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: monthly update
Weeks 35-36 (September 2023)

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, and started to decrease during week 37(Figure 1). The **mean positivity rate** over 7 sliding days also **peaked at 22%** at the end of week 36.
- **Similarly, the number of patients hospitalized with a positive SARS-CoV-2 test continued to increase during week 36**, mostly due to a large nosocomial cluster. 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 taking off in clinical specimens** (Figure 2, see below p.3 for more details); this is in line with wastewater surveillance data(https://cov-spectrum.org/stories/wastewater-in-switzerland)

- The number of sequences carrying the "FLip" mutations, arising in various backgrounds, is progressively increasing in Switzerland.

- **In the last sequencing batch, the large number of BA.2.75-like sequences can be linked to nosocomial clusters.**

- **Still no BA.2.86 has yet been retrieved in the Geneva area in clinical specimens**, although it has been detected in every canton at low levels in the wasterwater surveillance system The first swiss BA.2.86(1) sequence has been retrieved from a clinical specimen collected in the Vaud canton on September 7.

- On August 22, 2023, we resumed testing for the "S Drop out" (see methods section below), which serves as a proxy for BA.2.86. We had no positive result yet (over 109 specimen collected between August 22 and September 12, and 14 specimen collected between September 13 and September 19).

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.*

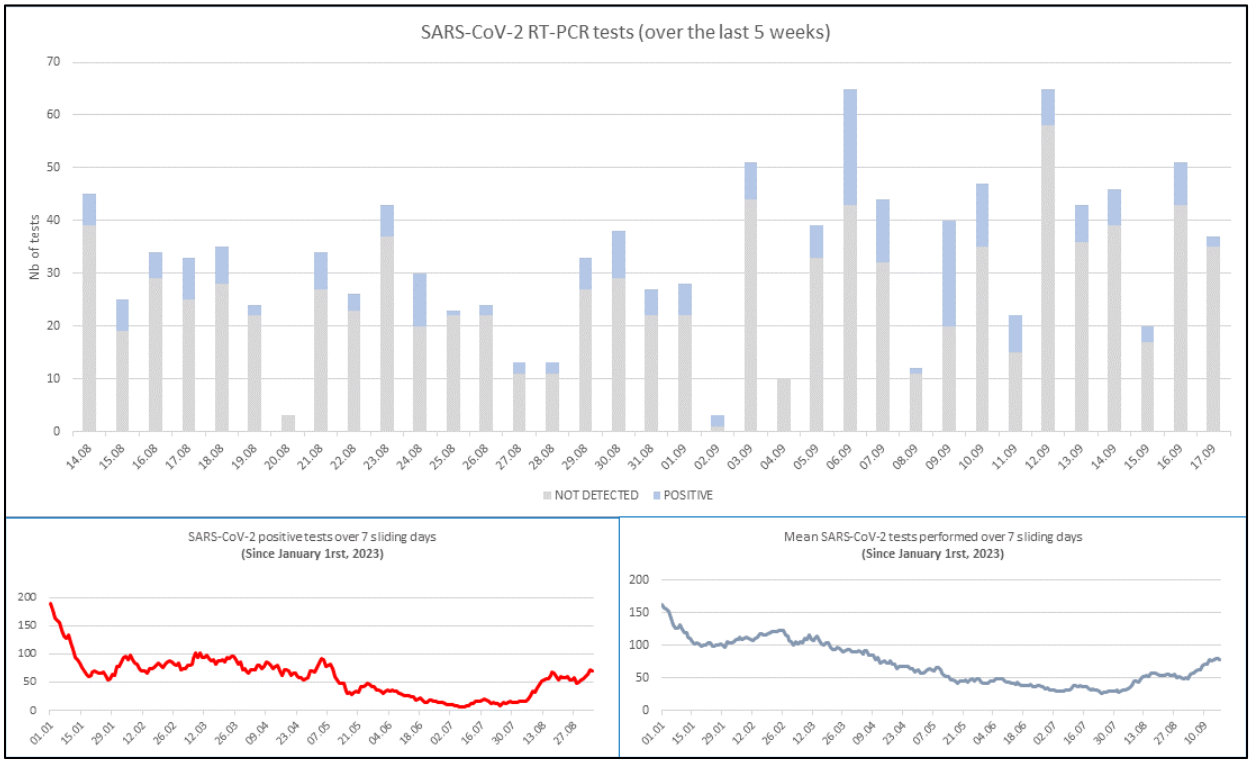
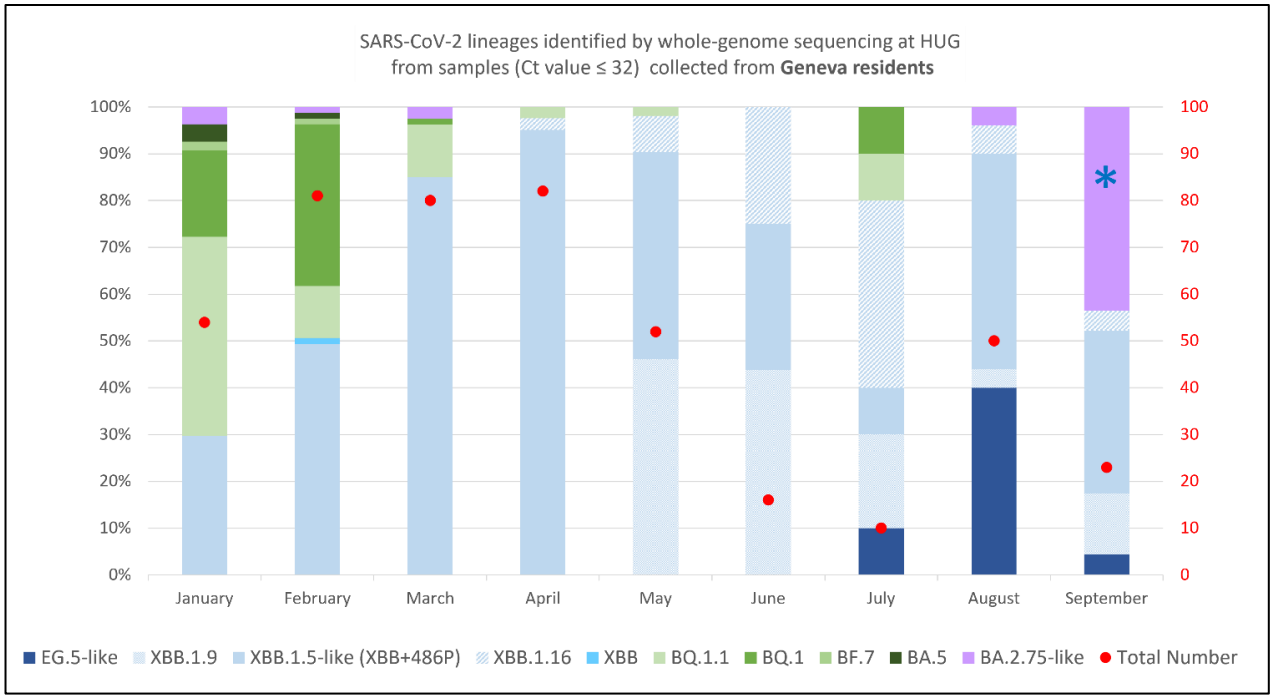


