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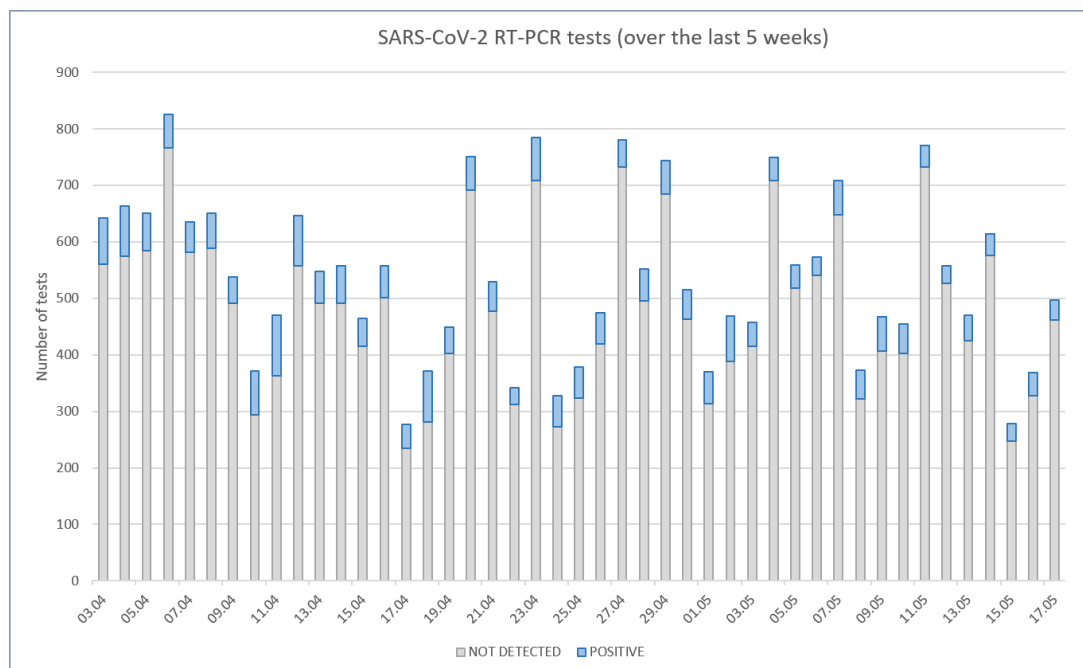
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Diagnostic Department

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

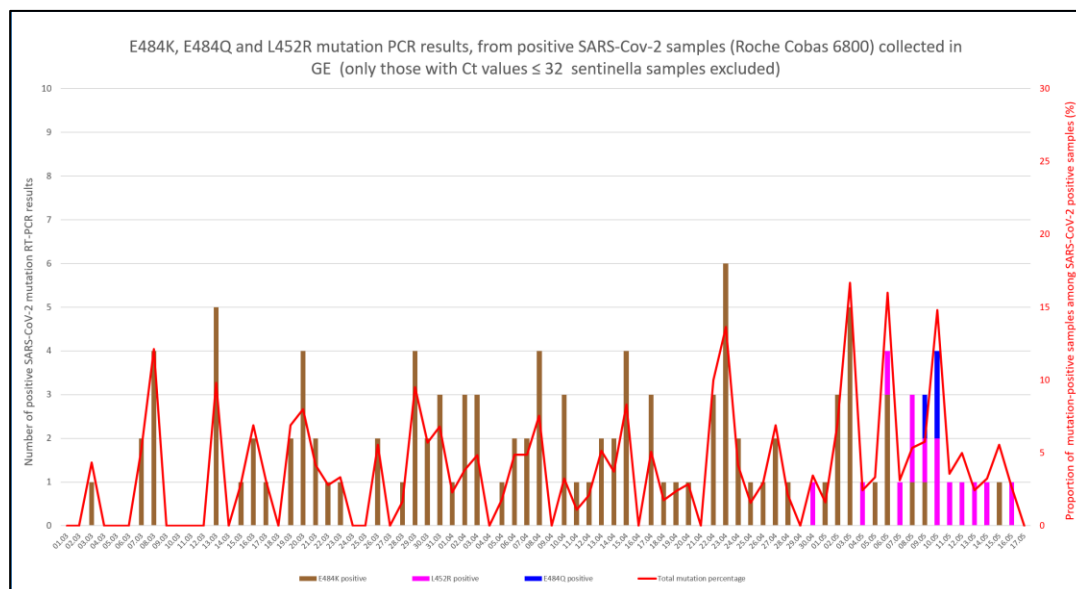
### The laboratory of virology of the Geneva University Hospitals as a sentinel site for the Geneva area

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. It is based on a daily random sampling of SARS-CoV-2 positive specimens by RT-PCR, with a Ct value  $\leq 32$  as the only selection criterion. 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 absolute number of positive cases diagnosed at HUG have been steadily diminishing over the last 20 days, to 30-40 cases per day over the last week.

### 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 is done on E484K-positive samples, and allows to presumably distinguish 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, and does not include mutations results obtained in SARS-CoV-2-positive samples sent from other laboratories.

Since the implementation of the systematic screening of the 452R mutation, 22 specimens carrying this mutation have been detected in the Geneva area (positive samples tested in our laboratory for primary diagnostic (pink bars) and external samples sent for specific mutation screening to HUG). This mutation, among others, is present, but not exclusively, in B.1.617 (Indian) variants. The increase in detection of the 452R mutation may be biased by the fact that this mutation has been retrospectively looked for during backward contact-tracing.

