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Division of Infectious Diseases

Department of Medicine

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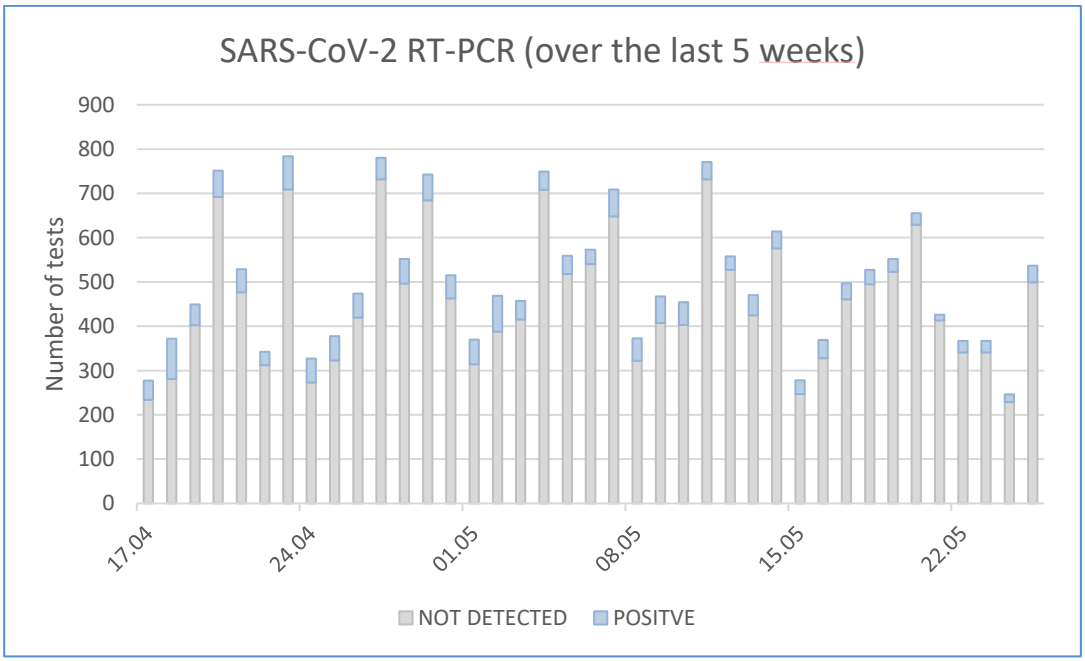
SARS-CoV-2 genomic and variants surveillance in Geneva: weekly update

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 ≤ 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 has continued its progressive decline since the beginning of May, with currently 10-40 cases per day over the last week.

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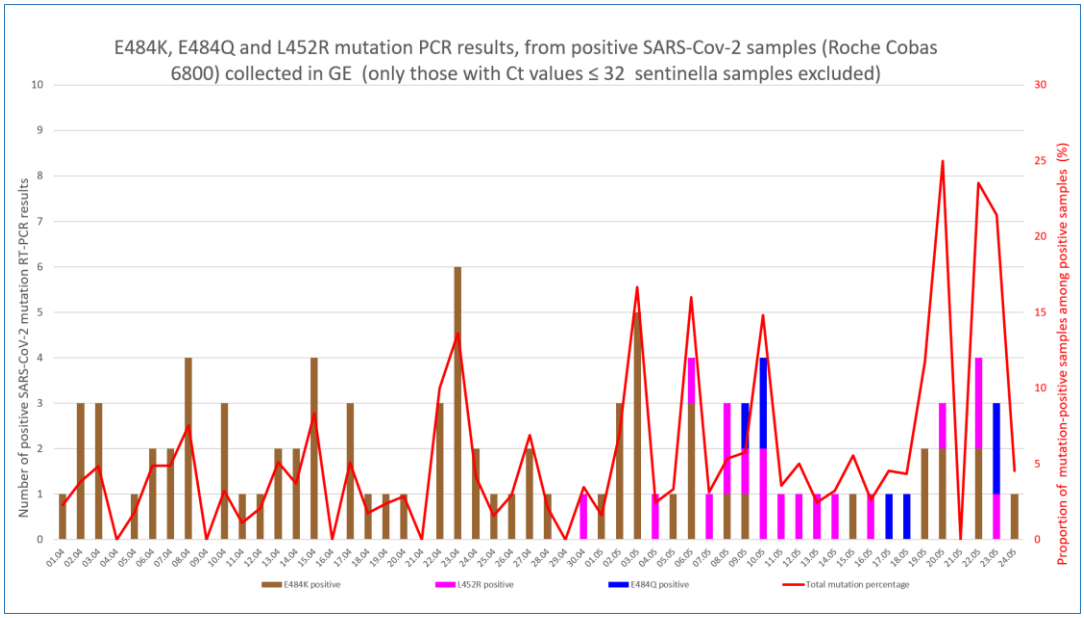
Specific mutations screening by RT-PCR among SARS-CoV-2 positive samples collected in GE and sent to our laboratory for primary diagnosis



