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Geneva Centre for
Emerging Viral Diseases

Division of Infectious
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**SARS-CoV-2 genomic surveillance in Geneva: monthly update
Weeks 4 - 9 2024**

Caveat: Data published by our laboratory might reveal some trends regarding local epidemiology. In terms of representability, this data should be interpreted cautiously due to possible cluster effects.

Highlights:

- The **number of positive tests** performed by our laboratory **continues to decrease** (Figure 1), with an absolute number of 28 positive specimen for week 9 of 2024. The positivity rate over 7 sliding days also fell below 5%.
- **With the decreasing number of positive tests, very few specimens were analyzed in the last 2 sequencing batches. They all were JN.1** (Figure 2). For more information, see (<https://cov-spectrum.org/stories/wastewater-in-switzerland>)

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>

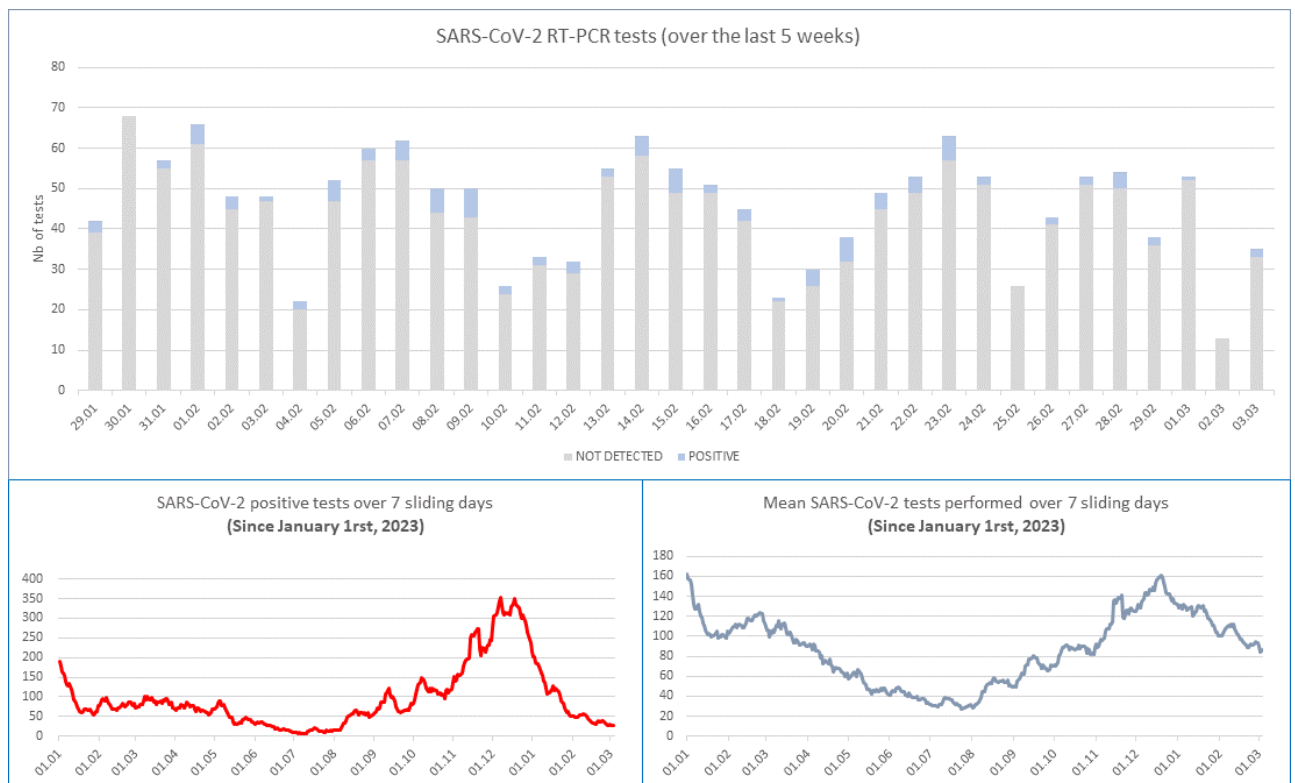


Figure 1: Number of SARS-CoV-2 tests performed at the HUG laboratory of virology (per day). Positive tests are displayed in light blue (top). Bottom left: SARS-CoV-2 positive tests over 7 sliding days. Bottom right: mean SARS-CoV-2 tests performed over 7 sliding days.

