Hôpitaux Universitaires Genève

REPUBLIQUE ET CANTON DE GENEVE
Département de la sécurité, de la population et de la santé
Direction générale de la santé
Service du médecin cantonal

UNIVERSITÉ DE GENÈVE
FACULTÉ DE MÉDECINE

Federal Office of Public Health FOPH
Public Health Directorate Communicable Diseases Division
Schwarzenburgstrasse 157
3003 Berne
Switzerland

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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: monthly update
Weeks 33-34 (August 2023)

Caveat:

- Data published by our laboratory might reveal some trends regarding local epidemiology but are not optimally representative, 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.

Highlights:

- The **number of positive tests** performed by our laboratory continued to **progressively increase**. (Figure 1). The **mean positivity rate is high, between 10 and 15% since week 30**.
- **Compared to week 33, the number of hospitalizations increased slightly during week 34.** For more information, please refer to the weekly CH-SUR report.
- **XBB.1.5-like, XBB.1.19 and XBB.1.16 variants and their derivatives are co-circulating in the Geneva area.** (Figure 2)
- **The EG.5 derivative sequences (e.g., EG.5.1, EG.6.1) increased in the Geneva area during August** (Figure 2)**.**
- **Of note, no BA.2.86 has yet been retrieved in the Geneva area nor in Switzerland in a clinical specimen. However, BA.2.86 was detected in wastewater surveillance in different parts of Switzerland, including Geneva during week 34.**

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

XBB is a recombinant of two Omicron sublineages: a BA.2 sublineage (BJ.1) and a BA.2.75 (BM.1.1.1) sublineage. Its breakpoint is located on the spike protein's RBD domain (Receptor Binding Domain). Different XBB sublineages are circulating worldwide, mainly **XBB.1.5-like** (acquired a mutation on the spike protein (486P) that increases its affinity to ACE-2 in vitro and therefore likely its transmissibility), **XBB.1.16** (similar genetic profile as XBB.1.5, with additional mutations (E180V and K478R) in the spike protein), and **XBB.1.9** (main differences with XBB.1.5 are mutations in the ORF1a gene, with XBB1.9 displaying two additional mutations (G1819S, T4175I)).

EG.5, a variant under monitoring with an increasing global prevalence, is an XBB.1.9.2 derivative that carries the additional mutation F456L.

BA.2.86 is descendent of BA.2. Despite the low number of sequences retrieved worldwide (n=9 as of August, 24, 2023), 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, as basal BA.2 has not been circulating for one year, worldwide.

