

Federal Office of Public Health FOPH
Public Health Directorate Communicable
Diseases Division
Schwarzenburgstrasse 157
3003 Berne
Switzerland

Geneva, December 13, 2023

Geneva Centre for
Emerging Viral Diseases

Division of Infectious
Diseases

Department of Medicine

Laboratory of virology

Division of Laboratory
Medicine

Diagnostic Department

SARS-CoV-2 genomic surveillance in Geneva: monthly update Weeks 46-49

Caveat: Data published by our laboratory might reveal some trends regarding local epidemiology but may not represent the situation well, as the number of available sequences has been low until mid-September 2023. 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 increase and reached 310 positives cases per week during week 49** (Figure 1). The mean positivity rate over 7 sliding days peaked at 42% at the end of week 48. Such numbers have not been observed since the last winter season. Note that the detection of other respiratory viruses, especially RSV (respiratory syncytial virus) is progressively increasing as well at our institution over the last 2 weeks. The detection of influenza remains low compared to previous seasons. (More information available at: <https://www.hug.ch/laboratoire-virologie/epidemiologie-virus-respiratoires>)
- **While several variants are co-circulating, EG.5-like sublineages are still the most identified variants** (Figure 2), however decreasing in frequency.
- **BA.2.86 and its derivative (such as JN.1) continue to progressively increase** in frequency and were identified in more than 1/3 of the sequences. Indeed, various JN sequences have been retrieved in the last sequencing batch, with JN.1 being the most frequent (Table 1). Of note, JN.1 is depicted to increase in the wastewater surveillance data (<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>

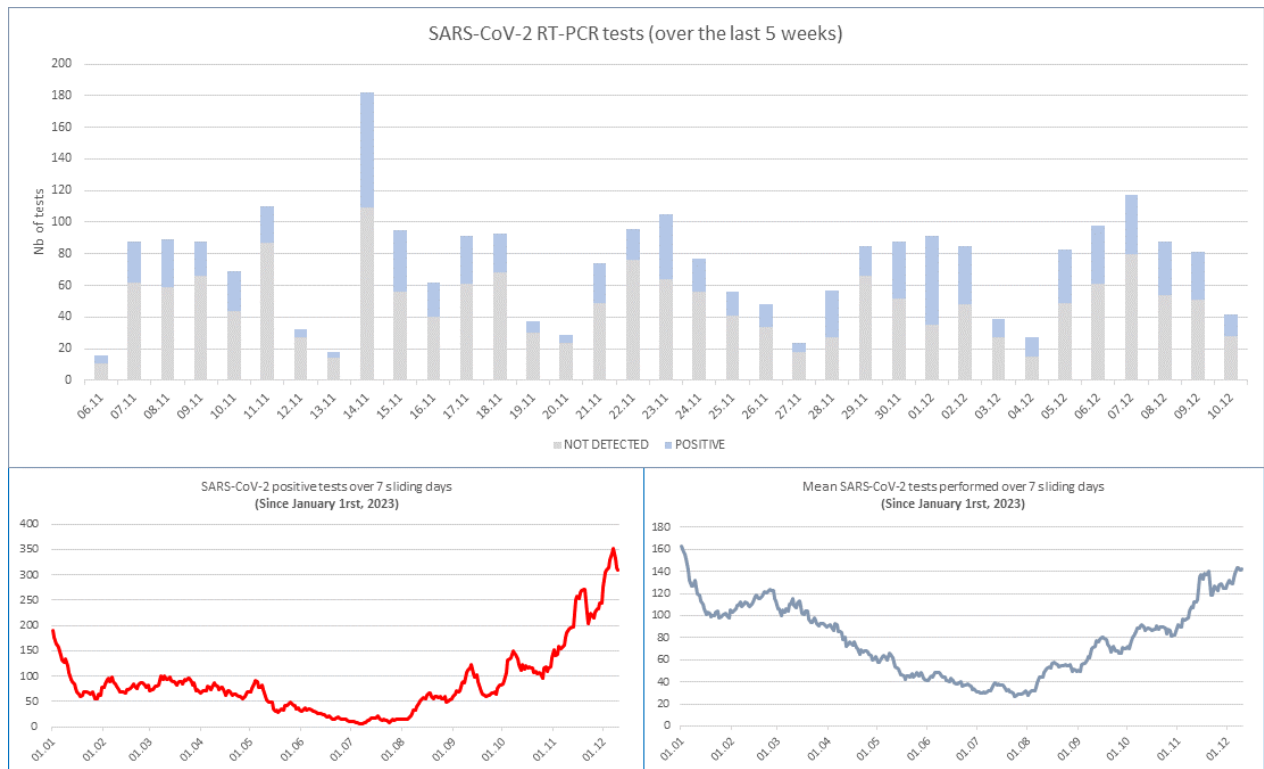


Figure 1: Number of SARS-CoV-2 tests performed at the HUG laboratory of virology (per day). Positive tests are displayed in light blue (top). Bottom left: SARS-CoV-2 positive tests over 7 sliding days. Bottom right: mean SARS-CoV-2 tests performed over 7 sliding days.

