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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 continued its steep decline (Figure 1). **The mean positivity rate at our outpatient symptomatic testing center also started to decrease, but still oscillated between 50 and 60%**
- **BA.2 infections** (assessed by S371L/S373P SNP RT-PCR) **continued to increase and represented more than 30% of the SARS-CoV-2 positive specimens tested** at the end of week 7 (see Figure 2). Samples not displaying the “S Drop out” are now almost exclusively BA.2 as Delta has been replaced by Omicron BA.1 and BA.2 (see Figure 3).
- **The progressive increase in BA.2 sequences was confirmed by WGS, which showed that the proportion of BA.2 sequences doubled between week 5 and week 6, reaching 7%** (Figure 4) (preliminary data, as sequencing is still ongoing for week 6).
- Note that among BA.1 sequences, more than 62% were carrying the R346K mutation, corresponding to the BA.1.1 sub-lineage. Diversity was also observed among BA.2 sequences: more than half 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.

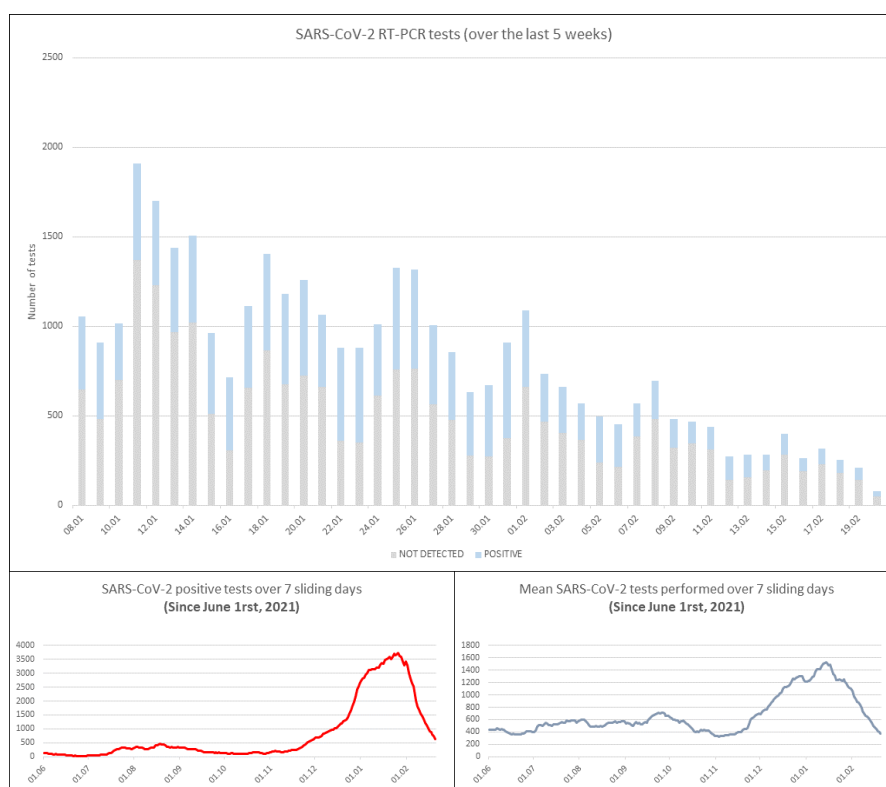


Figure 2: Daily evolution of the S Drop out among specimens collected at HUG (including both ambulatory and hospitalized patients). Note that because of the high number of positive samples, surveillance was shifted towards hospitalized patients during week 1, and only a random selection of specimens 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.

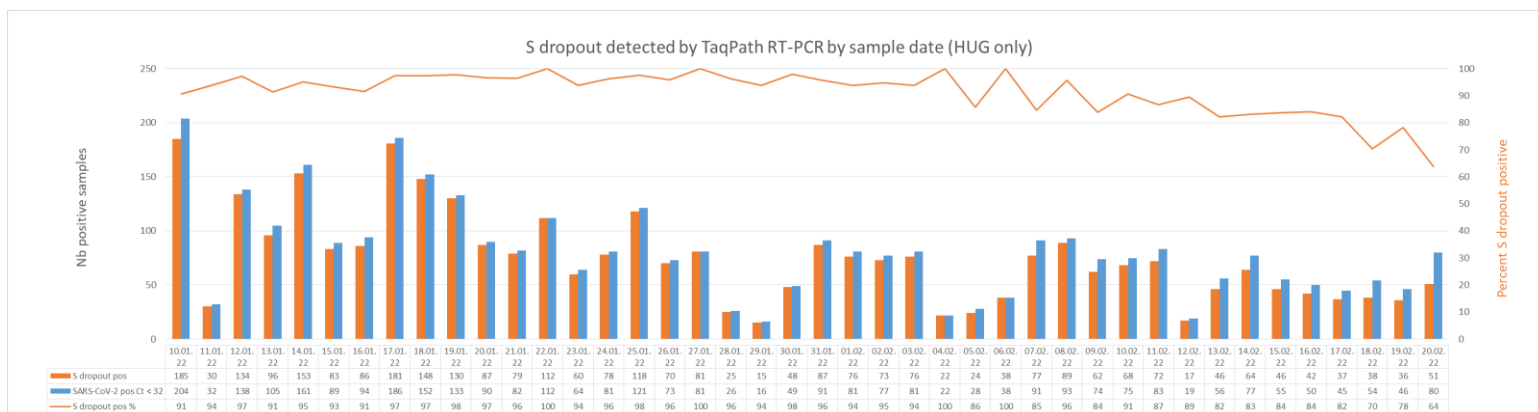


Figure 3: Weekly evolution of the different variants determined by RT-PCR: the presence of the S Drop out is used as a proxy for Omicron BA.1, and among samples not displaying the S Drop out, the S371L/S373P SNP RT-PCR allows for differentiation between Delta and BA.2. Note that specimen collection shifted towards hospitalized patients during week 1. 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.

