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Genomic surveillance report

Update for Belgium, 08/02/2022

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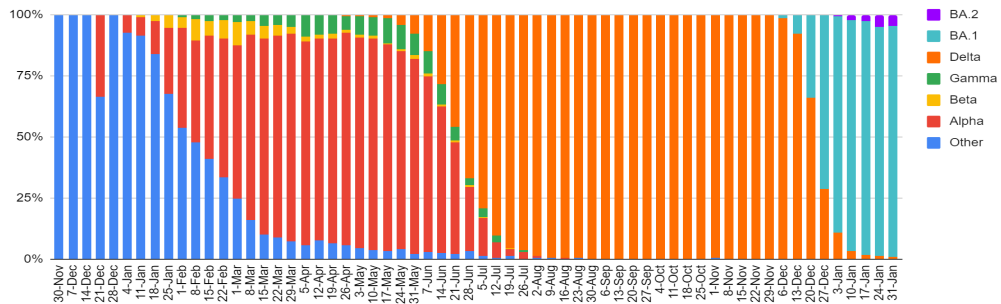
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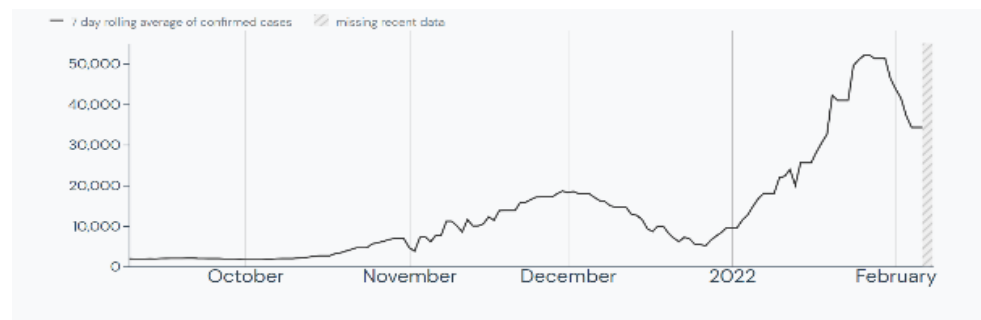
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Executive summary

During the last two weeks (24/1/2022 to 6/2/2022, representing 618 sequences at this stage), BA.1 and BA.1.1 jointly represented 93.5% of the circulating strains, while BA.2 and Delta represented respectively 5% and 1.5% (↘) of the strains sequenced as part of the baseline surveillance.



The peaks of BA.1 & BA.1.1 infections (dominant lineages) have been recently observed, leading to a decline in the total number of infections. The share of BA.2, although not fully visible through the (delayed) sequencing-based surveillance, is nevertheless increasing, as confirmed by the continuous decline of SGTF share among positive qPCR results. Nevertheless, this viral population replacement seems at this stage to be linked to a decrease in BA.1 & BA.1.1 rather than a tangible increase in the total number of BA.2 infections. The latter will probably become dominant in the coming month, but we currently observe no sign at this stage that this phenomenon will lead to a marked new wave of infections. The perspective for the coming weeks can therefore be considered as positive despite the current viral replacement phenomenon taking place. The evolution will nevertheless need to be continuously monitored.



1 Epidemiological context and indicators related to diagnostic activities

The current decline in the reported number of infections is associated with a continued decline in the positivity rate among diagnostic PCR tests performed in the Federal Platform Laboratories (Figure 1). This trend is consistent with a non-artificial decline, although the positivity rate remains high (40%).

