Hôpitaux Universitaires Genève

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FACULTÉ DE MÉDECINE

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Division of Infectious Diseases

Department of Medicine

Laboratory of virology

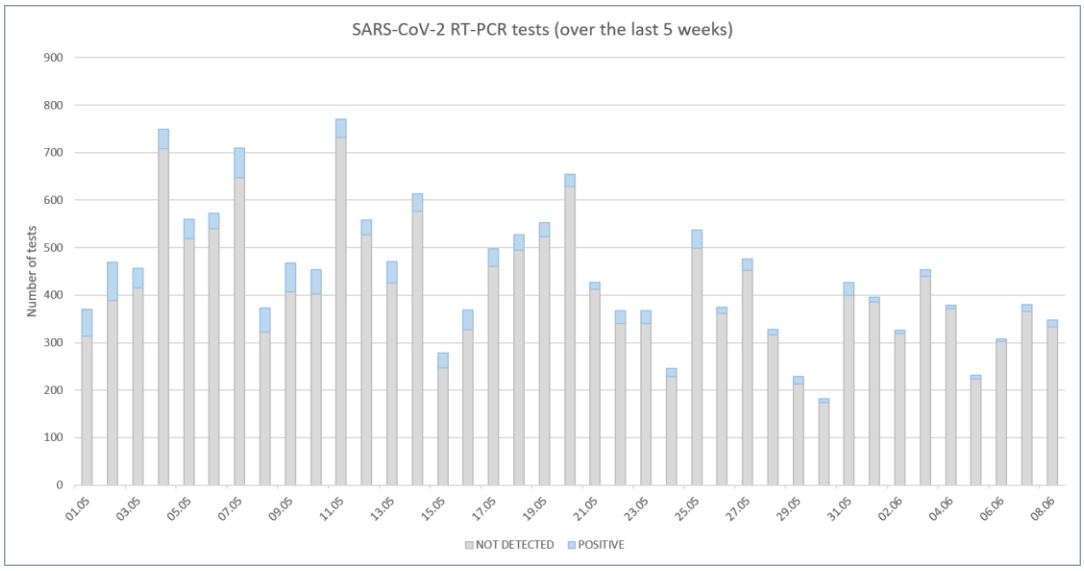
Division of Laboratory Medicine

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 1/4 of the total number of tests performed in the canton of Geneva. 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.



Both the absolute number of positive cases diagnosed at HUG and the positivity rate have continued their progressive decline since the beginning of May. Over the last week, the daily number of positive tests varied between 6 and 19 cases, and the positivity rate fell between 2 and 5%. Over the last week, HUG processed more than 1/3 of the positive tests of the canton (80/205).

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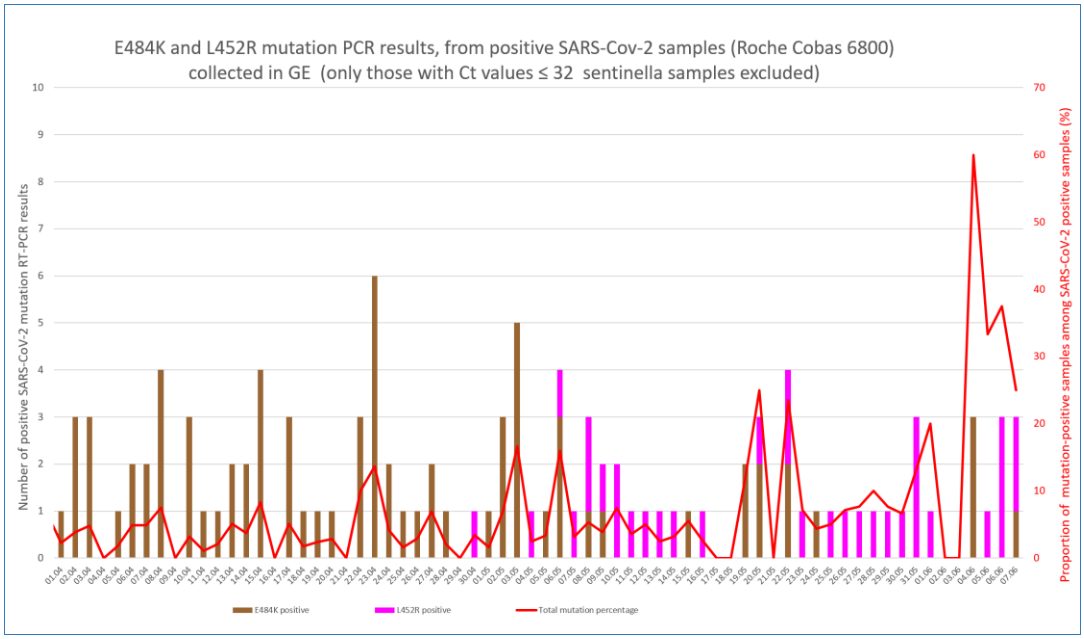
Specific mutations screening by RT-PCR among SARS-CoV-2 positive samples collected in GE and sent to our laboratory for primary diagnosis



