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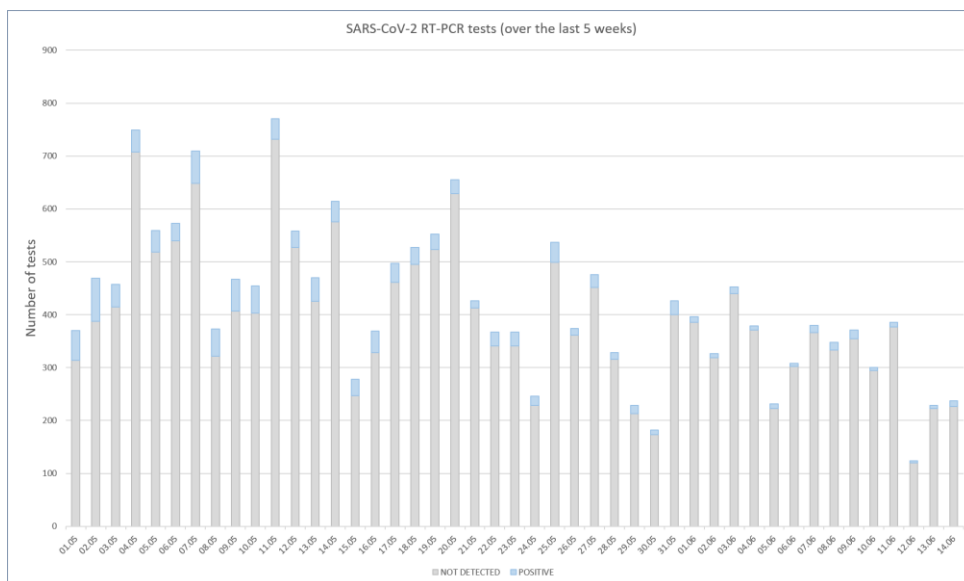
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Diagnostic Department

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

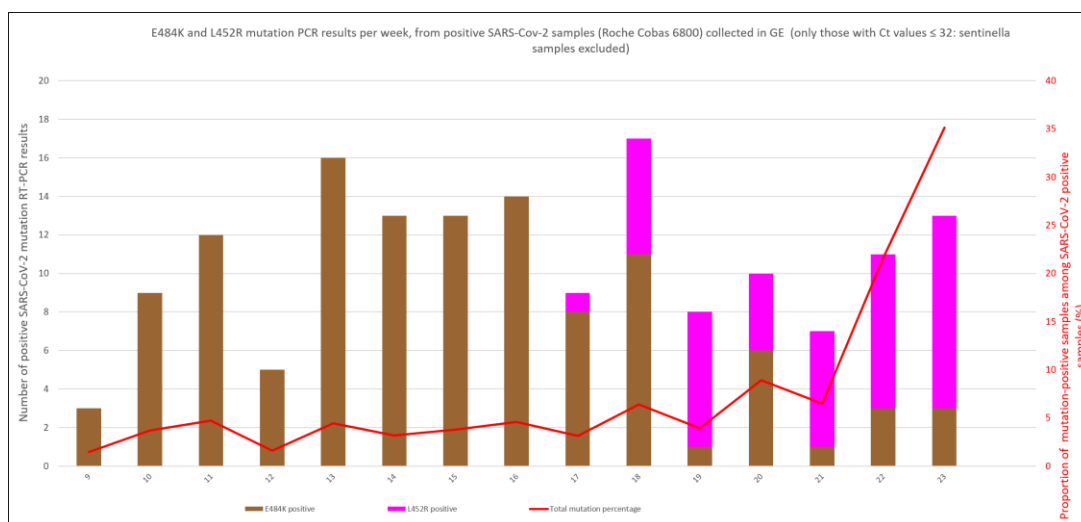
### The laboratory of virology of the Geneva University Hospitals as a sentinel site for the Geneva area

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  $\leq 32$  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. 80 positive tests have been processed at HUG over the last 7 days. The daily number of positive tests at HUG varied between 4 and 19 cases, and the mean positivity rate over the last 7 days fell between 2 and 3%.

### 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 (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. Results are presented by sampling date.

SARS-CoV-2 samples with mutations detected by PCR are now shown according to calendar weeks (including results from Monday to Sunday) and not on a daily basis anymore.

