Hôpitaux Universitaires Genève

REPUBLIQUE ET CANTON DE GENEVE
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Direction générale de la santé
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N/réf : PV/MS

SARS-CoV-2 genomic surveillance in Geneva: weekly update

Highlights:

- We start to observe both a decrease in the number of tests performed at our outpatient center, and a **decrease in the absolute number of positive SARS-CoV-2 tests**. However, we did not yet observe a decrease in the positivity rate, which is still relatively high (Figure 1).

- **BA.2** (assessed by the "S Drop out") **is now clearly dominant and represented more than 95% of the SARS-CoV-2 positive specimens tested** at the end of week 13 (see Figure 2). This is confirmed by WGS (Figure 3; preliminary data, as sequencing is still ongoing for week 12).

- We continue to observe a low variability among BA.2 sequences. 15/133 (11%) carried the H78Y mutation in the last sequencing batch. No BA.2 sub-lineage with additional L452R and F486V have yet been identified in the Geneva area.

- One possible BA.1/BA.2 recombinant (BA.2 backbone with a BA.1 insertion and a double breakpoint pattern), collected on March 21 from a Geneva resident without any recent travel history has been identified in the last sequencing batch (Figure 3). Up to now, this recombinant is a singleton, which has not been previously retrieved elsewhere.

- Because of the high prevalence of BA.2, our laboratory will stop screening all positive specimens for the S Drop out at the end of week 14. WGS will allow to differentiate the different variants.

- Note that as of the first week of April, fewer SARS-COV-2 sequences will be produced by the national genomic surveillance program. Therefore, the number of full length sequences from Geneva will decrease.

Figure 1: *Number of SARS-CoV-2 tests performed at the HUG laboratory of virology (per day). Positive tests are displayed in light blue (top). Bottom left: SARS-CoV-2 positive tests over 7 sliding days. Bottom right: mean SARS-CoV-2 tests performed over 7 sliding days.*

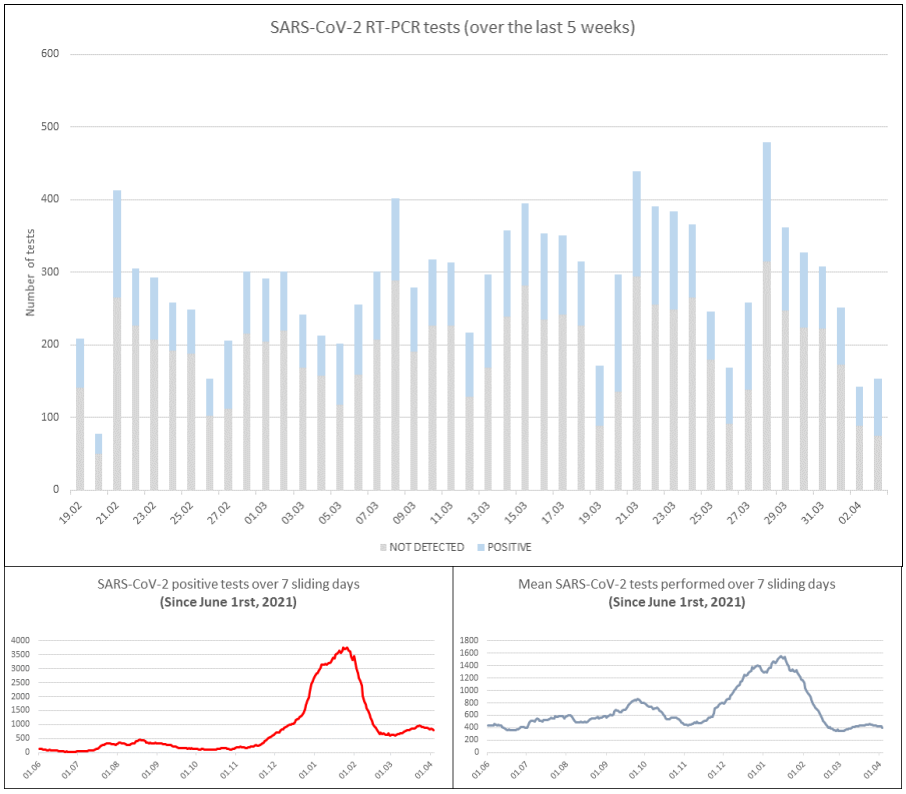


Figure 2: *Weekly evolution of the S Drop out among specimens collected at HUG (including both ambulatory and hospitalized patients). Note that because of the high number of positive samples, surveillance was shifted towards hospitalized patients during week 1, and only a random selection of specimens collected at our outpatient department was tested for the S Drop out between week 1 and 7. Since the beginning of week 7 (February 14), all positive samples collected at HUG (both in- and outpatients) with a Ct value < 32 are tested for the S Drop out. Acknowledgements: S Yerly.*

