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Geneva, February 22, 2023

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

### Highlights:

- After an initial decrease in the positivity rate and the number of tests done in the first weeks of January and a slight increase end of January/beginning of February, numbers tend to stabilize at low levels (Figure 1).
- Hospitalization rates at the HUG are stable (n=40-50).
- 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.
- For weeks 5 and 6 only 15 and 5 samples from Geneva residents were sequenced, respectively. Results from the 6<sup>th</sup> week will be completed with the following report.
- **XBB.1.5** appeared in week 3, representing 3/7 samples, and 10/14 samples in week 4. However, in week 5 and 6, 10/15 and 3/5 samples were represented by **BQ1.18** sublineages. Please note that these data should be interpreted cautiously, as clusters in geriatric and long-term care facilities have been reported.
- In week 5, the **XBB.3** subvariant was identified in one sample.
- In the wastewater-based surveillance of SARS-CoV-2 variants in the Geneva area, the relative proportion increased to 57.5% for XBB sublineages and decreased to 23.5% for BQ.1.1-sublineages, which had been the predominant variant until the 2<sup>nd</sup> week of January.\*
- The presence of XBB sublineages in wastewater was found in all other collection sites across Switzerland.\*

### More information:

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

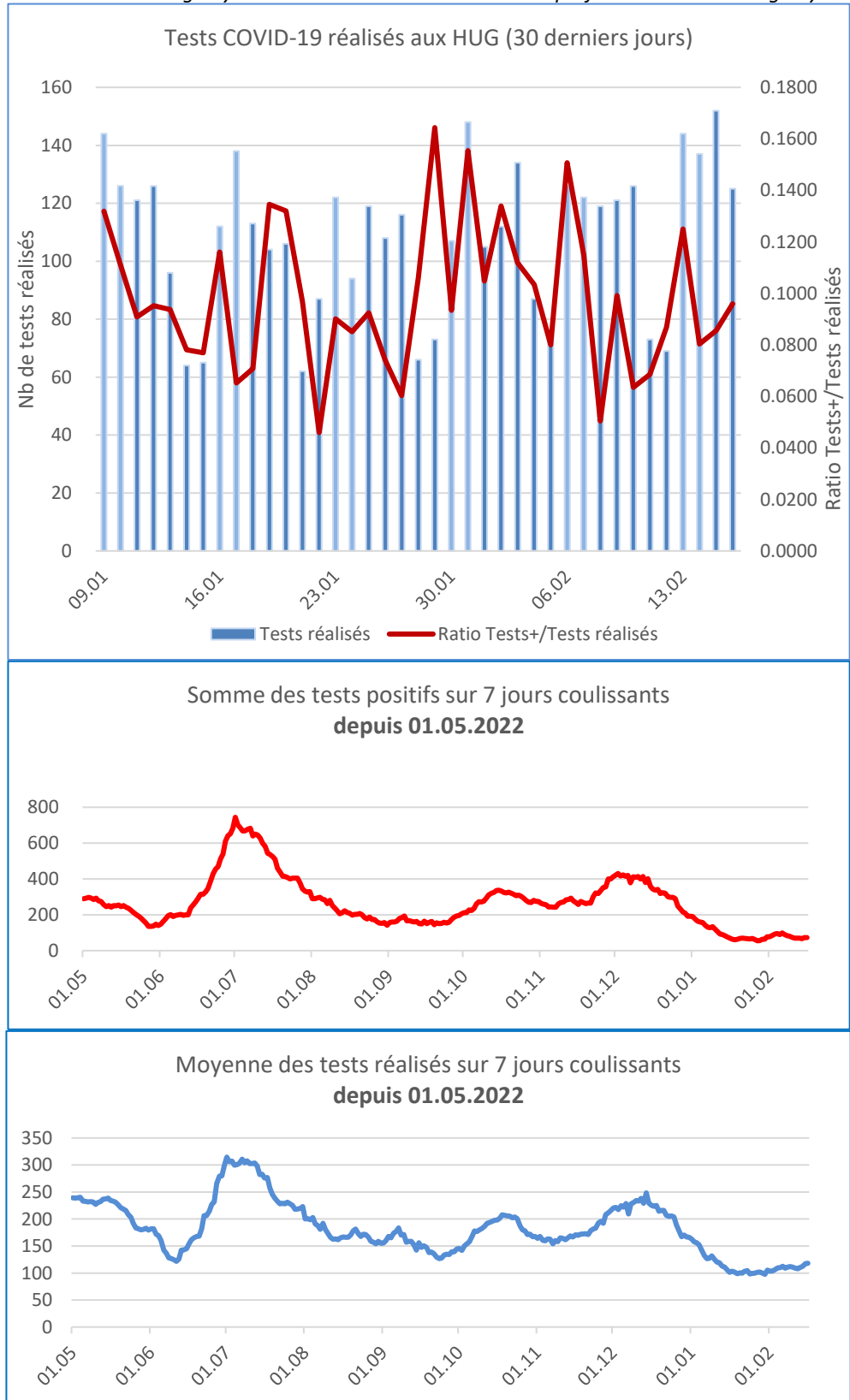
**XBB** is a recombinant of two Omicron sublineages : A BA.2 sublineage (BJ.1) and a BA.2.75 (BM.1.1.1) sublineage. Its breakpoint is located on the spike protein's RBD domain (Receptor Binding Domain).

