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

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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

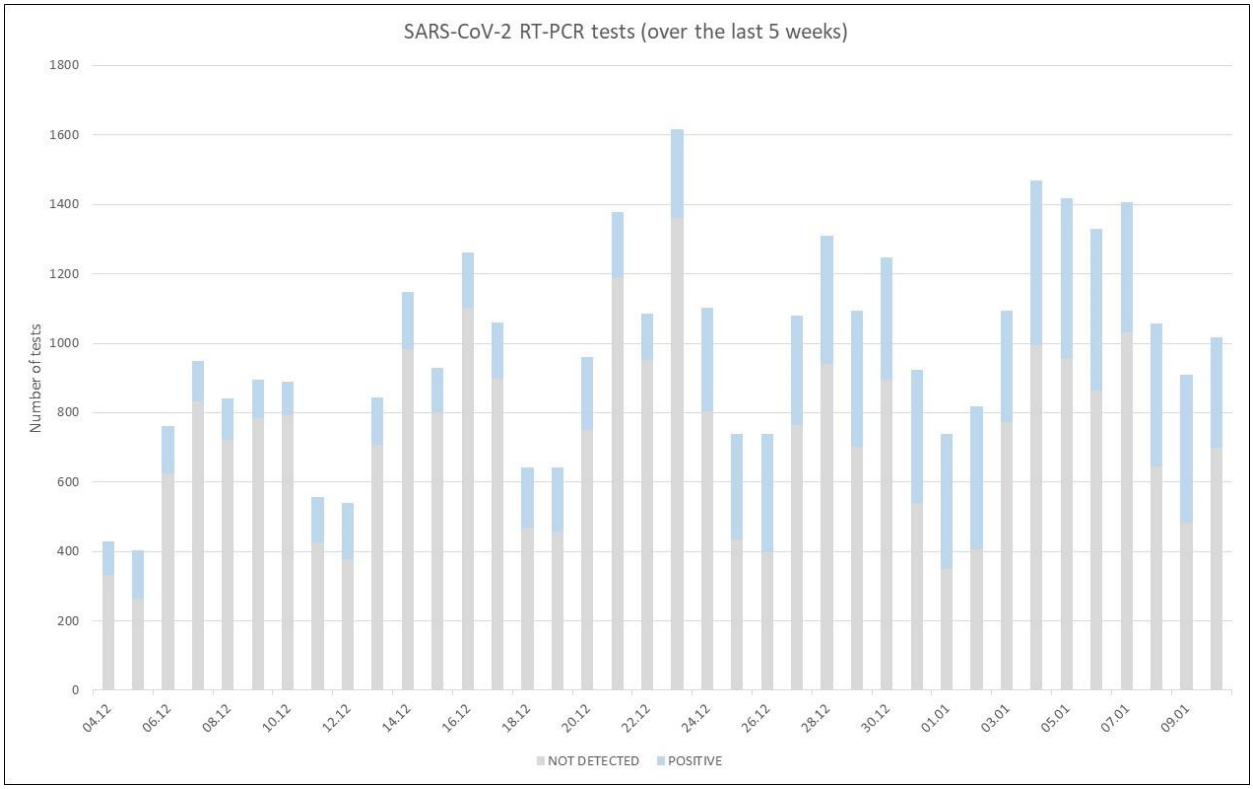
The number of tests (PCR and antigen tests) performed at the laboratory of virology of the Geneva University Hospitals represented around 32% of the total number of tests performed in the canton of Geneva during week 52 of 2021 and week 1 of 2022 (18528/58546). **Roughly 1/4** (26%) **of the positive specimens collected in the Geneva area were processed at HUG** (5954/22739) **during weeks 52 and 1**. Tests performed at our outpatient testing center are PCR-based for symptomatic individuals.
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 January 12, 2022, at 10:00.

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 were tested for the S drop out between December 1 and 31, 2021. Since January 2022, all specimens originating from hospitalized patients and a selection of specimens collected from ambulatory patients are tested for the “S Drop out”.

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.

