





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

Geneva, December 08, 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 Focus on Omicron B.1.1.529 (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 18% of the total number of tests performed in the canton of Geneva during week 48 (5330/29306). Roughly 21% of the positive specimens collected in the Geneva area were processed at HUG (754/3565) during week 48. 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 6, at 12 noon.

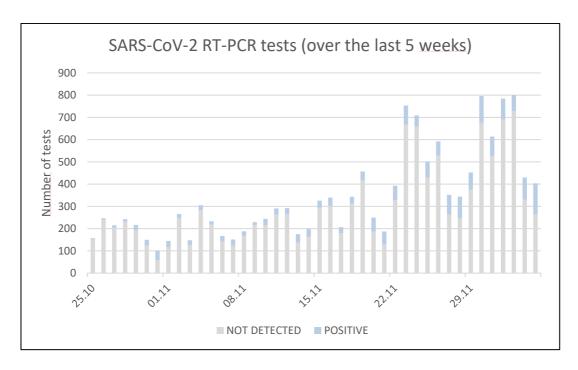
Methods and collaborations

The systematic 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.

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.

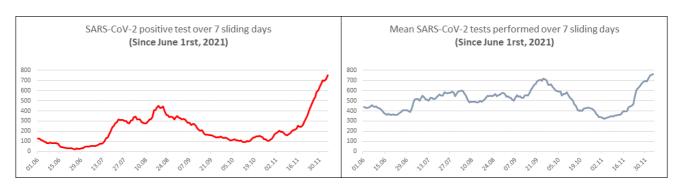
Geographic distribution, transmission advantage estimates and detailed number of available sequences over time in the canton of Geneva is available on the covSPECTRUM platform, run by Tanja Stadler's group at ETH Zurich.

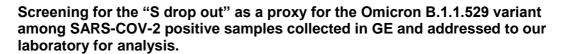
These reports are produced in collaboration with the Geneva Cantonal Physician team, which provides information on epidemiological links and post-vaccination infections (see below).

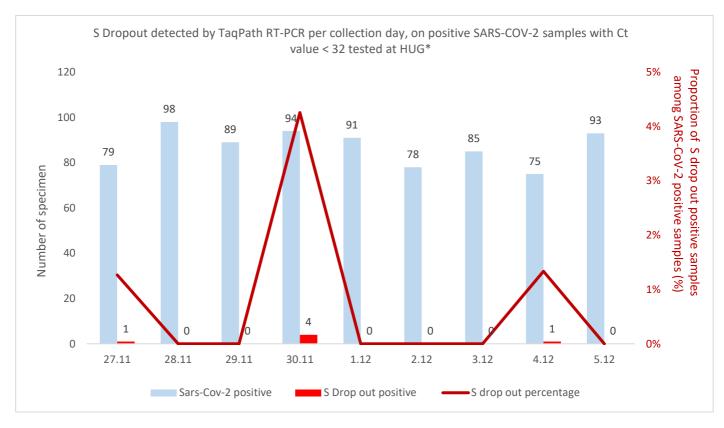


During week 48, the absolute number of positive SARS-CoV-2 tests increased substantially to 754, while the mean positivity rate over 7 sliding days remained stable at a high level around 14%.

Similarly, at our **outpatient symptomatic testing center**, the **mean positivity rate continued to increase and reached 28% on average**.







*Here are depicted all specimens tested for the "S Drop out" at HUG, collected from both Geneva residents and residents living outside the canton, tested either at our laboratory for primary diagnostic or diagnosed in another laboratory and sent for further testing at HUG.

The systematic screening for the "S drop out" by an additional RT-PCR (TaqPath, Thermofisher) was implemented at HUG on SARS-CoV-2 positive specimens with Ct value < 32 tested for primary diagnostic in our laboratory on November 27. In addition, this additional RT-PCR test is performed at the request of the cantonal physician team in positive specimen tested in other laboratories and repatriated to HUG.

All positive results are displayed here.

A total of 8 specimens were positive since the beginning of the screening. The first 2 positive cases were collected during week 47 and are described in the last weekly report, posted on Wednesday December 1, 2021 (not depicted in the graph).

Six additional specimens, one collected outside of HUG during week 47, and 5 collected at HUG during 48 were positive for the "S drop out". Note that all those samples were confirmed to be Omicron by partial S gene Sanger sequencing. Whole Genome Sequencing is ongoing.

