Hôpitaux Universitaires Genève

UNIVERSITÉ DE GENÈVE
FACULTÉ DE MÉDECINE

Federal Office of Public Health FOPH
Public Health Directorate Communicable Diseases Division
Schwarzenburgstrasse 157
3003 Berne
Switzerland

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Geneva Centre for Emerging Viral Diseases

Division of Infectious Diseases

Department of Medicine

Laboratory of virology

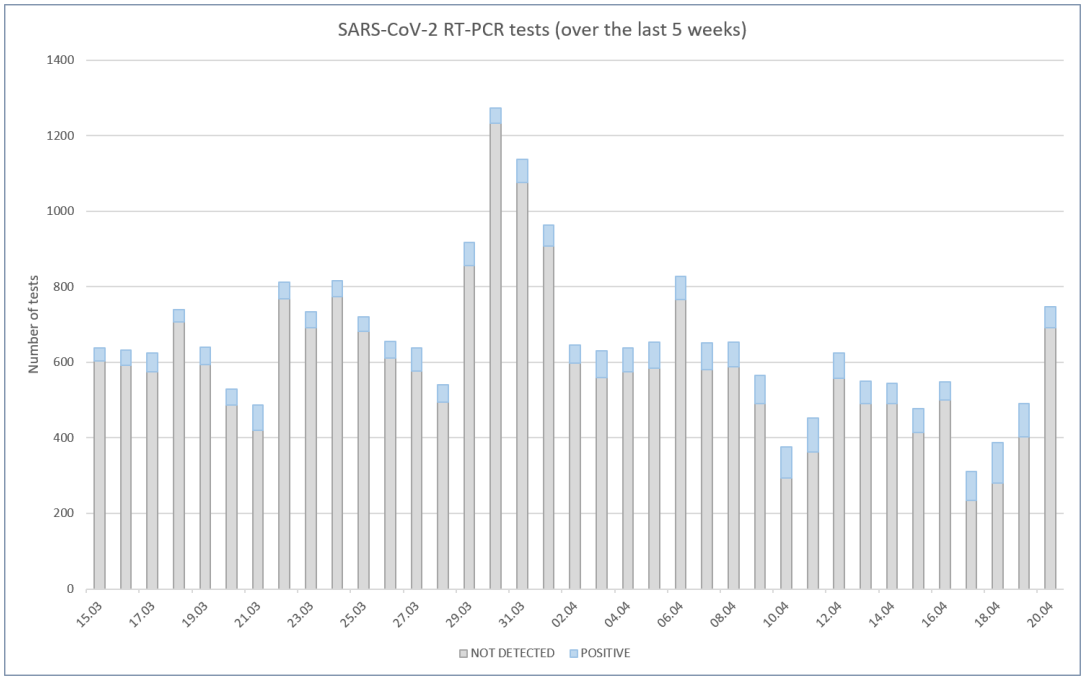
Division of Laboratory Medicine

Diagnostic Department

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

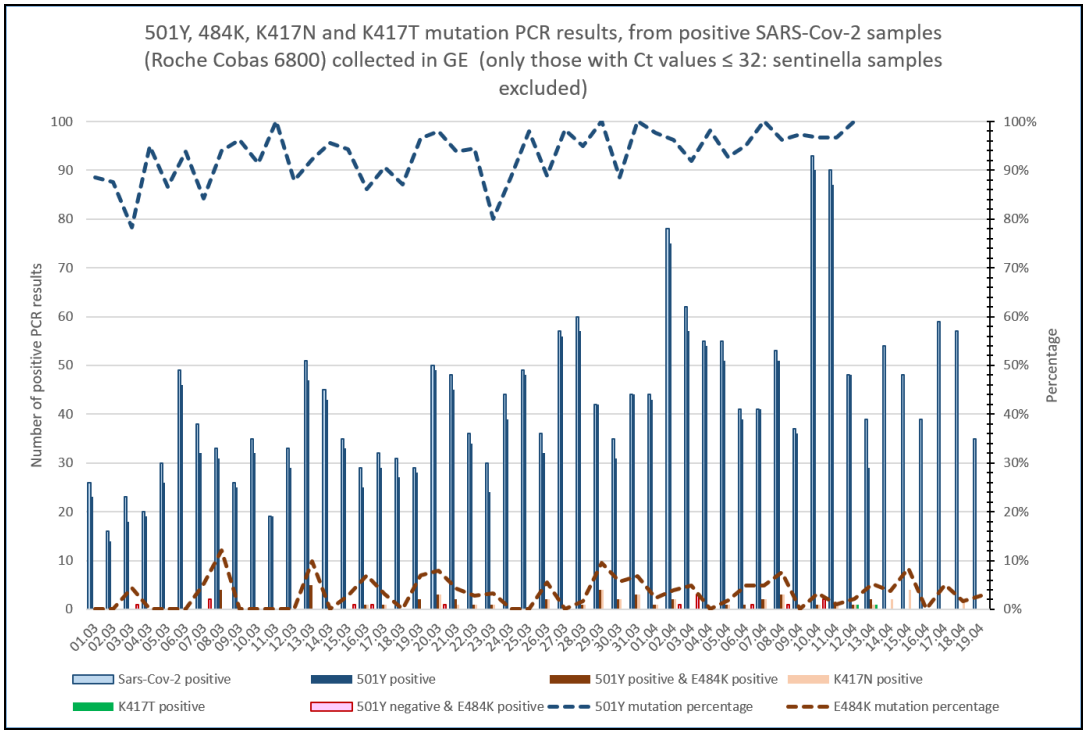
The laboratory of virology of the Geneva University Hospitals as a sentinel site for the Geneva area

