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

Highlights:

- The **absolute number of positive SARS-CoV-2 tests** at the HUG laboratory of virology stabilized over the last 2 weeks (Figure 1), while **the mean positivity rate at our outpatient symptomatic testing center continues to oscillate between 50 and 60%**
- Since Delta is virtually no longer circulating, SARS-CoV-2 positive samples not displaying the “S Drop out” can be considered as BA.2.
- **BA.2** (assessed by the “S Drop out”) **continued its increase and represented more than half (60%) of the SARS-CoV-2 positive specimens tested** at the end of week 8 (see Figure 2). This trend is being confirmed by WGS, with some delay (Figure 3; preliminary data, as sequencing is still ongoing for week 7).
- Among BA.1 sequences, two third (66%) corresponded to the BA.1.1. sub-lineage (presence of the R346K mutation) and half of BA.2 variants had lost the R408S mutation.

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.

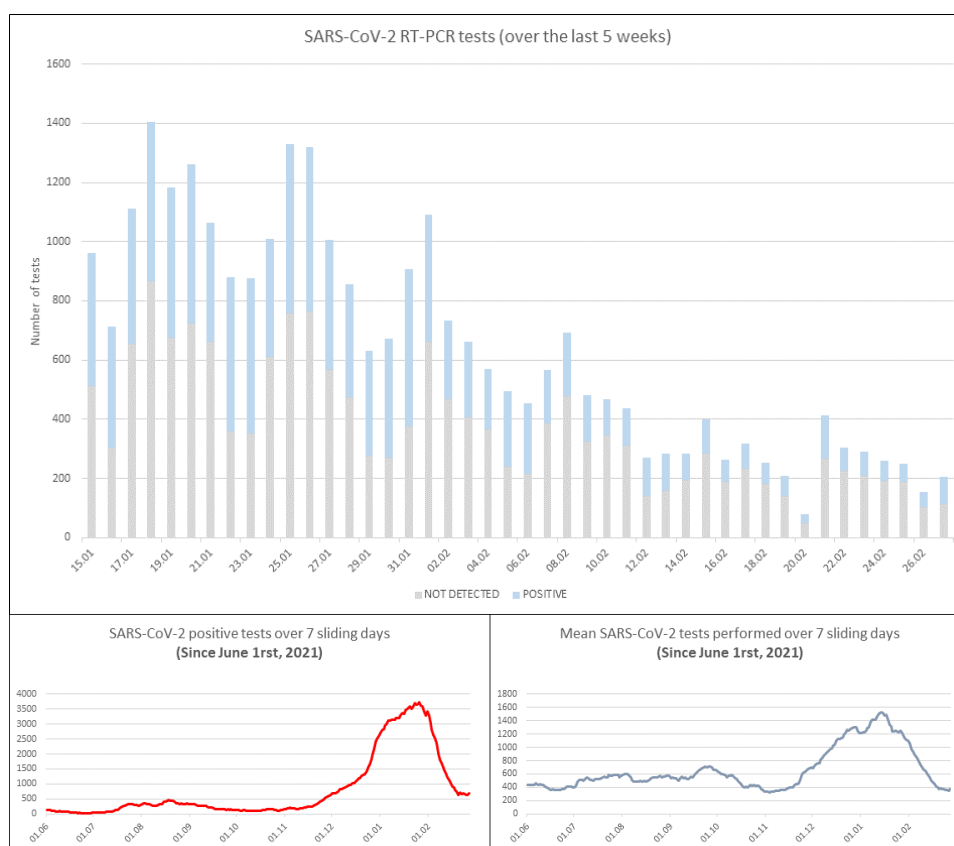


Figure 2: Daily evolution of the S Drop out among specimens collected at HUG (including both ambulatory and hospitalized patients). Note that because of the high number of positive samples, surveillance was shifted towards hospitalized patients during week 1, and only a random selection of specimens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

