KU LEUVEN

DEPARTMENT OF MICROBIOLOGY, IMMUNOLOGY AND TRANSPLANTATION

UZ LEUVEN | LABORATORIUMGENEESKUNDE

Genomic surveillance report

Update for Belgium, 29/03/2022

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Content

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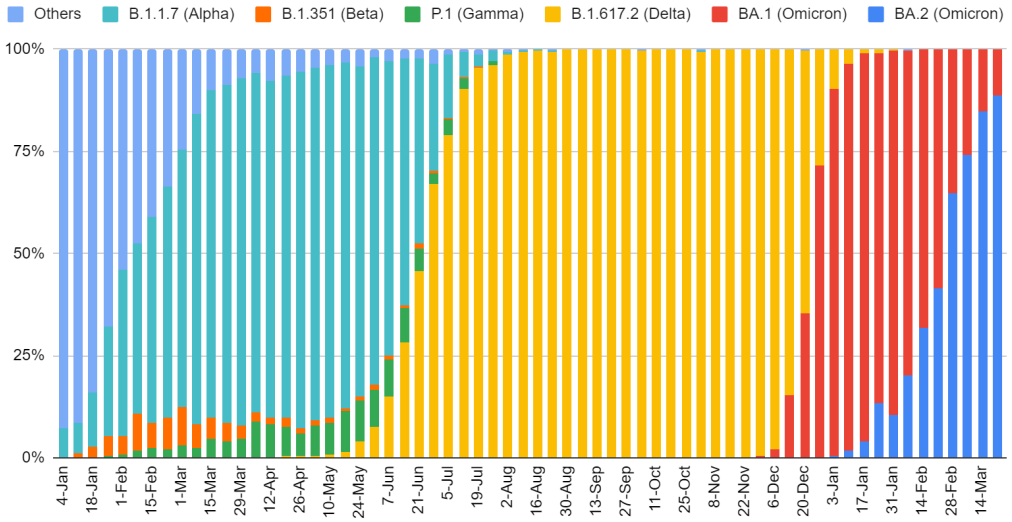
Executive summary

The share of BA.2 has reached 95% 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 86.0% (↗) of the infections diagnosed between 14/3/2022 and 27/3/2022 - 879 sequences analyzed at this stage).
During this same period, BA.1 and BA.1.1 jointly represented 13.9% (↘) of the circulating strains. Only one Delta case was 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 96% of positive samples diagnosed (Figure 1).

