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Geneva Centre for Emerging Viral Diseases

Division of Infectious Diseases

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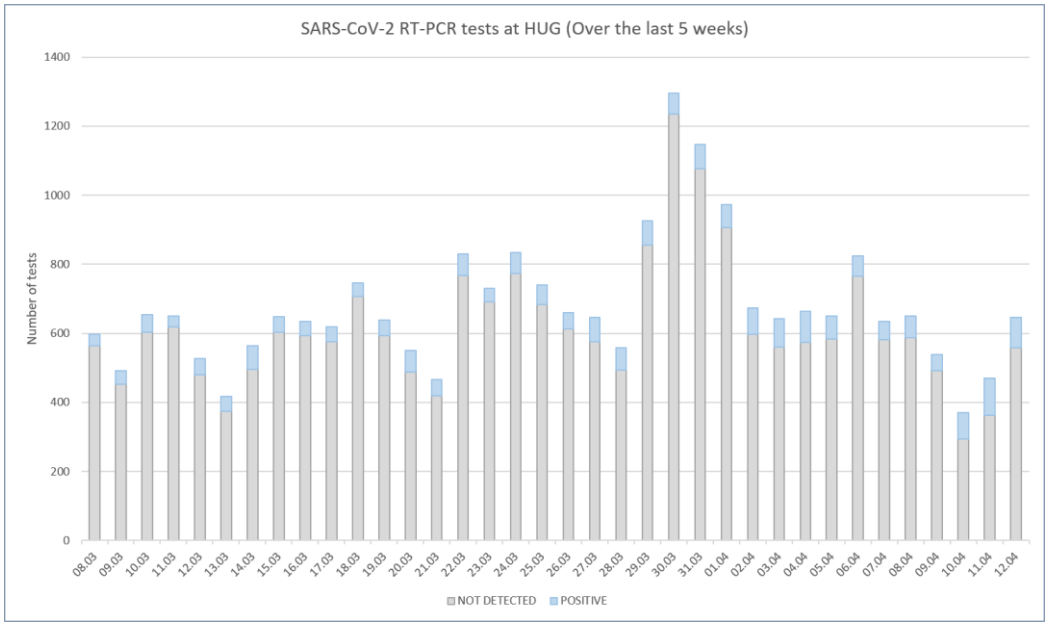
SARS-CoV-2 genomic and variants surveillance in Geneva: weekly update

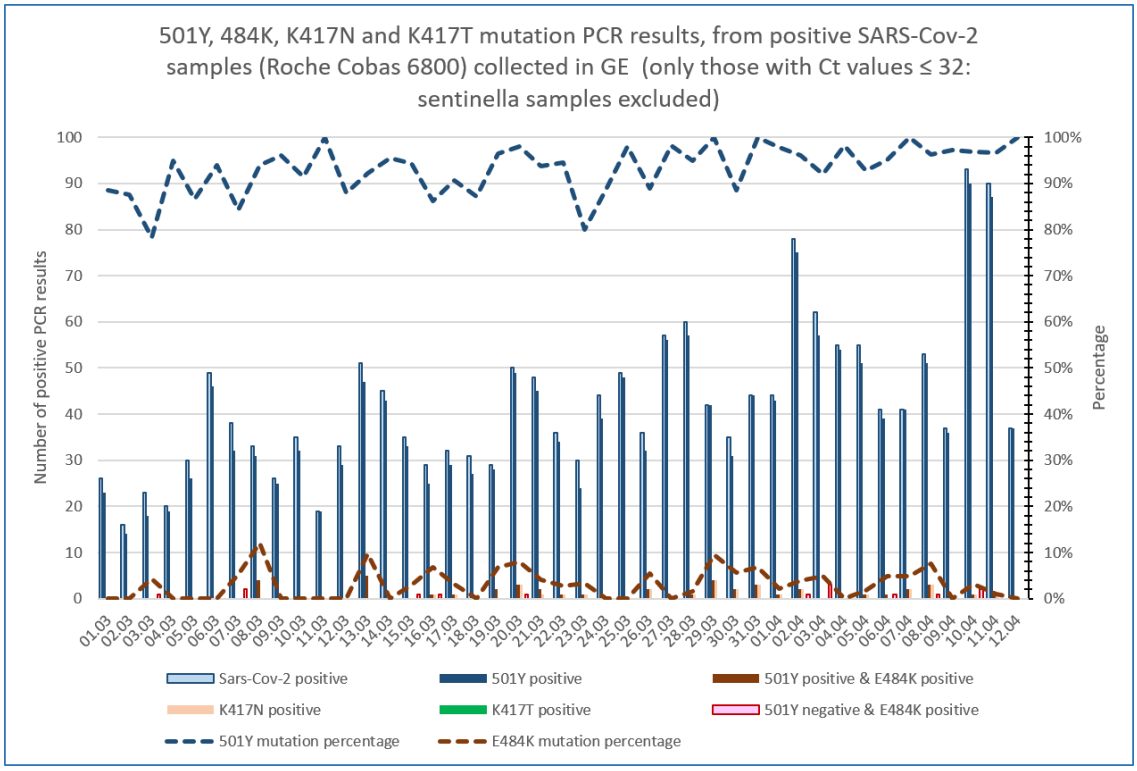
The laboratory of virology of the Geneva University Hospitals as a sentinel site for the Geneva area

