Hôpitaux Universitaires Genève

REPUBLIQUE ET CANTON DE GENEVE
Département de la sécurité, de la population et de la santé
Direction générale de la santé
Service du médecin cantonal

UNIVERSITÉ DE GENÈVE
FACULTÉ DE MÉDECINE

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

Geneva, December 14, 2021

N/réf : PV/LK

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: weekly update

The laboratory of virology of the Geneva University Hospitals as a sentinel site for the Geneva area

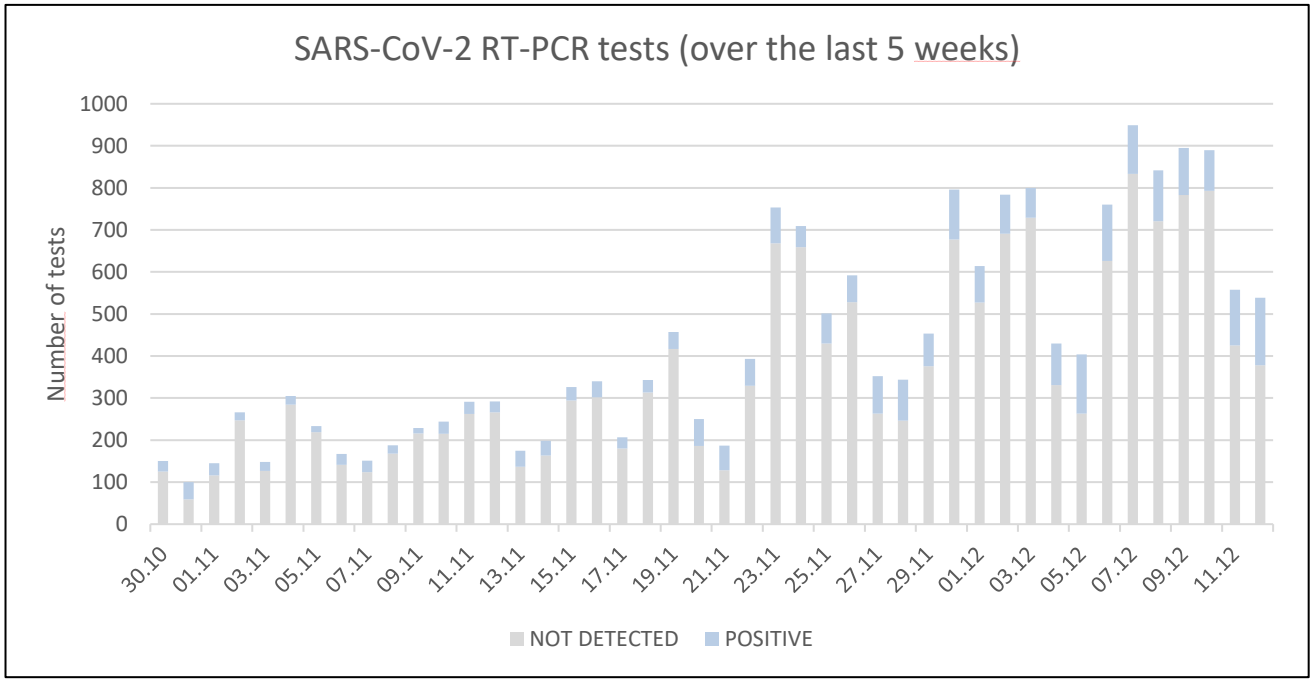
The number of tests (PCR and antigen tests) performed at the laboratory of virology of the Geneva University Hospitals represents around 19% of the total number of tests performed in the canton of Geneva during week 49 (6815/35078). **Roughly ¼** (24%) **of the positive specimens collected in the Geneva area were processed at HUG** (973/4062) **during week 49**. Tests performed at our outpatient testing center are either PCR-based or antigen-based. Most symptomatic patients are screened by RT-PCR and all positive antigen-based tests are confirmed by PCR, allowing screening for variants.
The number of positive tests in the canton and the total number of tests done during the surveilled week are derived from the website of the Direction Générale de la Santé in Geneva (available at https://infocovid.smc.unige.ch/), accessed December 13, at 14:20.