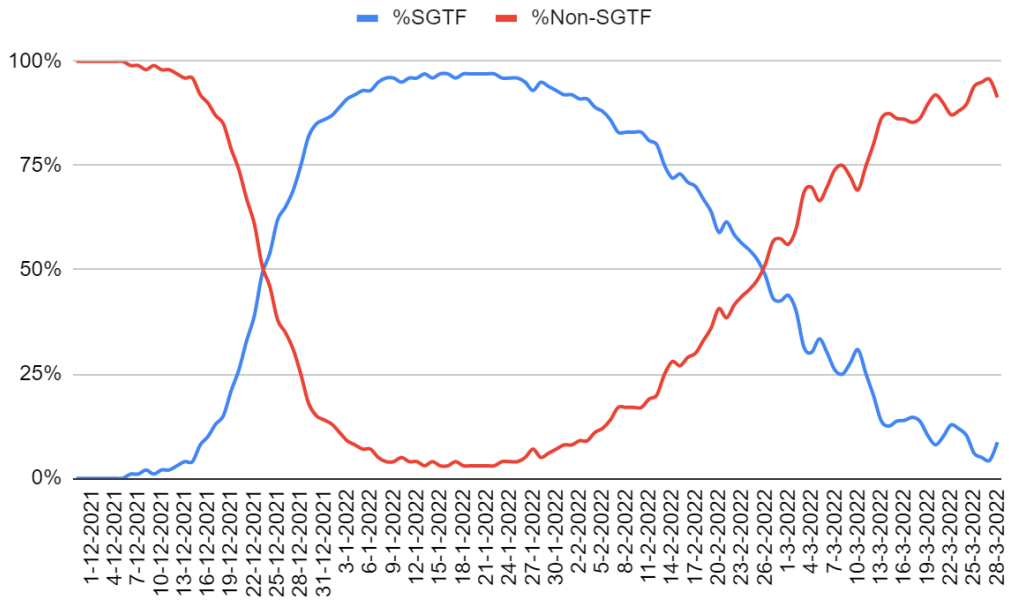


Figure 1: *S gene target failure (SGTF; blue: BA.1 & BA.1.1) and others (red: currently considered predominantly BA.2) among positive samples reported by the federal platform laboratories.*

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 and partial reflection of this surge of infections.

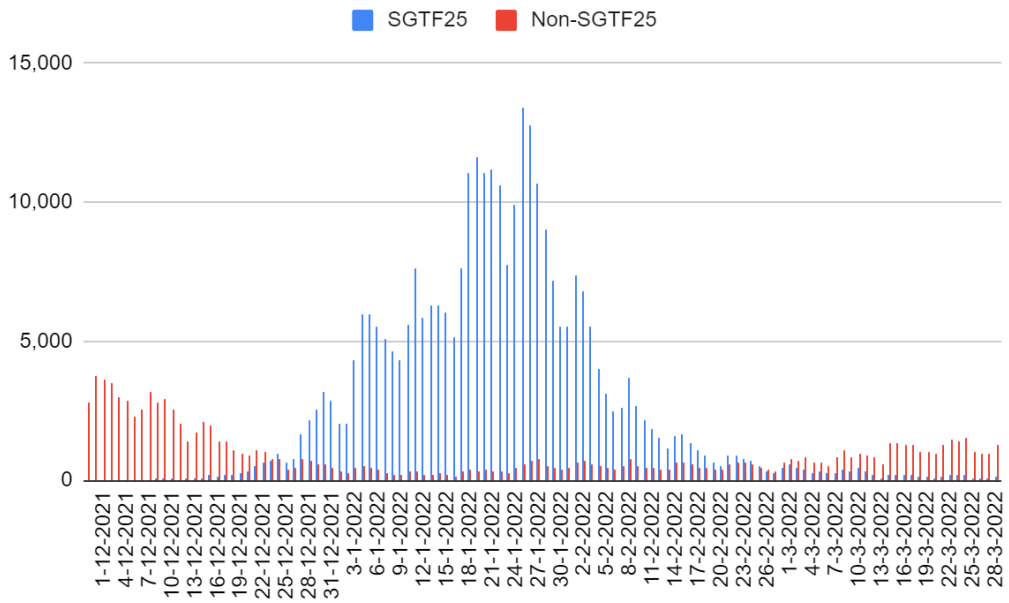


Figure 2: *Number of samples tested positive in the federal platform laboratories with S gene target failure (SGTF; blue) and without SGTF (non-SGTF; red). The absolute numbers are less representative of the actual epidemiology since a couple of weeks, as a result of a change in testing indications and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

2 Monitoring of Variants of Concern in Belgium

During the last two weeks of baseline surveillance - 14/3/2022 and 27/3/2022 - (879 sequences collected at this stage), BA.1 and BA.1.1 jointly represented 13.9% (↘) of the circulating strains, while BA.2 represented 86.0% (↗) of the strains. Only one Delta sequence was reported for the last two weeks (Figure 3).

