

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

N/réf : LK/MS/PV

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Geneva Centre for
Emerging Viral Diseases

Division of Infectious
Diseases

Department of Medicine

Laboratory of virology

Division of Laboratory
Medicine

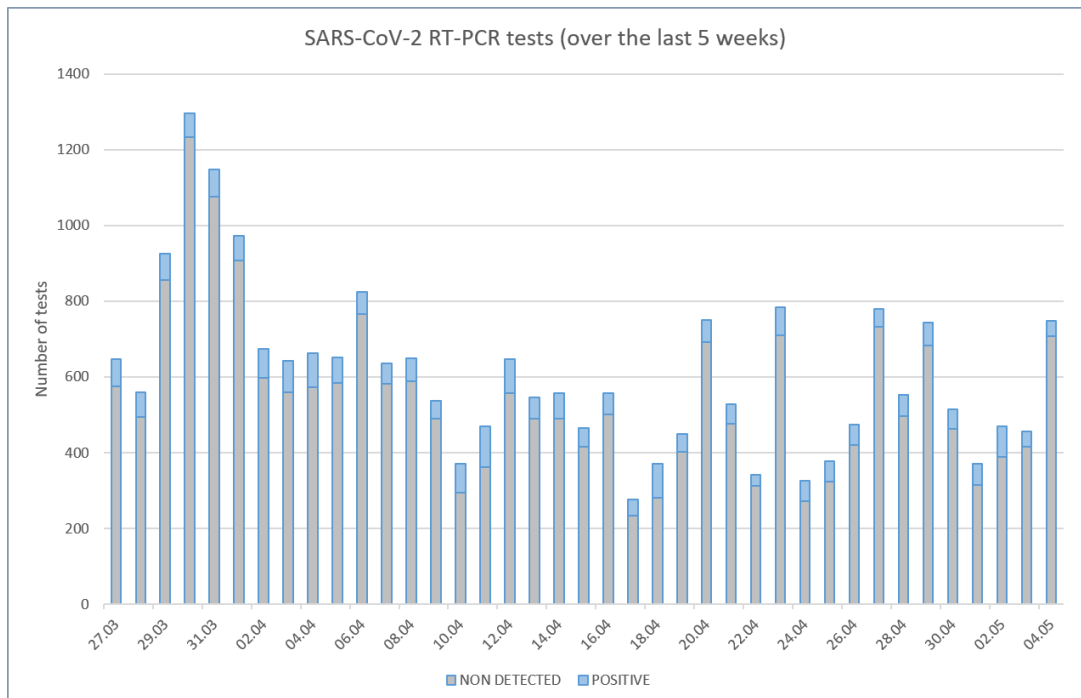
Diagnostic Department

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

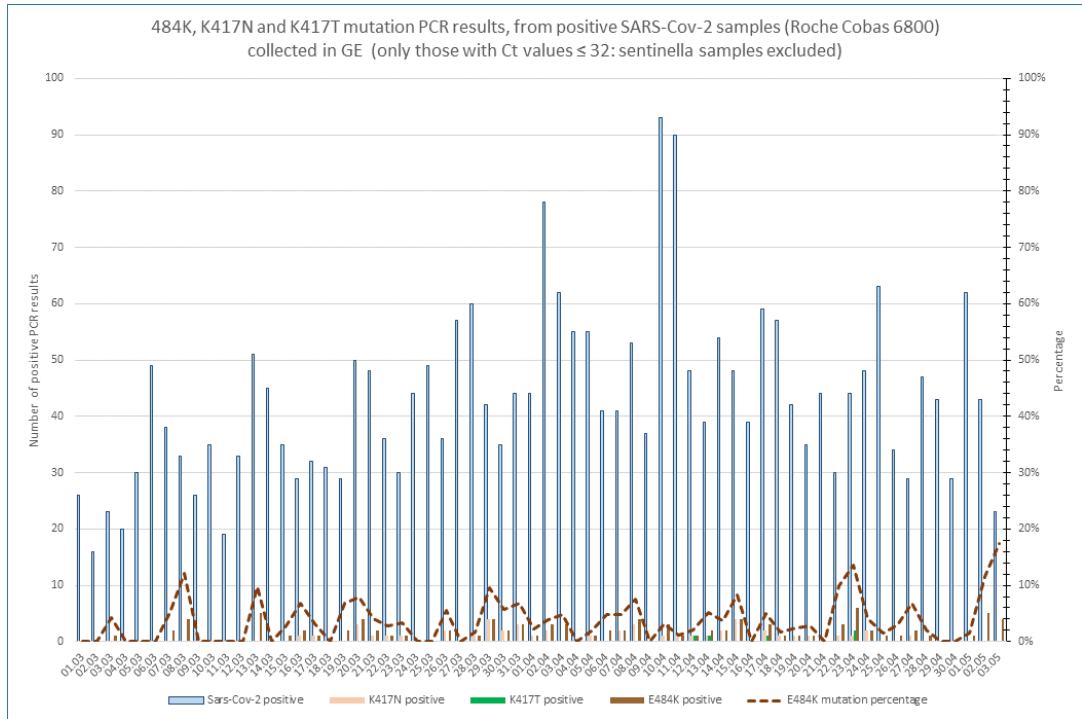
The number of tests performed at the laboratory of virology of Geneva University Hospitals represents around 1/3 of the total number of tests performed in the canton of Geneva. Specimens analyzed in our laboratory come from the community (the majority), from hospital workers (systematic screening in 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.



