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

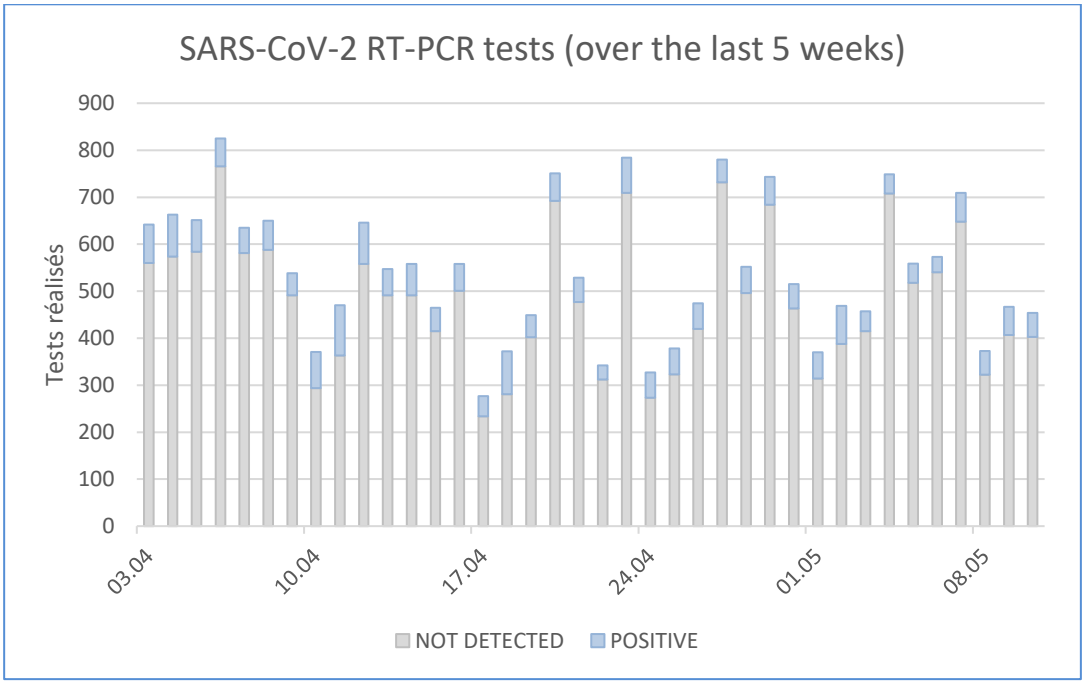
Division of Laboratory Medicine

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

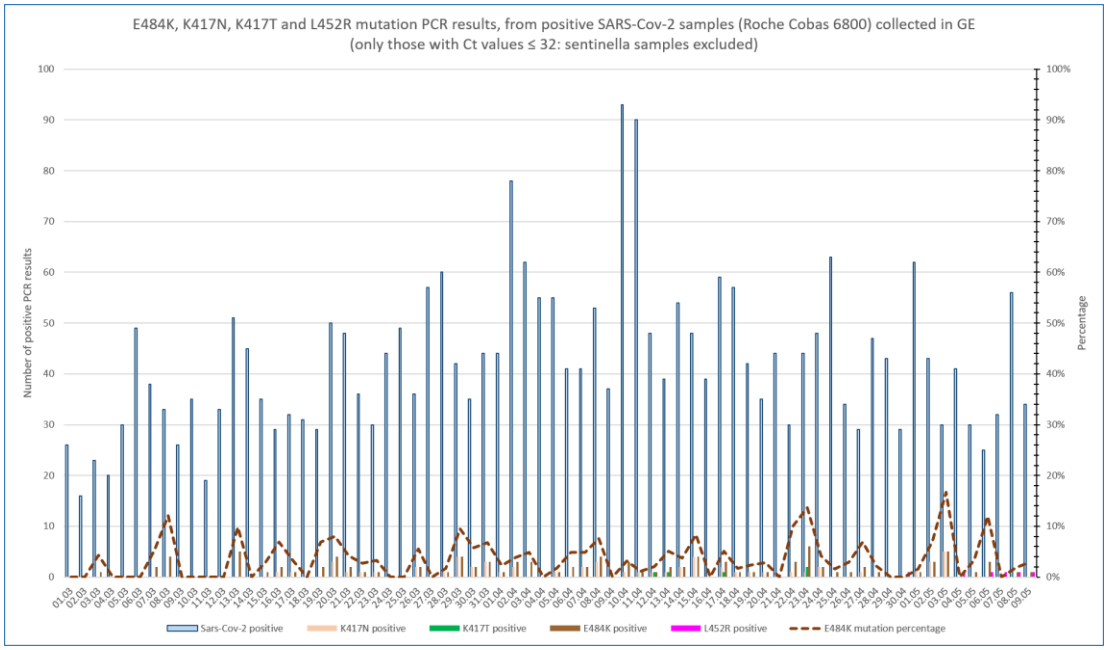
The number of tests performed at the laboratory of virology of Geneva University Hospitals represents around 1/3 of the total number of tests performed in the canton of Geneva. Specimens analyzed in our laboratory come from the community (the majority), from hospital workers (systematic screening in 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. It is based on a daily random sampling of SARS-CoV-2 positive specimens by RT-PCR, with a Ct value ≤ 32 as the only selection criterion. In some instances, sequencing can be done in specimens sent by other laboratories in Switzerland.



