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SARS-CoV-2 genomic surveillance in Geneva: bi-weekly update

Caveat:

- Since January 2023, only a limited number of samples (up to 30) from the Geneva area are sequenced weekly. Therefore, the data published by our laboratory might provide some trends regarding local epidemiology but are not optimally representative. Please note that in terms of representability, this data should be interpreted cautiously due to cluster effects.

Highlights:

- Over the last month, we observed a decrease in the **number of tests done at our laboratory. The positivity rate continues to progressively decrease** (Figure 1).
- **Similarly, hospitalization rates at the HUG continued to decrease over the last month.** Less than 10 hospitalized patients per week presented with a positive SARS-CoV-2 tests during the last month. For more information, please refer to the weekly CH-SUR report.
- **All sequences identified on specimen collected since the end of April were XBB.1.5-like variants.** (Figure 2)
- **Since the month of April, XBB.1.9 variants represent half of the sequences retrieved within the program in the Geneva area.**
- **XBB 1.16 is progressively increasing in proportion since the end of May**

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 XBB.1.9 displaying two additional mutations (G1819S, T4175I).

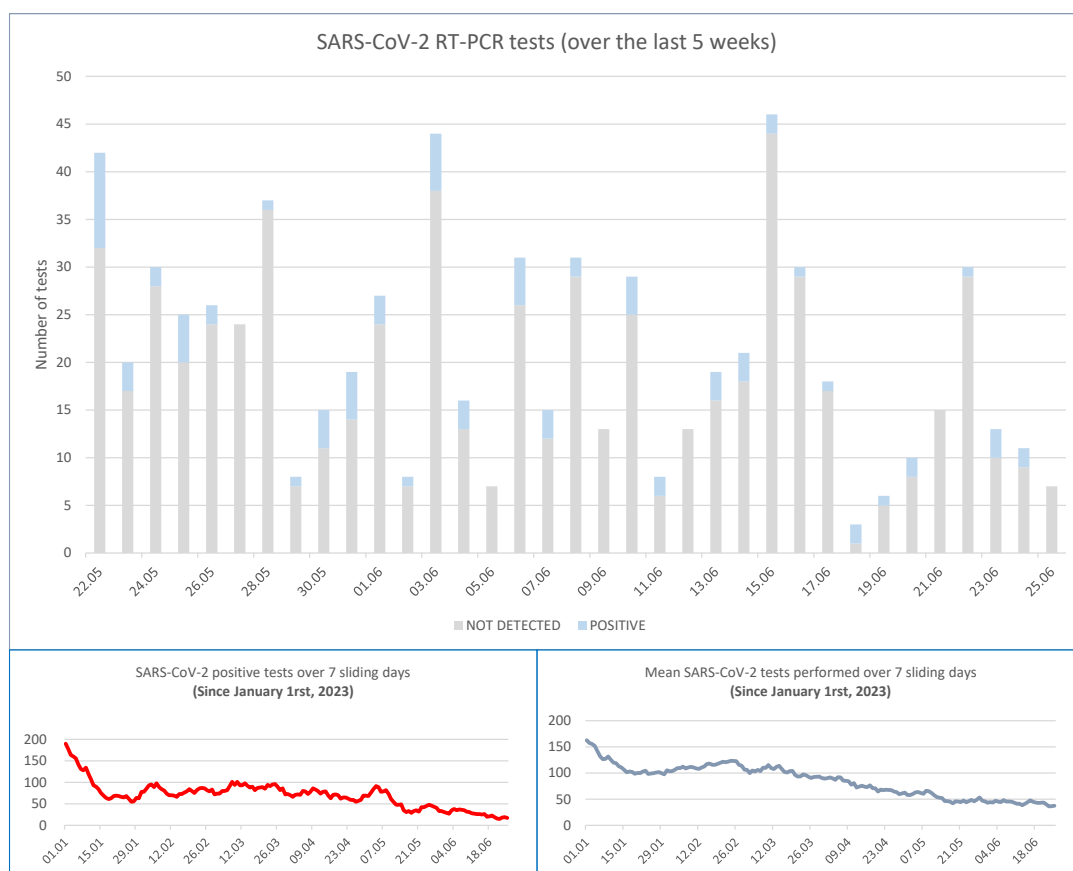