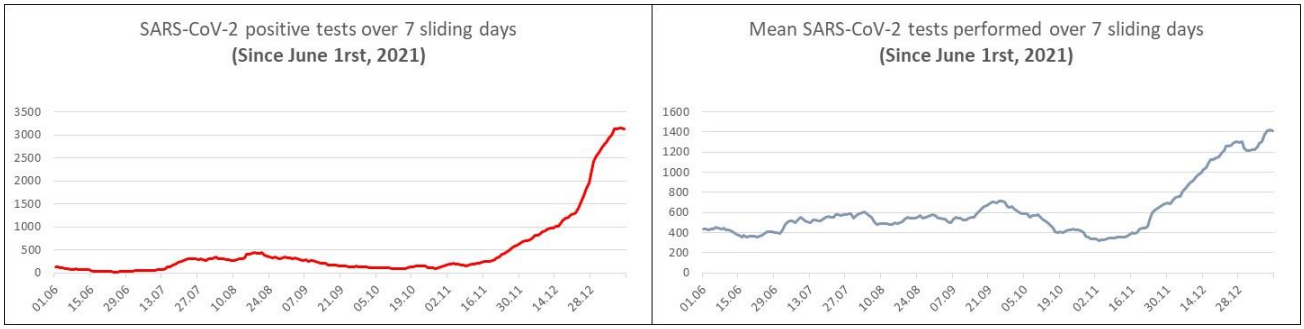
These reports are produced in collaboration with the Geneva Cantonal Physician team, which provides information on epidemiological links. Given the high number of post-vaccination infections due to Omicron, this information will no longer be displayed here (see weekly reports of the DGS).



During week 52 of 2021 and week 1 of 2022, the **absolute number of positive SARS-CoV-2 tests continued its steep increase**. The mean positivity rate of tests performed at our laboratory was around 33% on average during this period. This represent a doubling of the positivity rate compared to Christmas week 50 of 2021.

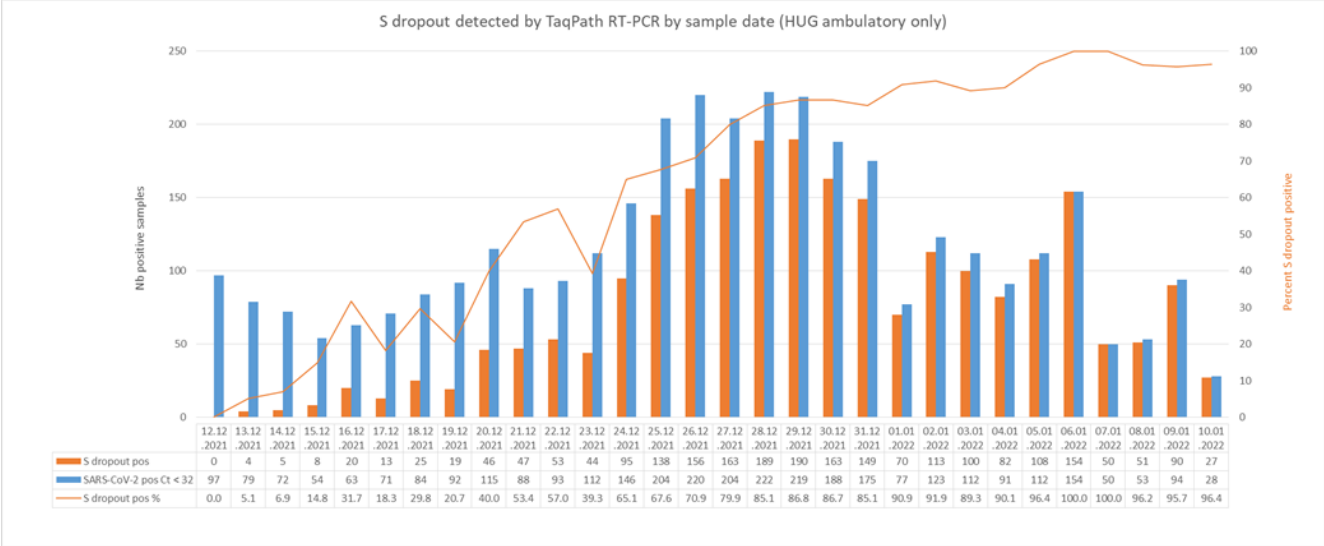
At our **outpatient symptomatic testing center**, the **mean positivity rate continued to increase and oscillated between 60 and 70% on average over the last 14 days**.

The positivity rate peaked at 84% on January 9 at our symptomatic outpatient testing center (228/272).



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.



