Hôpitaux Universitaires Genève

UNIVERSITÉ DE GENÈVE
FACULTÉ DE MÉDECINE

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

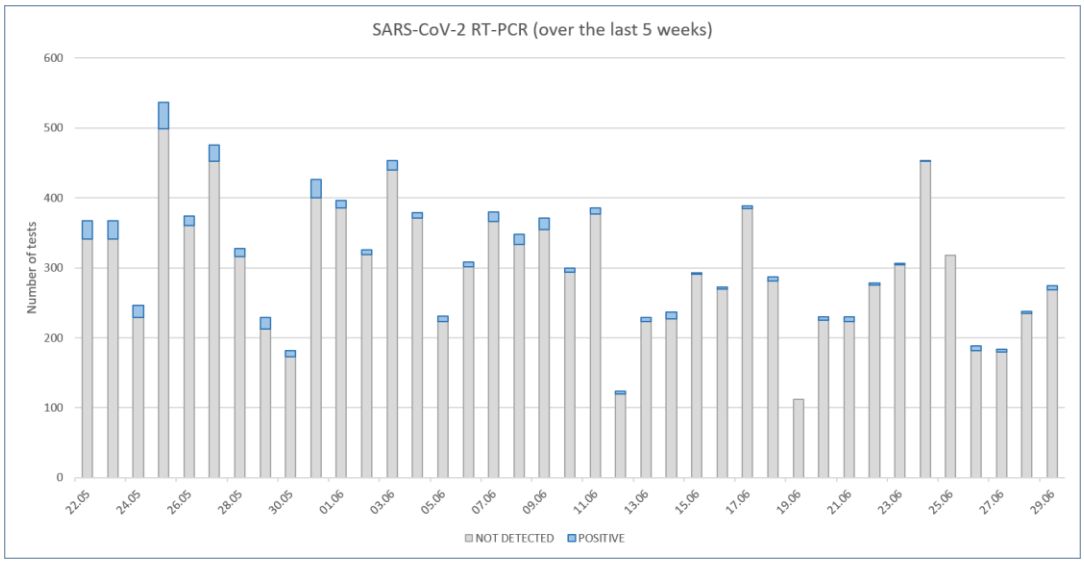
Diagnostic Department

SARS-CoV-2 genomic and variants surveillance in Geneva: weekly update

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

The number of tests performed at the laboratory of virology of Geneva University Hospitals represents around 1/3 of the total number of tests performed in the canton of Geneva during week 24. 1/3 to ¼ of the positive specimens collected in the Geneva area are processed at HUG for primary diagnostic. Specimens analyzed in our laboratory come from the community (the majority: symptomatic patients and asymptomatic contacts), from hospital workers (systematic screening in case of any symptoms, cluster investigations and asymptomatic HCWs as part of hospital surveillance system), from asymptomatic travelers needing a screening test, and from hospitalized patients. All tests performed at our outpatient testing center (located in the Hospital but open to anyone from the community) are PCR-based and not antigen-based; of course many centers in the canton are using antigen-based tests for primary screening.

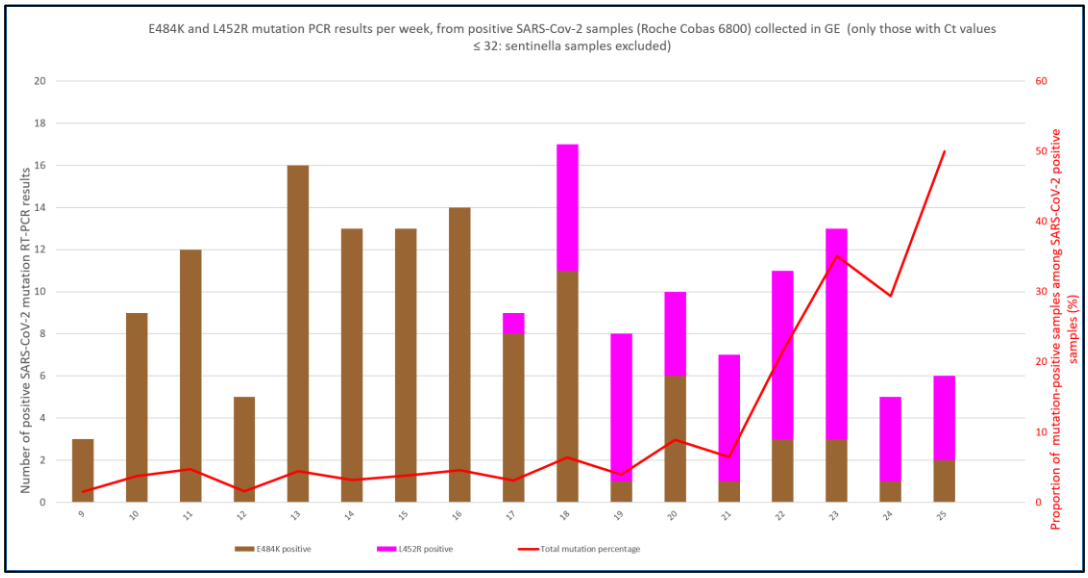
WGS is carried out in close collaboration with the Health 2030 Genome Center in Geneva and Philippe Le Mercier from the Swiss Institute of Bioinformatics. Since March 1, 2021, the sequencing is done within the Swiss national SARS-CoV-2 genomic and variants surveillance program. With the decreased number of SARS-CoV-2 positive cases, all specimens with a Ct value ≤ 32 are sequenced. In some instances, sequencing can be done in 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 cases diagnosed at HUG and the positivity rate seem to stabilize at a low level. The mean daily number of positive tests at HUG remained low, at 4 over the last 7 days.