**XBB.1.5** This sublineage 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>.

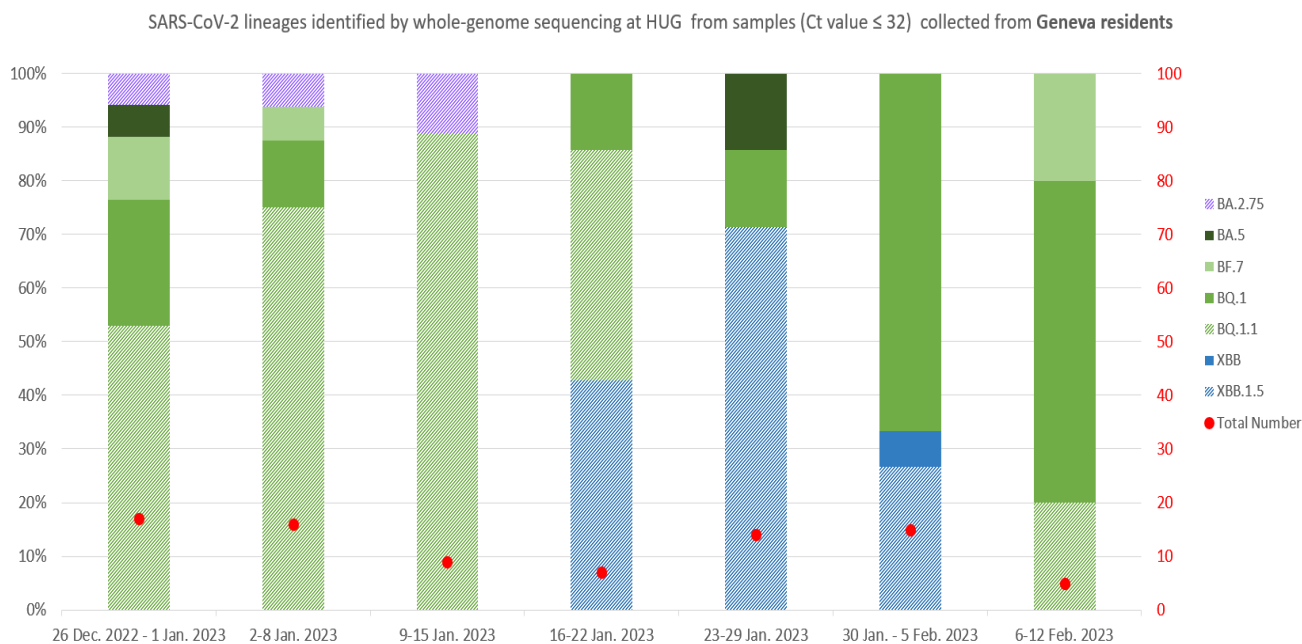
**XBB.3** This sublineage does not have the 486P mutation.

<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 positivity rate 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  $\leq 32$ ) collected from Geneva residents (Sentinella specimens excluded). A total of 157 sequences were included in this analysis. Please note the low sample number starting from Week 52 and reaching  $n=3$  on week 4 (samples from week 4 will be completed with the following report).



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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 **64.2%**(768/1196), and **68.6%**(756/1102) of the total number of tests performed in the canton of Geneva during weeks 5 and 6 of 2023, respectively. Roughly **74.2%**(89/120) and **77.8%**(70/99) of the positive specimens collected in the Geneva area were processed at HUG during weeks 5 and 6, 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-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  $\leq 32$ . 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 of 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 detailed 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. For epidemiological data, please refer to the report of the cantonal physician team.