Hôpitaux Universitaires Genève

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SARS-CoV-2 genomic surveillance in Geneva: monthly update
Weeks 25 to 28 (mid-June to mid-July) 2023

Caveat:

- Since January 2023, the number of samples available for sequencing is progressively decreasing. Therefore, the data published by our laboratory might provide some trends regarding local epidemiology but are not optimally representative. In terms of representability, this data should be interpreted cautiously due to cluster effects.

Highlights:

- Over the last month, we observed a **decrease** of the number of tests done at our laboratory and **of the positivity rate, which fell below 5% during weeks 26 to 28.** (Figure 1). This represented an **absolute number of positive tests of less than 10 per week** during weeks 26 and 27. Such low number of positive tests has not been observed since July 2020, when testing criteria were however larger.
- **Similarly, hospitalization rates at the HUG stayed very low** (≤5 per week over the last month, mostly patients with pauci-symptomatic or mild disease). For more information, please refer to the weekly CH-SUR report.
- **All sequences identified on specimen collected since the beginning of June were XBB derived variants.** (Figure 2)
- **XBB.1.5-like, XBB.1.19 and XBB.1.16 variants are co-circulating in the Geneva area.**
- **No EG.5 has yet been identified in the Geneva area.** One positive sample originating from a patient in the Canton of Luzern has been retrieved in the last sequencing batch.

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).

XBB.1.5-like These sublineages additionally 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 is currently displacing XBB.1.5 in many countries. It has a similar genetic profile as XBB.1.15, with additional mutations (E180V and K478R) in the spike protein.

XBB.1.9 is another variant displacing XBB.1.15 in many countries. The main differences in mutations lay in the ORF1a gene, with XBB1.9 displaying two additional mutations (G1819S, T4175I).

EG.5, an XBB.1.9.2 derivative that carries the additional mutation F456L, which has recently been appointed a new variant under monitoring by the WHO because of its global increasing prevalence.