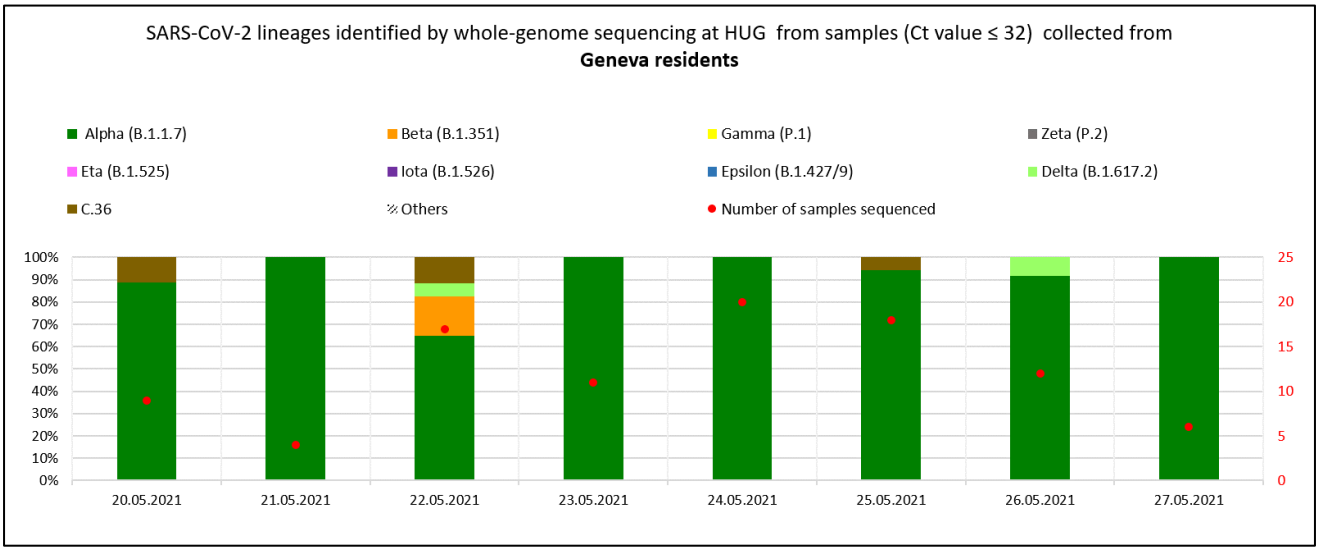
Starting date of E484K/Q mutation screening: January, 27, 2021. Starting date of 417N/T mutation screening: March, 3, 2021. This 417N/T screening is done on E484K-positive samples, and presumably allows distinguishing between B.1.351 and P.1 (not depicted on this graph). Starting date of L452R mutation screening: May, 4, 2021.
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. Results are presented by sampling date.

Note that the absolute number of new cases with Ct values <32 depicted on this graph is very low (below 12 specimens per day over the last week) and that proportions of mutations-positive samples carrying mutations may therefore be biased.

Amongst mutations of interest, since the beginning of May, the 452R mutation continues to be the most frequently detected. Almost all except one case identified during the last week are part of a known transmission chain or secondary cases linked to a new importation according to the cantonal physician team.
Variants carrying the 484K mutation are also detected at low level. Among the 4 cases identified over the last week, 2 are imported cases and 2 are linked together but come from an unknown transmission chain according to the cantonal physician team.