The number of tests performed at the laboratory of virology of Geneva University Hospitals represents around 1/3 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.



During the last 3 days, we have observed a sharp increase in the absolute number of positive SARS-CoV-2 specimens tested at our laboratory, with up to more than 100 new positive cases on April, 11. The last time such high numbers of positive tests was observed was in mid-January, 2021.

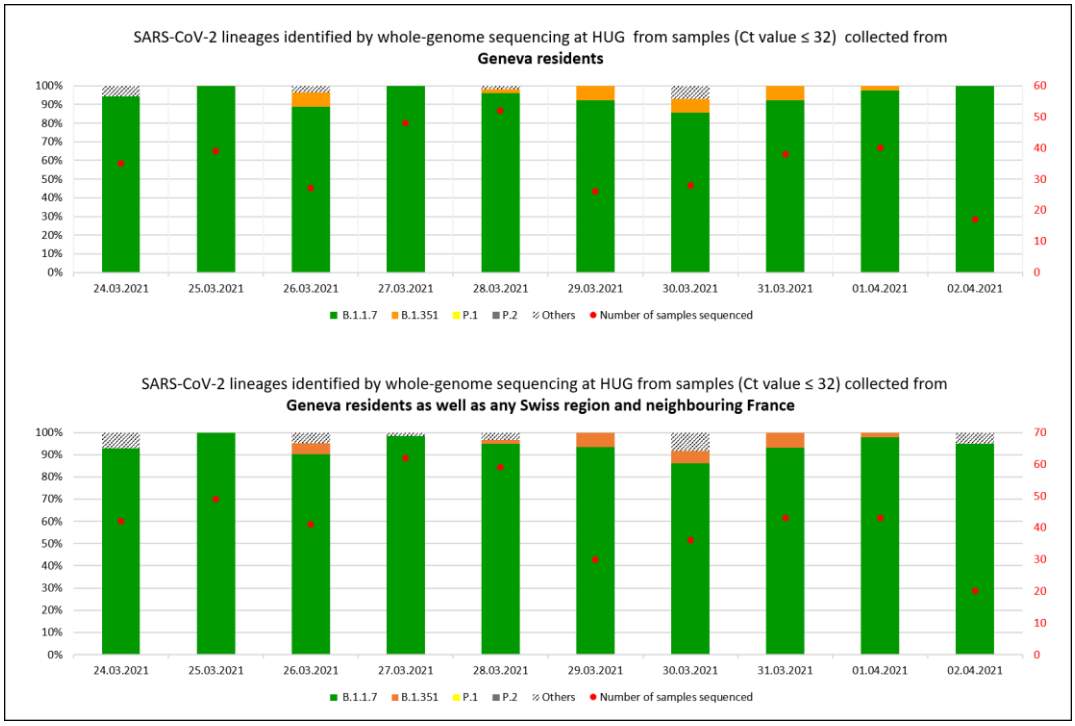
501Y and 484K mutation screening by RT-PCR among SARS-CoV-2 positive samples collected in GE and sent to our laboratory for primary diagnosis



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. Starting date of N501Y mutation screening: January, 5, 2021. Starting date of E484K mutation screening: January, 27, 2021. Starting date of 417N/T mutation screening: March, 3, 2021.

