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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 42-45

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 **progressively increased since mid-October and reached almost 200 positives cases per week during week 45** (Figure 1). The mean positivity rate over 7 sliding days followed the same trend and was above 20% during week 45. Such numbers have not been observed since the last winter season, when XBBs replaced previously circulating BA.5 derivatives.
- **In parallel, the number of patients hospitalized with a positive SARS-CoV-2 test is slowly but progressively increasing, staying however at a low level, compared to previous seasons.** For more information, please refer to the weekly CH-SUR report.
- **While several variants are co-circulating, EG.5-like sequences are identified in half of the specimens** (Figure 2); this is in line with the national wastewater surveillance data (<https://cov-spectrum.org/stories/wastewater-in-switzerland>).
- **BA.2.86 is progressively increasing** in frequency during the month of October and represented around 9% of the sequences. Note that no JN.1 has yet been identified in clinical specimen.
- The number of sequences carrying the “FLip” mutations, arising on various backgrounds, continues its slow but steady growth worldwide (Figure 3), and was present in 50% of the sequences collected since the beginning of October in the canton of Geneva (data originating from GISAID).

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>

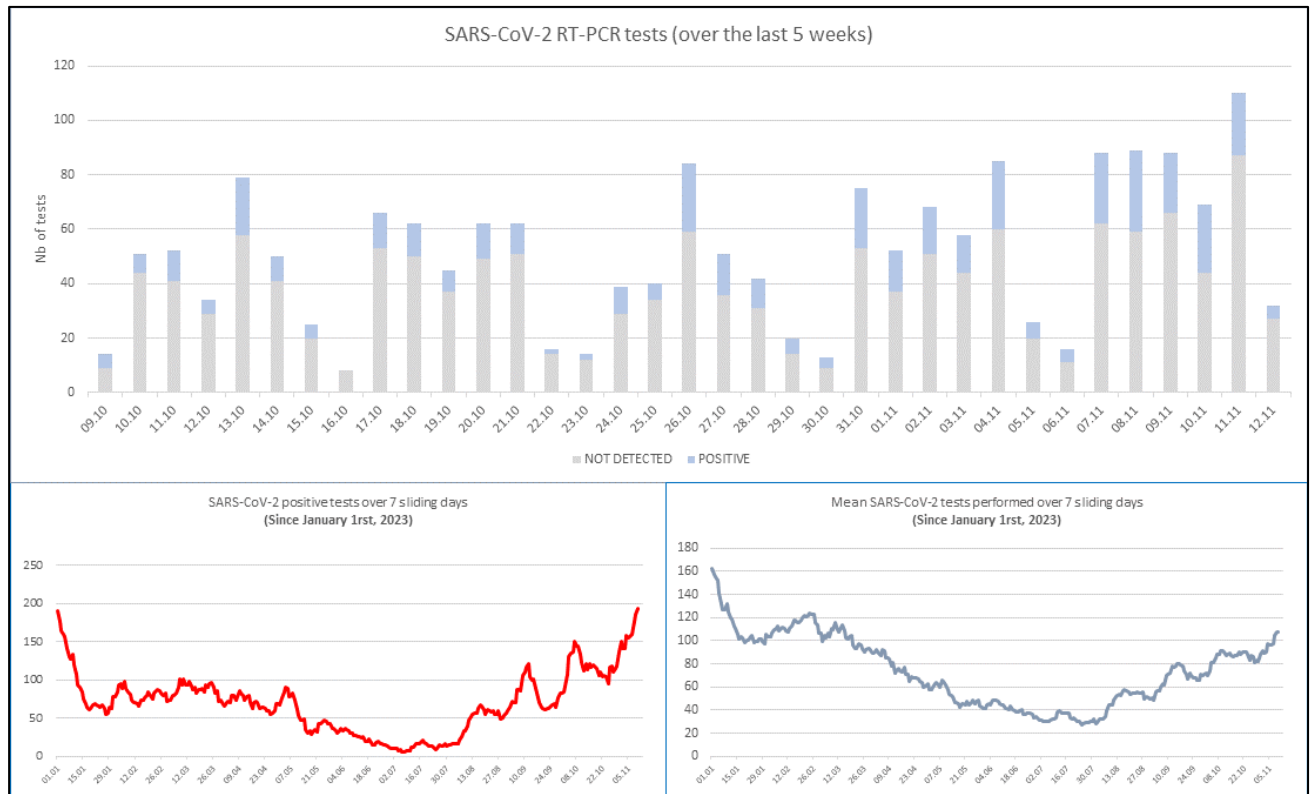


Figure 1: Number of SARS-CoV-2 tests performed at the HUG laboratory of virology (per day). Positive tests are displayed in light blue (top). Bottom left: SARS-CoV-2 positive tests over 7 sliding days. Bottom right: mean SARS-CoV-2 tests performed over 7 sliding days.

