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Geneva Centre for
Emerging Viral Diseases

Division of Infectious
Diseases

Department of Medicine

Laboratory of virology

Division of Laboratory
Medicine

Diagnostic Department

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

Highlights:

- The number of tests performed at our laboratory and at our outpatient testing center continues to progressively decline, along with the absolute number of positive SARS-CoV-2 tests. (Figure 1).
- **Only one BA.1** (sub-lineage BA.1.1) **was reported in the last sequencing batch** (Figure 2), with **BA.2 representing >98% of the tested specimens**.
- No BA.4 nor BA.5 have been yet detected in the Geneva area.
- Of note, WGS reports one **XE** recombinant (recombinant lineage of BA.1 and BA.2) in the Geneva area during week 15 of 2022 (Figure 2).

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.

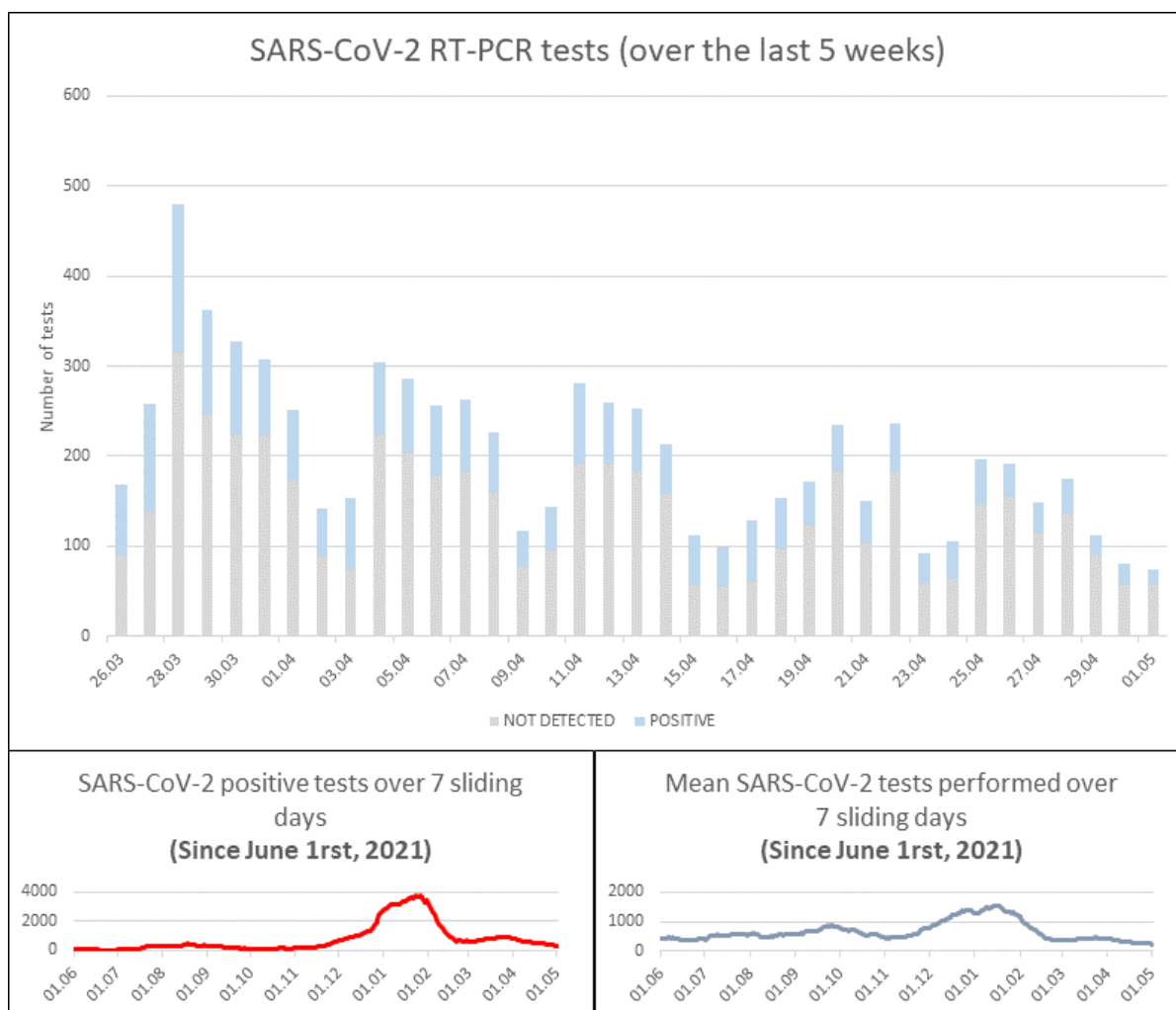
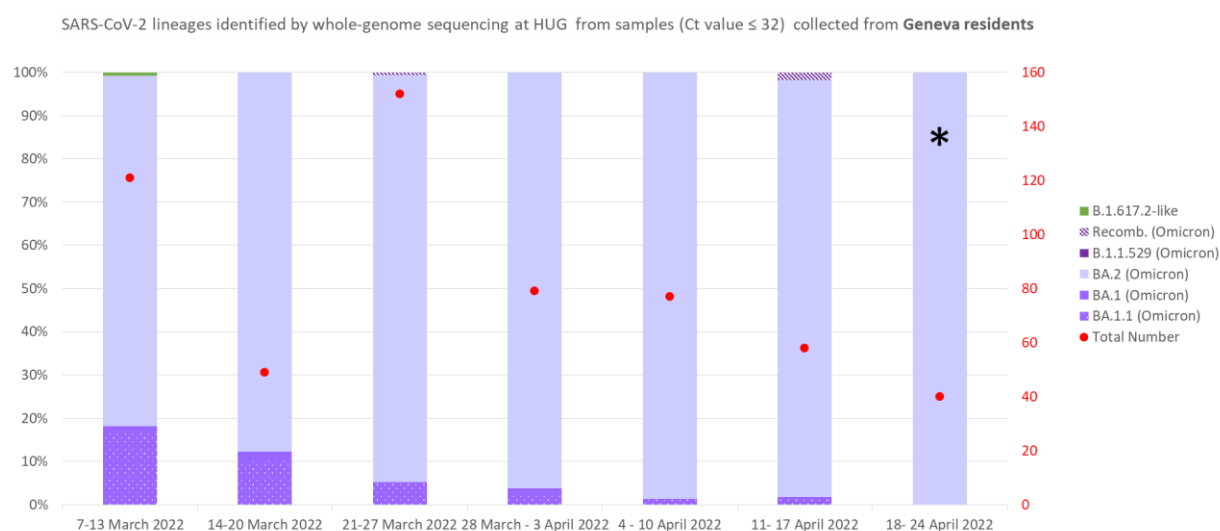


