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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 and the positivity rate continues to slowly but progressively decrease** since the beginning of the year. (Figure 1).
- **Hospitalization rates at the HUG are stable at low levels since mid-January.** Each week, between 5 and 15 patients are hospitalized directly due to a SARS-CoV-2 infection. For more information, please refer to the weekly CH-SUR report.
- **Most sequences identified on specimen collected since the end of February are XBB.1.5-like variants.** (Figure 2)
- **XBB.1.16** sequences have been identified in 2 samples in mid-April, but does not appear to be replacing XBB.1.5 yet in the Geneva area.

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.

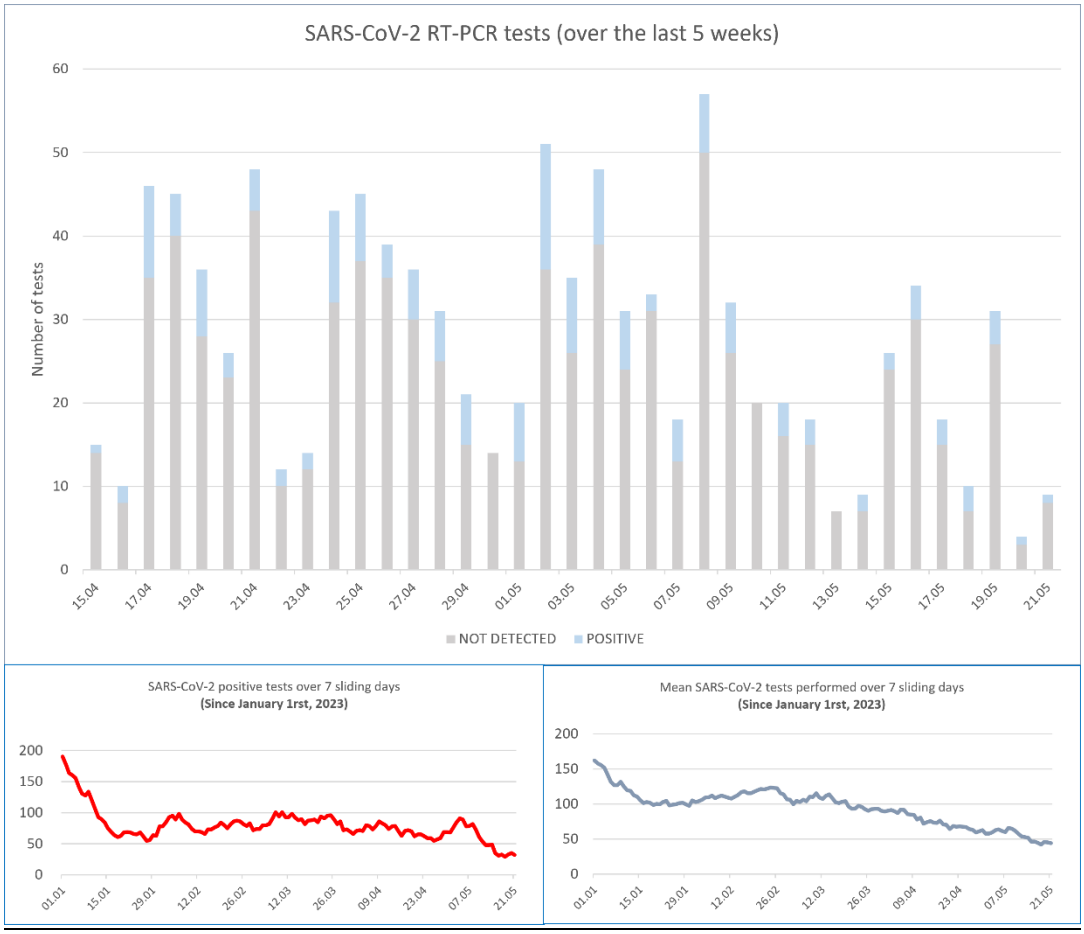

Figure 1: *Number of SARS-CoV-2 tests performed at the HUG laboratory of virology (per day). Positive tests are displayed in light blue (top). Bottom left: SARS-CoV-2 positive tests over 7 sliding days. Bottom right: mean SARS-CoV-2 tests performed over 7 sliding days.*

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 74**%** (421/569), and 76**%** (364/481) of the total number of tests performed in the canton of Geneva during weeks 18 and 19 of 2023, respectively. Roughly 77**%** (78/101) and 69**%** (49/71) of the positive specimens collected in the Geneva area were processed at HUG during weeks 18 and 19, 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)).

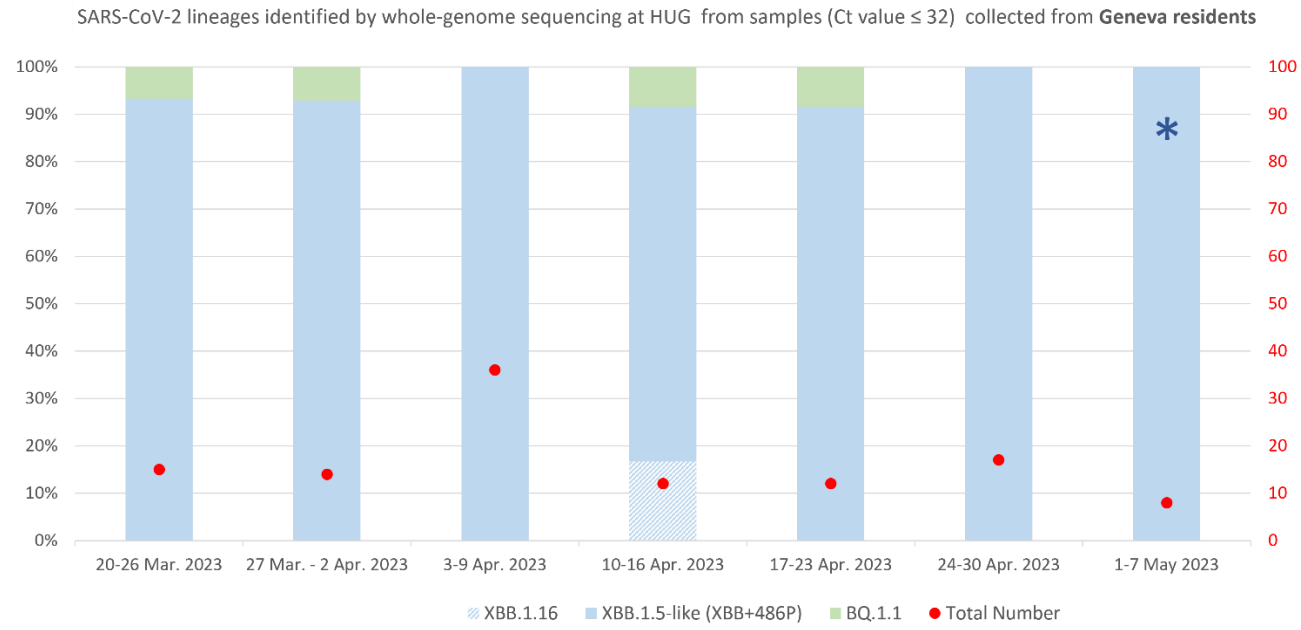

Figure 2: *SARS-CoV-2 lineages identified by whole-genome sequencing at HUG from samples (Ct-value ≤32) collected from Geneva residents (Sentinella specimens excluded). * Sequencing is still ongoing for week 18. A total of 114 sequences were included in this analysis. Note that sequencing has been shifted 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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Emma Hodcroft for the Geneva Center for Emerging Viral Diseases and University of Geneva.
Geraldine Duc for the Geneva Cantonal Physician team.