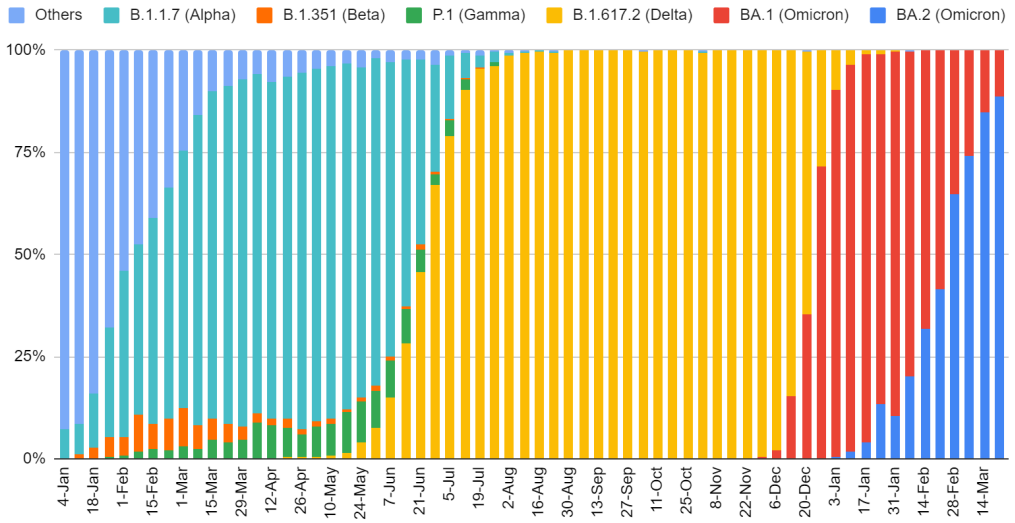


Figure 3: *Share of variants of concern per week in Belgium*

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).

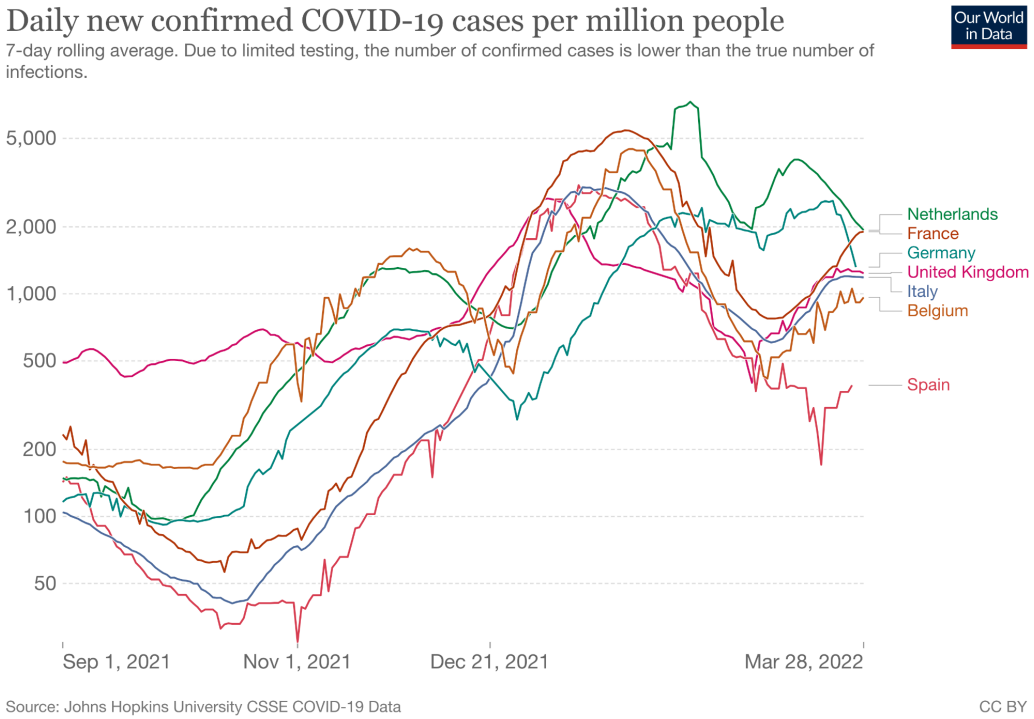


Figure 4: *Daily new confirmed COVID-19 cases per million people (source: ourworldindata.org)*