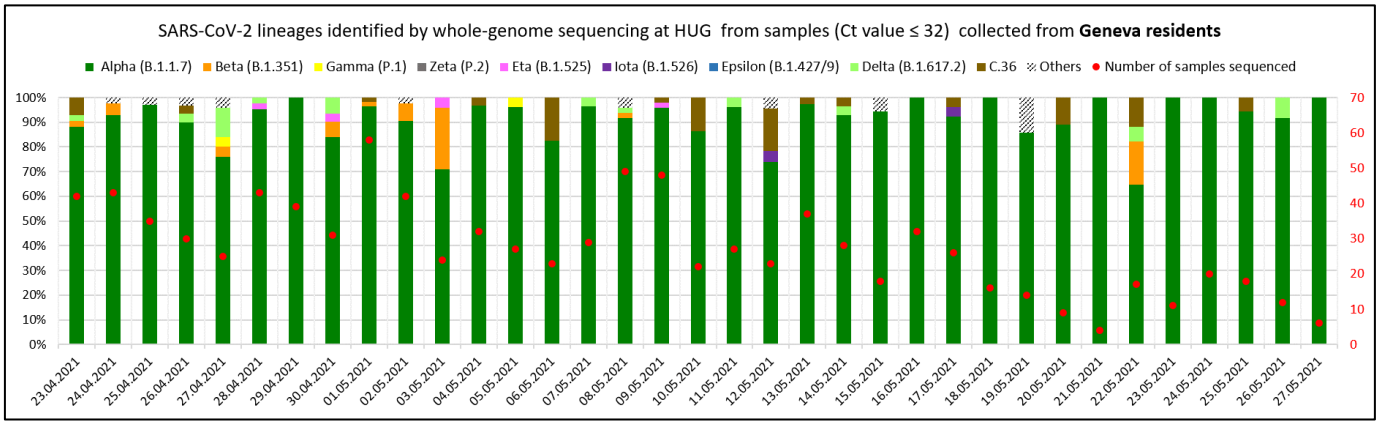
Whole genome sequencing results performed on SARS-CoV-2 positive samples collected in GE and sent to our laboratory

Figure A: data including the last whole genome sequencing series



This graph displays the sequences with 95% of positions covered ≥ 15x and submitted to GISAID (97 sequences obtained from samples collected from May, 20 to May, 27, 2021).

Figure B: whole genome sequencing results on SARS-CoV-2 positive samples over the last 5 weeks



This graph displays the sequences with 95% of positions covered ≥ 15x and submitted to GISAID (960 sequences obtained from samples collected from April, 23 to May, 27, 2021).

Note that due to the decreased number of new cases, the number of sequenced cases per day has substantially decreased (below 20 specimens per day since May 18, 2021). Dianalabs Genève is joining the Swiss national SARS-CoV-2 genomic and variants surveillance program in order to increase the coverage in the canton.

We continue to observe a decreased circulation of variants carrying the 484K mutation in the Geneva area, with only 3 B.1.351 (beta) sequences identified over the period of May 20 to May 27, 2021.

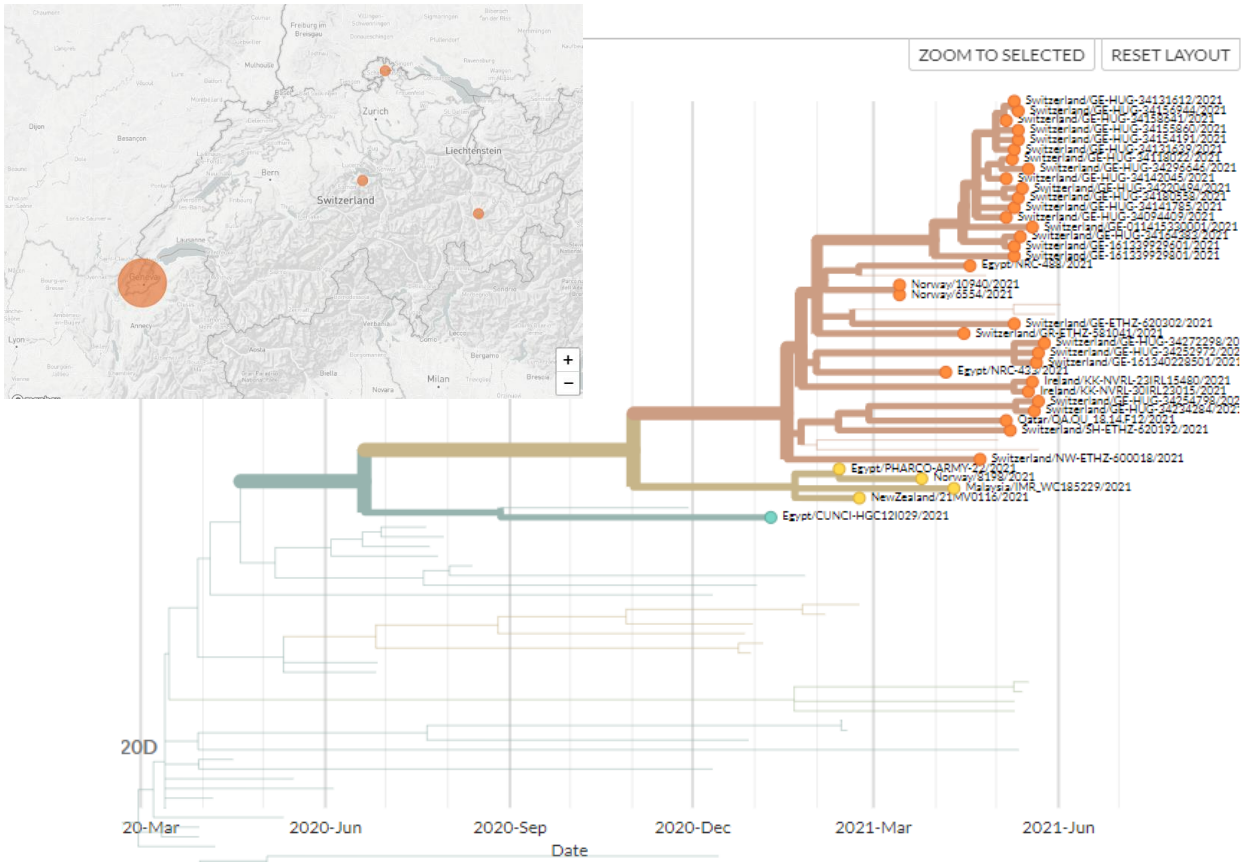
Most of the 452R positive circulating variants are C.36.3 variants, which have been detected circulating at a low level in the Geneva area since the beginning of this sequencing program in January 2021. The low number of sequenced cases, and the important contact tracing