Figure 2: *SARS-CoV-2 lineages identified by whole-genome sequencing at HUG from samples (Ct-value ≤32) collected from Geneva residents (Sentinella specimens excluded). *Sequencing is still ongoing for the month of August and September (last specimen included in this graph was collected on September 5, 2023). A total of 448 sequences were included in this analysis.*



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.

The BA.2.75-like sublineage identified in the nosocomial clusters are DV.7.1 sequences. This variant carries the FLip mutations, which until recently were only observed in the GK.2 (XBB.1.5.70) and HK.3 (XBB.1.9 derivative) backgrounds in Switzerland.
Of note, non-XBB BA.2 sublineages have not been widely circulating since the last year. DV.7.1 (CH.1.1 derivative) is among the few non-XBB variants still successfully circulating after XBB emerged.
BA.2.86 is also a descendent of BA.2. It has been appointed a new variant under monitoring on August 17, 2023 due to its high number of mutations leading to antigenic change and its identification in wide geographic area in the context of a decreased global genomic surveillance. Its origin is still unknown, with intermediaries missing.

As observed in the whole of Switzerland, as well as in Europe, the number of sequences carrying the FLip mutations is progressively increasing 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 80**%** (387/486) and 84**%** (495/592) of the total number of tests performed in the canton of Geneva during weeks 35 and 36 of 2023, respectively. Roughly 73**%** (72/99) and 83**%** (111/134) of the positive specimens collected in the Geneva area were processed at HUG during weeks 35 and 36, 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 and Diem-Lan Vu for the Geneva Cantonal Physician team.