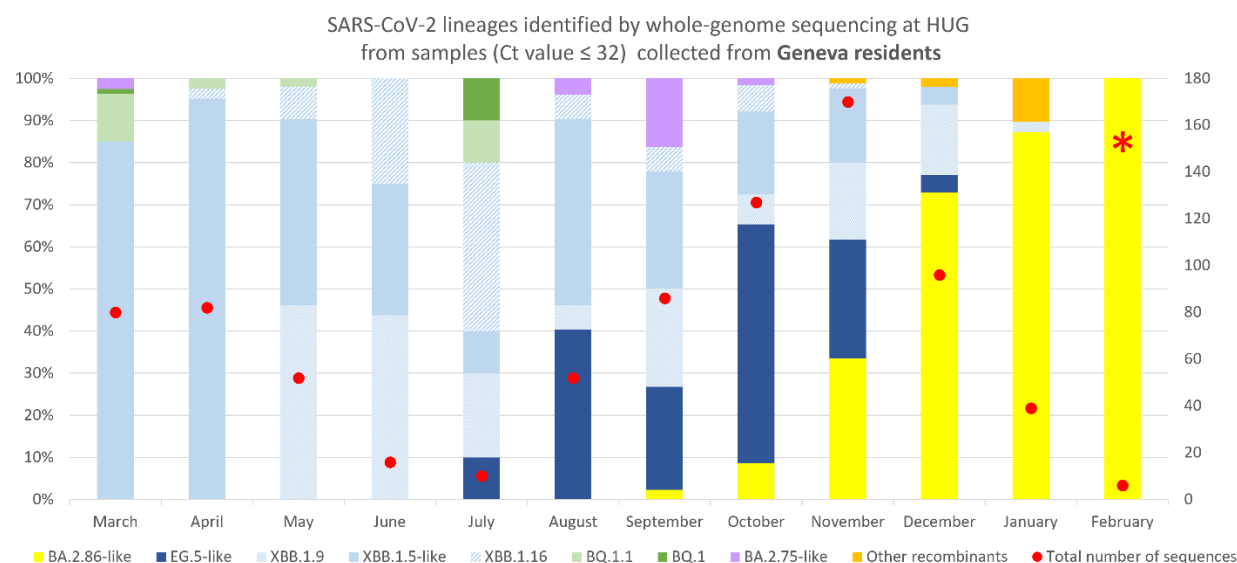


Figure 2: SARS-CoV-2 lineages identified by whole-genome sequencing at HUG from samples (Ct-value ≤32) collected from Geneva residents (*Sentinelia specimens excluded*). *Sequencing is still ongoing for the month of February. A total of 816 sequences were included in this analysis.

BQ.1 and BQ.1.1 (here depicted in green) are all BA.5 derivatives. EG.5-like variants are descendent lineages of XBB.1.9.2, which has the same spike amino acid profile as XBB.1.5. BA.2.86 is a highly divergent variant first identified in July 2023, carrying more than 30 different mutations in the Spike protein compared to the previous XBB lineages. JN.1, the most competitive of the BA.2.86 sublineages, displays an additional spike mutation (L455S).

The laboratory of virology of the Geneva University Hospitals as a sentinel site for the Geneva area

The number of SARS-CoV-2 RT-PCR tests performed at the Geneva University Hospitals (HUG) represented around 86% (782/914), 91% (659/728), and 91% (639/699) of the total number of tests performed in the canton of Geneva during weeks 6, 7 and 8 of 2024, respectively. Roughly 74% (50/68), 84% (31/37) and 95% (37/39) of the positive specimens collected in the Geneva area were processed at HUG during weeks 6, 7 and 8 of 2024, respectively. In addition, 28/668 specimens analyzed in our laboratory were positive during week 9 of 2024. 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](#).

Note that since January 1st, 2024, positive rapid antigenic tests are no longer mandatory to report to the health authorities.

Methods and collaborations

WGS is conducted in close collaboration with the Health 2030 Genome Center in Geneva. 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. Phylogenetic analysis data are produced by Nextstrain in collaboration with Richard Neher's group at the University of Basel. 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.