Methods and collaborations

Screening for the “S drop out” was implemented at HUG on SARS-CoV-2 positive specimens with Ct value < 32 tested for primary diagnostic in our laboratory on November 28. All positive specimen are tested for the S drop out since December 1, 2021.

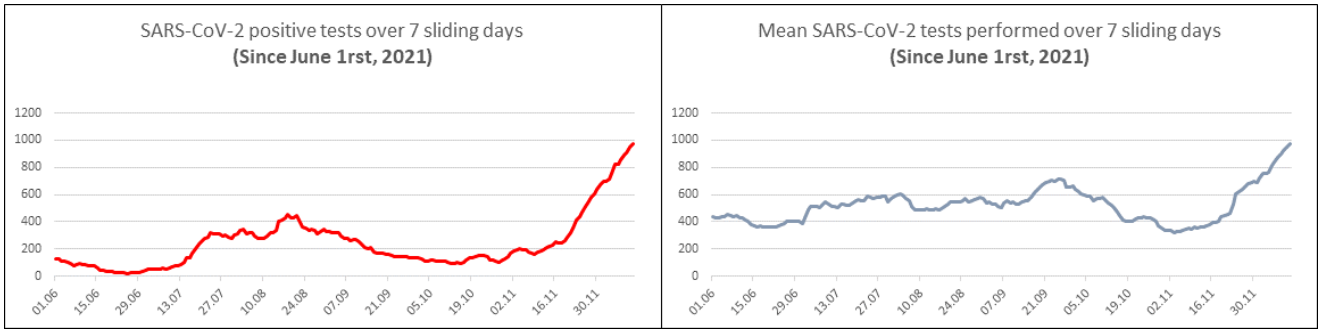
WGS is carried out in close collaboration with the Health 2030 Genome Center in Geneva and Philippe Le Mercier from the Swiss Institute of Bioinformatics. Since March 1, 2021, the sequencing has been done within the Swiss national SARS-CoV-2 genomic and variants surveillance program. Specimens collected at HUG with a Ct value ≤32 are sequenced. 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 detailed number of available sequences over time in the canton of Geneva is 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 and post-vaccination infections (see below).



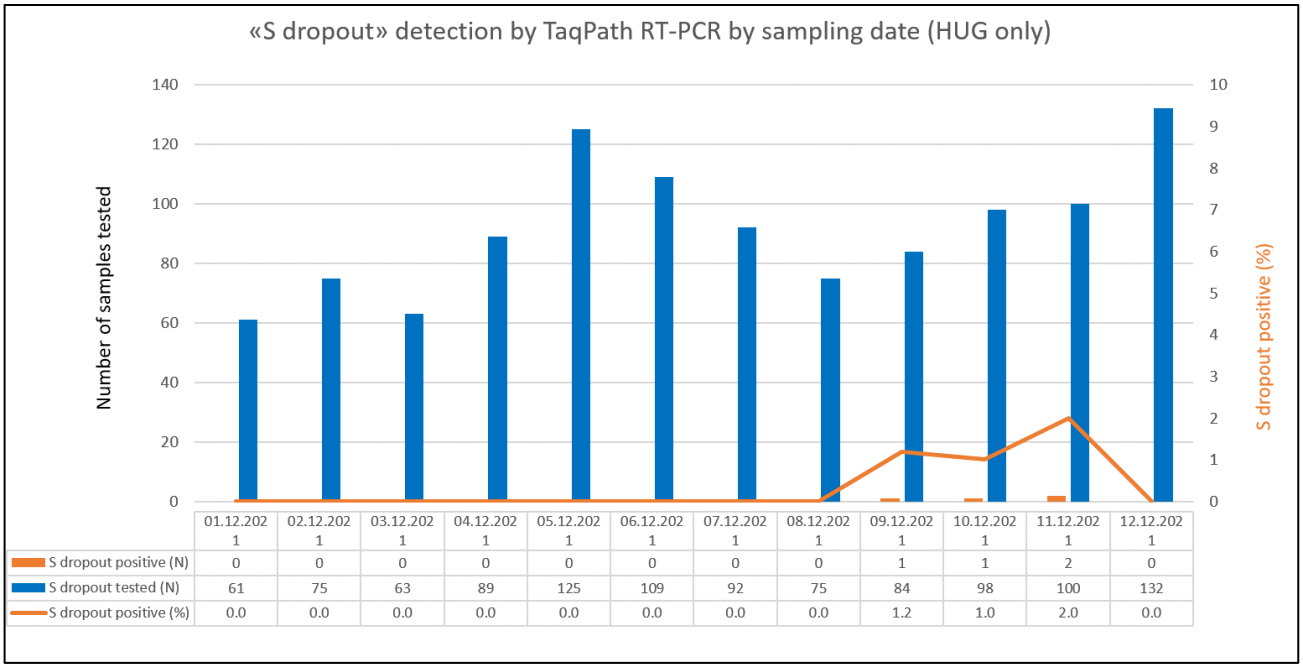
During week 49, the **absolute number of positive SARS-CoV-2 tests increased to approach a 1 000, a 30% increase from week 48**, while the mean positivity rate over 7 sliding days remained stable at a high level around 14%.