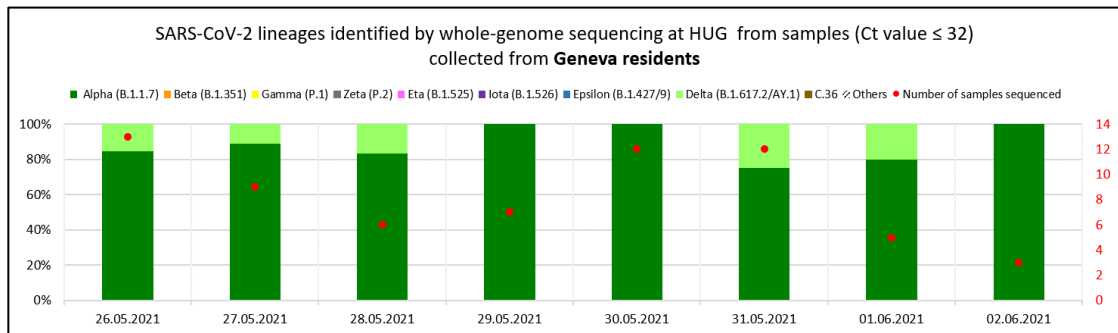
While the number of positive cases is decreasing, the proportion of variants carrying the 452R and 484K mutations is increasing.

The 452R mutation was the most frequently detected over the last three weeks. Importantly, all except one case identified during the last week were 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 were also detected at low level, and all are either linked to previously known transmission chains, or are newly imported.

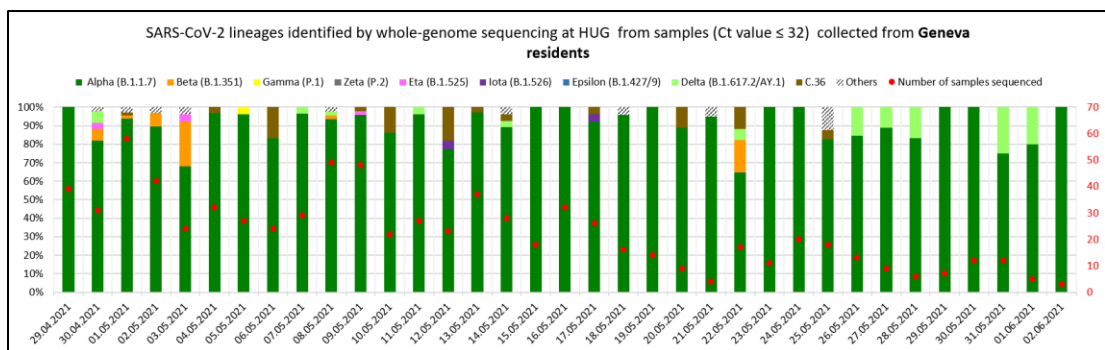
### Whole genome sequencing results performed on SARS-CoV-2 positive samples collected in GE and sent to our laboratory

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 (76 sequences obtained from samples collected from May 26 to June 2, 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 (792 sequences obtained from samples collected from April 29 to June 2, 2021).

While alpha was still the variant causing most of the new infections over the surveilled period, the proportion of delta variant is increasing. This increase in the proportion of the delta variant was not associated with an increase in the number of new cases.

Except for those 2 variants, one possible B.1.620 sequence has been identified (not a VOC but a VOI carrying the 484K mutation). This result is not represented in the graph, because the quality of the sequence was too low, and therefore it didn't meet the inclusion criteria.

Eight 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). Three cases falling in the same cluster were linked to an imported case according to the cantonal physician team. The 5 remaining cases were linked to the same previously known cluster, and their viral sequences contained the additional 417N mutation. The presence of the 417N mutation in the B.1.617.2 (delta) lineage is the hallmark of the AY.1 (or B.1.617.2.1) lineage, originating from B.1.617.2, and also considered a VOC (delta + 417N).

A total of 26 B.1.617.2 cases (with or without 417N) have been confirmed by whole-genome sequencing since mid-April (Figure B) in the Geneva area.

## 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 majority of new SARS-CoV-2 infections in the Geneva area.
- The proportion of positive tests carrying the 452R is progressively increasing over the last weeks. This is not associated with an increase in the number of new cases; importantly, all but one cases of new infections with variants carrying mutations of interest 452R or 484K in Geneva are linked to previously known clusters or to secondary cases linked to a new importation according to the cantonal physician team.
- Since its first identification in mid-April, a total of 26 B.1.617.2 (delta) sequences have been confirmed among samples collected from Geneva residents sent for primary diagnostic at HUG (over 792 sequences submitted to GISAID over the same period). Transmission chains were identified for all cases, according to the cantonal physician team.
- Both B.1.617.2 (delta) and AY.1 (delta + 417N) are circulating in the Geneva area.



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