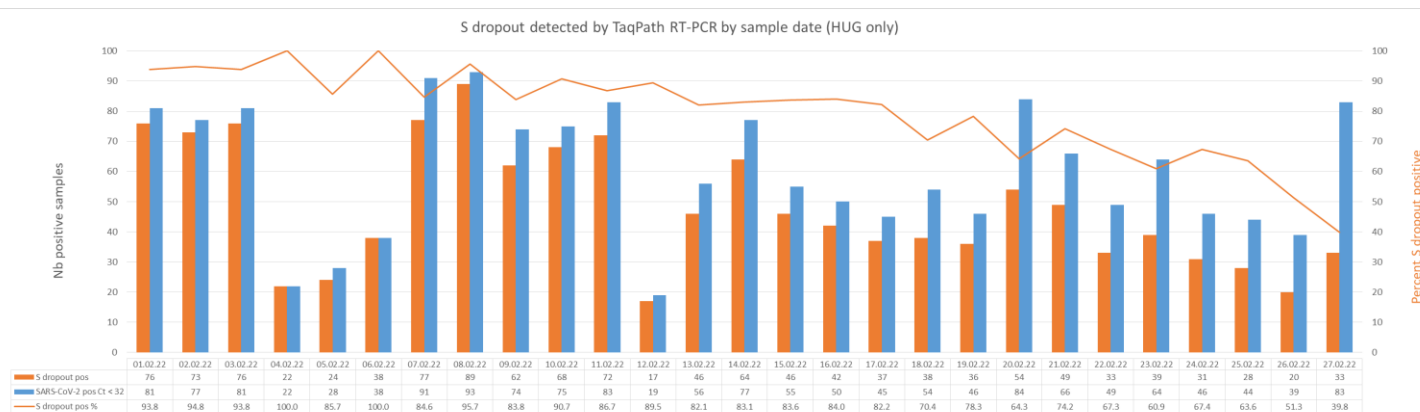
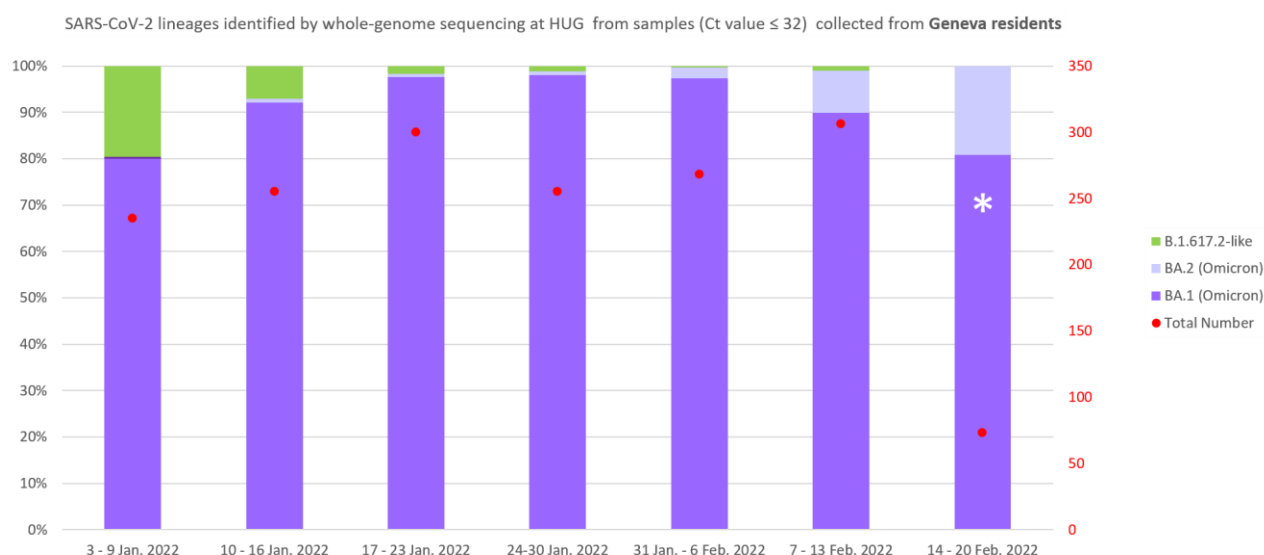


Figure 3: SARS-CoV-2 lineages identified by whole-genome sequencing at HUG from samples (Ct-value ≤ 32) collected from Geneva residents (Sentinella specimens excluded). Sequencing is still ongoing for week 7 (February 14 to February 20, 2022). A total of 1692 sequences are counted in this analysis. Note that specimen collection for WGS shifted towards hospitalized patients during week 1, explaining the rebound in the number of Delta cases over this week, due to the delay between what is observed in the community and hospitalizations.



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 2021 year. 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 specimen 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”.

Whole genome sequencing performed on SARS-CoV-2 positive samples allows for definitive sublineage/variant identification.

Geographic distribution, transmission advantage estimates and detailed number of available sequences over time in the canton of Geneva is 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.