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Geneva Centre for
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Division of Infectious
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SARS-CoV-2 genomic surveillance in Geneva: bi-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 May 16 and May 22 in the Geneva area (Figure 2). This included **two sequences of the BA.2.12.1 sublineage** (carrying the L452Q mutation). Only one BA.1.1.1 sequence has been identified in the last 2 sequencing batches.
- **BA.4 and BA.5 are increasing in frequency, and represented ~13% of the sequences collected between May 16 and 22**. This increase in proportion of the BA.4/BA.5 variants is also monitored through the S Drop out. **During week 21, 25% of all analyzed samples (all positive specimens with Ct values < 32) displayed the S Drop out** (Figure 3).
- In addition, WGS allowed to identify 2 additional **“XM” recombinants** (recombinant lineage of BA.1.1 and BA.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.

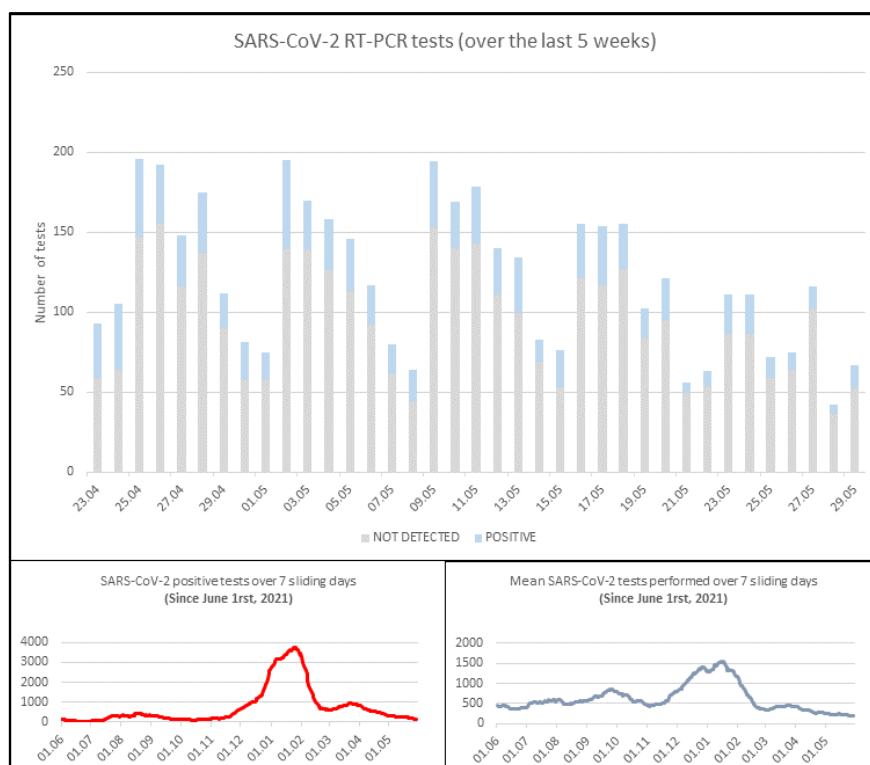


Figure 2: SARS-CoV-2 lineages identified by whole-genome sequencing at HUG from samples (C_t -value ≤ 32) collected from Geneva residents (*Sentinella* specimens excluded). *Sequencing is still ongoing for week 20 (May 16 to May 22, 2022). A total of 421 sequences are included in this analysis.