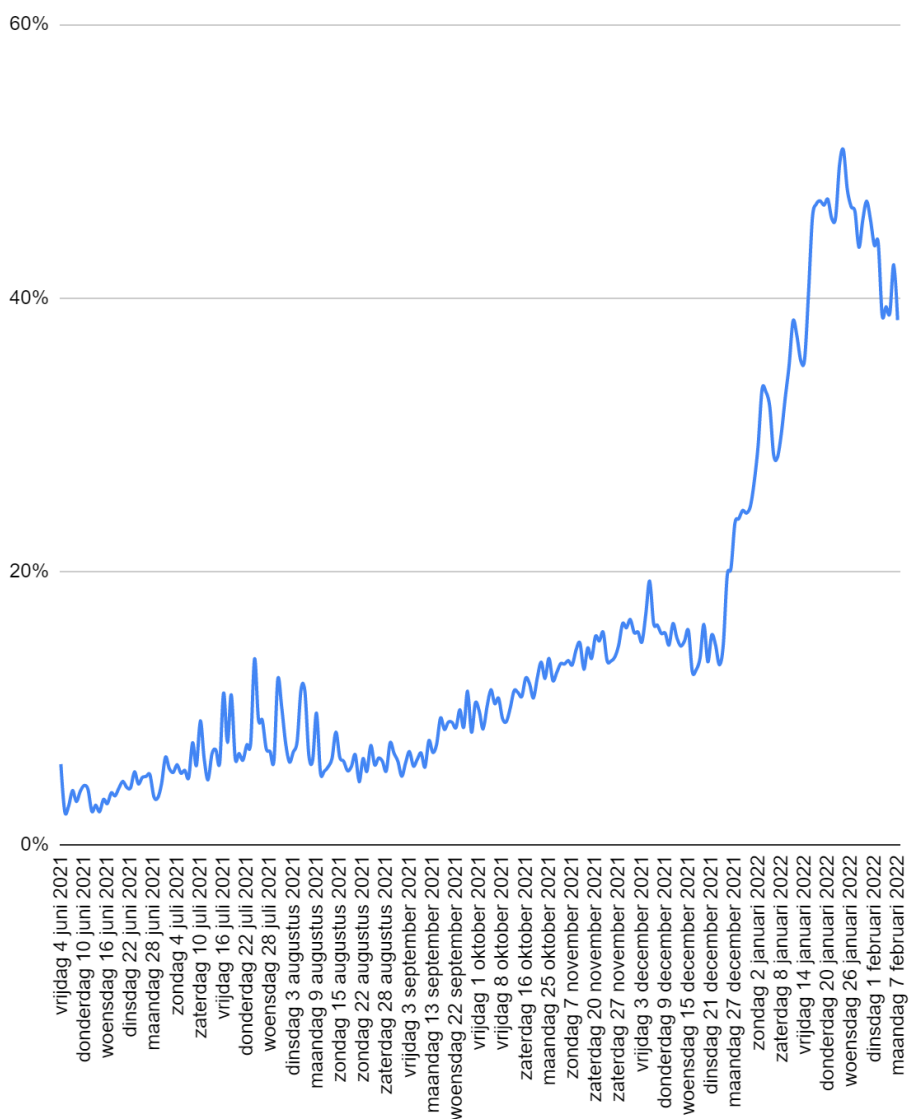


Figure 1: Positivity rate among the Federal Platform Laboratories.

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. Samples presenting SGTF currently represent 83% of positive samples diagnosed (Figure 2).