performed around infected persons carrying 452R mutations does not allow us to conclude anything regarding the dynamics between the different variants.

Two more cases of the B.1.617.2 (delta) variant collected over the time period surveilled in this report have been confirmed by sequencing (Figure A), and are linked to a previously known cluster, according to the cantonal physician team. A total of 18 B.1.617.2 cases have been confirmed by whole-genome sequencing since mid-April (Figure B). So far this variant does not seem to be outcompeting B.1.1.7 here in the Geneva area.

Note that a specific cluster of C.36 is observed in Geneva, which is not present in the rest of Switzerland (see below). Most sequences of the C.36 variants in Switzerland originate from the Geneva area.

Phylogenetic analysis on the C36.3 variant circulating in Switzerland



Dynamic interaction is available at https://nextstrain.org/groups/swiss/ncov/CH-geneva?c=gt-S_346,452&f_pango_lineage=C.36&label=clade:20D
On the map, the size of the dot is proportional to the number of sequences.
Colors depict the genotype at S site at the 346 and 452 positions: In blue: R/L; in yellow: R/R; in orange: S/R. Note a cluster in Geneva, not linked to other known clusters in other regions.

Post-vaccination infections

In collaboration with the Geneva cantonal physician team, genomic surveillance of post-vaccination breakthrough SARS-CoV-2 infections is ongoing. Around 60 breakthrough infections have been identified in the Geneva canton since the beginning of the vaccination program. The sequence of the SARS-CoV-2 causing the infection is available for more than 1/3 of them. In almost all cases (22/23), the variant B.1.1.7 (alpha) was responsible for the post-vaccination infections. Only one case was caused by variant B.1.351 (beta). This finding is in line with the local epidemiology of the circulating variants in the region of Geneva, and does not point to a particular VOC causing these infections. A separate detailed report on breakthrough vaccine infections has been transmitted this week to the FOPH.

Conclusions

- The absolute number of SARS-CoV-2-positive samples and the positivity rate since the end of April, 2021 in the Geneva area continues to decrease.
- The B.1.1.7 variant still represents the vast majority of new SARS-CoV-2 infections in the Geneva area.
-In almost all cases of infection with variants carrying mutations of interest 452R or 484K in Geneva, new cases are linked to previously known clusters or to secondary cases linked to a new importation according to the cantonal physician team.
- Variants carrying the 484K mutation are rare.
- As of today, 18 cases of B.1.617.2 have been identified in Geneva and confirmed by whole genome sequencing; the two additional cases confirmed this week were linked to a previously known cluster according to the cantonal physician team.
-Most breakthrough vaccine infections are due to B.1.1.7 in the Geneva area. This reflects the local epidemiology of the viruses circulating in Geneva. More details are available in the DGS/HUG report transmitted to FOPH on breakthrough SARS-CoV-2 infections.

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