Similarly, at our **outpatient symptomatic testing center**, the **mean positivity rate continued to increase and reached 29% on average**.



Screening for the "S drop out" as a proxy for the Omicron B.1.1.529 variant

1. Screening for the "S drop out" as a proxy for the Omicron B.1.1.529 variant among SARS-COV-2 positive samples collected from patients tested for primary diagnosis in our laboratory.



	01.12.2021	02.12.2021	03.12.2021	04.12.2021	05.12.2021	06.12.2021	07.12.2021	08.12.2021	09.12.2021	10.12.2021	11.12.2021	12.12.2021
S dropout positive (N)	0	0	0	0	0	0	0	0	1	1	2	0
S dropout tested (N)	61	75	63	89	125	109	92	75	84	98	100	132
S dropout positive (%)	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	1.2	1.0	2.0	0.0

Specimens tested for the "S Drop out" at HUG, tested at our laboratory for primary diagnostic.

The screening for the "S drop out" by an additional RT-PCR (TaqPath, Thermofisher) was implemented at HUG on November 27, and is systematically performed on all positive specimens, with Ct values <32, tested for primary diagnostic since December 1, 2021.
In addition, this additional RT-PCR test is performed at the request of the cantonal physician team on positive specimens tested in other laboratories and sent to HUG. In order to have a reproducible denominator to be used as sentinel surveillance, additional positive tests are not depicted in this graph.

Since the beginning of the systematic screening for the S Drop out on **December 1** until Sunday 12, 2021 included, **a total of 4 specimens collected at HUG were positive for the S Drop out. All were collected at our outpatient department.**

2. S drop out screening performed at the request of the cantonal physician team, in specimen tested outside of our laboratory for primary diagnosis and/or collected in non-Geneva residents

Thirteen additional specimens, collected from non-Geneva residents (n=5) or sent to our laboratory for S Drop out screening at the request of the cantonal physician team because of epidemiological link (n=8) **have been tested positive**. **The first positive specimen was collected on November 22.**

A total of 17 specimens tested positive for the S Drop out since November 22.

Confirmation by partial S gene Sanger sequencing

All the positive "S Drop out" specimens were confirmed to be Omicron when technically possible (ie: when Ct value is < 30) by partial S Sanger sequencing (n=10/14). 3 positive samples collected at the end of week 49 will be sequenced by Sanger during this week.

Epidemiological data (provided by the cantonal physician team)

All samples identified as Omicron over week 47 and 48 were epidemiologically linked to travel (see report of week 48).
Similarly, **all new cases identified during week 49 for whom data is available (5/8) are linked to travel** or to someone who traveled.