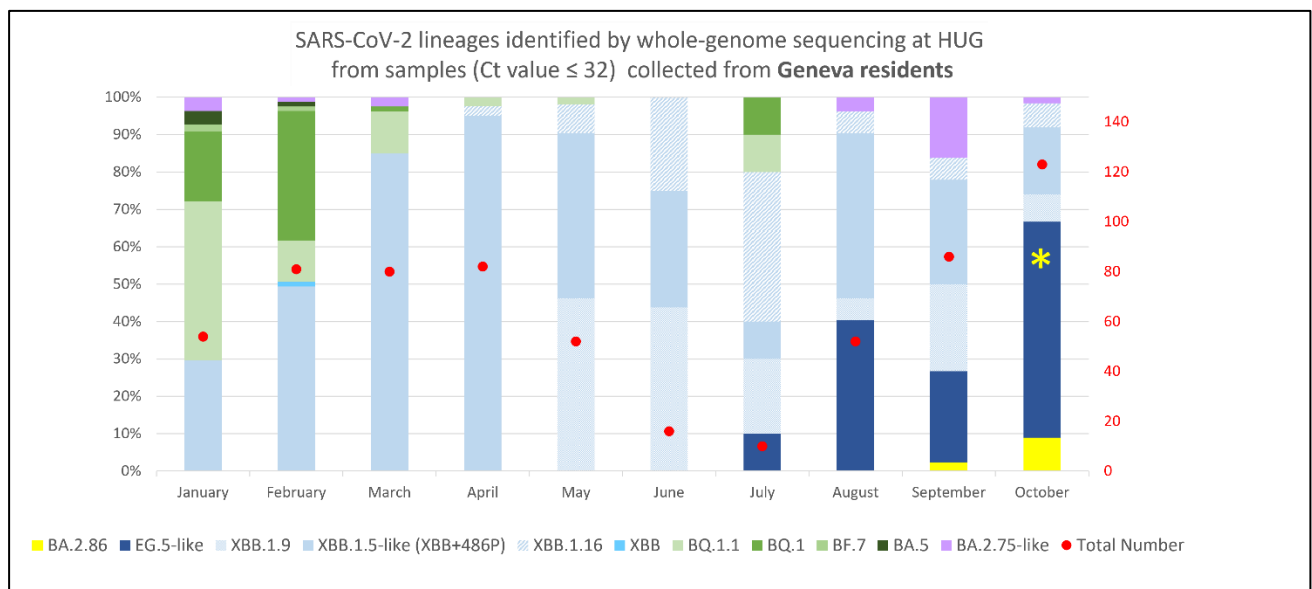


Figure 2: SARS-CoV-2 lineages identified by whole-genome sequencing at HUG from samples (Ct-value ≤32) collected from Geneva residents (*Sentinella* specimens excluded). *Sequencing is still ongoing for the month of October. A total of 636 sequences were included in this analysis.

Note that 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).

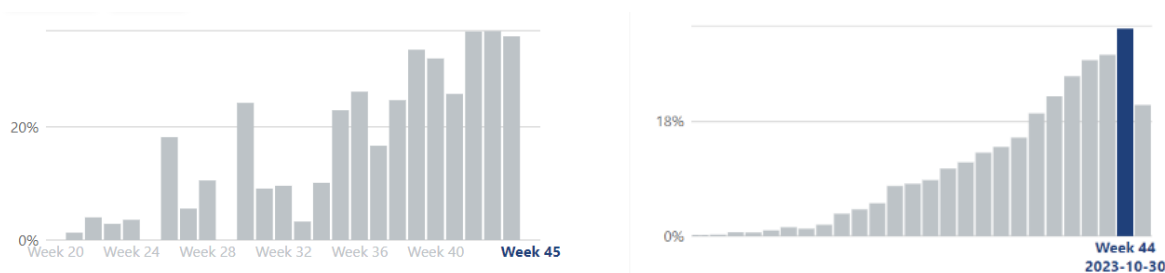


Figure 3: Proportion of the sequences carrying the “FLip” mutations (L455F and F456L) in Switzerland (left panel) and Europe (right panel). Constructed with CoVSpectrum, navigation available at <https://cov-spectrum.org/explore/Switzerland/AllSamples/Post5M>.

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% (630/846), 80% (579/726), 82% (672/818) of the total number of tests performed in the canton of Geneva during weeks 42, 43, 44 and 45 of 2023, respectively. Roughly 54% (105/193), 69% (115/166), 84% (155/185) of the positive specimens collected in the Geneva area were processed at HUG during weeks 42, 43 and 44, respectively. In addition, 196/787 specimen were analyzed in our laboratory were positive during week 45. 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) for epidemiological data.

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Geraldine Duc for the Geneva Cantonal Physician team.