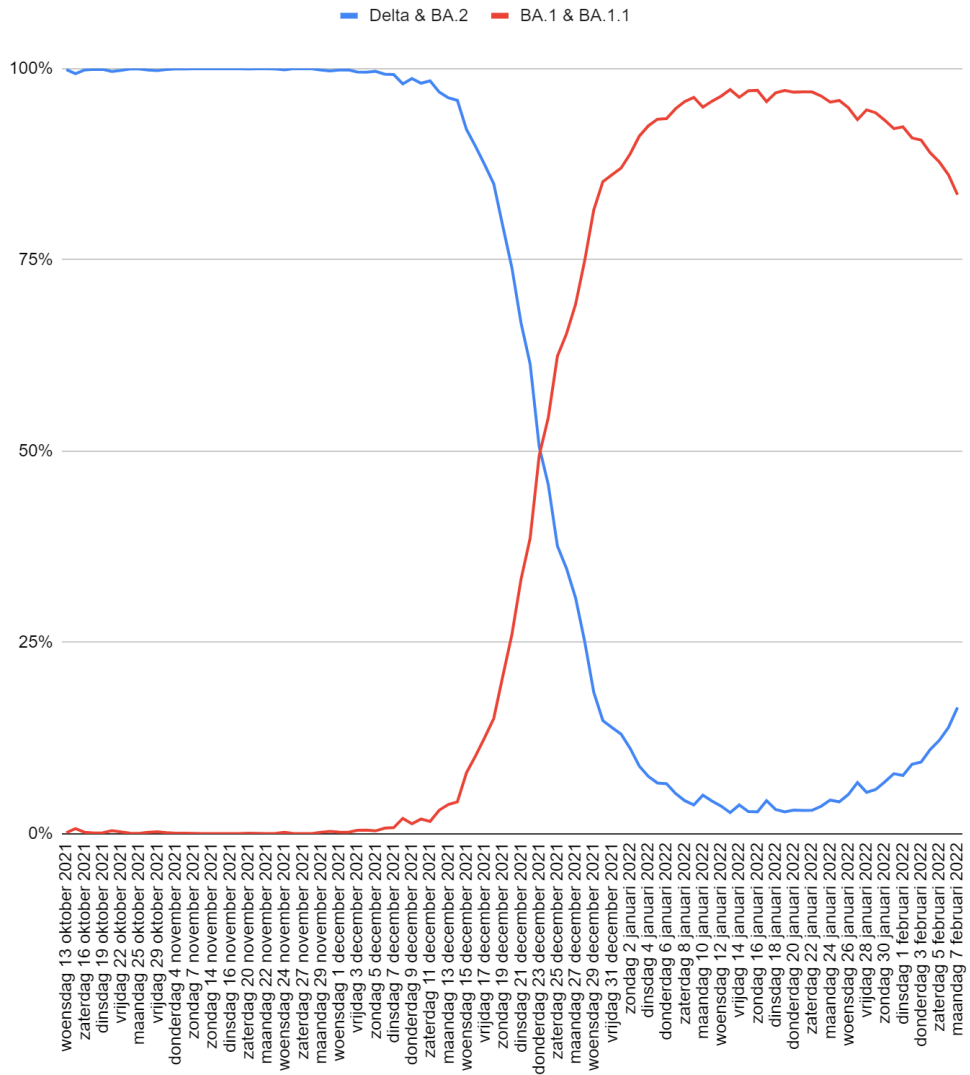


Figure 2: S Gene Target failure among positive samples reported by the Federal Platform laboratories

As shown in figure 3, the increasing share of non-SGTF positive PCR results is due to a steep decrease of SGTF samples, and not to an increase of non-SGTF samples. This implies that there is currently no marked increase of BA.2 infections in the population and that the epidemiological situation will therefore not be profoundly modified (new wave of infections) when BA.2 will become dominant. We can nevertheless not fully predict the impact of an increase in the total number of high risk social interactions (eg: stop all current measures).

