Hôpitaux Universitaires Genève

REPUBLIQUE ET CANTON DE GENEVE
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Direction générale de la santé
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SARS-CoV-2 genomic surveillance in Geneva: weekly update

Highlights:

- During week 4, we continued to observe a **stability in the absolute number of positive SARS-CoV-2 tests** at the HUG laboratory of virology (Figure 1), as well as in the **mean positivity rate at our symptomatic outpatients' testing center at around 70%**. During the whole month of January, 2022, 14 941 positive SARS-CoV-2 RT-PCR results have been produced at the HUG laboratory of virology. This represents around 25% of the total number of the positive results generated by the laboratory since the beginning of the pandemic.

- **The "S Drop out"** (a test used as a proxy for Omicron BA.1 detection) **is still displayed by more than 97% of the SARS-CoV-2-positive samples tested at our laboratory (see Figure 2).** We start to observe a trend towards an increase of S Drop out negative specimens, which will be monitored closely over the next weeks. As both Delta and the Omicron BA.2 sub-lineage don't display the S Drop out, we implemented a new SNPs RT-PCR aiming to differentiate between Delta and Omicron (S371L/S373P) among S Drop out negative samples. Numbers are too small to draw definitive conclusions, except that we are currently detecting BA.2 at a very low level.

- **Whole-genome sequencing confirmed the predominance of Omicron and showed that the vast majority of sequences retrieved from Geneva residents corresponded to the BA.1 sub-lineage**. (Figure 3). The S Drop out was still a good proxy for Omicron over this period.

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). SARS-COV-2 positive tests over 7 sliding days (bottom left) and mean SARS-COV-2 tests performed over 7 sliding days (bottom right).*

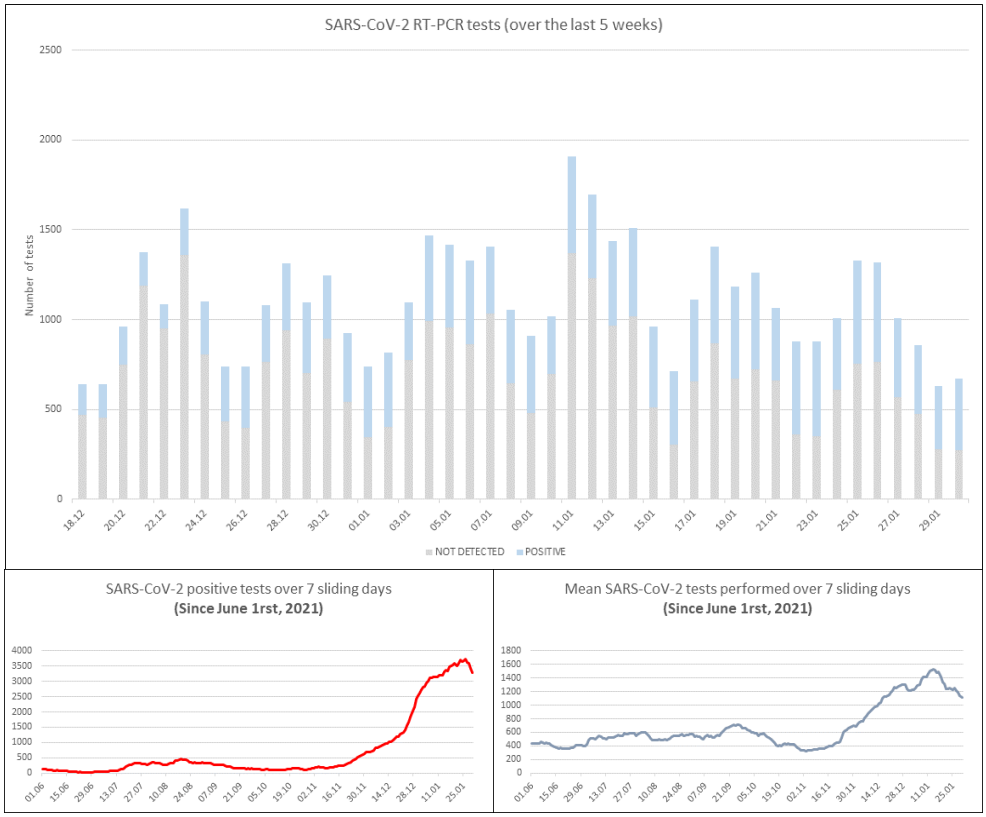


Figure 2: *Weekly evolution of the different variants determined by RT-PCR: the presence of the S Drop Out is used as a proxy for Omicron BA.1, and among samples not displaying the S Drop out, the S371L/S373P SNPs RT-PCR allows for differentiation between Delta and BA.2. Note that specimen collection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