Among new samples identified during week 49:

- 2 had travelled to South Africa. These travelers were fully vaccinated (second dose in June and December respectively), did not travel together and were not related to the other imported cases that were described in our previous reports.
- A third case, partially vaccinated (October 2021), was also imported and had close contact abroad with a symptomatic traveler from South Africa.
- The fourth case is a fully vaccinated person who did not travel and who is a family member of the third case.
- Lastly, one case is a Geneva resident, partially vaccinated with 1 dose, who is a family member of an imported case of S-drop out from South Africa (described in the report of week 48).

Update on B.1.1.529: the Omicron variant

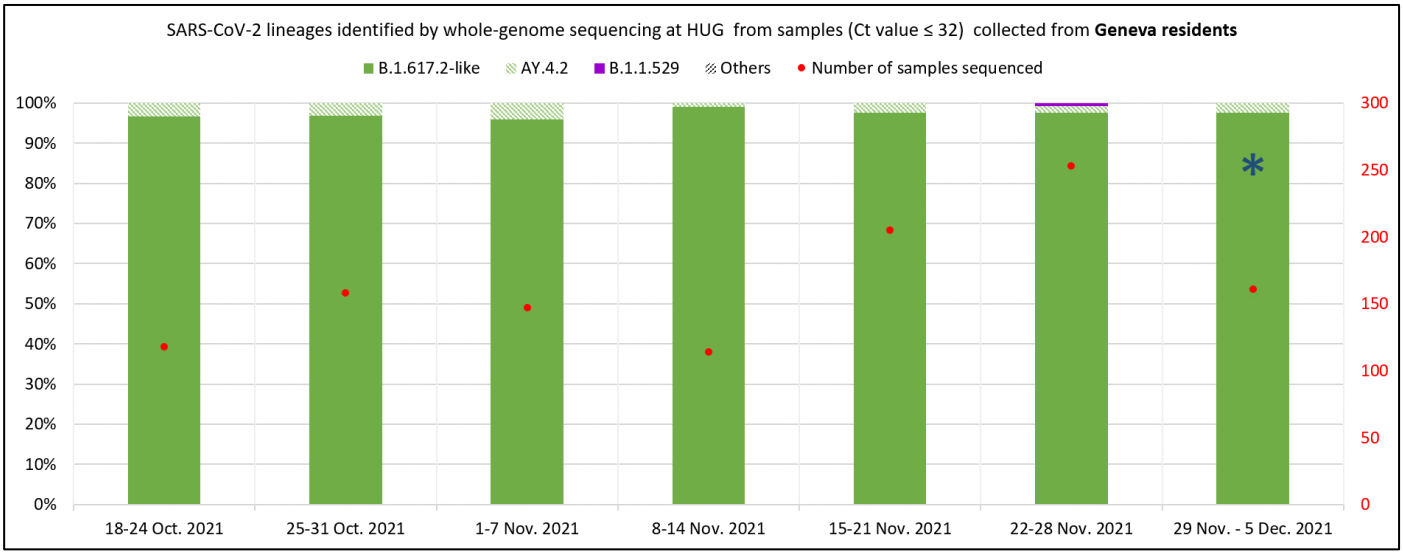
Data from countries where Omicron is circulating, and in vitro data, suggest a significant increase in transmissibility, but this has not been observed in Switzerland so far.

Community transmission has been announced in several countries, and the S drop out seems to be detected at increasing frequency in some countries, such as the UK, with a doubling time less than 3 days.

Preliminary data from the UK shows a vaccine effectiveness below 40% after 6 months post vaccination. Notably, a third/booster dose can partially offset this loss of effectiveness. Of note, the effect of cell mediated immunity in protection against severe disease should at least partially be conserved.

In addition, recent data with live virus clearly confirmed the lack of in vitro neutralization of Omicron by casirivimab/imdevimab. Pseudovirus lab experiments suggest that sotrovimab should retain most of its efficacy, with only a 2 fold reduction in IC_{50}. Confirmatiory data on live virus is pending.

SARS-CoV-2 lineages identified by whole-genome sequencing at HUG from samples (Ct value ≤32) collected from Geneva residents



Results of WGS of 1156 sequences submitted to GISAID between October 18 and December 5, 2021.