laurent.kaiser@hcuge.ch | T. +41 (0)22 372 98 00 | F. +41(0)22 372 98 30 | hug-ge.ch

Specific mutations screening by RT-PCR among SARS-CoV-2 positive samples collected in GE and sent to our laboratory for primary diagnosis, according to calendar weeks



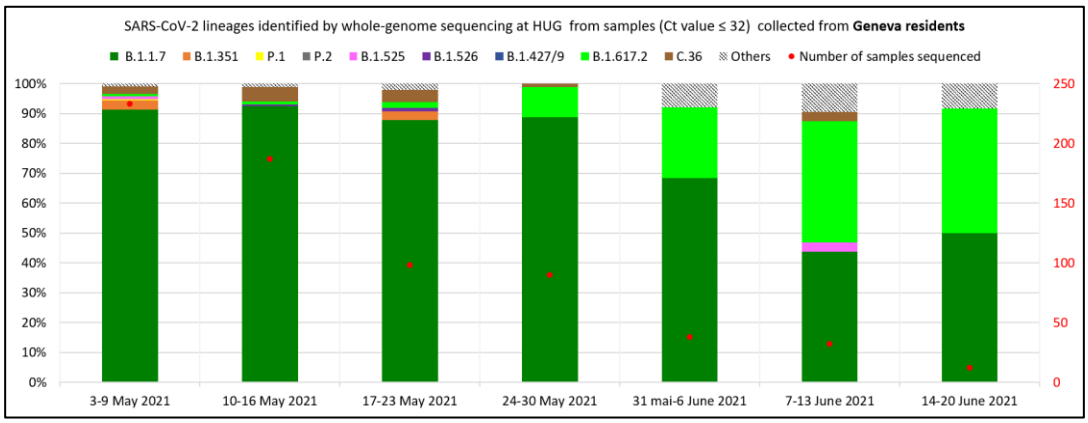
Starting date of E484K/Q mutation screening: January, 27, 2021. Starting date of 417N/T mutation screening: March, 3, 2021. This 417N/T screening is done on E484K-positive samples, and presumably allows distinguishing between B.1.351 (beta) and P.1 (gamma, not depicted on this graph). Starting date of L452R mutation screening: May, 4, 2021 (week 17). This graph only displays positive results of specific mutations looked for in samples sent for primary diagnostic with Ct values <32, and does not include mutation results obtained in SARS-CoV-2-positive samples sent from other laboratories.

Note:
The 484K mutation is mainly found, but not exclusively, on the B.1.351 (beta), the P.1 (gamma) variants, and various variants of interest.
The 452R mutation is mostly, but not exclusively, carried by the B.1.617.2 (delta) (and AY.1, which is B.1.617.2 with an additional 417N mutation) and the C.36.3 variants (not a VOC but a VOI).

Only 12 specimens were collected at HUG from persons living in the Geneva area, and allowing mutation screening (Ct values below 32), and are therefore included in this graph. This reflects the sharp decrease in incidence over the last month. Less than 50 new cases were reported by the cantonal physician team in the whole canton over the last week.
Of note, additional specimens originating from other laboratories and sent to HUG at the request of the cantonal physician team tested positive over the last week for the 452R mutation.

The proportion of specimens carrying the 452R mutation is progressively increasing over the last month. This mutation is now reported in half of the tested cases. However, mutation-harboring samples may be overrepresented due to aggressive contact tracing by the cantonal physician team, and the very low number of cases tested.

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



CAVEAT: Only 12 sequences were available for the surveilled period. Until mid-May, up to 200 sequences were analyzed each week. The proportion of the different variants should therefore be carefully interpreted in this context of low numbers.

The delta variant is progressively increasing in proportion, representing more than 40% of available sequences (5/12). Both specific mutation screening and sequencing reflect the progressive replacement of the B.1.1.7 (alpha) variant by the B.1.617.2 (delta) variant and its sublineage AY.1 (delta + 417N). Most identified cases are linked to known transmission chains or new importations. Only one cluster was linked to community transmission.

One B.1.525 sequence (not a VOC but a VOI because it carries the 484K mutation, has been identified first in Nigeria, also named eta) has been identified during the surveilled period. It was not linked to a previously known transmission chain, according to the cantonal physician team.

Conclusions

- The circulation of SARS-CoV-2 in the Geneva area remains low, with only less than 50 new cases reported by the cantonal physician team in the whole canton over the last week.
- Both specific mutation screening and sequencing reflect the progressive replacement of the B.1.1.7 (alpha) variant by the B.1.617.2 (delta) variant and its sublineage AY.1 (delta + 417N).
- B.1.617.2 (delta) and its sublineage AY.1 are circulating in the Geneva at the same proportion.
- This increase of detection of the delta variant in the Geneva area is until now not linked to a recrudescence of the new number of cases, nor to a recrudescence of the number of hospitalized patients.
- Most detected cases of variants are either linked to known clusters with identified transmission chains or to new importations with secondary clusters, according to the cantonal physician team.




Laurent Kaiser **Samuel Cordey** **Manuel Schibler** **Pauline Vetter**