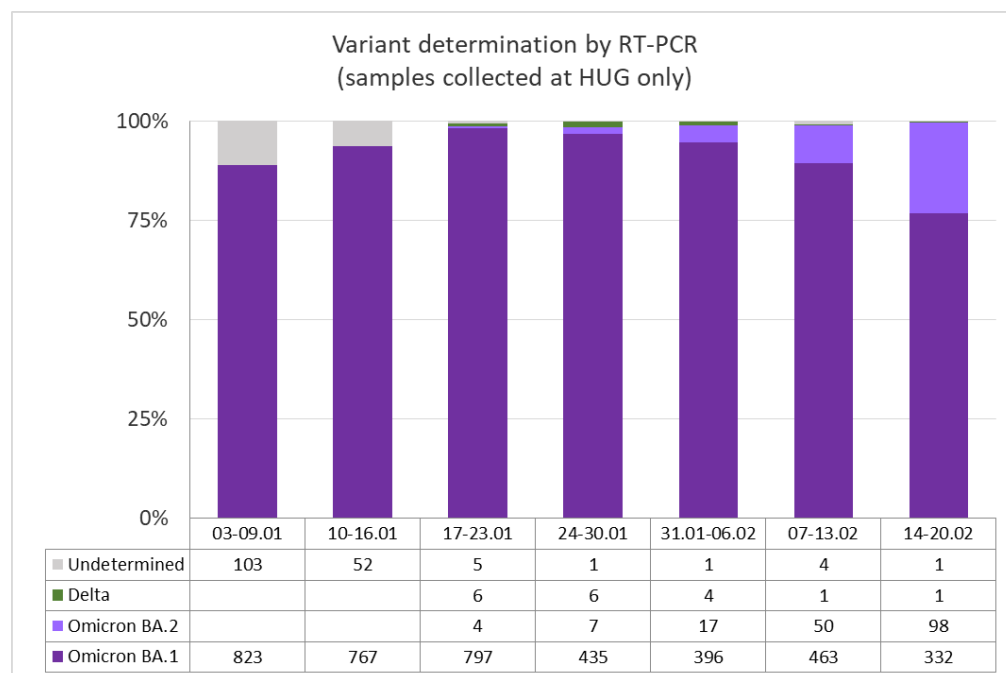
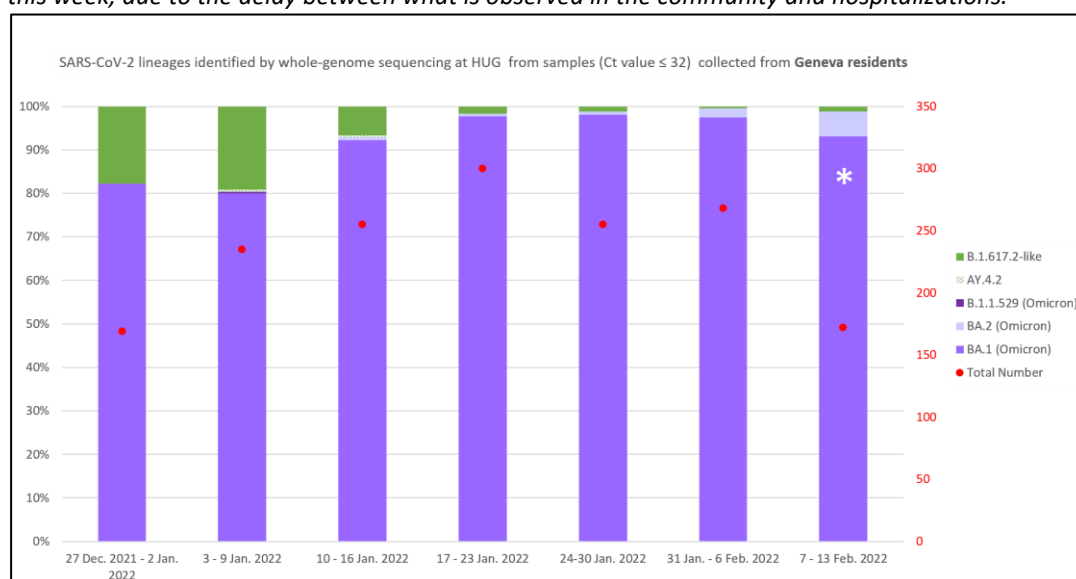


Figure 4: SARS-CoV-2 lineages identified by whole-genome sequencing at HUG from samples (Ct-value ≤32) collected from Geneva residents (Sentinella specimens excluded). Sequencing is still ongoing for week 6 (February 7 to February 13, 2022). A total of 1654 sequences are counted in this analysis. Note 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 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 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.

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 \(admin.ch\)](https://www.admin.ch/gov/fr/section/43139/index.html)). During week 7 in the canton of Geneva, both the number of RT PCR tests and the number of positive cases continued to decrease. The number of PCR tests per day decreased below 2000 per day. The proportion of positive tests also decreased to be around 30%.

Methods and collaborations

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 on November 28 (Taqpath RT-PCR assay). The “S drop out” corresponds to the S-gene PCR target being not amplified (“dropping out”), while the two other PCR targets are still detected, and serves as a proxy for Omicron.

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”.

The SNP RT-PCR S371L/S373P allows for differentiation between Delta, and the Omicron sublineages BA.1 and BA.2. This SNP RT-PCR was tested at HUG on a random selection (n=13) of SARS-CoV-2 “S Drop out” negative samples that were collected since week 3. It is currently used to screen for the Omicron BA.2 sublineage circulation.

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 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.