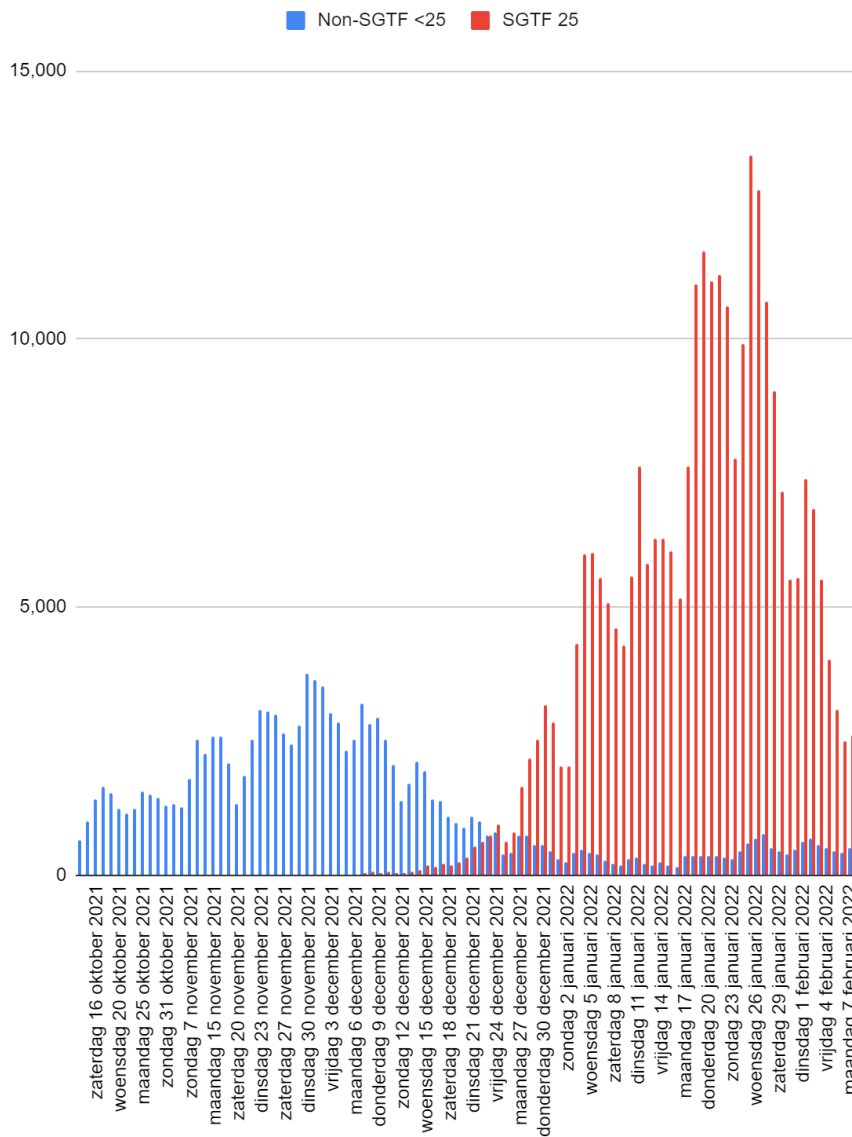


Figure 3: Number of samples tested positive in the Federal Platform Laboratories with S Gene target failure (SGTF, red) and with no S gene target failure (non-SGTF, blue).

2 Monitoring of Variants of Concern in Belgium

During the last two weeks of surveillance (24/1/2022 - 6/2/2022), BA.1 and BA.1.1 jointly represented 93.5% of the circulating strains, while BA.2 and Delta represented respectively 5% and 1.5%.

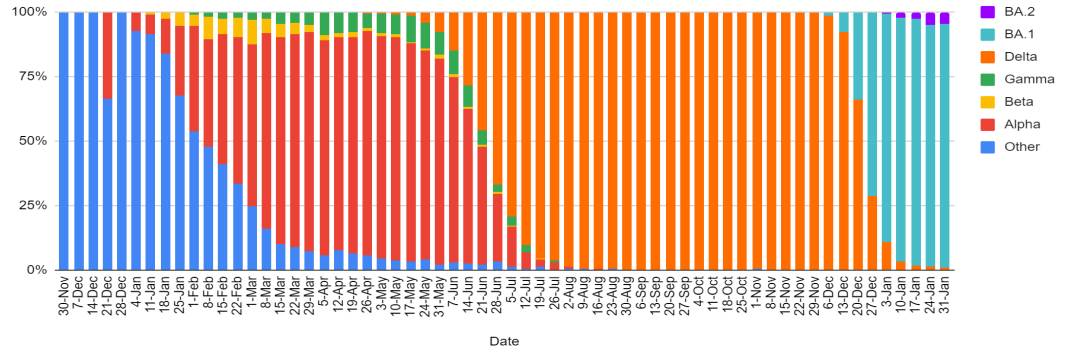


Figure 4: Share of variants of concern per week in Belgium

Omicron lineage currently consists of 4 main sublineages (BA.1, BA.1.1, BA.2 and BA.3) which present different evolutions. While BA.1 and BA.1.1 infections currently decline and BA.3 remains anecdotal, BA.2 continues to rise (Figure 5).

