



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

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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: bi-weekly update

Highlights:

- We observe a relative stability with a mild tendency of decrease of the number of positive tests and of the overall positivity rate over the last two weeks (Figure 1).
- BA.5 sublineage remains the most prevalent in the Geneva area during weeks 42-43.

BQ.1 and BQ.1.1 have been detected among hospitalized cases (Figure 2). The prevalence of BQ.1.1 is increasing. However, the high prevalence reported by WGS during week 41 is overestimated as a result of a large intra-hospital cluster (the surveillance program prioritizes hospitalized patients) and probably does not reflect that observed yet in the community at the same time.

- During week 42, BF.7 sublineage has been detected in nearly 10% of the analyzed samples.

Important: There is a clear and present danger that all available monoclonal antibodies available in Switzerland will soon be ineffective against the majority of circulating variants. In particular, the current increase in BQ.1.1 is of concern as it will likely be dominant in Switzerland by the end of the year.

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.

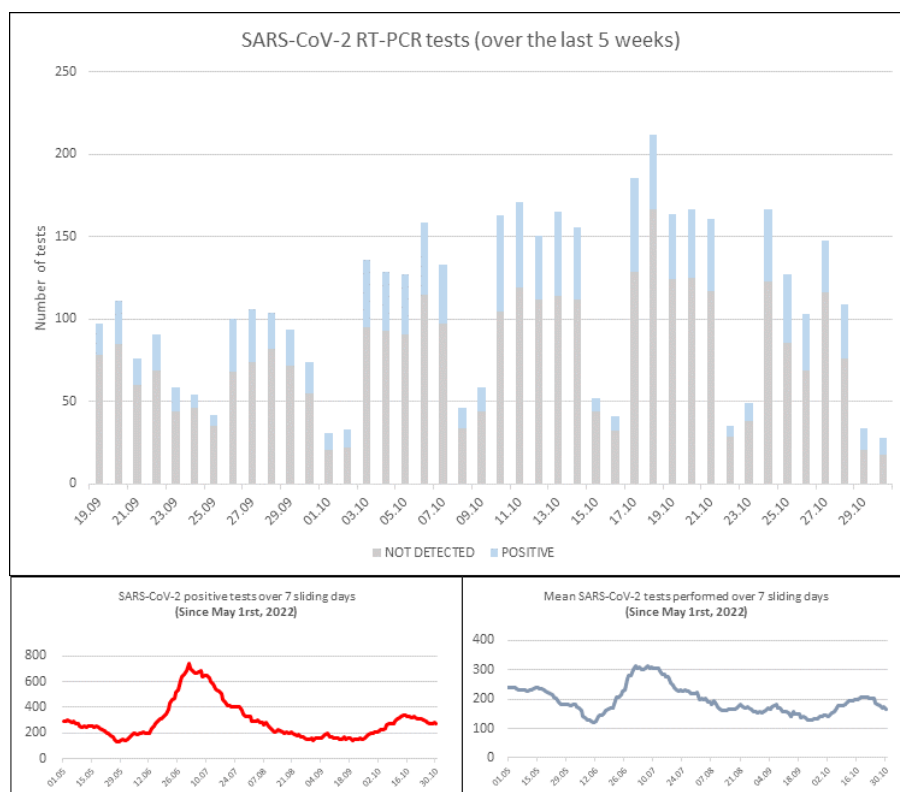
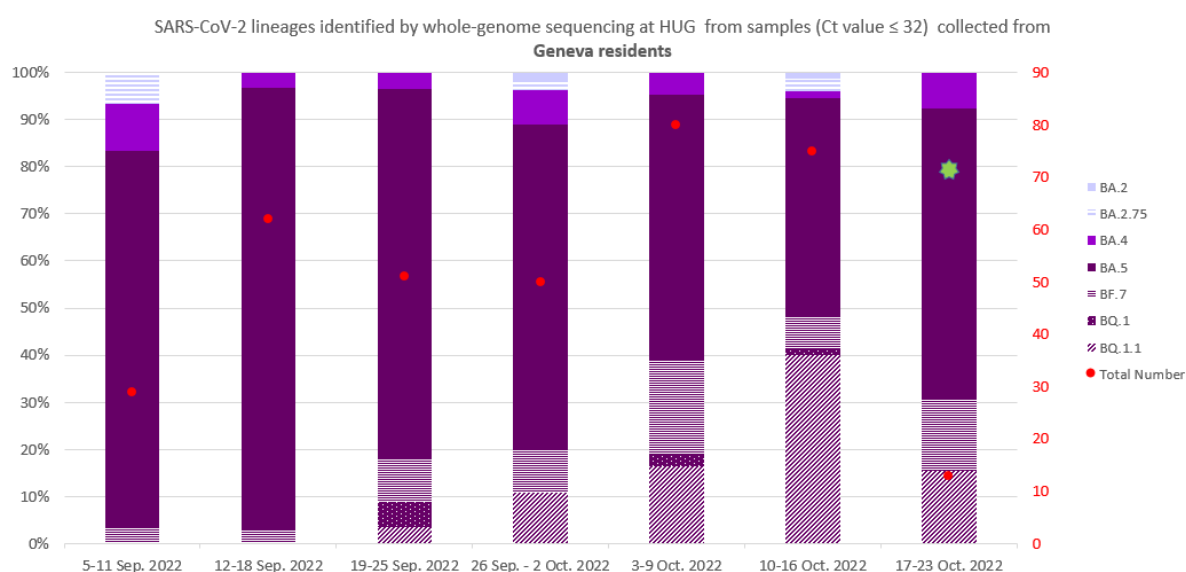


