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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 biweekly 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:

- The number of tests done at our laboratory tends to stabilize at low levels since mid-January. There has been a slight decrease in the positivity rate since mid-March (Figure 1).
- Hospitalization rates at the HUG are stable at low levels since mid-January. For more information, please refer to the weekly CH-SUR report.
- For weeks 10 and 11 only 23 and 13 samples from Geneva residents were sequenced, respectively. Results from the 11th week will be completed with the following report.
- XBB.1.5-like variants represented 19/23 and 11/13 samples in weeks 10 and 11, respectively. Considering all samples sequenced in Switzerland since the beginning of February, XBB.1.5-like variants have progressively replaced the previously circulating BQ.1 sub-lineages.
- Such replacement of BQ.1 by XBB sublineages is also observed in the wastewater-based surveillance*.
- No XBB.1.16 sequence was identified.

More information:

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

*Information from <https://bsse.ethz.ch/cbg/research/computational-virology/sarscov2-variants-wastewater-surveillance.html>

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).

¹Can Yue et al. Enhanced transmissibility of XBB.1.5 is contributed by both strong ACE2 binding and antibody evasion. biorxiv.org

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 transmissibility¹.

Figure 1: Total number of SARS-CoV-2 tests performed at the HUG per day and over 30 days (PCR and antigenic tests). The mean positivity rate over 7 sliding days is displayed as a red curve. **Middle:** SARS-CoV-2 positive tests over 7 sliding days. **Bottom:** mean SARS-CoV-2 tests performed over 7 sliding days.

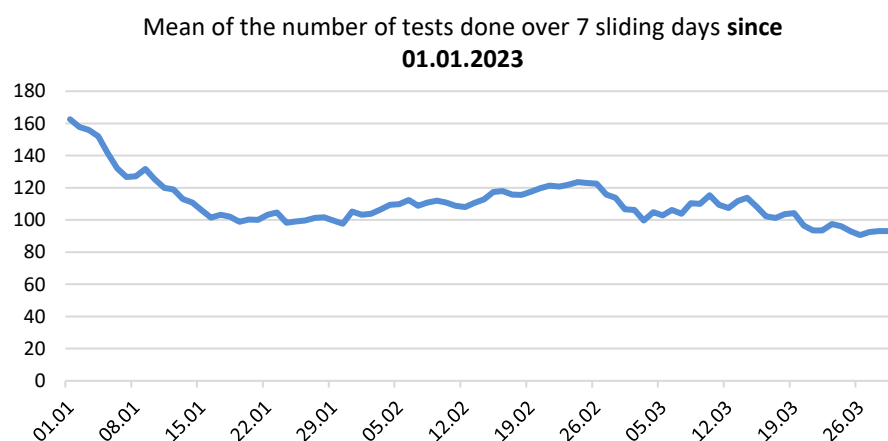
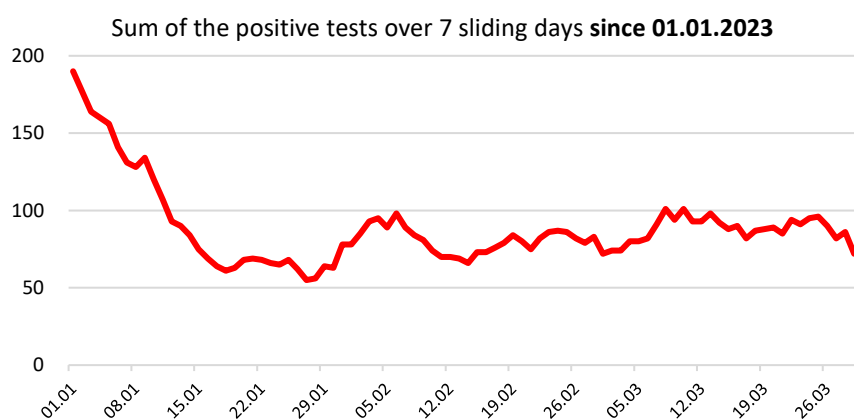
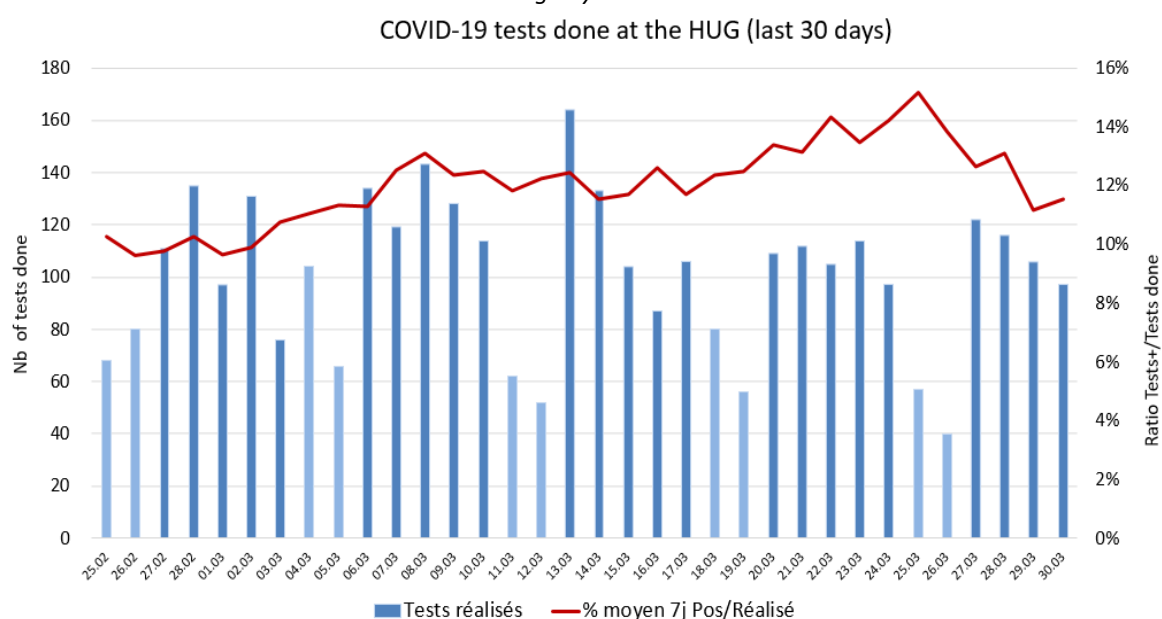


Figure 2: SARS-CoV-2 lineages identified by whole-genome sequencing at HUG from samples (Ct-value ≤ 32) collected from Geneva residents (*Sentinella specimens excluded*). A total of 145 sequences were included in this analysis.



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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 66% (659/1001), and 70% (642/921) of the total number of tests performed in the canton of Geneva during weeks 11 and 12 of 2023, respectively. Roughly 77% (93/121) and 75% (88/118) of the positive specimens collected in the Geneva area were processed at HUG during weeks 11 and 12, 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/covid-19/covid-19-suisse-coronavirus-dashboard-admin.ch)).

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](https://epi.scope.ge.ch)) for epidemiological data.