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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: monthly update Weeks 37-39

Caveat: Data published by our laboratory might reveal some trends regarding local epidemiology but may not represent the situation well, as the number of available sequences has been low since the beginning of 2023. In terms of representability, this data should be interpreted cautiously due to possible cluster effects (see below).

Highlights:

- The **number of positive tests** performed by our laboratory **peaked during week 36, progressively decreased** until week 38, when it started to slightly increase again (Figure 1). The mean positivity rate over 7 sliding days followed the same variations.
- **In parallel, the number of patients hospitalized with a positive SARS-CoV-2 test peaked during week 36 and is progressively decreasing since then.** For more information, please refer to the weekly CH-SUR report.
- **Currently, several variants are co-circulating in the Geneva area, with no specific variant becoming dominant** (Figure 2, see below p.3 for more details); this is in line with the national wastewater surveillance data (<https://cov-spectrum.org/stories/wastewater-in-switzerland>).
- The number of sequences carrying the “FLip” mutations, continues to progressively increase in Switzerland. It arises on different backgrounds, both BA.2.75 and XBB derivatives.
- **Still no BA.2.86 has been identified in the Geneva area in clinical specimens.** Its proportion remains low in the wastewater surveillance system. As of beginning of October, only 3 sequences have been made available in the SARS-CoV-2 national sequencing program in Switzerland in clinical specimens so far.

More information can be found in the monthly national surveillance report available at <https://www.hug.ch/centre-maladies-virales-emergentes/programme-sequencage-national-du-sars-cov-2>

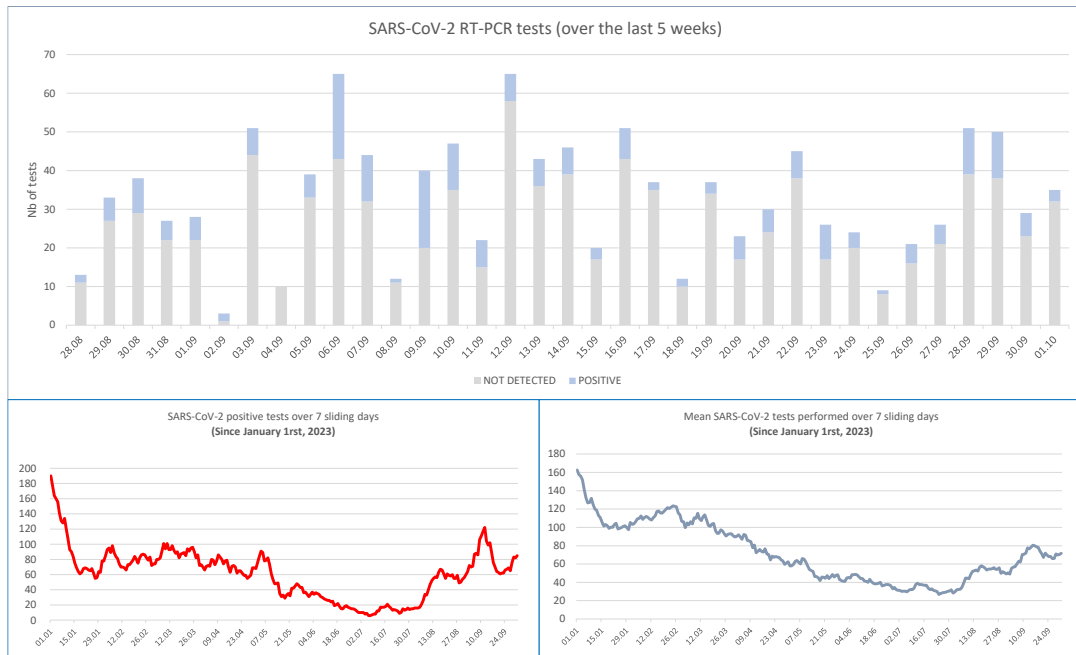


Figure 1: Number of SARS-CoV-2 tests performed at the HUG laboratory of virology (per day). Positive tests are displayed in light blue (top). Bottom left: SARS-CoV-2 positive tests over 7 sliding days. Bottom right: mean SARS-CoV-2 tests performed over 7 sliding days.