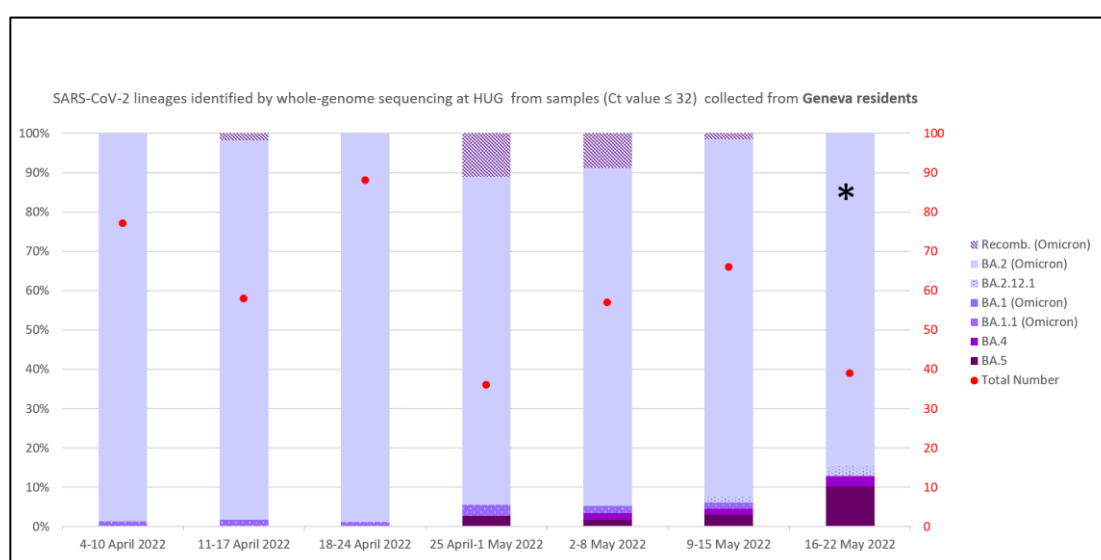
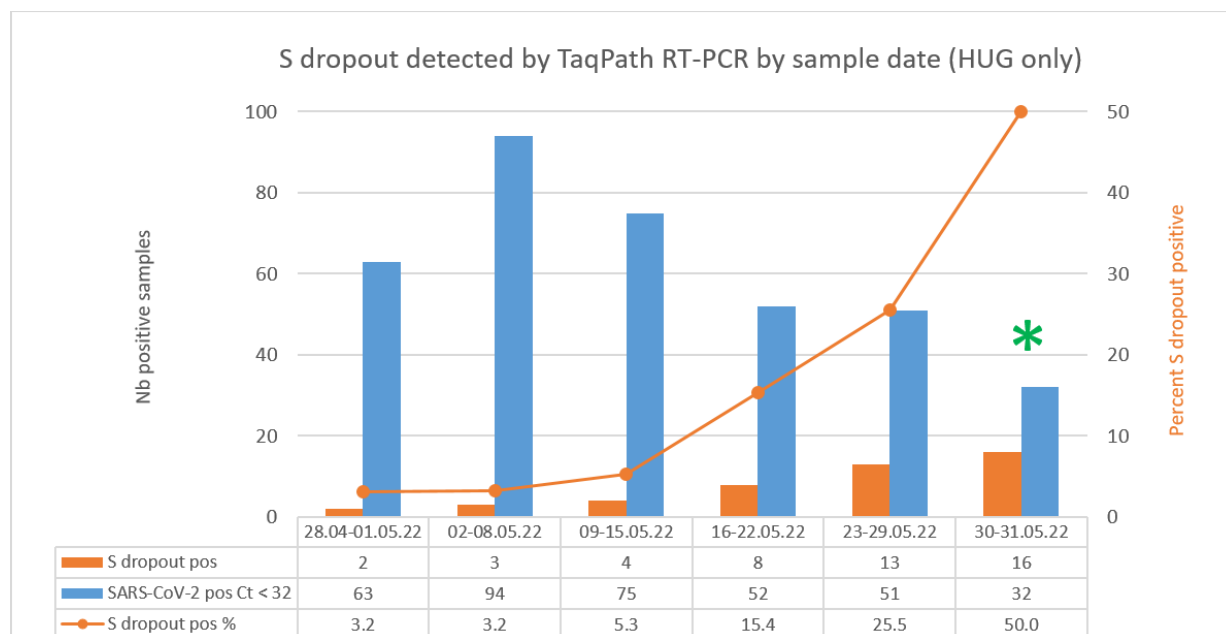


Figure 3: Weekly evolution of the S Drop out among specimens collected at HUG (including both ambulatory and hospitalized patients). All positive samples collected at HUG (both in in- and outpatients) with a Ct value < 32 are tested for the S Drop out. Green star: Note that only preliminary results are available for week 22, on samples collected on May 30 and 31 (first 2 days of the week).



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 Emma Hodcroft for the Geneva Center for Emerging Viral Diseases.
 Pauline Brindel for the Geneva Cantonal Physician team.

The number of tests (PCR and antigen tests) performed at the Geneva University Hospitals represented around 26% (1513/5746) and 28% (1267/4567) of the total number of tests performed in the canton of Geneva during weeks 20 and 21 of 2022, respectively. Roughly 29% and 24% of the positive specimens collected in the Geneva area were processed at HUG during weeks 20 and 21 (202/703 and 137/579), 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.

Methods and collaborations

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 and analyzed by Emma Hodcroft, from the Geneva Center of Emerging Viral Diseases and University of Geneva. In addition, partial Sanger sequencing may be done by our laboratory.

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.