Figure 2: SARS-CoV-2 lineages identified by whole-genome sequencing at HUG from samples (Ct-value ≤ 32) collected from Geneva residents (*Sentinella specimens excluded*). *Sequencing is still ongoing for week 16 (April 18 to April 24, 2022). A total of 576 sequences are included in this analysis.



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 27% (1876/6885) and 26% (1674/6378) of the total number of tests performed in the canton of Geneva during weeks 16 and 17 of 2022, respectively. Roughly 24% and 22% of the positive specimens collected in the Geneva area were processed at HUG during weeks 16 and 17 (433/1801 and 289/1336), respectively. 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 \(admin.ch\)](https://www.admin.ch/gov/fr/section/1331/section/13311/section/133111)). During weeks 16 and 17 in the canton of Geneva, the number of RT-PCR tests and the number of positive cases continued to decrease compared to the previous week. The proportion of positive tests also continues to decline and was below 30% during week 17.

Methods and collaborations

The laboratory has stopped the screening for the “S Drop out” (Taqpath RT-PCR assay) at the end of week 14 of 2022, after the replacement of BA.1 by BA.2. However, in order to monitor the potential arrival of BA.4/BA.5 variants in the Geneva area, the “S Drop out” analysis will be reintroduced from week 18 on a selection of community positive samples (for any “S Drop out” detected, a screening for the 452R mutation will be then carried out). Whole genome sequencing (WGS) performed on SARS-CoV-2 positive samples within the Swiss national SARS-CoV-2 genomic and variants surveillance program 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. The national genomic surveillance program is ongoing in Switzerland since March 1, 2021 and includes specimens collected at HUG with a Ct-value ≤ 32 . 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 report of the cantonal physician team.