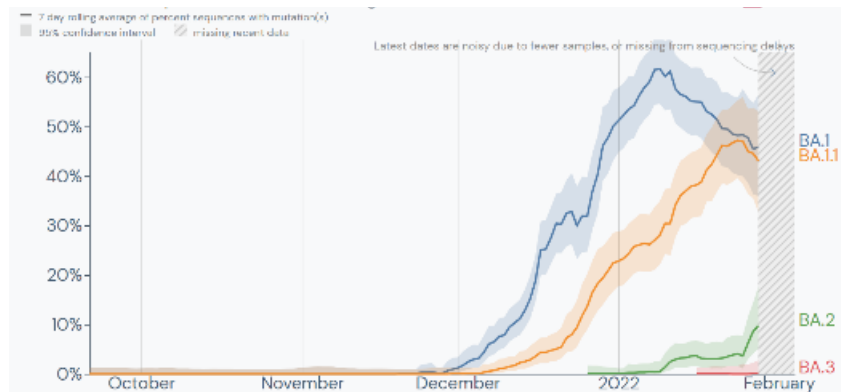


Figure 5: Share of Omicron sublineages in Belgium ([source](#))

3 Situation in Denmark

The epidemiological situation in Denmark (where BA.2 has become the dominant lineage) can provide useful insights on the impact of the release of contact-restriction policies. In this country, the total number of infections seems to decline since a few days. Compared to the current situation in Belgium, this decline nevertheless seems less sharp (Figure 6) and would need to be consolidated in the coming days.

It should further be noticed that none of these two countries have yet observed a decline in the number of daily COVID-related deaths (Figure 7).

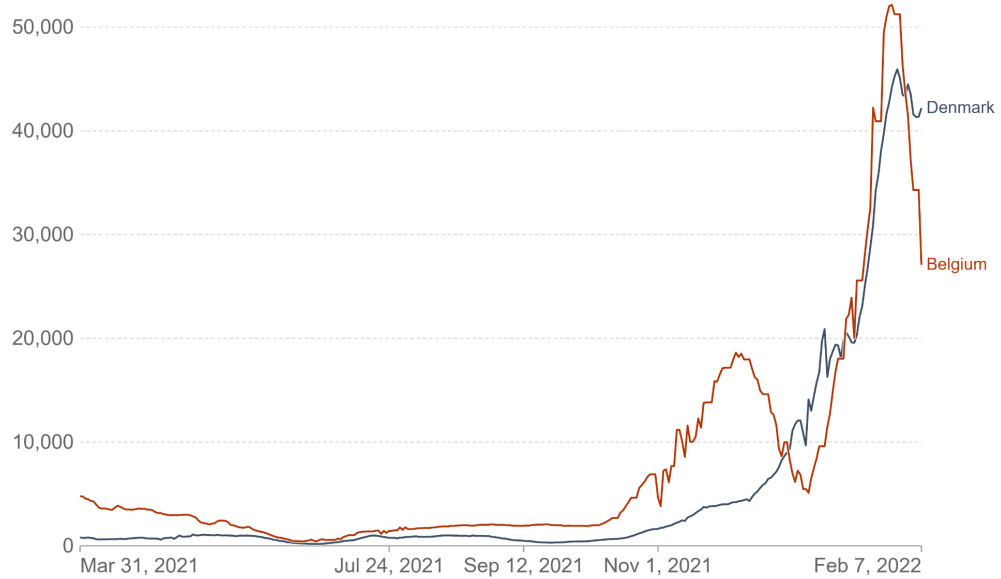


Figure 6: Daily confirmed COVID-19 cases in Belgium and Denmark. (Source : Our World in Data)

