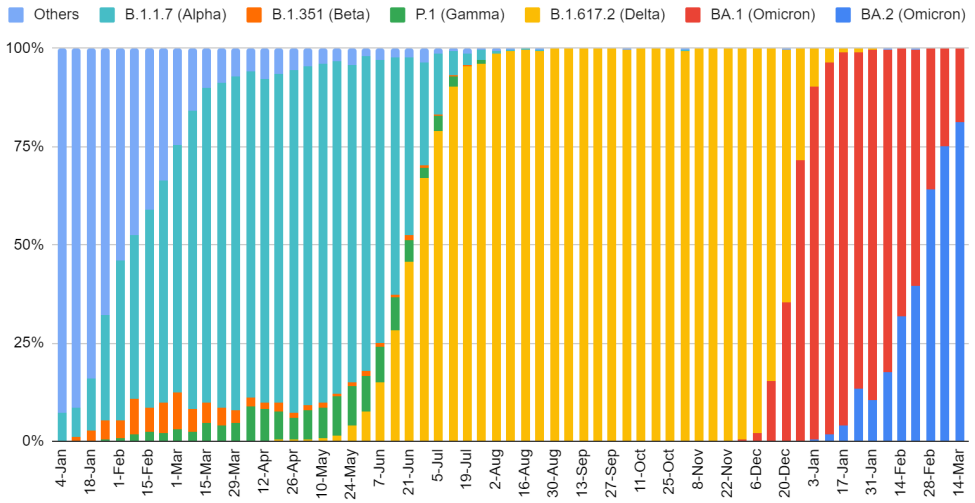
Previous reports are available online using this link.

Executive summary

The share of BA.2 has reached 90% of new infections diagnosed in Belgium, as suggested by the share of SGTF among positive qPCR results (data federal platform labs), and supported by sequencing-based surveillance (BA.2 was responsible for 76.7% (↗) of the infections diagnosed between 07/3/2022 and 20/3/2022 - 602 sequences analyzed at this stage).
During this same period, BA.1 and BA.1.1 jointly represented 23.3% (↘) of the circulating strains. Delta was not reported during the last two weeks.

This phenomenon is concomitant with a recent surge of reported infections.



1 Epidemiological context and indicators related to diagnostic activities

The share of positive samples (Cq <25) presenting an S gene target failure (SGTF) reflects the share of BA.1 and BA.1.1 samples circulating in the country. Samples which are negative for this marker can be Delta or BA.2, although from genomic baseline surveillance we know that Delta is only sporadically detected for more than one month (two genomes for the last month through the baseline surveillance initiative). Samples without SGTF (most likely to be BA.2 infections) have taken over, now representing 92% of positive samples diagnosed (Figure 1).