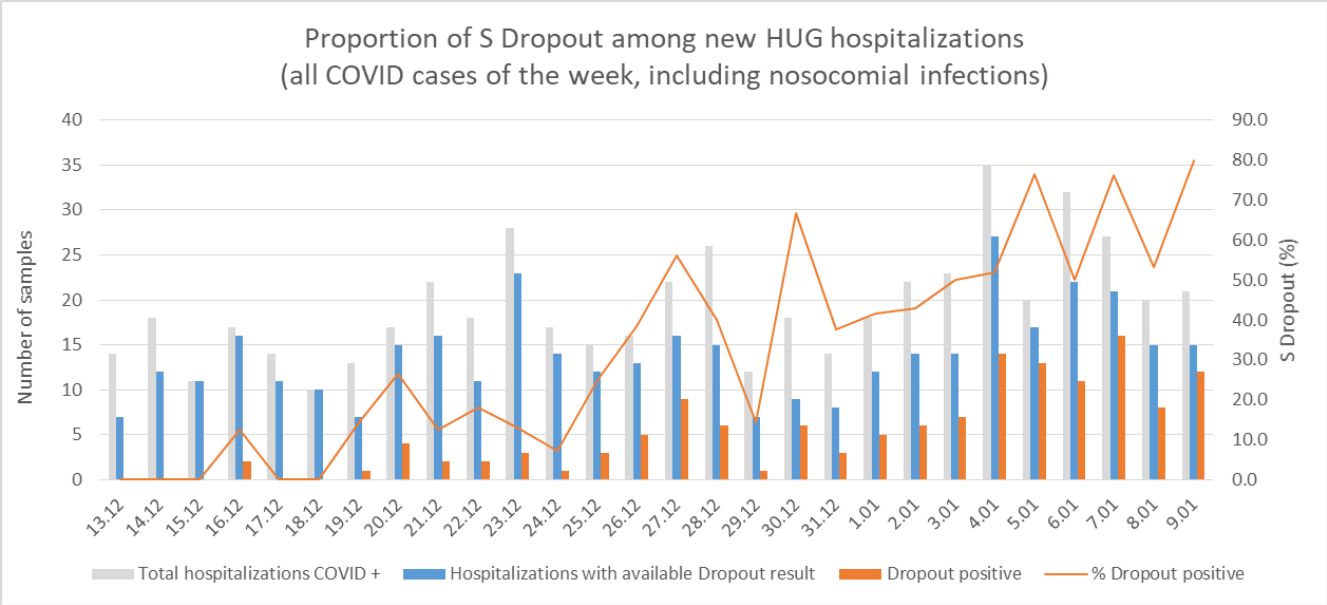
	12.12.2021	13.12.2021	14.12.2021	15.12.2021	16.12.2021	17.12.2021	18.12.2021	19.12.2021	20.12.2021	21.12.2021	22.12.2021	23.12.2021	24.12.2021	25.12.2021	26.12.2021	27.12.2021	28.12.2021	29.12.2021	30.12.2021	31.12.2021	01.01.2022	02.01.2022	03.01.2022	04.01.2022	05.01.2022	06.01.2022	07.01.2022	08.01.2022	09.01.2022	10.01.2022
S dropout pos	0	4	5	8	20	13	25	19	46	47	53	44	95	138	156	163	189	190	163	149	70	113	100	82	108	154	50	51	90	27
SARS-CoV-2 pos Ct < 32	97	79	72	54	63	71	84	92	115	88	93	112	146	204	220	204	222	219	188	175	77	123	112	91	112	154	50	53	94	28
S dropout pos %	0.0	5.1	6.9	14.8	31.7	18.3	29.8	20.7	40.0	53.4	57.0	39.3	65.1	67.6	70.9	79.9	85.1	86.8	86.7	85.1	90.9	91.9	89.3	90.1	96.4	100.0	100.0	96.2	95.7	96.4

We use the Taqpath RT-PCR assay on SARS-CoV-2 positive samples with Ct value < 32 to detect the so called "S gene dropout" (the S gene PCR target is not amplified, while the two other targets are detected). This constellation currently indicates the presence of the Omicron variant with a high probability. Whole genome sequencing performed on SARS-CoV-2 positive samples allows for definitive confirmation. The daily evolution of the proportion of the "S gene dropout" among SARS-CoV-2 samples tested with the Taqpath assay is displayed in the graph above. Since January 1st, 2022 samples included come exclusively from adult people screened at our outpatient testing centers.

Omicron replaced Delta over a period of 3-4 weeks in the Geneva area, as shown by the proportion of the samples displaying the "S drop out" and therefore suspected as **Omicron specimens**.