As observed since the end of February, almost all new positive cases are due to variants carrying the 501Y mutation. Variants carrying the 484K mutation (mainly B.1.351 and P.1, see below) have been circulating at a low level in the community in the Geneva area since mid-March.
We plan to stop the testing of the 501Y mutation by the end of the week because of its high prevalence in the community. We will however continue to screen specimens for the E484K mutation, considering its potential for immune escape.

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



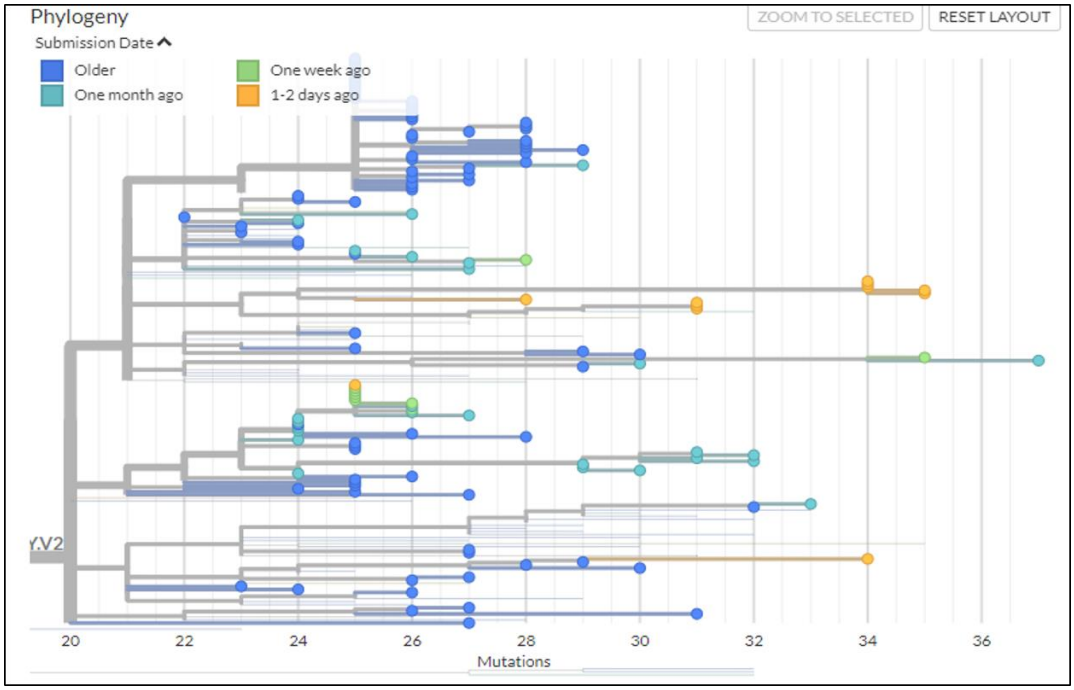
This graph displays the sequences with 95% of positions covered ≥ 15x and submitted to GISAID (425 sequences obtained from samples collected from March, 24 to April, 2 2021).

B.1.1.7 has been generating almost all new SARS-CoV-2 infections since the end of February, as confirmed by whole genome sequencing.

B.1.351 is still circulating at a low level in the community. No new P.1 sequence has been retrieved over the surveilled period.
No other VOC/VOI has been identified over this period of time.

The B.1.214.2 variant (not a VOC - coming from Belgium) is still being observed circulating at low level in the community, mostly affecting children below 15 years old; its circulation has been observed since mid-March.

Phylogenetic analysis produced by Nextstrain based on those data showed that most (9/11) new B.1.351 specimens identified during the surveyed period (here in orange) are not linked to previously known transmission chains in Geneva, but fall into a new cluster.
For information, the Whole Genome Sequencing national surveillance program is now active, which will significantly increase in the coming weeks the number of SARS-CoV-2 sequences generated from the different Swiss regions.



https://nextstrain.org/groups/swiss/ncov/501Y.V2?c=recency&f_country=Switzerland&label=clade:20H/501Y.V2&m=div

Conclusions

-The B.1.1.7 variant is still representing almost all new SARS-CoV-2 contaminations in the Geneva area.
-Testing for the 501Y mutation will be stopped at the end of this week because of its high prevalence.
-Variants carrying the 484K mutations (especially B.1.351) are circulating at a low level in Geneva.
-Monitoring 484K and avoid its spread is of importance, due to its potential for immune/vaccine escape, and we will continue to test for the mutation.
-The whole genome sequencing national program is now active.

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