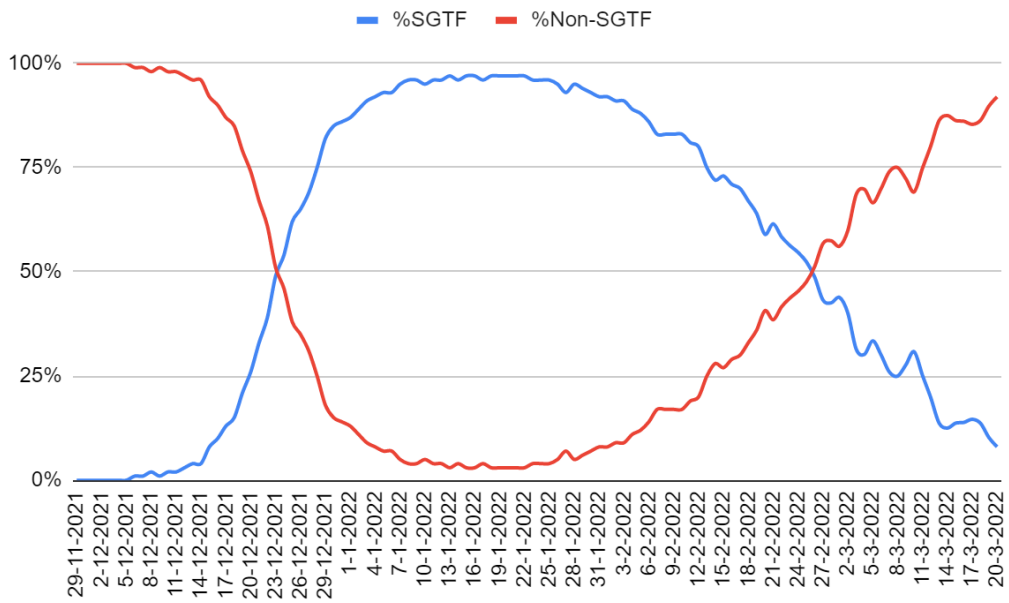


Figure 1: *S gene target failure (SGTF; blue: BA.1 & BA.1.1) and others (red: currently considered predominantly BA.2) among positive samples reported by the federal platform laboratories.*

As shown in Figure 2, the increasing share of non-SGTF positive PCR results was first associated with a steep decrease in SGTF samples (BA.1, BA.1.1 and BA.3). More recently, and despite de-intensification of PCR testing at national level, we observe a rise in the number of non-SGTF infections (BA.2). This viral population replacement, together with the recent release of general disease control measures most likely have led and will further lead to an increase of infections and hospital admissions.

A recent change in testing indications has led to a delayed observation of this surge of infections. In the future, we recommend to avoid changing testing indications during the weeks following a release of control measures, as a decreased testing intensity may hide an early surge of the real number of infections.

These observations are also reflected in the recent increase of infections and hospitalizations at national level.

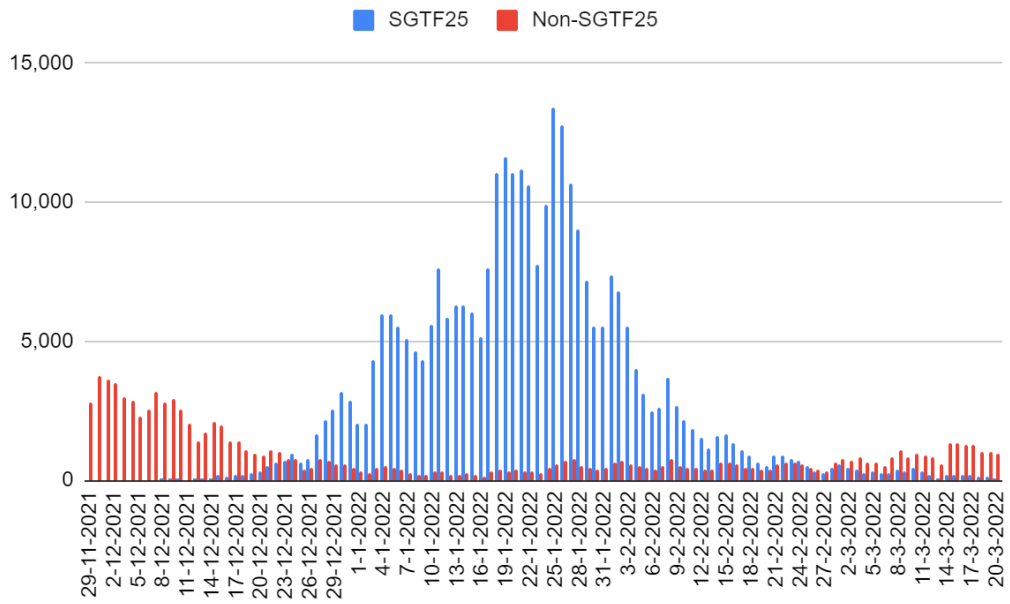


Figure 2: *Number of samples tested positive in the federal platform laboratories with S gene target failure (SGTF; blue) and without SGTF (non-SGTF; red). The absolute numbers are less representative of the actual epidemiology since a couple of weeks, as a result of a change in testing indications and a lower testing intensity.*

2 Monitoring of Variants of Concern in Belgium

During the last two weeks of baseline surveillance - 7/3/2022 and 20/3/2022 - (602 sequences collected at this stage), BA.1 and BA.1.1 jointly represented 23.3% (↘) of the circulating strains, while BA.2 represented 76.7% (↗) of the strains. No Delta sequence was reported for the last two weeks (Figure 3).

Partners of the national sequencing consortium have reported potential "recombinant" sequences, of which four isolates have so far been confirmed as recombinants of BA.1(.1) and BA.2 with a breakpoint located at the end of ORF1b. Additional analyses are currently ongoing, after which a complete assessment can be communicated, hopefully in next week's report.