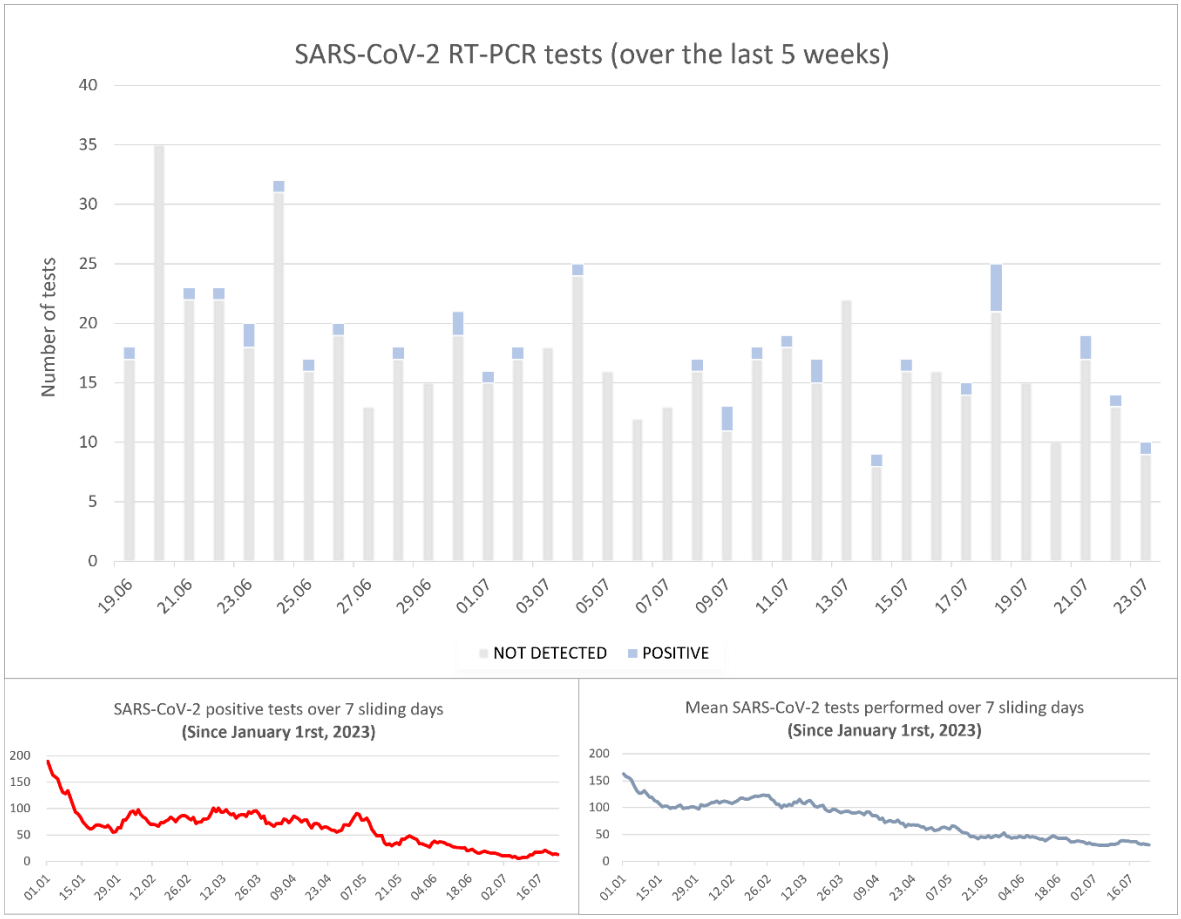

Figure 1: *Number of SARS-CoV-2 tests performed at the HUG laboratory of virology (per day). Positive tests are displayed in light blue (top). Bottom left: SARS-CoV-2 positive tests over 7 sliding days. Bottom right: mean SARS-CoV-2 tests performed over 7 sliding days.*

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 75**%** (263/353), 75**%** (220/292), 76**%** (226/298) and 78**%** (260/333) of the total number of tests performed in the canton of Geneva during weeks 25, 26, 27 and 28 of 2023, respectively. Roughly 57**%** (17/30), 77**%** (10/13), 70**%** (7/10) and 81**%** (17/21) of the positive specimens collected in the Geneva area were processed at HUG during weeks 25, 26, 27 and 28, 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)).

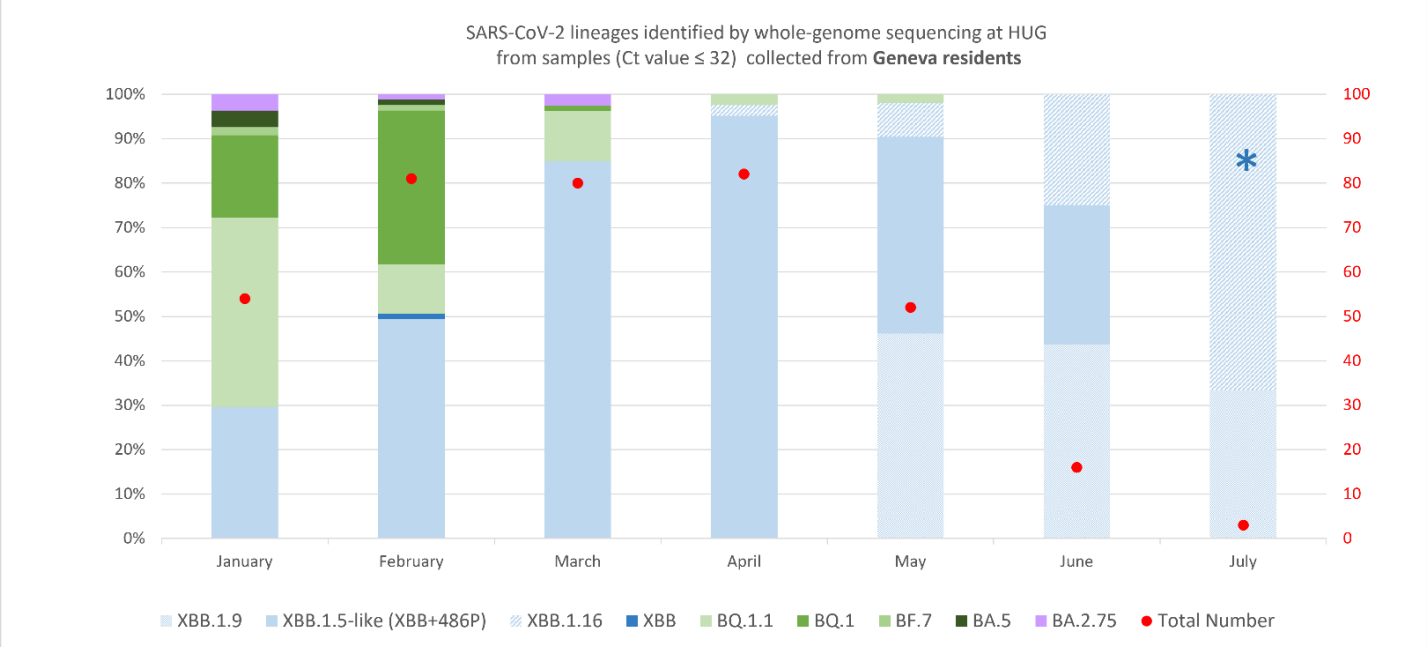

Figure 2: *SARS-CoV-2 lineages identified by whole-genome sequencing at HUG from samples (Ct-value ≤32) collected from Geneva residents (Sentinella specimens excluded). *Sequencing is still ongoing for the month of July. A total of 368 sequences were included in this analysis.*

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.