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Geneva Centre for  
Emerging Viral Diseases

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## SARS-CoV-2 genomic surveillance in Geneva: bi-weekly update

### Highlights:

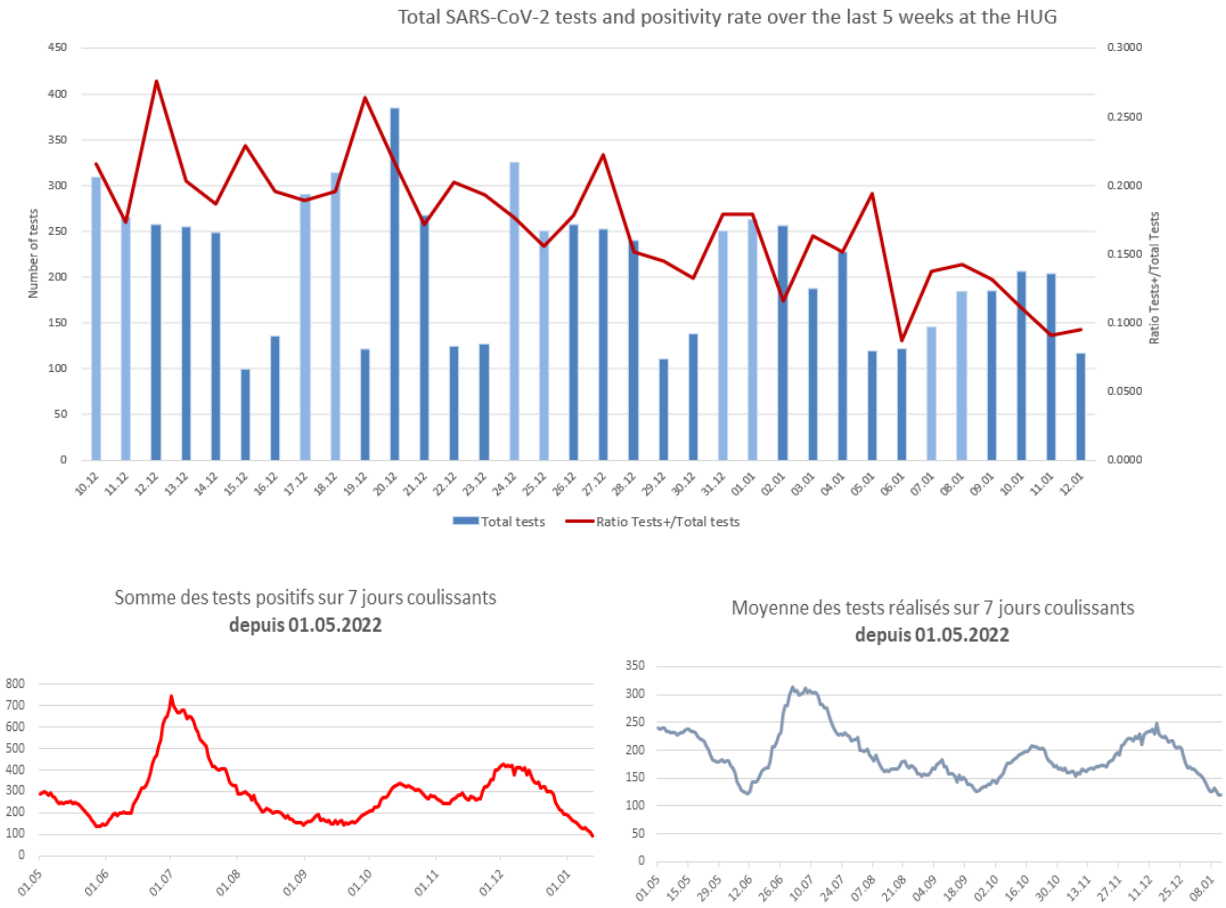
- In the last weeks of December, we have seen a decrease in the number of tests done and a decrease in the positivity rate (Figure 1).
- Starting 1 January 2023, only 30 samples will be sequenced weekly in the Geneva region. Statistics and trends published by our laboratory biweekly might give some hints about the local epidemiology but are not representative.
- **BQ.1/BQ.1.1** sublineages still represent most of the sequenced samples, though they might have reached their peak.
- **No XBB.1.5** sublineages were found in the sequences of week 50, 51 and 52.
- **BA.2.75** sublineages represent less than 10% of the sequenced samples.
- The proportion of SARS-CoV2 samples with the 346T mutation continues to increase to more than 80% in week 52, 2022 and week 1, 2023. (Figure 3)\*

### More information \*:

Since week 45/2022, the laboratory has introduced the screening of the S:346T mutation (one batch per week; one batch usually contains samples from the week before). The prevalence of the 346T mutation has been increasing: batch 49 (78.7%), 50 (79.6%), 51 (87.1%), 52 (83.9%), 1 (92.6%).