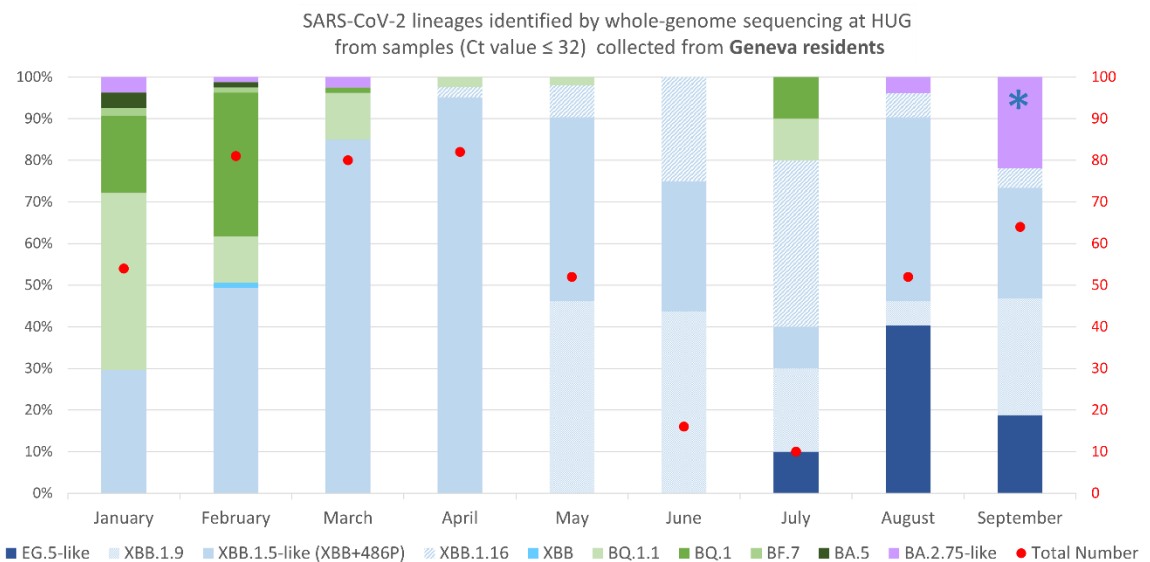


Figure 2: SARS-CoV-2 lineages identified by whole-genome sequencing at HUG from samples (Ct-value ≤ 32) collected from Geneva residents (Sentinella specimens excluded). *Sequencing is still ongoing for the month of September (last specimen included in this graph was collected on September 19, 2023). A total of 491 sequences were included in this analysis. Note that the large BA.2.75 number of sequences retrieved during the month of September can be attributed to a cluster effect.

SARS-CoV-2 sequences identified in the Geneva area

XBB.1.5-like, XBB.1.16 and XBB.1.9 variants and their derivatives (including EG.5 and derivative sublineages, mostly EG.5.1 and EG.5.1.1) are co-circulating in the Geneva area, along with BA.2 derivatives such as DV.7.

As observed in the whole of Switzerland, as well as in Europe, the number of sequences carrying the FLip mutations continues to increase in the Geneva area.

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 75% (552/732) and 72% (477/660) of the total number of tests performed in the canton of Geneva during weeks 37 and 38 of 2023, respectively. Roughly 57% (76/133) and 55% (66/120) of the positive specimens collected in the Geneva area were processed at HUG during weeks 37 and 38, respectively. Specimens analyzed at the HUG originate mainly from hospitalized patients.

The number of positive tests in the canton and the total number of tests done during the surveilled weeks are available on the [website of the Federal Office of Public Health](#).

Methods and collaborations

Screening for the “S drop out” was resumed at HUG on SARS-CoV-2 positive specimens with a Ct-value ≤ 32 that were tested for primary diagnosis in our laboratory on August, 22, 2023 (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. In the current context of circulating variants, the presence of the “S Drop out” serves as a proxy for BA.2.86. Note that other BA.2 derivatives, such as DV.7.1 (BA.2.75 derivative), and XBB derivatives don't display the “S Drop out”.

WGS is conducted 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 has been ongoing in Switzerland since March 1, 2021, and includes specimens collected at the 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 Centre for Emerging Viral Diseases and the University of Geneva. In addition, partial Sanger sequencing may be done by our laboratory.

Geographic distribution, transmission advantage estimates and exact 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. Please refer to the EpiScope report (EpiScope | [ge.ch](#)) for epidemiological data.

Laurent Kaiser, Samuel Cordey, Manuel Schibler, Francisco Perez Rodriguez and Pauline Vetter for the HUG and the Geneva Centre for Emerging Viral Diseases.

Geraldine Duc for the Geneva Cantonal Physician team.