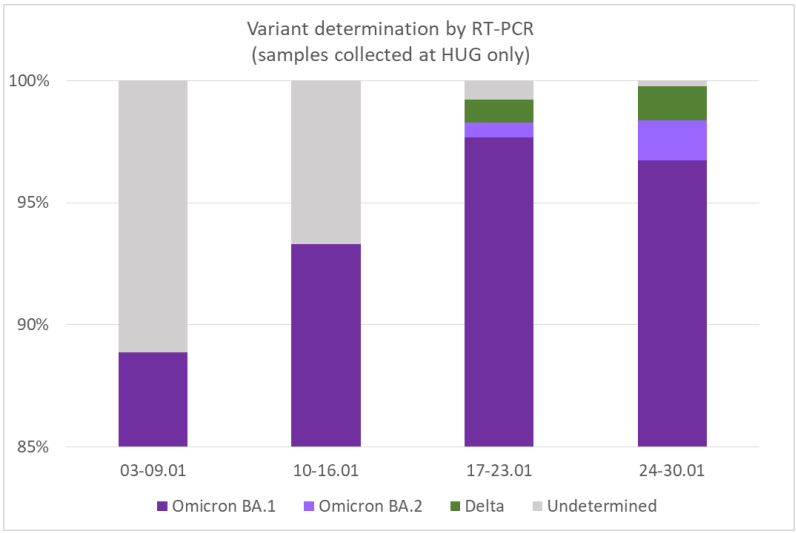
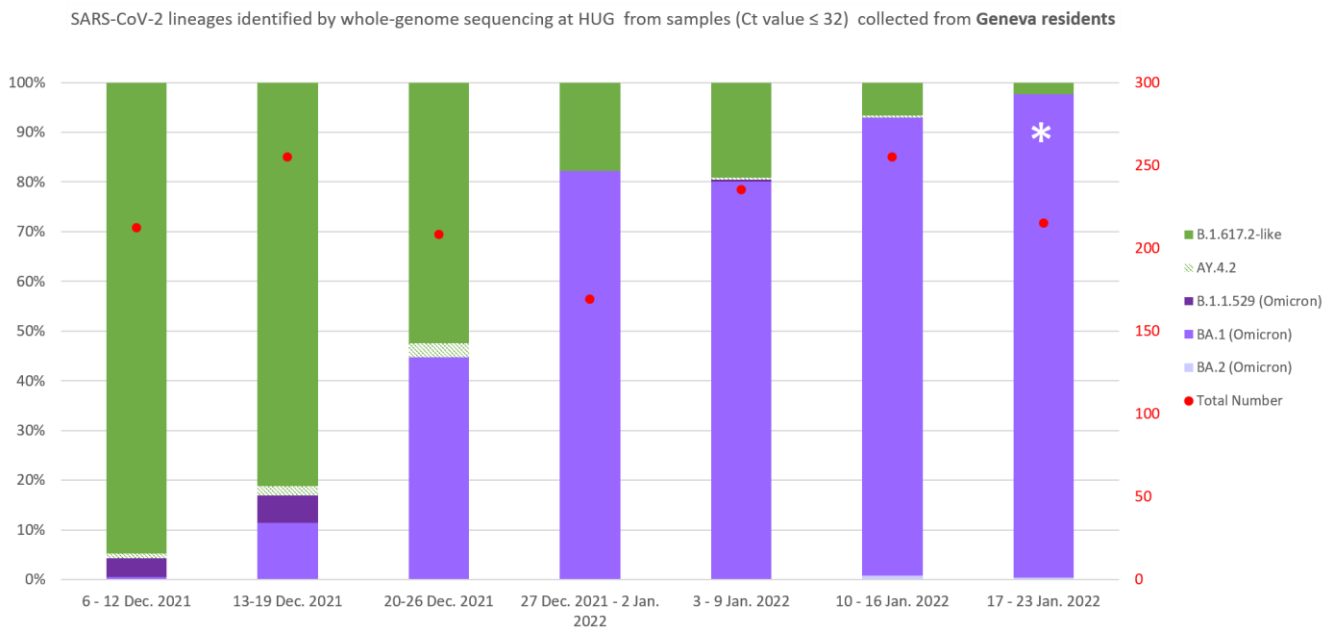


Figure 3: *SARS-CoV-2 lineages identified by whole-genome sequencing at HUG from samples (Ct-value ≤32) collected from Geneva residents (Sentinella specimens excluded). Sequencing is still ongoing for week (January 17 to 23, 2022). A total of 1549 sequences are counted in this analysis. Note that specimen collection for WGS shifted towards hospitalized patients since 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)). During week 4 in the canton of Geneva, the number of RT-PCR tests remained very high - reached between 5000 and 7000 tests per day for several days in a row - and the proportion of positive tests continued to be around 50%. For further epidemiological data, please refer to the weekly report of the cantonal physician team.

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 S371L/S373P SNPs RT-PCR allows for differentiation between Delta, BA.1 and BA.2 Omicron sublineages, and was tested at HUG on a random selection (n=13) of SARS-CoV-2 "S Drop out" negative samples collected since week 3. It will be used to screen for BA.2 Omicron sublineage circulation.
Whole-genome sequencing performed on SARS-CoV-2 positive samples allows for definitive sublineage/variant identification.

Whole-genome sequencing 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.