



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

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Geneva Centre for Emerging Viral Diseases

Division of Infectious Diseases

Department of Medicine

Laboratory of virology

Division of Laboratory Medicine

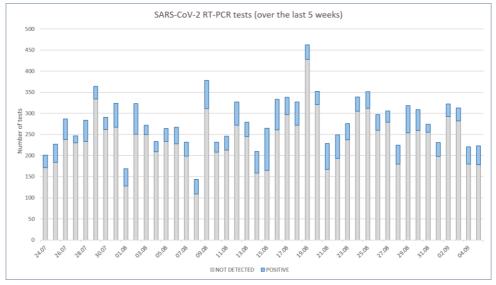
Diagnostic Department

SARS-CoV-2 genomic 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

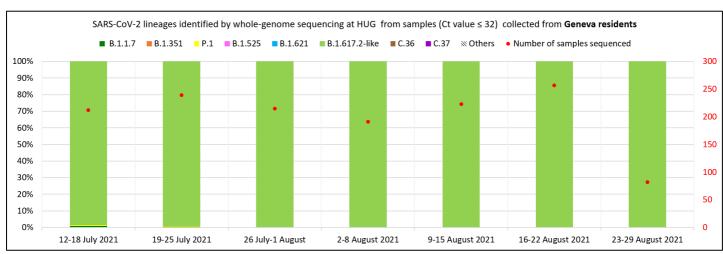
The number of tests (PCR and antigen tests) performed at the laboratory of virology of the Geneva University Hospitals represents more than a quarter of the total number of tests performed in the canton of Geneva during weeks 34 and 35 (7638/27587). Roughly 35% of the positive specimens collected in the Geneva area were processed at HUG (N=626/1743) during weeks 34 and 35. 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 September 6, at 10:00 am.



Both the number of weekly positive cases and the mean positivity rate (8.1%) have stabilized at a high level over the last 2 weeks.

Of note, the mean positivity rate at the dedicated outpatient department (secteur E' – which tests only symptomatic patients) started to decline over the last 14 days, and was on average at 28% over this period. (As a reminder, it peaked above 50% twice during 2 consecutive days over week 32, and was around 40% between weeks 29 and 32).



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

Results of WGS of 1419 sequences submitted to GISAID between July 12 and August 29, 2021.

Since mid-July, Delta or one of its sub-lineages has almost exclusively been retrieved from sequences collected from Geneva residents.

A variety of Delta sub-lineages has started to be observed. However, those lineages are still new and their definitions are still not fixed. We then chose not to represent Delta's sub-lineage divisions until clear definitions are available. There is no evidence that any clade within Delta is of greater concern. Similarly, no special issues regarding transmissibility, immune escape, clinical severity or diagnostic failure between Delta and its various sub-lineages have been identified yet. Data are currently scarce, and more information will follow.

Since the last report, WHO elevated B.1.621 to the new status of "variant of interest", and assigned it the Greek letter of Mu. It shares the N501Y mutation, linked to greater ACEII affinity with the VOCs Alpha, Beta, and Gamma. Similarly it shares the E484K mutation, linked to partial immune escape, with the VOCs Beta and Gamma. It additionally has few mutations in the N-terminus that may be associated with partial immune escape, and a P681H mutation near the furincleavage site that is also seen in Alpha and at the same position as a mutation in Delta (P618R). This variant has apparently reached high prevalence in some south American countries.

A total of 6 sequences were reported in the Geneva area at the end of June/beginning of July, 2021 (see update of August 12, 2021 for the overview of the sequences and update of July 13, 2021 for the description of the cases). Those cases were linked together, according to the cantonal physician team. Since then, no additional Mu sequences have been retrieved in the Geneva area.

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 1025 and 835 new COVID-19 cases reported by the Direction Générale de la Santé in Geneva respectively over week 34 and 35, 14% and 15% have respectively been identified as post-vaccination infections for sequencing.

A total of 534 post-vaccination infections have been identified in the Canton of Geneva among 4161 cases during the month of August. Over the same period of time, only 31 fully vaccinated patients have been hospitalized at HUG**. Among them, 35% had mild disease and were hospitalized because of comorbidities/concomitant disease (but not severe COVID).

**Available data from the Geneva University Hospitals COVID-19 surveillance, available in detail in a separate report.

Conclusions

- The positivity rate among symptomatic outpatients tested at HUG has stabilized at a high level, around 28% on average over the last 2 weeks.
- Meanwhile, the absolute number of newly hospitalized people at Geneva University Hospitals has remained high over the last 2 weeks. The vast majority are young and not vaccinated.
- WGS confirmed that exclusively the Delta variant (B.1.617.2 and its sub-lineages) has been identified since the end of July, 2021.
- Most positive tests (85%) occurred in non-vaccinated individuals. Those numbers are in line with existing data on mRNA vaccine effectiveness against infection by the Delta variant.
- Since the last report, the WHO elevated the classification of B.1.621 as a new variant of interest, which was named Mu. A total of 6 sequences were reported in the Geneva area at the end of June beginning of July, 2021. Since then, no new Mu sequences have been retrieved in the Geneva area.

Laurent Kaiser

Wrisu

Samuel Cordey

Sol

Manuel Schibler

Pauline Vetter