All 6 new cases were linked to travel in a country where the variant is widely circulating in the community:

- One case was imported from a returning traveler back from South Africa at the end of November, but did not have any link with the first two cases described in our previous report. This person was fully vaccinated.
- Four cases are related since they belong to the same family. One of the member was returned from South Africa at the end of November and contaminated the rest of the family. All were vaccinated, although 2 received only one dose the month before diagnosis.
- The most recent case is an imported case returning from South Africa end of November who was fully vaccinated. This person had no link with the previously identified cases.

Of note, all imported cases described in this report traveled on separate flights.

Update on B.1.1.529: the Omicron variant

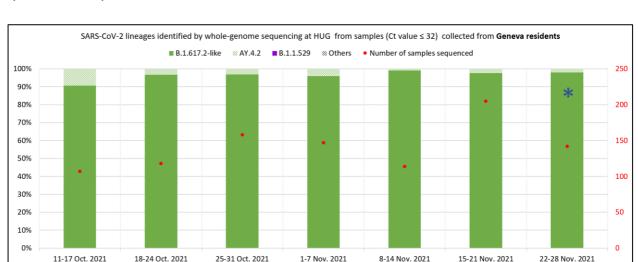
For the summary of the current knowledge on Omicron, please refer to the weekly report of week 47, posted on Wednesday, December 1, 2021. In addition, few (2) Omicron-like lineages have been reported in South Africa that lack the deletion causing S drop out, confirming the necessity of pursuing sequencing surveillance in Switzerland.

Data are still not clear enough regarding Omicron's emergence, its transmissibility, and its severity.

However, this variant is quickly expanding in southern Africa. Community transmission has been announced in several countries at low level, and the S drop out seems to be detected at increasing frequency in some countries, such as the UK. However critical epidemiological data are still lacking to determine with certainty if Omicron can outcompete Delta. Delta is still the variant leading the fifth wave in Europe and in Switzerland.

Preliminary data on neutralization capacity of sera from vaccinees show an extended loss of neutralization against Omicron, which increases with time since the last received dose. However, 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 keep its efficacy. 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 991 sequences submitted to GISAID between October 11 and November 28, 2021.

Delta or one of its sub-lineage has been identified in all the available SARS-CoV-2 sequences collected over the last 2 months. Worldwide, this variant and its sub-lineages are retrieved in more than 99% of available sequences.

Note that this percentage is lower in Africa, where genomic surveillance is particularly low.

AY.4.2 is still circulating in the community since the beginning of October. It hasn't been increasing in frequency in the canton of Geneva over the last 6 weeks and remains under 1% of all retrieved sequences.

We still observe a large variety of different Delta sub-lineage, with AY.43 and AY.122 being the most frequently identified over the last 2 sequencing batches (not depicted here). No Delta sub-lineage identified for now is suspected to have any additional property.

Note that the Omicron variant has been confirmed by Sanger sequencing on 6 occasions since November 28 (see above).

^{*}Partial data for week 47 (November 22 to November 28), as sequencing is still ongoing. Numbers will be updated in the next report.

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 3718 new COVID-19 cases reported by the Direction Générale de la Santé in Geneva over week 48, 1007 (32%) 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 48.

Conclusions

- The absolute number of positive tests continued to increase over week 48, as well as the mean positivity rate over 7 sliding days, which reached 28% in our symptomatic outpatient testing center.
- Delta or its sub-lineage were the only variants identified by whole genome sequencing in the canton of Geneva since mid-September, in specimen collected until November 28. Note that sequencing is still ongoing on some specimen collected between November 21 and 28. The Delta sub-lineage AY.4.2 is circulating in the community at a low level. AY.43 and AY.122 were the Delta-lineages identified most frequently. None is supposed to have any specific additional property.
- As of December 6, 2021, a total of 8 positive specimens have tested positive for the S drop out since the beginning of the screening. Six were confirmed by Sanger sequencing to be Omicron; one could not be confirm because of low viral load, and the last one is ongoing sequencing. Three were collected during week 47, from Geneva residents, and 4 of them were collected from residents of Vaud during week 48. All were closely linked to travel in a country where Omicron is widely circulating. WGS is ongoing.
- While Omicron is spreading fast in southern Africa and was detected in many countries mostly in returning travelers, it is still too soon to make conclusions regarding its transmissibility pattern compared to Delta. Preliminary data on neutralization capacity of sera from vaccinees show an extended loss of neutralization against Omicron, which increases with time since the last received dose. In addition, recent data confirmed the lack of in vitro neutralization of casirivimab/imdevimab against Omicron.

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

Pauline Brindel for the Geneva Cantonal Physician team.