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Geneva, November 17, 2022

Geneva Centre for
Emerging Viral Diseases

Division of Infectious
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SARS-CoV-2 genomic surveillance in Geneva: bi-weekly update

Highlights:

- We observe a relative stability with a mild tendency of increase of the number of positive tests and of the overall positivity rate over the last two weeks (Figure 1).
- Although BQ.1/BQ.1.1 almost reach a prevalence of 50%, others BA.5 sublineages remain the most prevalent in the Geneva area during weeks 44-45 (Figure 2).

Important:

The laboratory has introduced from week 45 the screening of the S:346T mutation (one series/week). Series from weeks 45 and 46 showed prevalences of 54.4 (43/79) and 63.2% (55/87), respectively. It is important to note that the presence of this mutation is not restricted to BQ.1/BQ.1.1 and is also reported in others lineages.

Importantly, this mutation is linked to abolition in neutralization *in vitro* by all currently available monoclonal available in Switzerland. In other words, there is a clear signal that these antibody-based treatments, including cilgavimab, will soon be completely ineffective. 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.

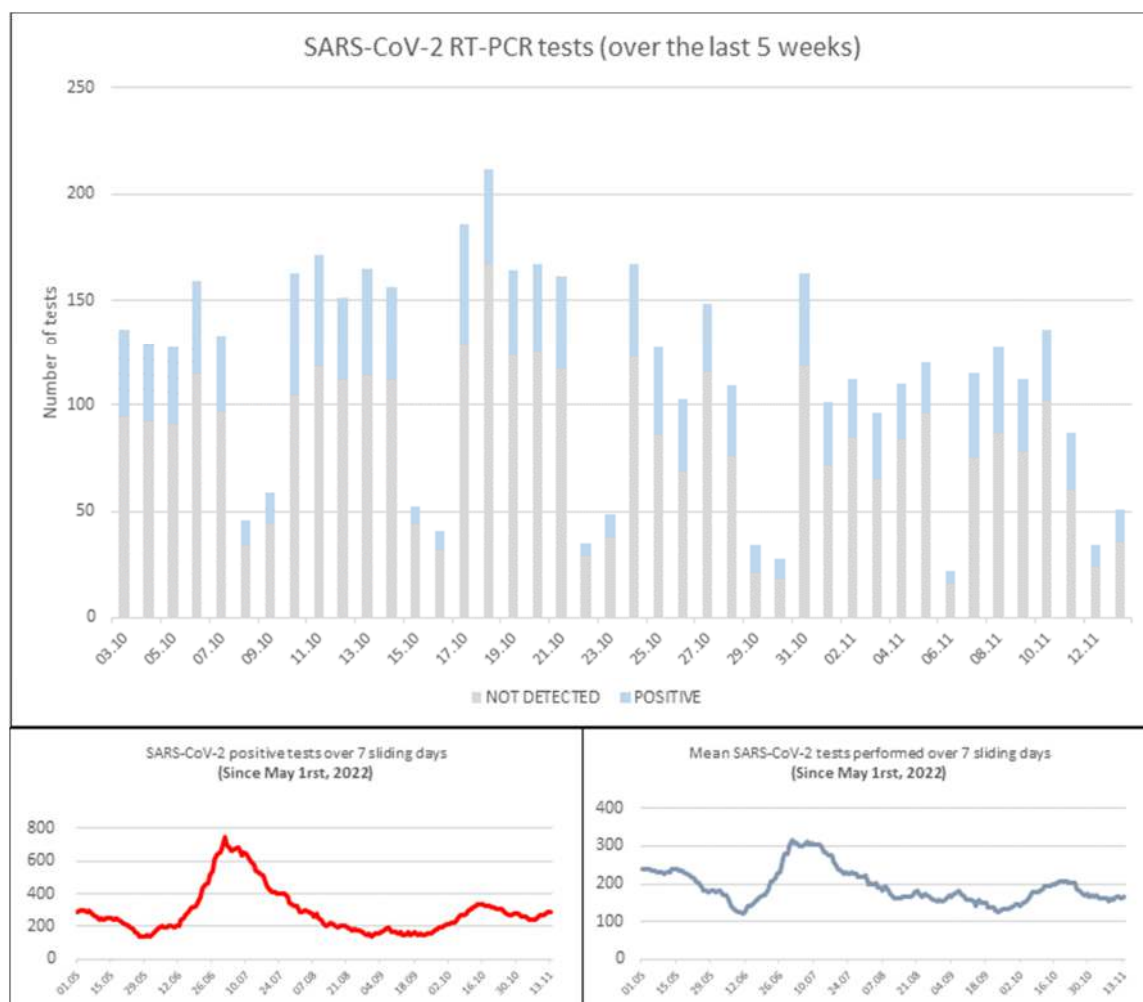