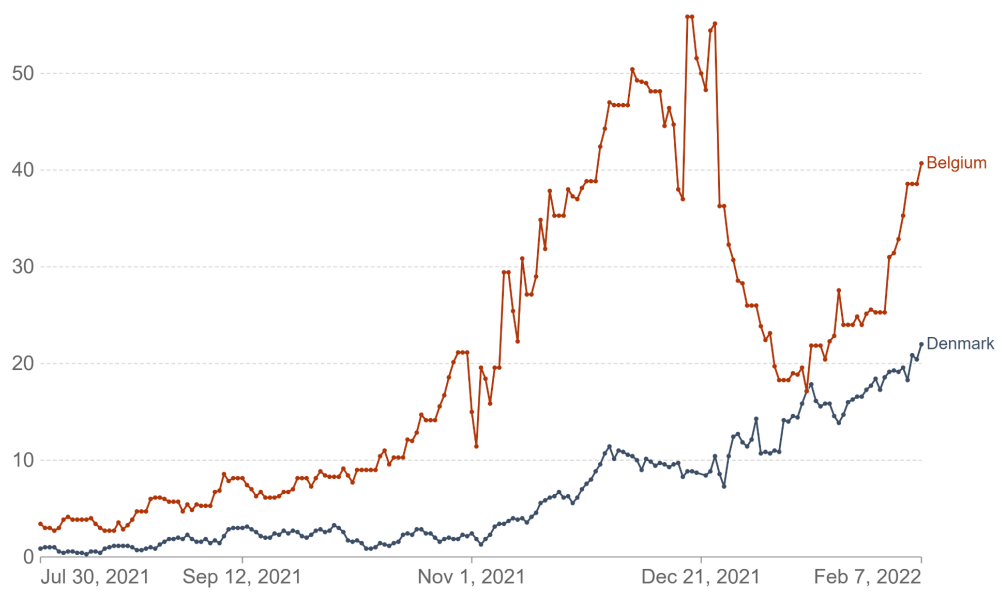


Figure 7: Daily confirmed COVID-19 deaths in Belgium and Denmark. (Source : Our World in Data)

4 Cross-immunity associated with Omicron

Several recent studies (published or in preprint) analyzed the cross-immunity associated with Omicron. For instance, in their preprint, Rössler and colleagues report analyzed samples from BA.1 (Omicron) convalescent patients with different constellations of prior SARS-CoV-2 immunity regarding vaccination and previous infection with a non-Omicron variant and determined titers of neutralizing antibodies against different SARS-CoV-2 variants (D614G, Alpha, Beta, Delta, Gamma, Omicron). They found high neutralizing antibody titers against all variants for vaccinated individuals after BA.1 breakthrough infection or for individuals after infection with a pre-omicron variant followed by BA.1 infection. In contrast, samples from naive unvaccinated individuals after BA.1 infection mainly contained neutralizing antibodies against BA.1 but only occasionally against the other variants.