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



We observed a decrease in the total number of tests performed at our laboratory over the last week. The overall positivity rate is stable, and is between 10 and 15%.

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

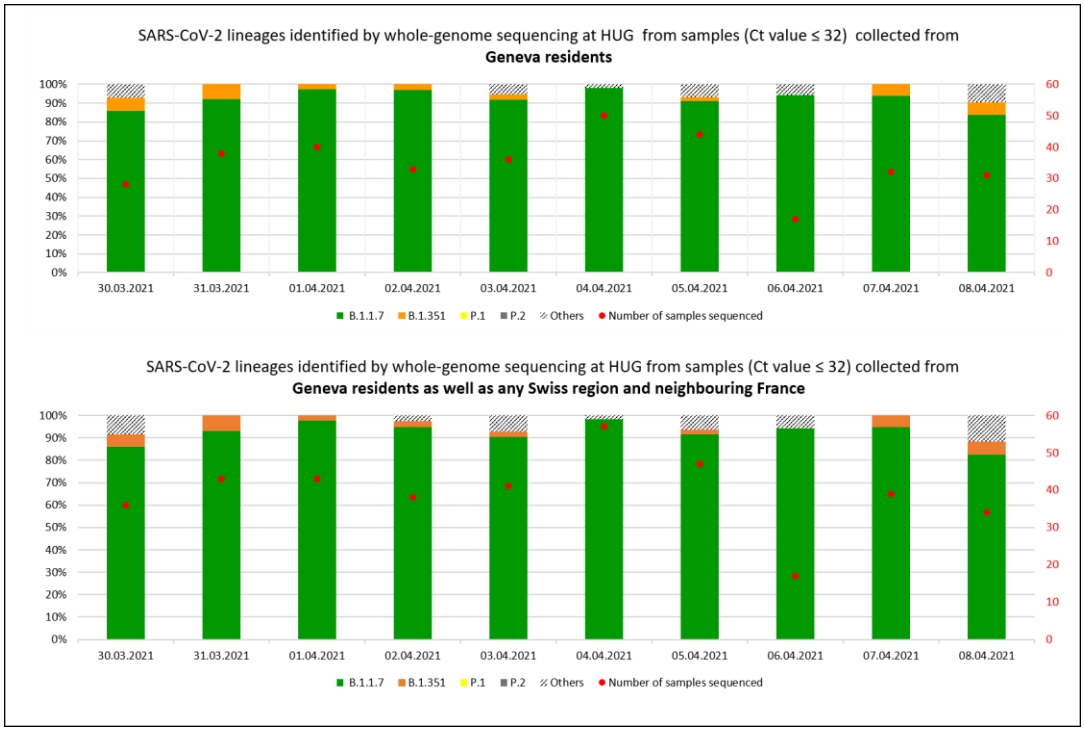


Among all SARS-CoV-2 RT-PCR-positive samples identified in our laboratory, all those with a Ct value ≤ 32 are subsequently screened for the 501Y and 484K mutations by specific RT-PCR assays. Specimens carrying the 484K and the 501Y mutations are subsequently tested for the 417N/T mutation. Period of N501Y mutation screening: January, 5, 2021 to April, 13, 2021. Starting date of E484K mutation screening: January, 27, 2021. Starting date of 417N/T mutation screening: March, 3, 2021.

Because almost all new positive cases are due to variants carrying the 501Y mutation, our laboratory stopped the screening for this mutation on April 13, 2021. We are continuing to screen specimens for the E484K mutation, considering its potential for immune escape.

As shown by the brown dotted-line, variants carrying the 484K mutation (mainly B.1.351, see below for details) have been circulating at a low level in the community in the Geneva area since mid-March. The proportion of variants carrying the 484K mutation is stable over time, and these don't seem to be able to outcompete B.1.1.7 so far.

