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

Highlights:

- Both the **absolute number of positive SARS-CoV-2 tests** and the mean positivity rate at the HUG laboratory of virology have **stabilized over the last 3 weeks** (Figure 1). **The mean positivity rate at our outpatient symptomatic testing center continues to oscillate between 50 and 60%.**
- **BA.2** (assessed by the “S Drop out”) **continued its increase and represented 75% of the SARS-CoV-2 positive specimens tested** at the end of week 9 (see Figure 2). This trend is being confirmed by WGS (Figure 3; preliminary data, as sequencing is still ongoing for week 8). Note that since Delta is essentially no longer circulating, SARS-CoV-2 positive samples not displaying the “S Drop out” can be considered to be BA.2.
- Among BA.1 sequences, 3/4 (73%) corresponded to the BA.1.1 sub-lineage (with the R346K mutation). Among BA.2 variants, we also observe an increasing diversity: half of the sequences lost the R408S mutation, and 12% carry the H78Y mutation observed in ORF3a, first described in Denmark.

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.

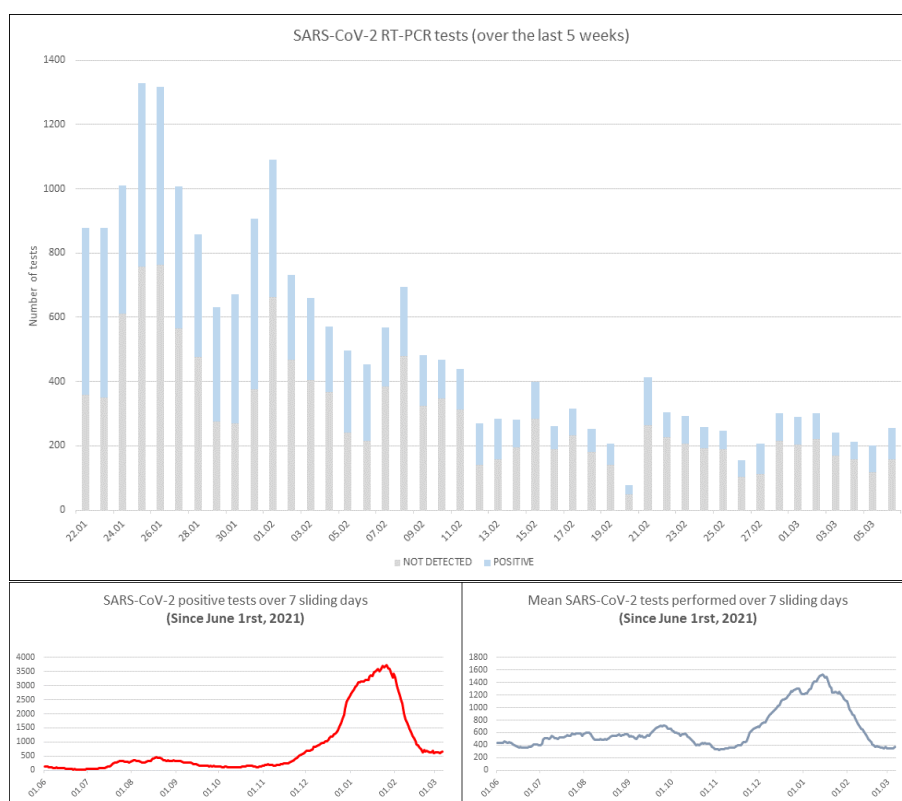


Figure 2: Weekly evolution of the S Drop out among specimens collected at HUG (including both ambulatory and hospitalized patients). Note that because of the high number of positive samples, surveillance was shifted towards hospitalized patients during week 1, and only a random selection of specimens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