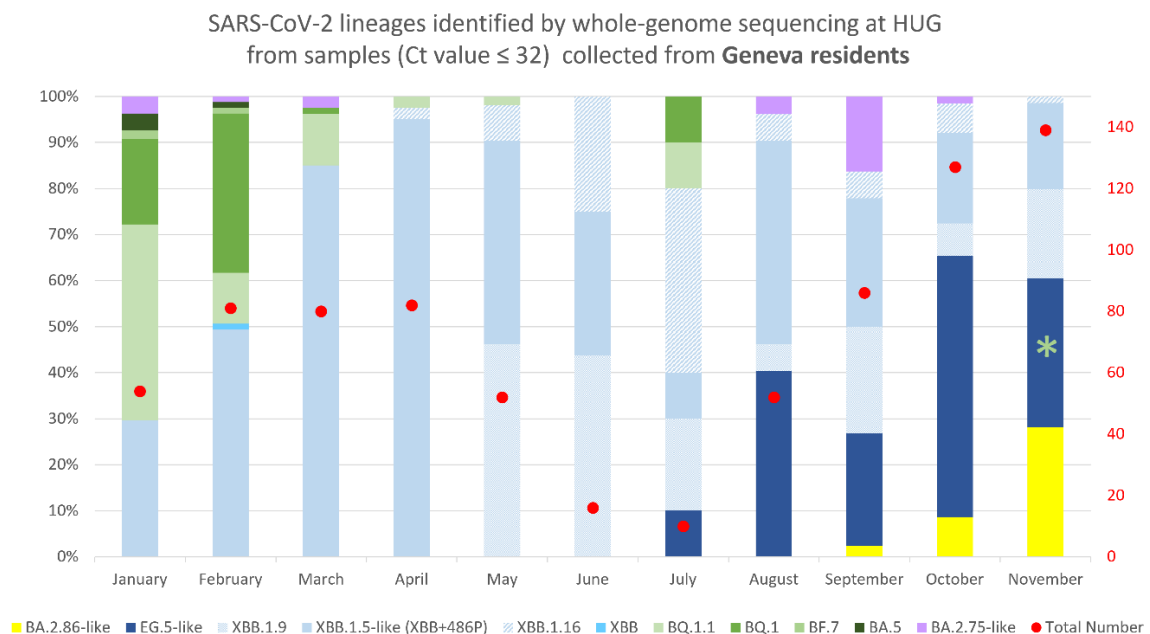


Figure 2: SARS-CoV-2 lineages identified by whole-genome sequencing at HUG from samples (Ct-value ≤ 32) collected from Geneva residents (Sentinella specimens excluded). *Sequencing is still ongoing for the month of November. A total of 779 sequences were included in this analysis.

BQ.1, BQ.1.1 and BF.7 (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 than the circulating XBB lineages. JN.1, the most competitive of the BA.2.86 sublineages, displays an additional spike mutation (L455S).

Table 1: Details of the BA.2.86 sublineages retrieved since the end of October.

	BA.2.86	BA.2.86.1	JN.1	JN.2	JN.3	JN.5
Week 44	1	1	2	1	0	1
Week 45	0	3	2	0	1	5
Week 46	0	7	3	1	0	0
Week 47	0	2	8	0	1	0
Week 48	0	0	1	0	0	0

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 83% (867/1045), 80% (892/1112), 43% (910/2119) of the total number of tests performed in the canton of Geneva during weeks 46, 47, and 48 of 2023, respectively. Roughly 88% (272/310), 66% (226/342), 62% (309/498) of the positive specimens collected in the Geneva area were processed at HUG during weeks 46, 47 and 48, respectively. In addition, 310/994 specimen were analyzed in our laboratory were positive during week 49. 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](#).

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. 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://www.episcope.ch)) for epidemiological data.

Laurent Kaiser, Samuel Cordey, Manuel Schibler, Erik Boehm, Francisco Perez Rodriguez and Pauline Vetter for the HUG and the Geneva Centre for Emerging Viral Diseases.

Geraldine Duc for the Geneva Cantonal Physician team.