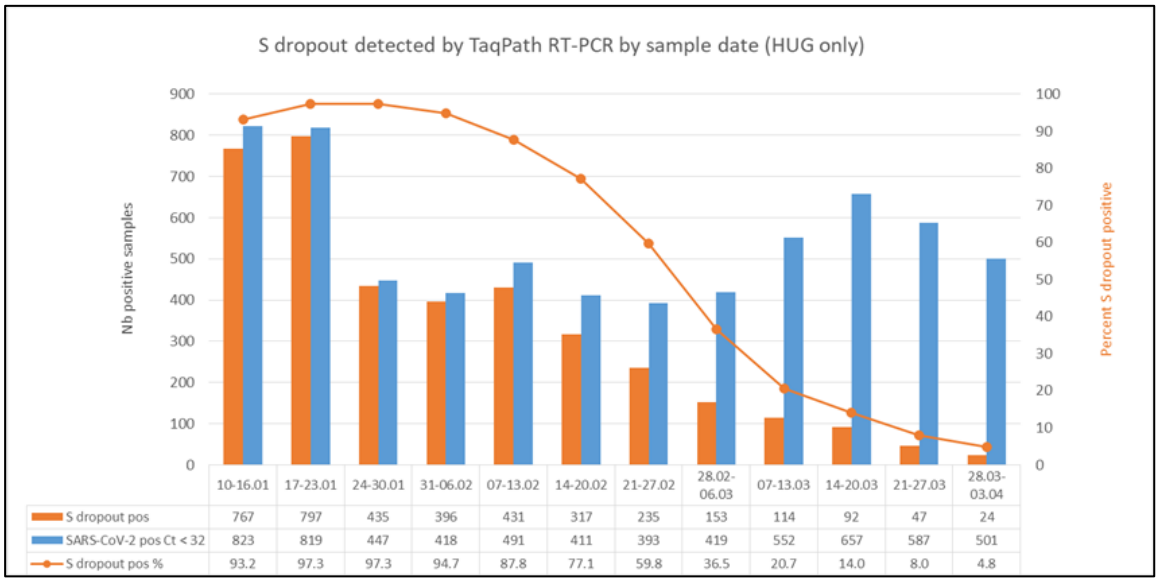
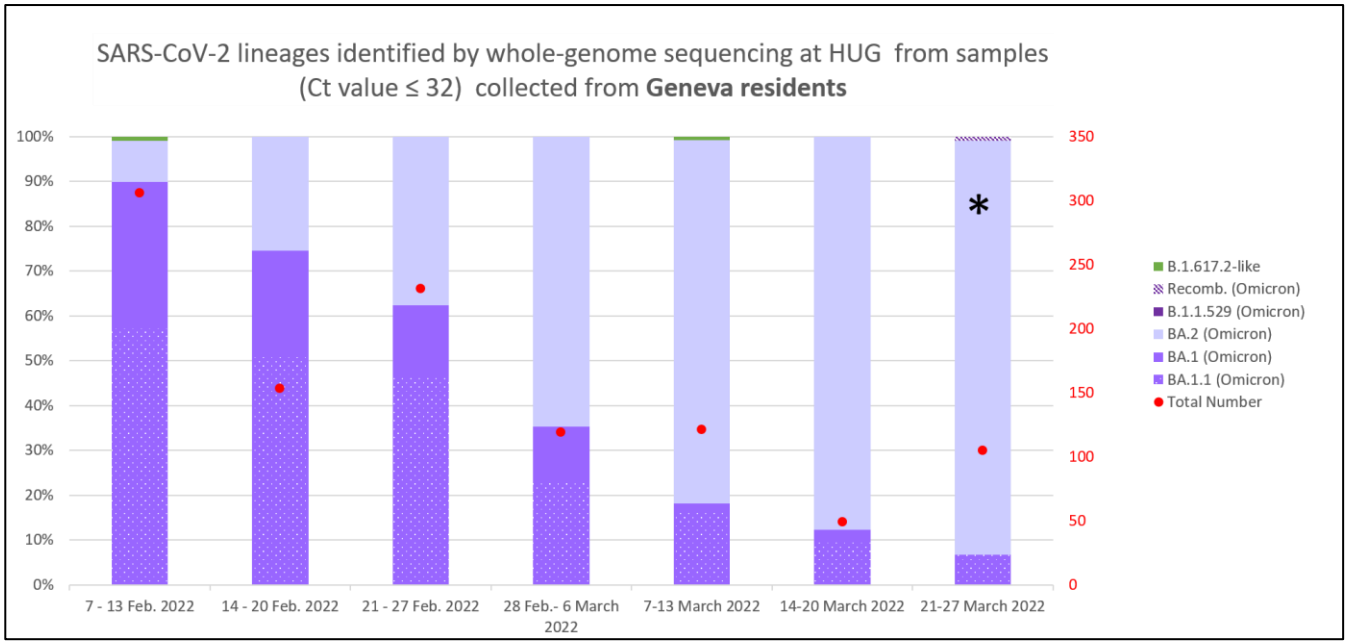