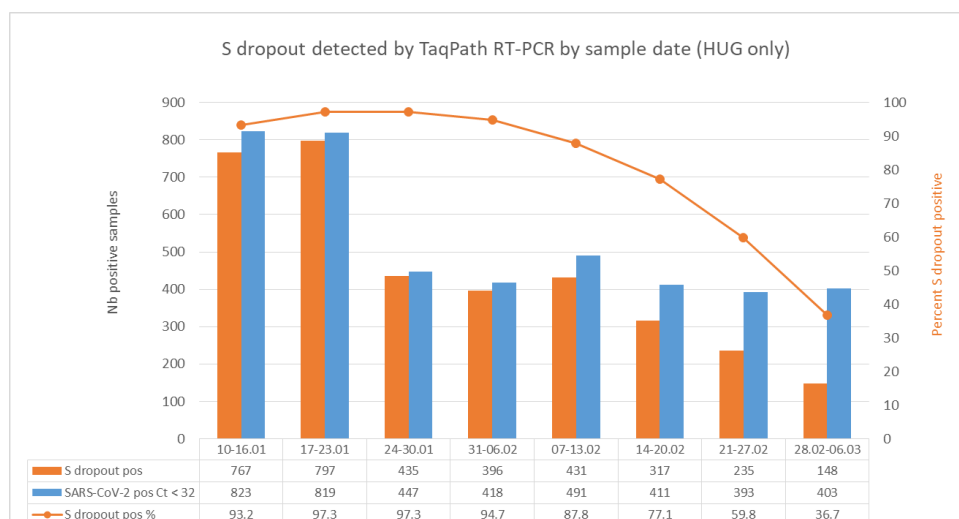
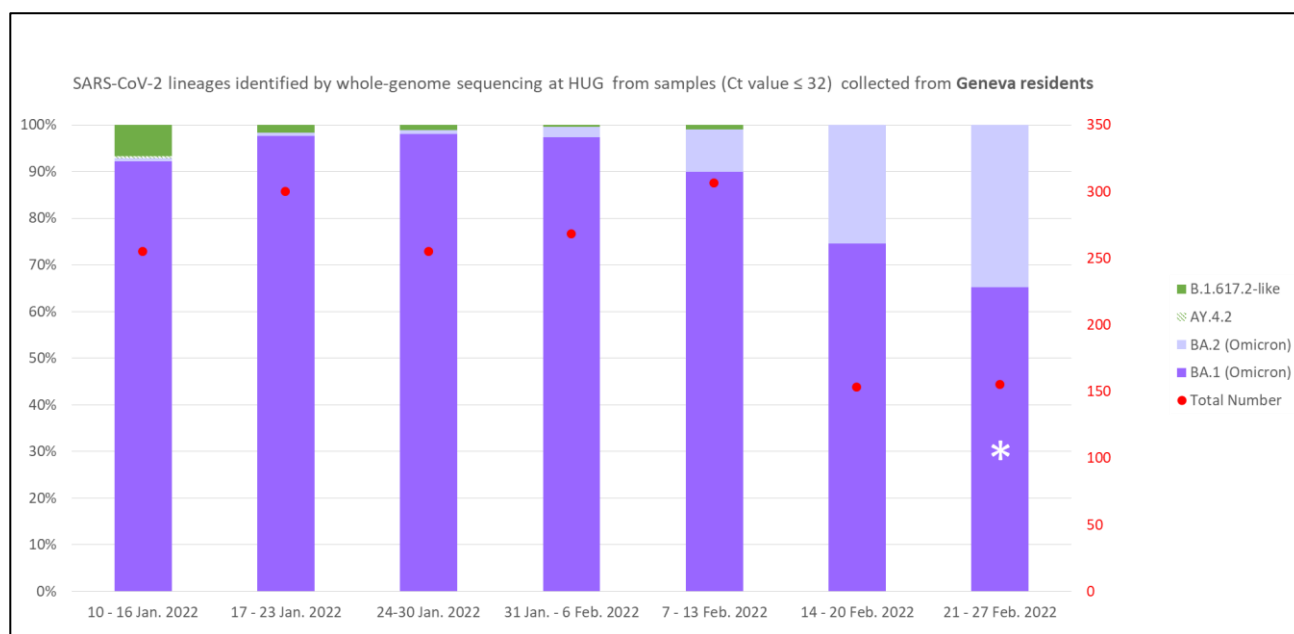


Figure 3: SARS-CoV-2 lineages identified by whole-genome sequencing at HUG from samples (Ct-value ≤ 32) collected from Geneva residents (Sentinella specimens excluded). Sequencing is still ongoing for week 8 (February 21 to February 27, 2022). A total of 1692 sequences are counted in this analysis.



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

The number of tests (PCR and antigen tests) performed at the Geneva University Hospitals represented around 20% of the total number of tests performed in the canton of Geneva during the whole year of 2021. Roughly 25% of the positive specimens collected in the Geneva area were processed at HUG during this period. Samples collected at our outpatient testing center are RT-PCR-based for symptomatic individuals. Specimens analyzed in our laboratory originate from ambulatory and hospitalized patients as well as symptomatic and/or asymptomatic health care workers.

Methods and collaborations

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 in- and outpatients) with a Ct value < 32 and processed at our laboratory are tested for the S Drop out.

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.

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.