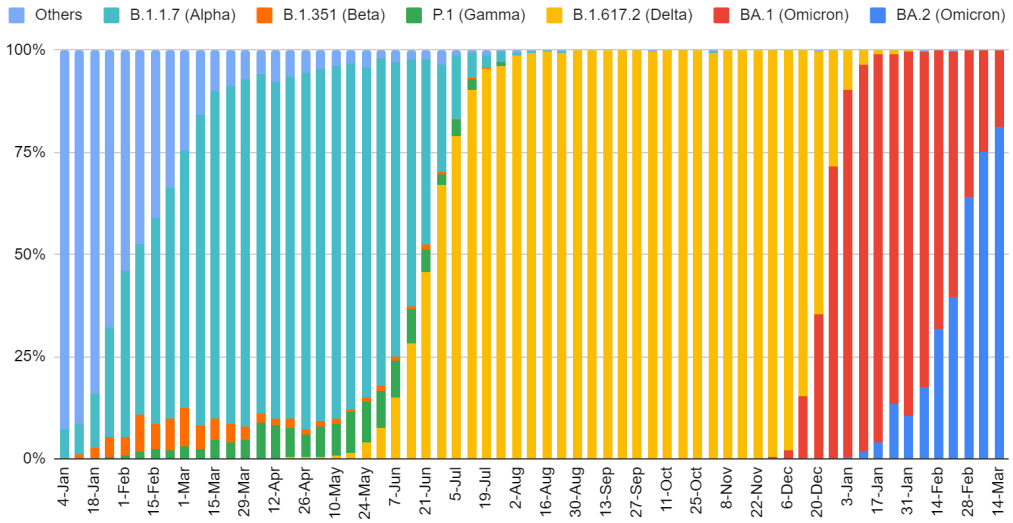


Figure 3: *Share of variants of concern per week in Belgium*

3 International situation

Several European countries have recently observed a recent rise of infections which, in terms of timing, is concomitant with the dominance of BA.2 and follows national releases of disease-control measures (Figure 4). For some European countries, this recent increase of cases is already followed by an increase in new hospital admissions (Figure 5).

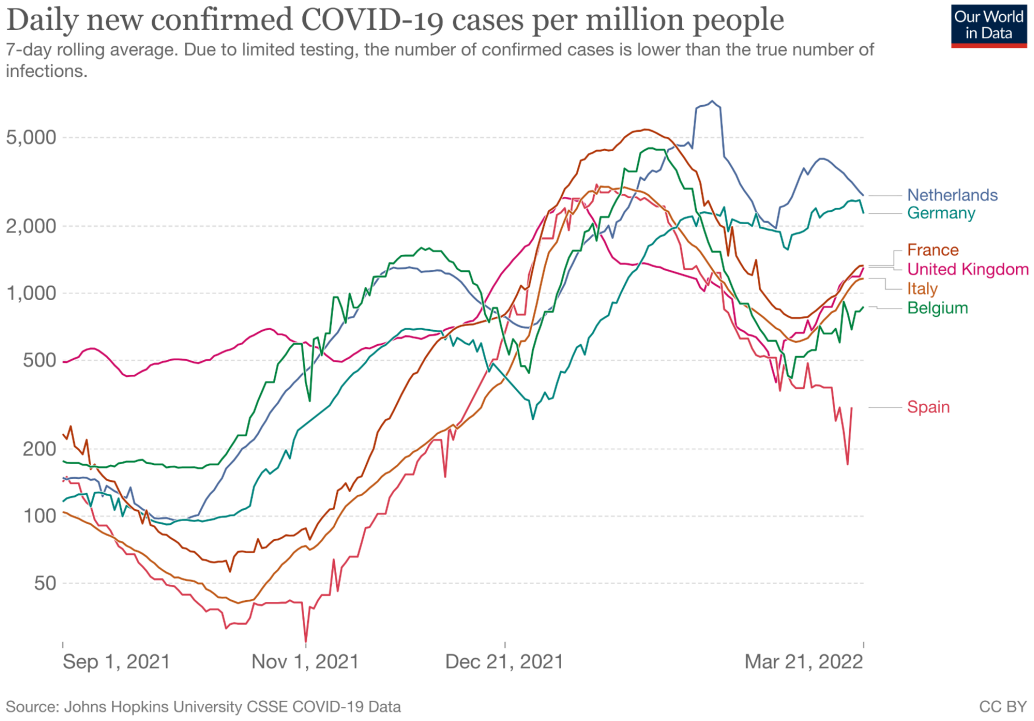


Figure 4: *Daily new confirmed COVID-19 cases per million people (source: ourworldindata.org)*