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 (395 sequences obtained from samples collected from March, 30 to April, 8 2021).

Because the whole genome sequencing national surveillance program has begun as well as the fact that we no longer perform the PCR 501 routinely, only a few samples are now collected from other Swiss regions and sent to our laboratory, which explains why both graphs are nearly identical.

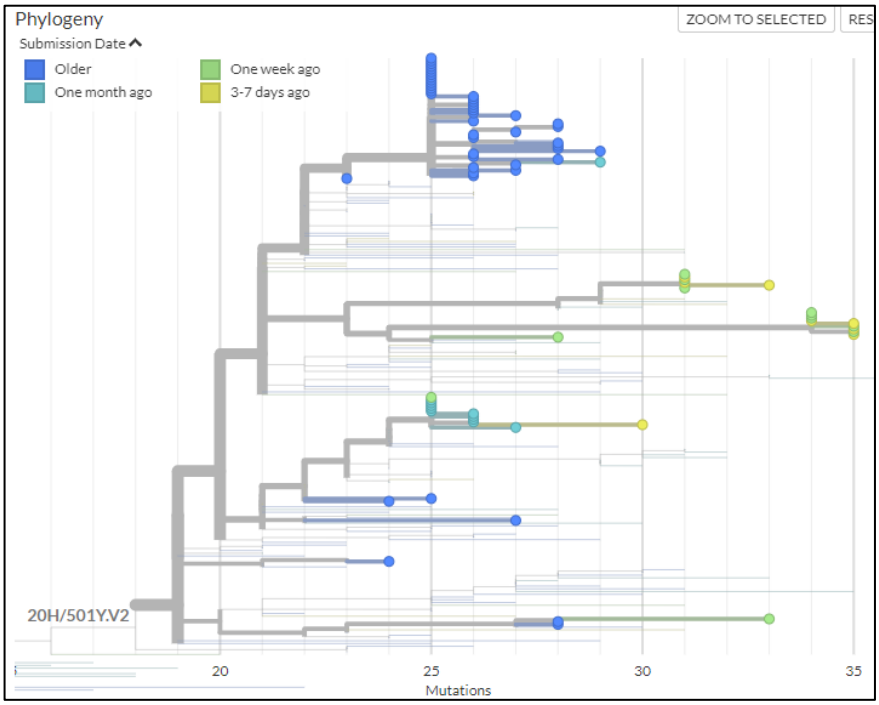
B.1.1.7 has been causing almost all new SARS-CoV-2 infections since the end of February, as confirmed by whole genome sequencing.

Over the surveilled period, a higher diversity of variants carrying the 484K mutation have been identified than previously:
-B.1.351 is still circulating at a low level in the community. Almost all new sequences submitted this week to GISAID fall into the new cluster identified last week (see below).
-a variant originating from the B.1 lineage has been identified in Geneva in 3 persons without known epidemiological link according to the cantonal physician team. This variant carrying the 484K mutation has already been identified in Switzerland, in the Neuchatel area.
-a new sequence not described previously, with 6 point mutations on the S gene and one deletion, carrying the 484K mutation, has been retrieved from one adult living in the Geneva area.
-another new sequence, which may have resulted from a recombination event has been identified in a child in the Geneva area.
-no new P.1 sequence has been retrieved over the period of surveillance.

No other VOC/VOI has been identified over this period of time.

More sequences of the B.1.214.2 variant (not a VOC - coming from Belgium and circulating in the Geneva area at very low level since mid-March) is still being observed.

Phylogenetic analysis of SARS-CoV-2 genomes retrieved in the Geneva area in their context (data shown for the B.1.351 lineage)



https://nextstrain.org/groups/swiss/ncov/501Y-V2?c=recency&f_country=Switzerland&f_division=Geneva&label=mlabel:20C/C28253T&m=div

Phylogenetic analysis data are produced by Nextstrain, in collaboration with Richard Neher's group at the University of Basel.

Conclusions

-The B.1.1.7 variant still represents almost all new SARS-CoV-2 infections in the Geneva area.
-Variants carrying the 484K mutation are currently not able to outcompete B.1.1.7.
-We are starting to observe the emergence of the 484K mutation in a background of sequences in which it has not been described previously in our area. Two new variants carrying the 484K mutation have been identified and will be watched closely over the next weeks.
-No infection by P.1 has been identified in the Geneva area in the last 2 surveilled periods.
-no other VOCs/VOIs have been identified over the period of surveillance.

Laurent Kaiser **Samuel Cordey** **Manuel Schibler** **Pauline Vetter**