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Geneva Centre for
Emerging Viral Diseases

Division of Infectious
Diseases

Department of Medicine

Laboratory of virology

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Diagnostic Department

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

Highlights:

- Both the number of tests performed at our laboratory and the absolute number of positive SARS-CoV-2 tests **continues to decline**. (Figure 1).
- **BA.2 was still the most frequent** variant retrieved in specimens collected between April 25 and May 8 in the Geneva area (Figure 2). **Only one BA.2.12.1 sublineage** (carrying the L452Q mutation) was identified in a Swiss patient living outside the canton of Geneva, who traveled abroad shortly before the appearance of symptoms.
- **One BA.5 sequence** collected at the end of April was retrieved in a symptomatic returning traveler (Figure 2). This variant remains rare in Switzerland, with only 2 BA.5 sequences identified so far in the whole country.
- In addition, WGS allowed to identify 8 **"XM" recombinants** (recombinant lineage of BA.1.1 and BA.2) collected during weeks 17 and 18 from a cluster of 5 patients (Figure 2).
- In order to monitor the arrival of BA.4/BA.5 in the Geneva area, the HUG laboratory of virology is performing additional RT-PCRs (S Dropout +/- L452R/Q SNPs) in all positive SARS-COV-2 specimens with Ct value <32 since week 18. **At least 7 additional putative BA.4/BA.5 specimens** have been identified among 260 specimens tested. WGS will allow for definitive confirmation.

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.

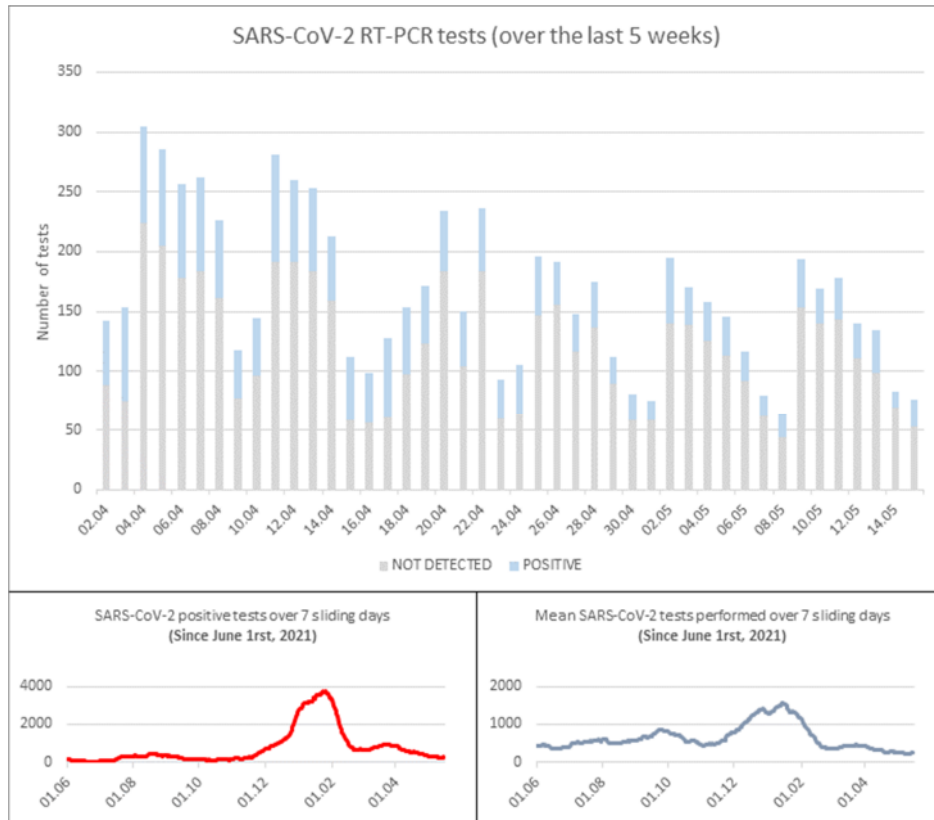
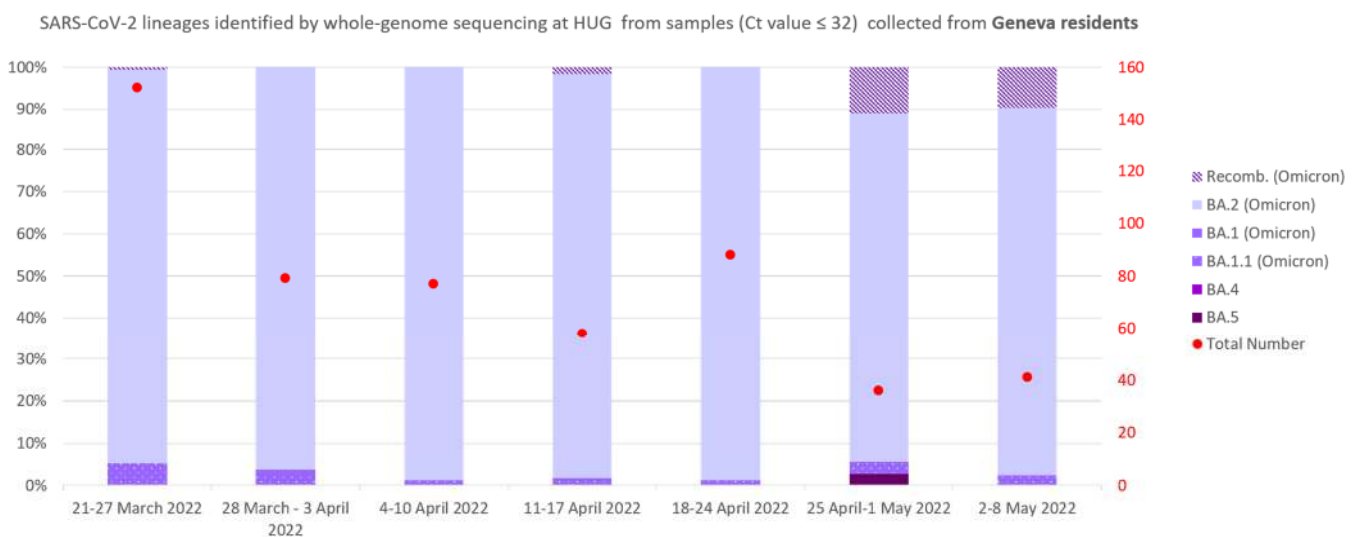


Figure 2: SARS-CoV-2 lineages identified by whole-genome sequencing at HUG from samples (Ct-value ≤ 32) collected from Geneva residents (Sentinella specimens excluded). *Sequencing is still ongoing for week 18 (May 2 to May 8, 2022). A total of 531 sequences are included in this analysis.



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% (1625/5995) and 28% (1673/5969) of the total number of tests performed in the canton of Geneva during weeks 18 and 19 of 2022, respectively. Roughly 28% and 30% of the positive specimens collected in the Geneva area were processed at HUG during weeks 18 and 19 (274/977 and 255/859), 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/de/section/04601/index.html?id=13632)). During weeks 18 and 19 in the canton of Geneva, the number of RT-PCR tests and the number of positive cases continued to decrease. The proportion of positive tests also continues to decline and was below 20% during week 19.

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 has been reintroduced from week 18 on a selection of community positive samples (for any “S Drop out” detected, a screening for the 452R mutation is 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.