*Partial data for week 48 (November 29 to December 5), as sequencing is still ongoing. Numbers will be updated in the next report.

The first Omicron sequences collected from Geneva residents have been identified by WGS and have been submitted to GISAID. Those sequences were collected during week 47 from travelers coming back from South-Africa, and were already confirmed by partial Sanger sequencing to be Omicron (please refer to weekly reports of week 47 and 48 for more details). Those samples originate from patients who have been tested in external laboratories, and sequenced at the request of the cantonal physician team.

Delta or one of its sub-lineage are still the most frequently identified variants collected over the last 2 months.

Of note, we start to observe a more diverse variability among Delta sequences.

- Notably, 3 of the 314 Delta and Delta sub-lineages identified in the last sequencing batch carried the E484Q mutation. Those sequences are not genetically closed to the E484Q containing sequences observed last month.
- In general, we observe an increase in the number of other Delta or Delta sub-lineages containing 3 or more mutations in the Spike protein. This could reflect the fact that the virus is more widely circulating in the community.
- AY.4.2 is still circulating at a very low level in the community.

Post-vaccination infections in the canton of Geneva

Post-vaccination infection is defined here as a positive SARS-CoV-2 test occurring more than 14 days after the second vaccine dose. This surveillance is done in collaboration with the Direction Générale de la Santé (DGS) of Geneva. Data are collected by the DGS of Geneva during contact tracing calls after having obtained informed consent from SARS-CoV-2 positive patients. The list of patients with post-vaccination infections is sent weekly to HUG virology laboratory, which makes an effort to retrieve initial diagnostic samples in order to ensure sequencing, as recommended by FOPH.

Among the 4202 new COVID-19 cases reported by the Direction Générale de la Santé in Geneva over week 49, 1220 (29%) have been identified as post-vaccination infections.

Of note, because more than 80% of the population is vaccinated in the Canton, the incidence is largely higher (more than 7 times) in non-vaccinated patients, which represented more than 2/3 of infected patients in the Canton during week 49.

Vaccination status is available for 15 of the 17 specimen positive for the S Drop out, among which 10 have been confirmed by Sanger sequencing and/or WGS to be Omicron.
All but 2 of those 15 samples positive for the "S Drop out" have been collected in vaccinated individuals:
- Regarding the 2 unvaccinated individuals, no data is available concerning a possible previous infection.
- 4 were only partially vaccinated (only received one dose)
- 9 received 2 doses of vaccine (delay between the last received dose and the positive test ranging from a few weeks to more than 6 months).

Conclusions

- The absolute number of positive tests both collected at our institution and in the canton of Geneva continued to increase over week 49.

- A total of 17 specimens have tested positive for the “S Drop out” since November 22. Among them, only 4 have been collected at HUG. All were collected at our outpatient testing center. Thirteen additional specimens, collected from non-Geneva residents (n=5) or sent to our laboratory for “S Drop out” screening at the request of the cantonal physician team because of epidemiological link (n=8) have been tested positive. The first positive specimen was collected on November 22. None of those patients are known to be hospitalized.

All positive “S Drop out” specimens were confirmed to be Omicron when technically possible (ie: when Ct value is < 30) by partial S Sanger sequencing.

All cases for whom data is available (13/17) are linked to travel.
Among cases for whom vaccination status is available (15/17), 2 were unvaccinated, 4 received only 1 dose of vaccine, and 7 received 2 vaccine doses.

- Two full-length sequences of Omicron collected from Geneva residents have been submitted to GISAID. WGS is ongoing for other specimens.

- Among Delta and Delta-lineages identified by WGS, we start to observe more sequence variability. This includes a higher number of mutations on the Delta background. This may reflect the higher circulation of SARS-CoV-2 in the community. No specific identified sub-lineage is known to have any specific additional property.

Laurent Kaiser, Samuel Cordey, Manuel Schibler, Erik Boehm and Pauline Vetter for HUG.

Pauline Brindel for the Geneva Cantonal Physician team.