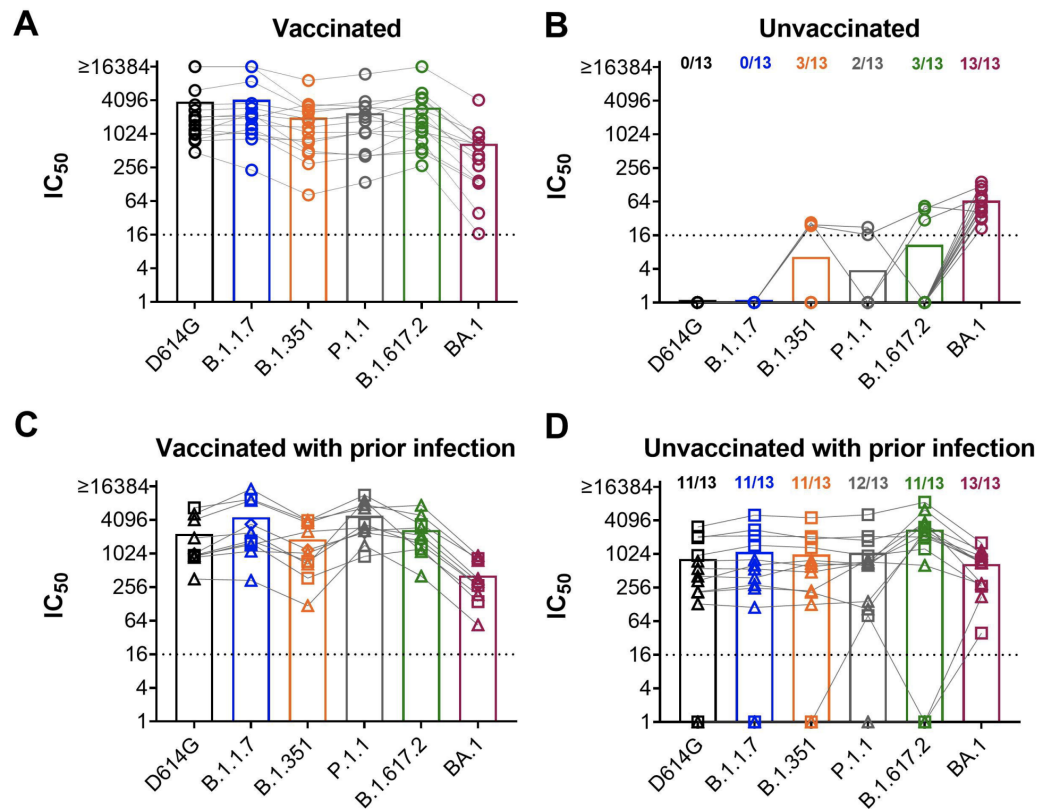


Figure 8: Neutralization capacity of plasma samples from BA.1 (Omicron) convalescent patients. Plasma samples were collected from BA.1 convalescent patients; Panel A vaccinated individuals with no prior infection (n=15), Panel B unvaccinated individuals with no prior infection (n=13), Panel C vaccinated individuals with a prior history of D614G (squares), B.1.1.7 (diamonds), or B.1.617.2 (Delta variant, triangles) SARS-CoV-2 infection (n=10), Panel D unvaccinated individuals with a prior history of either D614G (squares) or B.1.617.2

(triangles) SARS-CoV-2 infection (n=13). Plasma was collected 5-35 days after first positive PCR (BA.1 infection). Samples were analyzed for 50 % neutralization titers (IC50) using life D614G, B.1.1.7 (Alpha), B.1.351 (Beta), P.1.1 (Gamma), B.1.617.2 (Delta), or BA.1 SARS-CoV-2 isolates. Individual values and mean titers (bars) are shown. Samples for each individual patient analyzed with the different virus variants are connected by lines. Titers below 1:16 are regarded as negative (dotted line). Source: Rössler et al., preprint (<https://www.medrxiv.org/content/10.1101/2022.02.01.22270263v1.full.pdf>).

Results reported by Walls and colleagues (2022, *Cell*) are in the same line: they demonstrate that breakthrough infections induce serum-binding and -neutralizing antibody responses that are markedly more potent, durable, and resilient to spike mutations observed in variants than those in subjects who received only 2 doses of vaccine. However, they show that breakthrough cases, subjects who were vaccinated after infection, and individuals vaccinated three times have serum-neutralizing activity of comparable magnitude and breadth, indicating that an increased number of exposures to SARS-CoV-2 antigen(s) enhance the quality of antibody responses.

In their recent preprint entitled “Limited cross-variant immunity after infection with the SARS-CoV-2 Omicron variant without vaccination”, Suryawanshi and colleagues investigated those cross-immunity aspects with some experiments on mice sera. They show that infection with Delta, but not Omicron, induces broad immunity in mice. While sera from Omicron-infected mice only neutralize Omicron, sera from Delta-infected mice are broadly effective against Delta and other VOCs, including Omicron. Analysis of human sera from Omicron and Delta breakthrough cases reveals effective cross-variant neutralization induced by both viruses in vaccinated individuals. Together, their results indicate that Omicron infection enhances preexisting immunity elicited by vaccines, but on its own may not induce broad, cross-neutralizing humoral immunity in unvaccinated individuals.