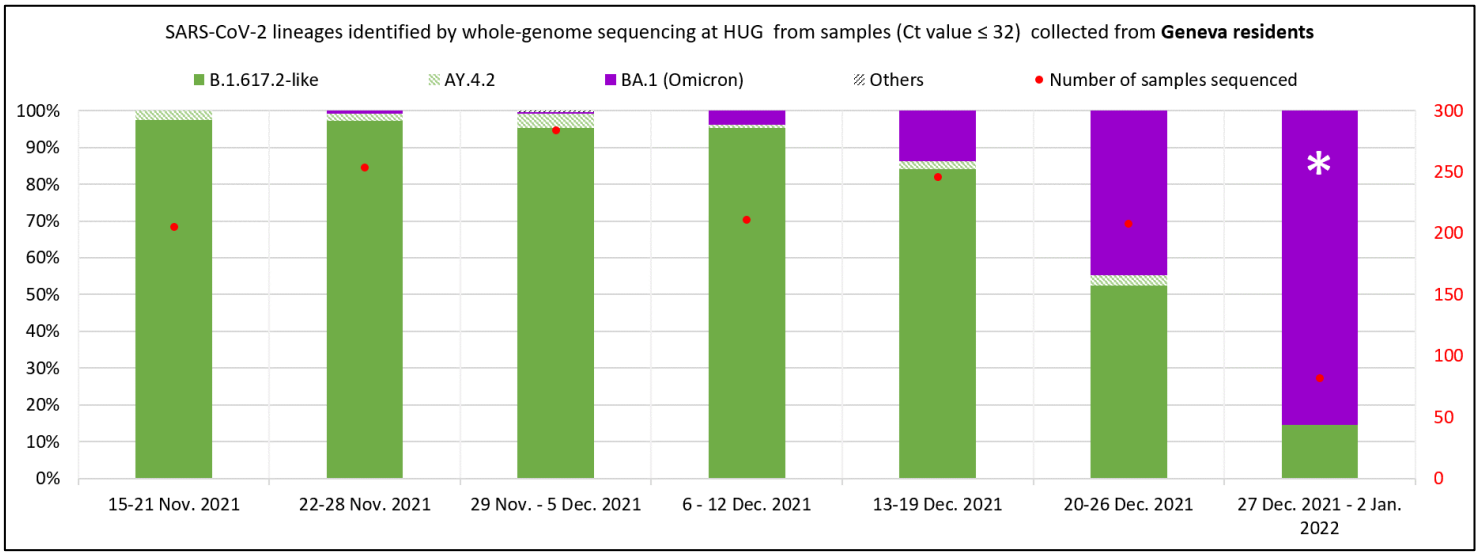
For epidemiological data, please refer to the weekly report of the cantonal physician team. Omicron is largely circulating in the community, and the very high positivity rate observed among symptomatic patients reflects the saturation of testing centers capacities and thus underdiagnosis of SARS-CoV-2 infections in the community.

2. 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 hospitalized at HUG and tested for primary diagnosis at our laboratory.



Among hospitalized patients, as expected due to the delay between infection and hospital admission due to COVID complications, **the proportion of samples positive for Omicron reached 80% at the end of week 1.**

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



Results of WGS of 1490 sequences submitted to GISAID between October 18 and December 5, 2021.

*Partial data for week 52 (December 27, 2021 to January 2, 2022), as sequencing is still ongoing. Numbers will be updated in the next report.

Whole genome sequencing confirmed the progressive replacement of Delta by Omicron.

Omicron sequences were detected since week 47, at a proportion progressively increasing over time. More results are awaited for week 52, due to the intrinsic delay of sequencing.

All Omicron sequences belonged to the BA.1 sub-lineage (and therefore displayed the S Dropout), confirming that the “S Dropout” can still be used as a proxy for Omicron.

Note that 31% (73/231) Omicron sequencing available from the last sequencing batch carried the R346K polymorphism, which is a marker of Omicron diversity and sub-lineage spread, which will be closely surveilled.

Available Delta sequences were much more variable, as was previously observed, with over 25% of the sequences displaying at least 2 mutations compared to the Delta reference. This reflects the progressive accumulation of selected mutations of a variant which evolved over time. Among them, 9 sequences carried the E484Q mutation within the AY.70 Delta sub-lineage.

Conclusions

- The **absolute number of positive tests** collected at our institution **continued to increase, and the positivity rate among symptomatic outpatients peaked at 84% on January 9, 2022.** This reflects the saturation of testing capacities in the Canton and the underidentification of SARS-COV-2 infections in the canton.

- **Over a period of 3-4 weeks,** as shown by the progressive increase in the S Drop out feature among tested specimens from the community, **Delta was replaced by Omicron.**

- **The S drop out reached close to 100% in the community, and is detected among 80% of hospitalized patients.**

- Whole genome sequencing confirmed that the “S Dropout” can still be used as a proxy for Omicron in the Geneva area, as all Omicron sequences identified belonged to the BA.1 sub-lineage.

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Pauline Brindel for the Geneva Cantonal Physician team.