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Geneva Centre for  
Emerging Viral Diseases

Division of Infectious  
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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 increase in the positivity rate since the beginning of 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 9 and 10 only 28 and 9 samples from Geneva residents were sequenced, respectively. Results from the 10<sup>th</sup> week will be completed with the following report.
- XBB.1.5-like variants represented 21/28 and 6/9 samples in weeks 9 and 10, 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\*.

### **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>

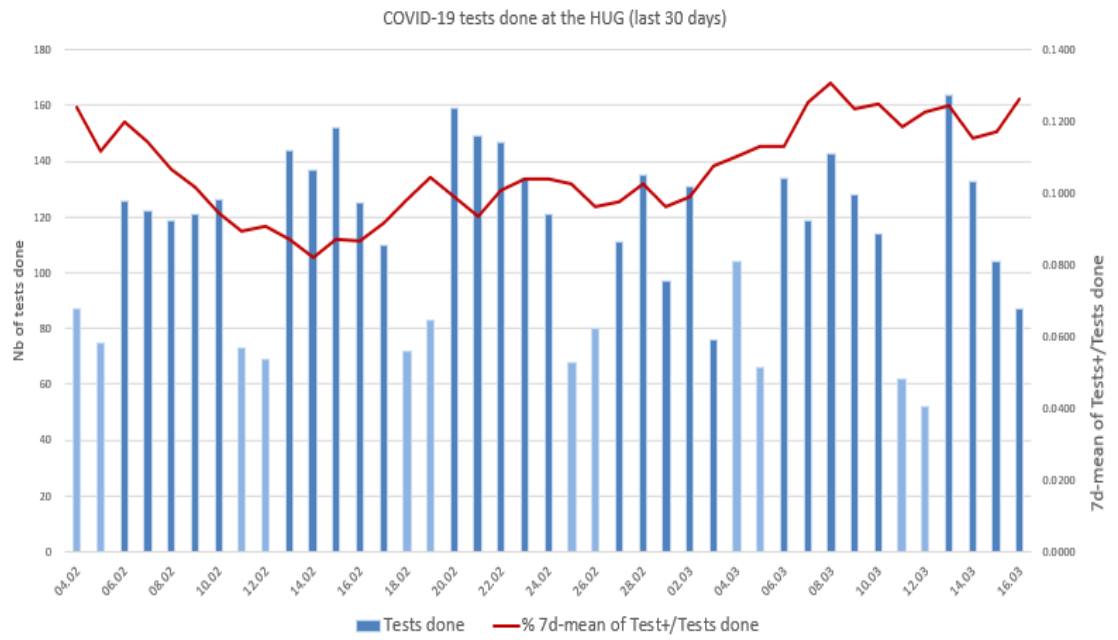
\*Information from <https://bsse.ethz.ch/cbg/research/computational-virology/sarscov2-variants-wastewater-surveillance.html>

**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).

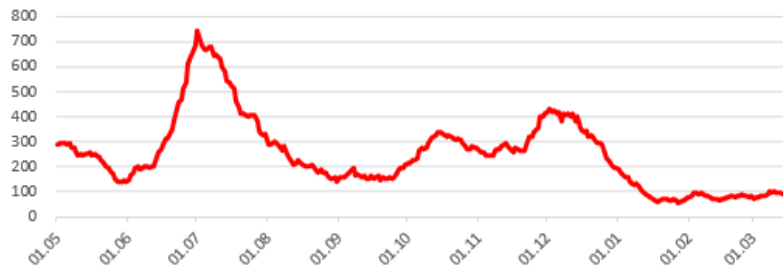
**XBB.1.5-like** These sublineages additionally acquired a mutation on the spike protein (486P) that increases its affinity to ACE-2 in vitro and therefore likely its transmissibility<sup>1</sup>.

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

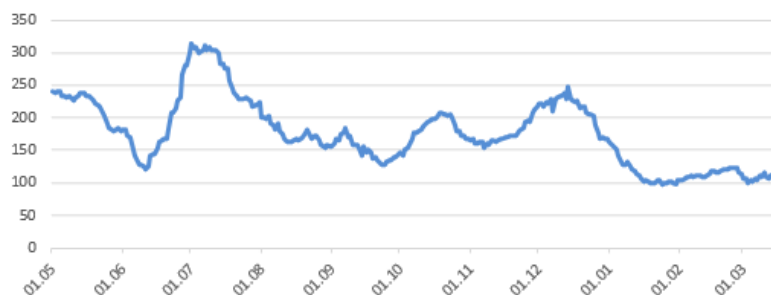
**Figure 1:** Total number of SARS-CoV-2 tests performed at the HUG per day and over 30 days (PCR and antigenic tests). The mean positivity rate over 7 sliding days is displayed as a red curve. **Middle:** SARS-CoV-2 positive tests over 7 sliding days. **Bottom:** mean SARS-CoV-2 tests performed over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



Sum of the positive tests over 7 sliding days since 01.05.2022



Mean of the number of tests done over 7 sliding days since 01.05.2022



**Figure 2:** SARS-CoV-2 lineages identified by whole-genome sequencing at HUG from samples (Ct-value  $\leq 32$ ) collected from Geneva residents (Sentinella specimens excluded). A total of 132 sequences were included in this analysis.



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Emma Hodcroft for the Geneva Center for Emerging Viral Diseases.  
Geraldine Duc, for the Geneva Cantonal Physician team.

### 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 69% (720/1048), and 74% (752/1020) of the total number of tests performed in the canton of Geneva during weeks 9 and 10 of 2023, respectively. Roughly 72% (80/111) and 68% (93/137) of the positive specimens collected in the Geneva area were processed at HUG during weeks 9 and 10, 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-2023-09-10.html)).

### 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  $\leq 32$ . 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://ge.ch)) for epidemiological data.