The absolute number of positive cases has been stable over the last 10 days, between 40 and 60 positive cases per day.

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

484K mutation screening by RT-PCR among SARS-CoV-2 positive samples collected in GE and sent to our laboratory for primary diagnosis



Among all SARS-CoV-2 RT-PCR-positive samples identified in our laboratory, all those with a Ct value ≤ 32 are subsequently screened for the 501Y and 484K mutations by specific RT-PCR assays. Specimens carrying the 484K and the 501Y mutations are subsequently tested for the 417N/T mutation. Period of N501Y mutation screening: January, 5, 2021 to April, 13, 2021. Starting date of E484K/Q mutation screening: January, 27, 2021. Starting date of 417N/T mutation screening: March, 3, 2021. Starting date of L452R mutation screening: May, 4, 2021.

After the first identification of B.1.617 variant in Switzerland, we implemented the systematic screening of the 452R mutation on May, 4, 2021. Its presence is shown in the graph by the pink bars. This mutation is present, among others, in the B.1.427/429 (Californian) and the B.1.617 (Indian) variants.
Since January, 2021 and the beginning of the sequencing surveillance program in Geneva, no B.1.427/429 has been identified in the Geneva area. The first case of B.1.617.2 was detected on April 17, 2021 in the Geneva area, in a returning traveler from Russia.

We detected the 452R mutation at low levels over the last week. Precise variant typing will be provide by whole genome sequencing, which is ongoing.

Variants carrying the 484K mutation are still circulating at a low level in the community, with a seemingly stable proportion over time.

Most recent whole genome sequencing results performed on SARS-CoV-2 positive samples collected in GE and sent to our laboratory

This graph displays the sequences with 95% of positions covered ≥ 15x and submitted to GISAID (385 sequences obtained from samples collected from April, 20 to April, 29, 2021).

A higher diversity of different variants was observed during the surveilled period relative to the preceding periods. B.1.1.7 is still causing almost all new SARS-CoV-2 infections, as confirmed by whole genome sequencing.

Among variants carrying the 484K mutation:
- B.1.351 is still circulating at a low level in the community, and 6 sequences were retrieved during the surveilled period
- three P.1 sequences were identified
- four B.1.525 sequences were detected (not considered a VOC, but a VOI).

The number of B.1.617.2 (first identified in India) cases is increasing: 4 specimens were identified during the surveilled period. According to the cantonal physician team, 3 of those new positive samples were retrieved from people belonging to the same family. These cases are linked to a school cluster, which is presumably consecutive to transmission from a traveler returning from India in mid-April.

B.1.617.2 is now considered a VOC by WHO, because of its probable higher transmissibility. No data are yet available to evaluate its severity. Preliminary *in vitro* data suggest a modest potential for immune escape; no *in vivo* data is yet available on mRNA vaccine efficacy on this variant, but *in vitro* studies demonstrate that sera from vaccinated subjects retains (somewhat reduced) neutralizing activity. Of note, available mRNA vaccines in Switzerland are still expected to protect against severe disease caused by this variant. Based on *in vitro* studies conducted with pseudoviruses not carrying the full set of mutations, efficacy of some monoclonal antibodies cocktails may be reduced (bamlanivimab and etesevimab); the combination casirivimab/imdevimab is expected to keep its neutralizing activity. Diagnostic test failure is not expected (no data yet on antigenic tests, but not expected).

Conclusions

- The absolute number of positive SARS-CoV-2 cases has been stable over the last 10 days in the Geneva area.
- The B.1.1.7 variant still represents the vast majority of new SARS-CoV-2 infections in the Geneva area.
- B.1.351 is still circulating at a low level.
- Other variants carrying the 484K mutation have been detected, such as B.1.525 and P.1
- B.1.617.2, first identified in India, has been detected in the Geneva since April 17, 2021. More cases have been detected since then. Most identified cases so far are linked to imported cases from returning travelers and to a subsequent cluster, according to the cantonal physician team.
- We implemented the systematic screening of the 452R mutation since May, 4, 2021, in order to rapidly identify suspected B.1.617.2 variants.




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