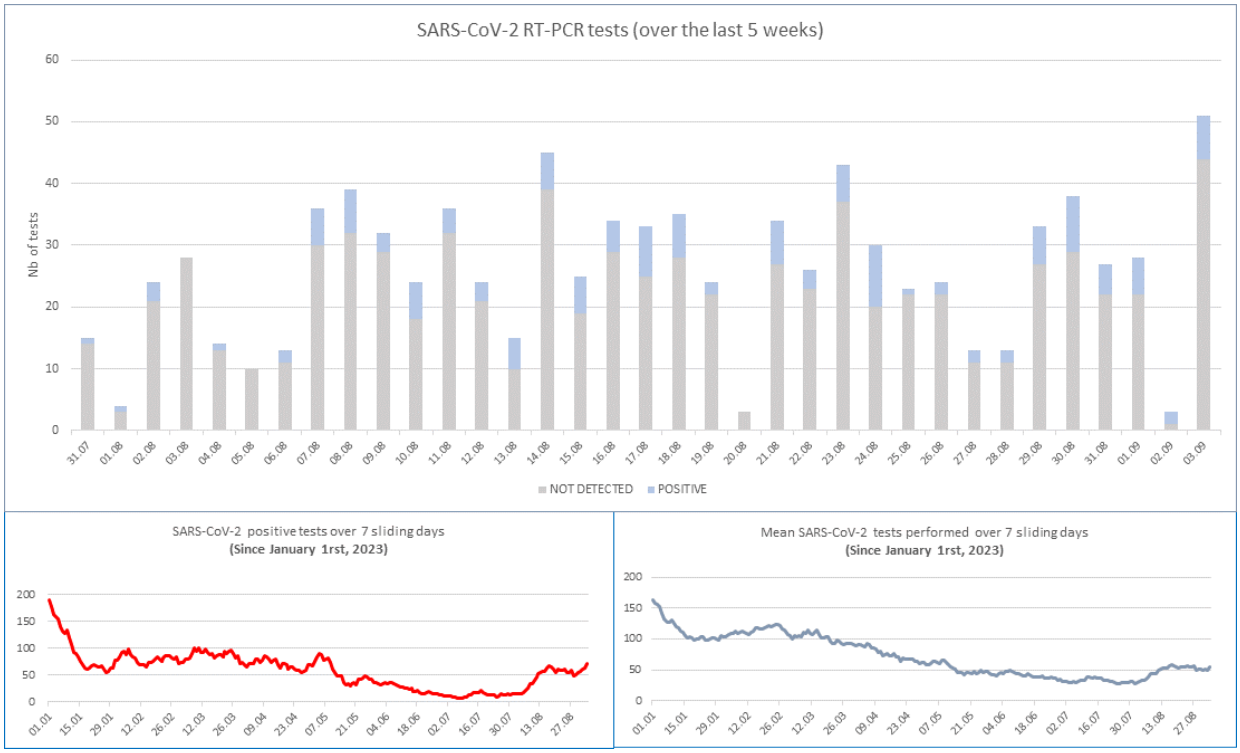

Figure 1: *Number of SARS-CoV-2 tests performed at the HUG laboratory of virology (per day). Positive tests are displayed in light blue (top). Bottom left: SARS-CoV-2 positive tests over 7 sliding days. Bottom right: mean SARS-CoV-2 tests performed over 7 sliding days.*

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 79**%** (374/476) and 79**%** (391/498) of the total number of tests performed in the canton of Geneva during weeks 33 and 34 of 2023, respectively. Roughly 63**%** (55/88) and 69**%** (59/85) of the positive specimens collected in the Geneva area were processed at HUG during weeks 33 and 34, 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 (COVID-19 Suisse | Coronavirus | Dashboard (admin.ch)).

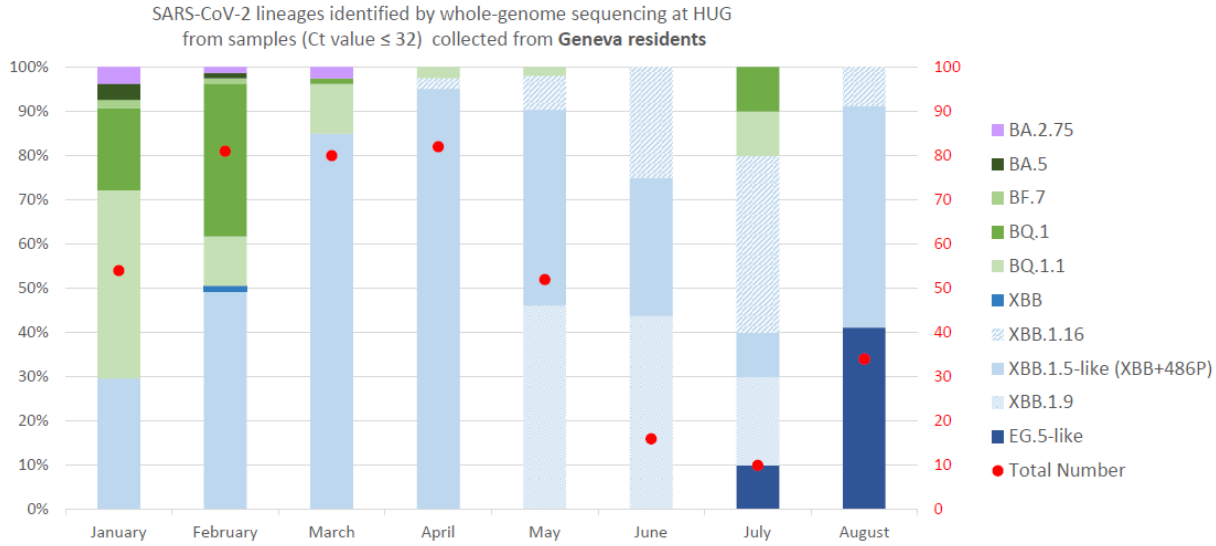

Figure 2: *SARS-CoV-2 lineages identified by whole-genome sequencing at HUG from samples (Ct-value ≤32) collected from Geneva residents (Sentinella specimens excluded). *Sequencing is still ongoing for the month of August. A total of 409 sequences were included in this analysis.*

Methods and collaborations

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.