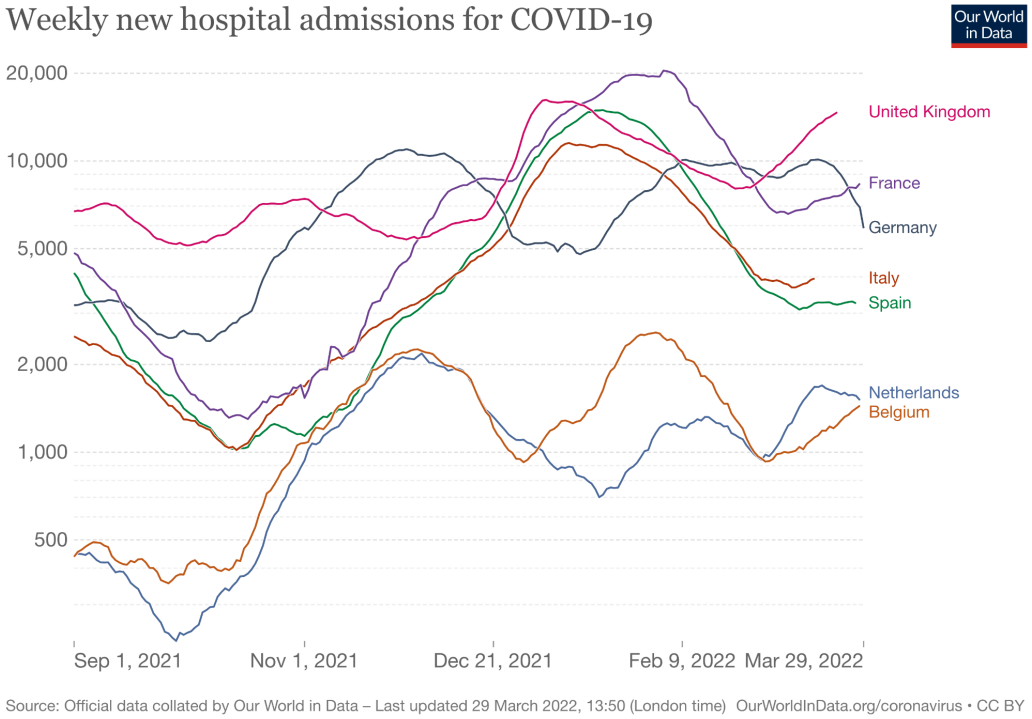


Figure 5: *Weekly new hospital admission for COVID-19 (source: ourworldindata.org)*

4 Comparison of the risk of hospitalization associated with BA.2 (Omicron lineage BA.2)

In its last technical briefing (#39, 25/03/22) on the SARS-CoV-2 variants of concern in England, the UK Health Security Agency (UKSHA) reports the results of updated comparative analyses on the risk of hospitalization associated with BA.2: "*Analyses of sequenced cases up to 8 March 2022 have been undertaken to compare the risk of hospitalisation, as defined by admission as an inpatient, or presentation to emergency care that resulted in admission, transfer or death, following BA.2 compared to BA.1. This analysis adjusted for age, reinfection status, sex, ethnicity, local area deprivation and vaccination status. It also controlled for the effect of geography and specimen date. The risk of hospitalisation does not appear to be higher following a BA.2 infection than following a BA.1 infection (hazard ratio 0.94 95% CI: 0.88-1.00).*"

Source:
https://assets.publishing.service.gov.uk/government/uploads/system/uploads/attachment_data/file/1063424/Tech-Briefing-39-25March2022_FINAL.pdf

5 SARS-CoV-2 recombinant lineages

Recombination is a frequent and well documented feature of the molecular evolution of coronaviruses, including SARS-CoV-2. Recombination likely occurs in many of the infected individuals, however in the large majority of the cases it will involve nearly identical genomes which makes it difficult to detect. The detection of clear examples of recombinant SARS-CoV-2 genomes is an interplay between the distinctness of the lineages that are involved, the intensity of the genomic surveillance system that is in place in a country, the frequency of co-infections and the incidence and lineage co-circulation in the region. When intensive genomic sequencing is undertaken, it is expected that recombinant strains will be more commonly detected. Already during the Alpha wave, recombinant strains that were assigned as B.1.1.7, contained mosaic structures of other lineages in their genome.