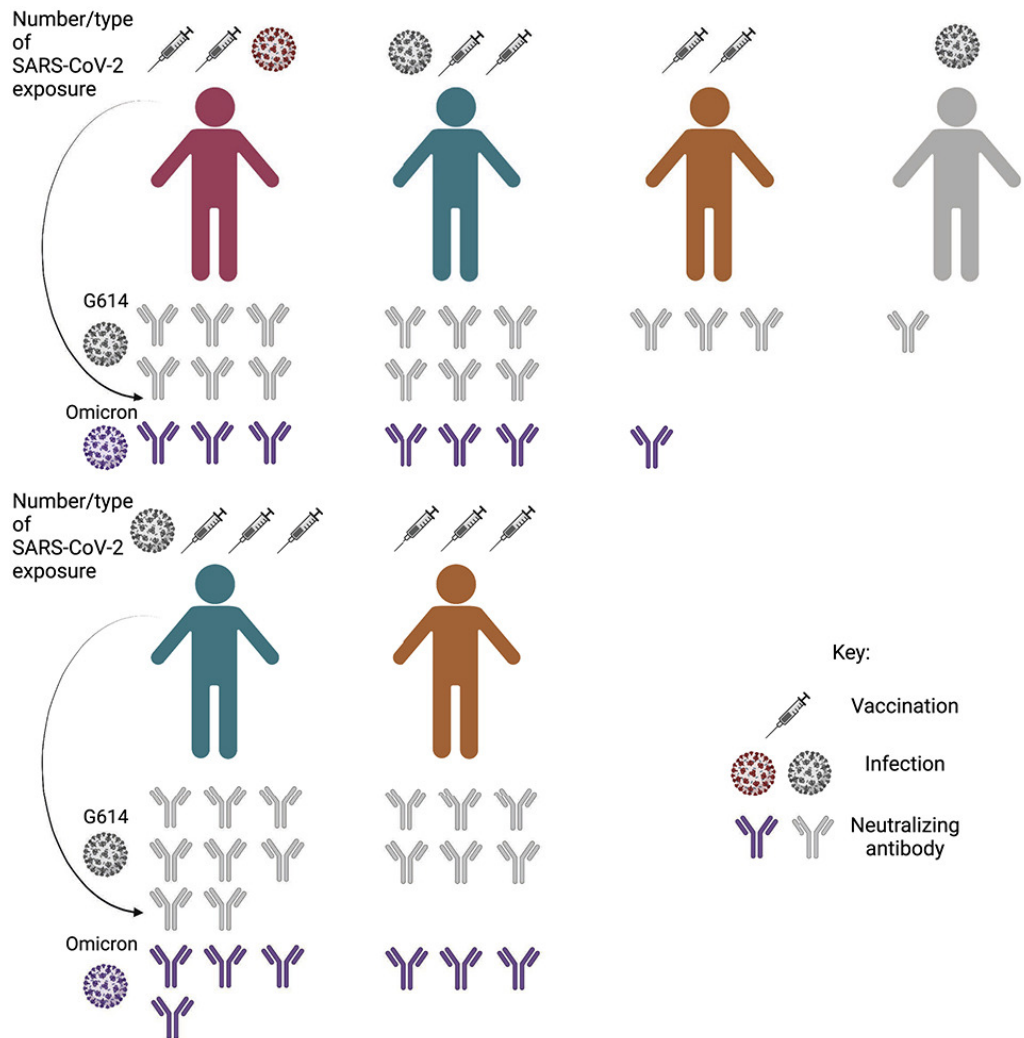


Figure 9: Graphical abstract of the study of Walls et al. (2022, “SARS-CoV-2 breakthrough infections elicit potent, broad, and durable neutralizing antibody responses”, <https://www.cell.com/action/showPdf?pii=S0092-8674%2822%2900076-9>).

Sources:

- <https://www.sciencedirect.com/science/article/pii/S0092867422000691>
- <https://www.medrxiv.org/content/10.1101/2022.01.25.22269794v1.full.pdf>
- <https://www.medrxiv.org/content/10.1101/2022.01.13.22269243v1.full.pdf>