Figure 2: SARS-CoV-2 lineages identified by whole-genome sequencing at HUG from samples (Ct -value ≤ 32) collected from Geneva residents (*Sentinella* specimens excluded). *Sequencing is still ongoing for week 42 (from October 17 to October 23, 2022). A total of 360 sequences were included in this analysis.



Laurent Kaiser, Samuel Cordey, Manuel Schibler, Ioannis Evgenidis and Pauline Vetter for HUG and the Geneva Center for Emerging Viral Diseases.

Emma Hodcroft for the Geneva Center for Emerging Viral Diseases.

Pauline Brindel 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 29.5% (1428 /4833) and 32.5% (1170 /3605) of the total number of tests performed in the canton of Geneva during weeks 42 and 43 of 2022, respectively. Roughly 22% and 25% of the positive specimens collected in the Geneva area were processed at HUG during weeks 42 and 43 (310 /1385 and 275 /1118), respectively. Samples collected from symptomatic individuals at our outpatient testing center are tested by RT-PCR. Specimens analyzed in our laboratory originate from ambulatory and hospitalized patients as well as symptomatic and/or asymptomatic health care workers.

The number of positive tests in the canton and the total number of tests done during the surveilled weeks are available on the website from Federal Office of Public Health ([COVID- 19 Suisse | Coronavirus | Dashboard \(admin.ch\)](https://www.bfs.admin.ch/bfs/fr/topics/santite/infec/coronavirus/covid-19/suisse/covid-19-suisse-dashboard-admin)).

During weeks 42 and 43 in the canton of Geneva, a decrease was observed for the number of RT-PCR tests and the number of positive tests compared to the two previous weeks. The proportion of positive tests was stable. .

Methods and collaborations

The laboratory has reintroduced from week 37 the screening for the “S Drop out” (Taqpath RT-PCR assay) in order to monitor BA.2.75. Considering the low prevalence of BA.2.75 variant in the Geneva area (Figure 2), S Drop out screening has been stopped from week 42.

WGS is carried out 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 is ongoing in Switzerland since March 1, 2021 and includes specimens collected at 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 Center of Emerging Viral Diseases and 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.