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Geneva Centre for Emerging Viral Diseases

Division of Infectious Diseases

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SARS-CoV-2 genomic and variants surveillance in Geneva: Bi-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 a fifth of the total number of tests performed in the canton of Geneva during weeks 40 and 41 (6955/34109). Roughly 33% of the positive specimens collected in the Geneva area were processed at HUG (231/704) during weeks 40 and 41. Tests performed at our outpatient testing center (located in the Hospital but open to anyone from the community) 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.

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. All specimens with a Ct value ≤32 are sequenced. In some instances, sequencing can be done on specimens sent by other laboratories in Switzerland. Phylogenetic analysis data are produced by Nextstrain, in collaboration with Richard Neher's group at the University of Basel. The number of positive tests in the canton and the total number of tests done during the surveilled week come from the website of the Direction Générale de la Santé in Geneva (available at https://infocovid.smc.unige.ch/), accessed October 19, at 10:00 am.





Both the absolute number of positive SARS-CoV-2 tests and the percentage of positive results have continued to decrease until the middle of week 41 (mean positivity rate over 7 sliding days of less than 3), with a new increase at the end of week 41 (positivity rate of 10% on Sunday, October 17) while the number of tests performed decreased.

The increase in the positivity rate was also obvious at our outpatient symptomatic testing center at the end of week 41 (sector E'), where the positivity rate reached more than 20% again for the first time since mid-September.



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

Results of WGS of 794 sequences submitted to GISAID between August 23 and October 10, 2021.

B.1.617.2 (Delta, or one of its sub-lineages) represented the only SARS-CoV-2 variant identified in samples collected from Geneva residents over the last 4 weeks.

No other VOC/VOIs have been retrieved in the last sequencing batch. Of note, no B.1.621 (Mu) or B.1.620 variant have been identified since mid-September.

Numerous Delta sub-lineages have been identified and some mutations can accumulate in the Delta background. Sub-lineages are not depicted here.

Currently, one Delta sub-lineage called AY.4.2, carrying 2 additional mutations Y145H and A222V is rapidly increasing in frequency in the UK, where a growth advantage of 10-15% has been observed. It is too soon however to conclude that this corresponds to an intrinsic increased transmissibility of this sub-lineage or to increased spread led by behavioral events.

In Geneva, this sub-lineage has only been identified once in late July, in an individual having experienced a SARS-CoV-2 infection despite vaccination.

Of note, more information will follow in the next reports regarding any potential increased risk associated with Delta sub-lineages.

Additional remark: due to a technical problem encountered during the WGS process, a total of 76 SARS-CoV-2 positive samples collected between September 23 and 28 could not be sequenced. This partly explains the drop in the number of sequences available during this period. Please note that the data collected on week 39 (from 4 to 10 October) are still incomplete, as sequencing is still ongoing.

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 304 and 423 new COVID-19 cases reported by the Direction Générale de la Santé in Geneva respectively over week 40 and 41, respectively, 21% and 25% have been identified as post-vaccination infections.

A total of 166 post-vaccination infections have been identified in the Canton of Geneva among 723 cases during the first two weeks of October, 2021 (week 40 and 41). Over the same time period, only 5 fully vaccinated patients have been hospitalized at HUG**. Among them, one was hospitalized because of comorbidities/concomitant disease and not because of severe COVID-19, another was severely immunocompromised.





Of note, available data show that post vaccination infection epidemiology follows the epidemiology of circulating variants in the community. Preliminary analysis of available sequences from SARS-CoV-2 breakthrough vaccine infections since the beginning of 2021 in the Geneva area show no specific mutation selected. Consolidated data will follow.

Conclusions

• Both the absolute number of positive SARS-CoV-2 tests and the percentage of positive results decreased until the middle of week 41, with a new increase at the end of week 41 while the number of tests performed decreased. Whether this reflects a significant epidemiological trend or the awaited instability of an early endemic phase will be carefully monitored over the next weeks.

• The majority of new SARS-CoV-2 cases arose in unvaccinated individuals.

• Delta (or one of its sub-lineages) has continued to be the sole SARS-CoV-2 variant identified among sequences collected from Geneva residents, with no other VOC/VOI sequences retrieved in the Geneva over the surveilled period.

• Of note, among Delta sub-lineages worth mentioning, only one AY.4.2 sequence was retrieved in the Geneva area since the beginning of the genomic surveillance program. It has been identified from a vaccine breakthrough infection at the end of July and has not been retrieved anymore since.

• Preliminary results of the analysis of full sequences retrieved from post vaccination infection cases do not show any specific mutations along the genome.

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