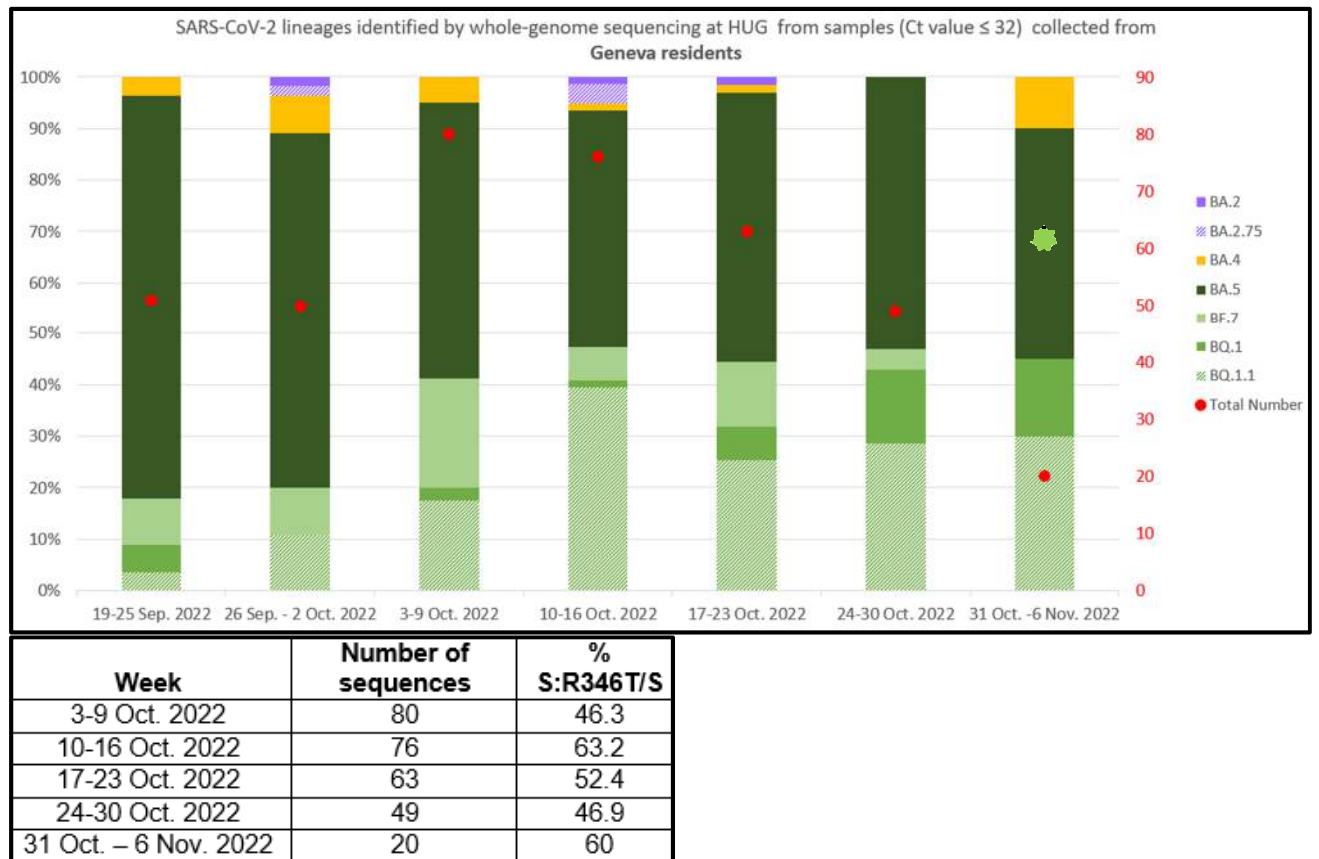


Figure 2: SARS-CoV-2 lineages identified by whole-genome sequencing at HUG from samples (Ct-value ≤32) collected from Geneva residents (Sentinella specimens excluded). A total of 389 sequences were included in this analysis. **Bottom Left:** Percentage of SARS-CoV-2 sequenced samples with the S:R346T/S.

*To be noted that sequencing is still ongoing for week 44 (from October 30 to November 6, 2022).



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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 32% (1137 /3555) and 31% (1158 /3693) of the total number of tests performed in the canton of Geneva during weeks 44 and 45 of 2022, respectively. Roughly 24% and 25% of the positive specimens collected in the Geneva area were processed at HUG during weeks 44 and 45 (243/1004 and 292/1161), 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.admin.ch/gov/de/section/04601/index.html)).

During weeks 44 and 45 in the canton of Geneva, the number of RT-PCR tests and the proportion of positive tests remained stable. The number of confirmed cases also seems so stabilize.

Methods and collaborations

Of note, the laboratory has introduced from week 45 the screening of the S:346T mutation using the SARS Spike R346T kit (TIB Molbiol).

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.