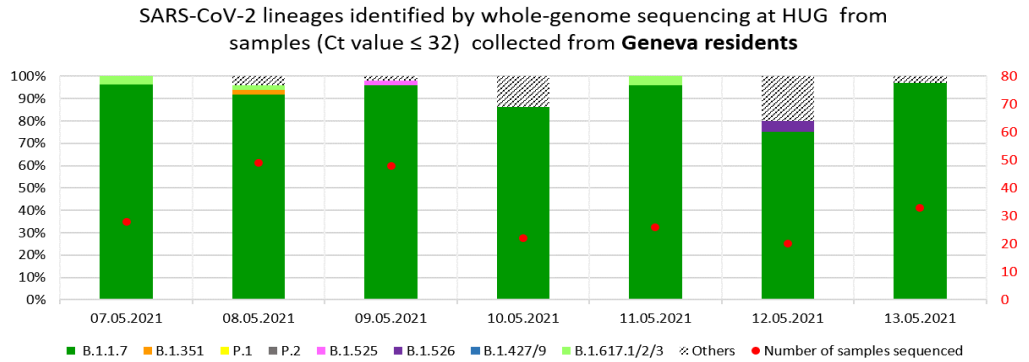
Starting date of E484K/Q mutation screening: January, 27, 2021. Starting date of 417N/T mutation screening: March, 3, 2021. This 417N/T screening is done on E484K-positive samples, and presumably allows distinguishing between B.1.351 and P.1 (not depicted on this graph). Starting date of L452R mutation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

The proportion of positive samples carrying a mutation of interest (E484K, E484Q and/or L452R) is increasing, in parallel to the decrease in the number of positive cases. The absolute number of positive cases carrying a mutation of interest has stayed stable over the last weeks.

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

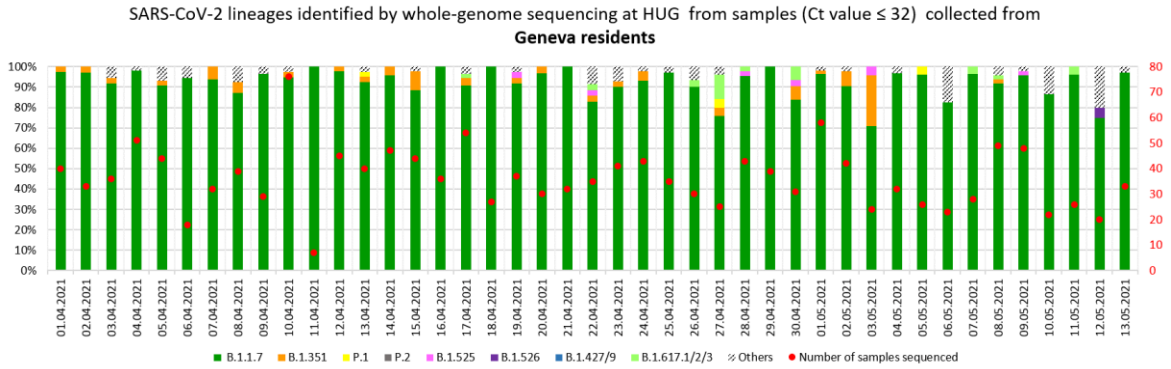
Whole genome sequencing results performed on SARS-CoV-2 positive samples collected in GE and sent to our laboratory

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 (233 sequences obtained from samples collected from May, 7 to May, 13, 2021).

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



This graph displays the sequences with 95% of positions covered ≥ 15x and submitted to GISAID (1 550 sequences obtained from samples collected from April, 1 to May, 13, 2021).

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

We continue to observe a low-level circulation of variants carrying the 484K mutation in the last sequencing batch, but spread across more lineages:
-1 new B.1.351 (first detected in South-Africa) sequence has been identified
-no new P.1 (originating from Brazil) sequences have been identified in the last series
-1 B.1.525 (first detected in Nigeria, now circulating worldwide) sequence, not considered as a VOC but a VOI, has been identified
-1 B.1.565 (New-York) variant, also considered a VOI and not a VOC, has been identified.

Six more cases of the B.1.617.2 (first detected in India) variant have been confirmed by sequencing (Figure A), for a total of 13 B.1.617.2 cases confirmed by whole-genome sequencing since mid-April. The increase in the number of new positive cases is biased due to intensive contact tracing investigations, including backward tracing.

We still occasionally detect the C.36 variant (not a VOC but a variant under monitoring, also carrying the 452R mutation), which has been circulating at low level in Geneva since the beginning of March. It is represented in hatched grey among “others” variants. Since, like the B.1.617.2 variant, it carries the 452R mutation, its detection has benefited from an intensive contact tracing investigation.

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. No variant seems to be able to outcompete it so far. The absolute number of cases infected by the B.1.617.2 (Indian) variant is too low to be able to draw solid conclusions regarding its transmission dynamics.
- 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 B.1.526.
- As of today, 13 cases of B.1.617.2 have been identified in Geneva and confirmed by whole genome sequencing.
-Specimens identified carrying the 452R mutation also include a large cluster of the C.36 variant, which is not considered as a VOC, nor a VOI, but a variant under monitoring.

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