This mutation, among others, is found on several Omicron sub-variants, and is phenotypically associated with immune escape, notably regarding mAb treatments.

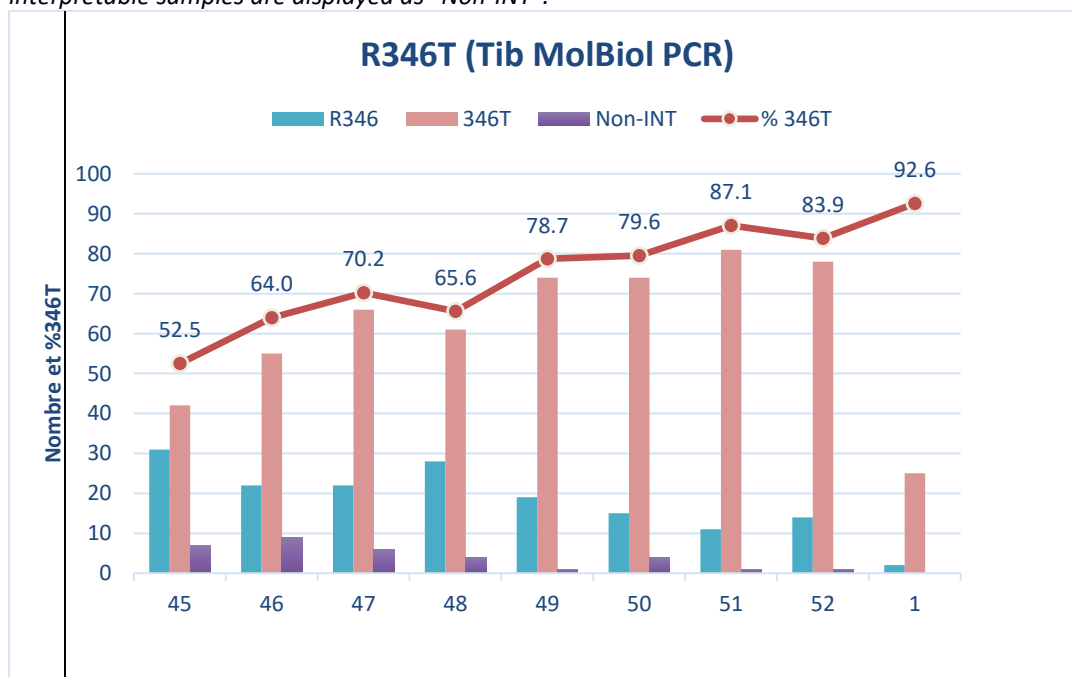
**Figure 1:** Total number of SARS-CoV-2 tests performed at the HUG per day and over 5 weeks (PCR and antigenic tests). The positivity rate is displayed as a red curve. **Bottom left:** SARS-CoV-2 positive tests over 7 sliding days. **Bottom right:** mean SARS-CoV-2 tests performed over 7 sliding days.



**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 440 sequences were included in this analysis. **Bottom Left:** Percentage of SARS-CoV-2 sequenced samples with the S:R346T/S.



**Figure 3:** Number and proportion of SARS-CoV-2 screened samples with and without the 346T mutation. Non-interpretable samples are displayed as "Non-INT".



Laurent Kaiser, Samuel Cordey, Manuel Schibler, Miguel Carvalho, Yerly Sabine and Iris Najjar for the HUG and the Geneva Centre for Emerging Viral Diseases.  
 Emma Hodcroft for the Geneva Center for Emerging Viral Diseases.  
 Geraldine Duc, 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 **31%**(1327/4317), **35%**(1426/4051), and **49%**(1138/2332) of the total number of tests performed in the canton of Geneva during weeks 50, 51 and 52 of 2022, respectively. Roughly **27%**(342/1262), **29%**(289/1002) and **43%**(190/444) of the positive specimens collected in the Geneva area were processed at HUG during weeks 50, 51 and 52, respectively. Specimens analyzed at the HUG originate from ambulatory and hospitalized patients and symptomatic and/or asymptomatic healthcare 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 of the Federal Office of Public Health ([COVID-19 Suisse | Coronavirus | Dashboard \(admin.ch\)](#)).

During weeks 50, 51, and 52 in the canton of Geneva, the total number of RT-PCR tests, confirmed cases, and positivity rate **decreased** compared to the previous weeks.

### **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 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  $\leq 32$ . 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 Centre of Emerging Viral Diseases and the 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.