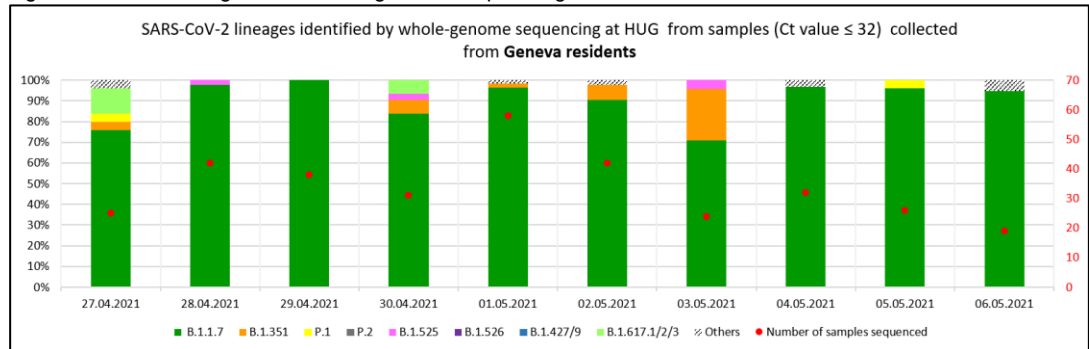
Precise variant typing will be provided by ongoing whole genome sequencing.

Variants carrying the 484K mutation have been and still are circulating at a low level in the community since the implementation of their screening at the end of January, and seem to be decreasing over the last few days.

The first three cases of variants carrying the 484Q mutation, without the 452R mutation have been identified. Sequencing is ongoing to determine the lineage.

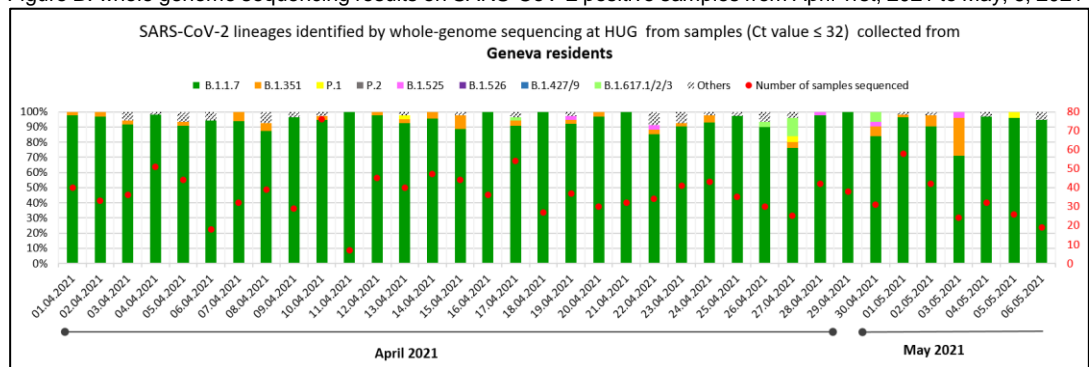
## Whole genome sequencing results performed on SARS-CoV-2 positive samples collected in GE and sent to our laboratory

Figure A: data including the last whole genome sequencing series



This graph displays the sequences with 95% of positions covered  $\geq 15x$  and submitted to GISAID (369 sequences obtained from samples collected from April, 27 to May, 6, 2021).

Figure B: whole genome sequencing results on SARS-CoV-2 positive samples from April 1st, 2021 to May, 6, 2021



This graph displays the sequences with 95% of positions covered  $\geq 15x$  and submitted to GISAID (1317 sequences obtained from samples collected from April, 1 to May, 6, 2021).

B.1.1.7 is still causing almost all new SARS-CoV-2 infections.

We continue to observe a low circulation of variants carrying the 484K mutation in the last sequencing batch, which covers the period from April, 27 to May, 6, 2021:

- 13 new B.1.351 (first detected in South-Africa) sequences have been identified (sharp increase in absolute number for the first time; however the proportion of variants carrying the 484K mutations the following assessed by specific RT-PCR assay is again low, see above)
- 1 new P.1 (originating from Brazil) variant
- 2 B.1.525 (first detected in Nigeria, now circulating worldwide) variant, not considered as a VOC but a VOI.

Two more cases of the B.1.617.2 (first detected in India) variant have been confirmed by sequencing (Figure A). Since the first case of B.1.617.2 was detected on April 17, 2021 in the Geneva area, in a returning traveler, a total of 7 different people have been confirmed by sequencing to have a SARS-CoV-2 infection due to B.1.617.2. More cases, for which sequencing is still ongoing or impossible due to technical reasons, are epidemiologically linked to the same cluster according to the cantonal physician team. When available, testing for the 452R mutation is positive in those linked cases.

Of note, the last WGS series revealed 3 cases of the C.36 variant (country of first detection Egypt), which, like B.1.617.2, carries the 452R mutation. This variant is not yet considered as a VOC/VOI, but is a variant under monitoring. Cases are linked to a cluster, according to the cantonal physician team.

## Conclusions

- The absolute number of SARS-CoV-2-positive samples and the positivity rate since the end of April, 2021 in the Geneva area are decreasing.
- The B.1.1.7 variant still represents the vast majority of new SARS-CoV-2 infections in the Geneva area.
- Variants carrying the 484K mutation have been detected. This includes B.1.351, which is circulating at a low level, and B.1.525 and P.1.
- As of today, 7 cases of B.1.617.2 have been identified in Geneva and confirmed by whole genome sequencing. While most cases are epidemiologically linked together within the same cluster or have been diagnosed in returning travelers, in 1 isolated case investigation is still ongoing to determine the source of the infection, according to the cantonal physician team.
- Another variant carrying the 452R mutation, C.36, considered as a variant under monitoring, is circulating in the Geneva area.



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