More recently, an AY.4/BA.1 (Delta/Omicron) recombinant was first detected in France, and was identified to be circulating in several regions of the country since early January 2022. Genomes with a similar profile have been also identified in the United Kingdom, Denmark, the Netherlands and Belgium. Further investigations are currently ongoing to determine if these recombinants derive from a single common ancestor or could result from multiple similar recombination events.

So far, we are aware of 11 recombinant lineages that have been defined by Pangolin and are implemented in Nextclade. Most likely more recombinant lineages will be identified and receive a formal classification in the upcoming weeks. The current defined recombinant lineages are named from XA to XL, excluding XI.

> Source:
> https://virological.org/t/recombinant-sars-cov-2-genomes-involving-lineage-b-1-1-7-in-the-uk/658

Recombinant lineage XK, a recombination event between Omicron BA.1 and BA.2 with the breakpoint located at the end of the gene ORF1b, is a so-called Belgian lineage, as it was first identified by the sequencing lab of the hospital AZ Delta Roeselare. Evaluation of the sequencing data obtained in this center since the start of January 2022, shows that the detection of a recombinant lineage is a rare event. For the 4452 sequences generated over the course of 12 weeks time, the lab only identified 22 XK recombinant lineages (0.5%) and 3 XE recombinants (0.07%, a UK lineage). Looking at the detailed sequencing data per week, the percentage of recombinant lineages (XE and XK) did not exceed 2%, with for week 8 the highest percentage of 1.9% identified (Figure 6).

Since classification tools have just started updating their framework to ensure the correct classification of recombinant lineages, currently, the members of the Belgian SARS-CoV-2 sequencing consortium are reanalysing the sequences obtained during the last weeks to make sure no recombinant strains have been missed.

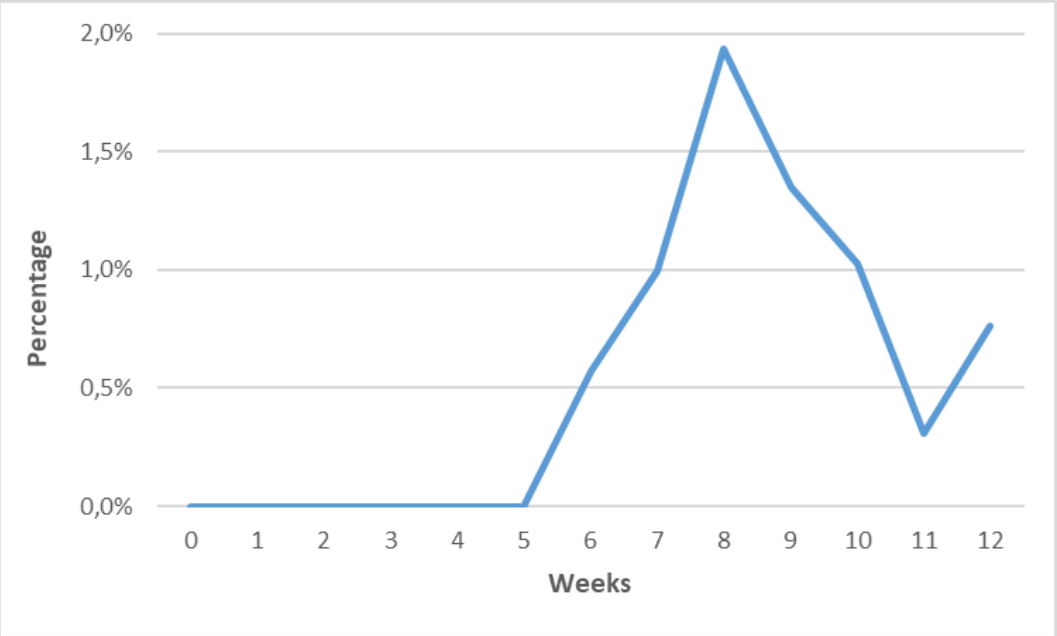


Figure 6: *Weekly detection of recombinant lineages (XE and XK) at the sequencing laboratory of the hospital AZ Delta Roeselare, since January 2022.*