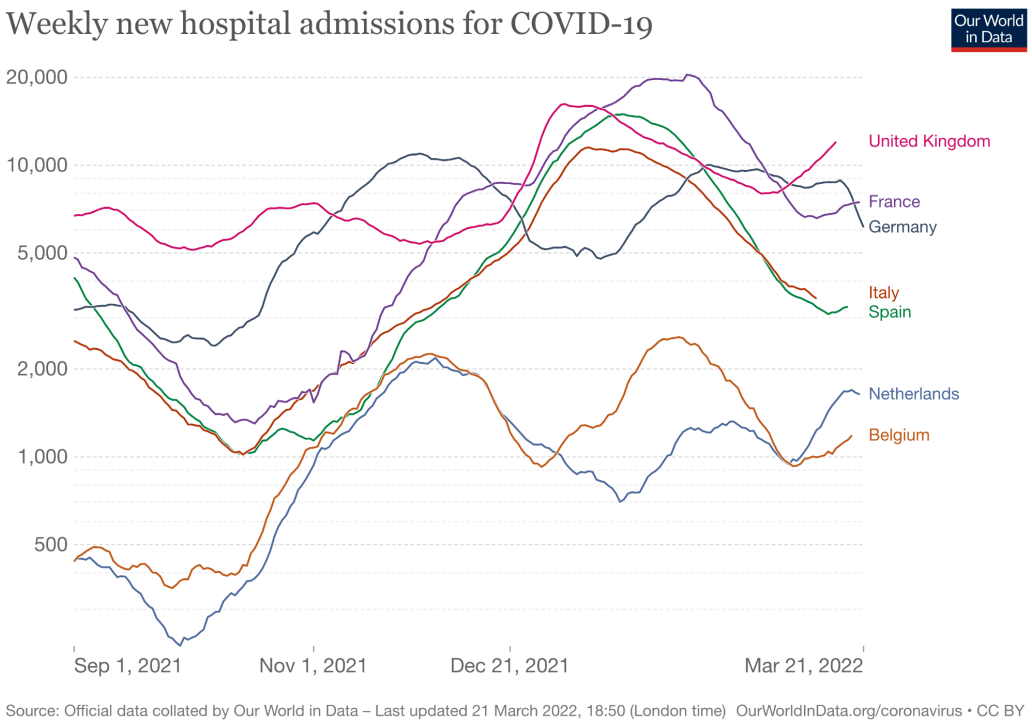


Figure 5: *Weekly new hospital admission for COVID-19 (source: ourworldindata.org)*

4 Cryptic SARS-CoV-2 lineages detected in NYC wastewater

In a recent study published in *Nature*, Smyth and colleagues report the circulation and increasing frequency of several cryptic lineages of SARS-CoV-2 in the New York City (NYC) metropolitan area; cryptic lineages which have not been detected by standard genomic surveillance. Indeed, these lineages contain mutations that had been rarely observed in clinical samples (including Q493K, Q498Y, E484A, and T572N) and share many mutations with the Omicron variant of concern. Some of these mutations expand the tropism of SARS-CoV-2 pseudoviruses by allowing infection of cells expressing the human, mouse, or rat ACE2 receptor. The authors also demonstrated that pseudoviruses containing the spike amino acid sequence of these lineages were resistant to different classes of receptor binding domain neutralizing monoclonal antibodies. The authors offer several hypotheses for the anomalous presence of these lineages, including the possibility that these lineages are derived from unsampled human COVID-19 infections or that they indicate the presence of a non-human animal reservoir. Their study also highlights the interest of a genomic surveillance based on wastewaters and its complementary to a clinical (standard) genomic surveillance.

Source: https://www.nature.com/articles/s41467-022-28246-3