Figure 1: Number of SARS-CoV-2 tests performed at the HUG laboratory of virology (per day). Positive tests are displayed in light blue (top). Bottom left: SARS-CoV-2 positive tests over 7 sliding days. Bottom right: mean SARS-CoV-2 tests performed over 7 sliding days.

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 81% (316/391), 76% (289/381), 88% (305/347) of the total number of tests performed in the canton of Geneva during weeks 22, 23, 24 and 25 of 2023, respectively. Roughly 81% (38/47), 80% (28/35), 60% (21/31) of the positive specimens collected in the Geneva area were processed at HUG during weeks 22, 23, 24 and 25, 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 \(admin.ch\)](https://www.bfs.admin.ch/bfs/fr/home/actualites/actualites-2023/actualites-2023-06-01.html)).

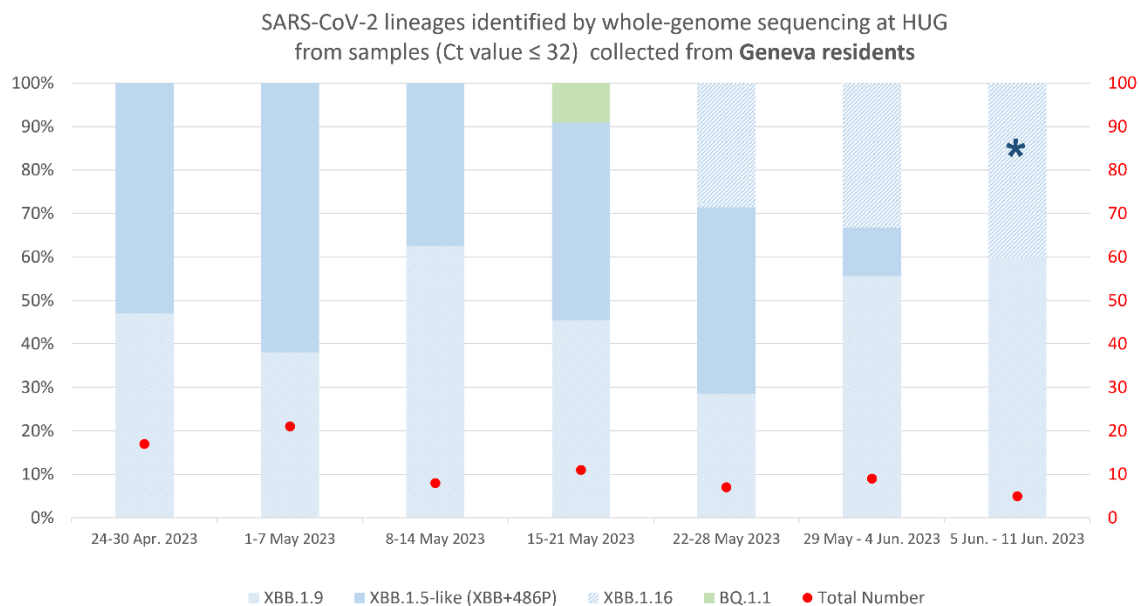


Figure 2: SARS-CoV-2 lineages identified by whole-genome sequencing at HUG from samples (Ct-value ≤ 32) collected from Geneva residents (*Sentinella* specimens excluded). *Sequencing is still ongoing for week 23. A total of 78 sequences were included in this analysis. Note that sequencing has been shifted towards hospitalized patients since the beginning of 2023.

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.

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Geraldine Duc for the Geneva Cantonal Physician team.