Figure 3: *SARS-CoV-2 lineages identified by whole-genome sequencing at HUG from samples (Ct-value ≤32) collected from Geneva residents (Sentinella specimens excluded). *Sequencing is still ongoing for week 12 (March 21 to March 27, 2022). A total of 1084 sequences are included in this analysis.*



Laurent Kaiser, Samuel Cordey, Manuel Schibler and Pauline Vetter for HUG.
Pauline Brindel for the Geneva Cantonal Physician team.

The laboratory of virology of the Geneva University Hospitals as a sentinel site for the Geneva area

The number of tests (PCR and antigen tests) performed at the Geneva University Hospitals represented around 21% (2813/12955) of the total number of tests performed in the canton of Geneva during week 13 of 2022. Roughly 20% of the positive specimens collected in the Geneva area were processed at HUG during this period (790/3826). Samples collected from symptomatic individuals at our outpatient testing center are tested by RT-PCR. Specimens analyzed in our laboratory originate from ambulatory and hospitalized patients as well as symptomatic and/or asymptomatic health care workers.
The number of positive tests in the canton and the total number of tests done during the surveilled week are available on the website from Federal Office of Public Health (COVID-19 Suisse | Coronavirus | Dashboard (admin.ch)). During week 13 in the canton of Geneva, the number of RT-PCR tests and the number of positive cases slightly decreased compared to the previous week, with a lower number of people getting tested. The proportion of positive tests also shows the first signs of decline.

Methods and collaborations

On November 28 2021, screening for the "S drop out" was implemented at HUG on SARS-CoV-2 positive specimens with a Ct-value ≤ 32 that were tested for primary diagnosis in our laboratory (Taqpath RT-PCR assay). The "S drop out" corresponds to the S-gene PCR target not being amplified("dropping out"), while the two other PCR targets are still detected, and serves as a proxy for Omicron BA.1.
All positive specimens were tested for the S drop out between December 1 and 31, 2021. Since January 2022, all specimens originating from hospitalized patients and a selection of specimens collected from ambulatory patients are tested for the "S Drop out". With the decrease in the number of new cases since the beginning of week 7 (February 14), all positive samples collected at HUG (both in- and outpatients) with a Ct value < 32 and processed at our laboratory are tested for the S Drop out.
Whole genome sequencing performed on SARS-CoV-2 positive samples allows for definitive sublineage/variant identification.

WGS is carried out in close collaboration with the Health 2030 Genome Center in Geneva and Philippe Le Mercier from the Swiss Institute of Bioinformatics. Since March 1, 2021, the sequencing has been done within the Swiss national SARS-CoV-2 genomic and variants surveillance program. Specimens collected at HUG with a Ct-value ≤32 are sequenced. In some instances, sequencing can be done on specimens sent by other laboratories in Switzerland within the surveillance program or by request of the cantonal physician team. Phylogenetic analysis data are produced by Nextstrain, in collaboration with Richard Neher's group at the University of Basel. In addition, partial Sanger sequencing may be done by our laboratory.
Geographic distribution, transmission advantage estimates and detailed numbers of available sequences over time in the canton of Geneva are available on the covSPECTRUM platform, run by Tanja Stadler's group at ETH Zurich.

These reports are produced in collaboration with the Geneva Cantonal Physician team, which provides information on epidemiological links. For epidemiological data, please refer to the weekly report of the cantonal physician team.