A trend towards a slight decrease in the positivity rate is observed, and is currently between 5 and 15%.

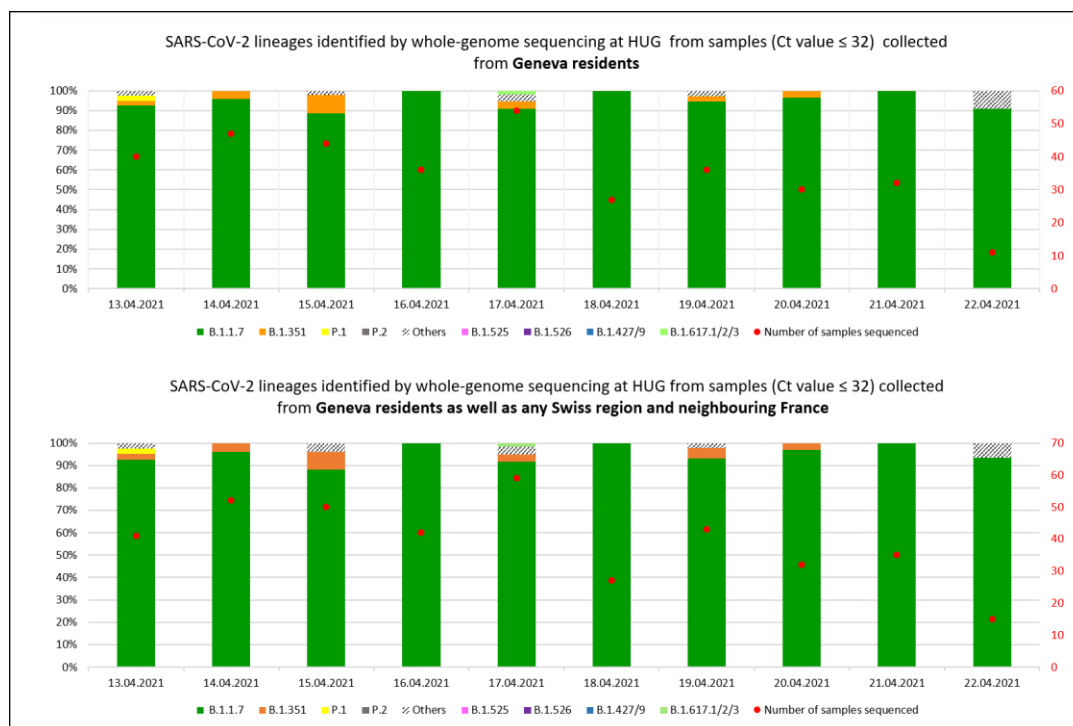
484K mutation screening by RT-PCR among SARS-CoV-2 positive samples collected in GE and sent to our laboratory for primary diagnosis



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

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 globally stable; an isolated increase is on May 3, 2021 (17,3%), without an increase in the absolute number of 484K-positive cases. This finding is currently isolated, and observed on a day during which the number of SARS-CoV-2-positive samples denominator was low. It should therefore not be over interpreted.

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



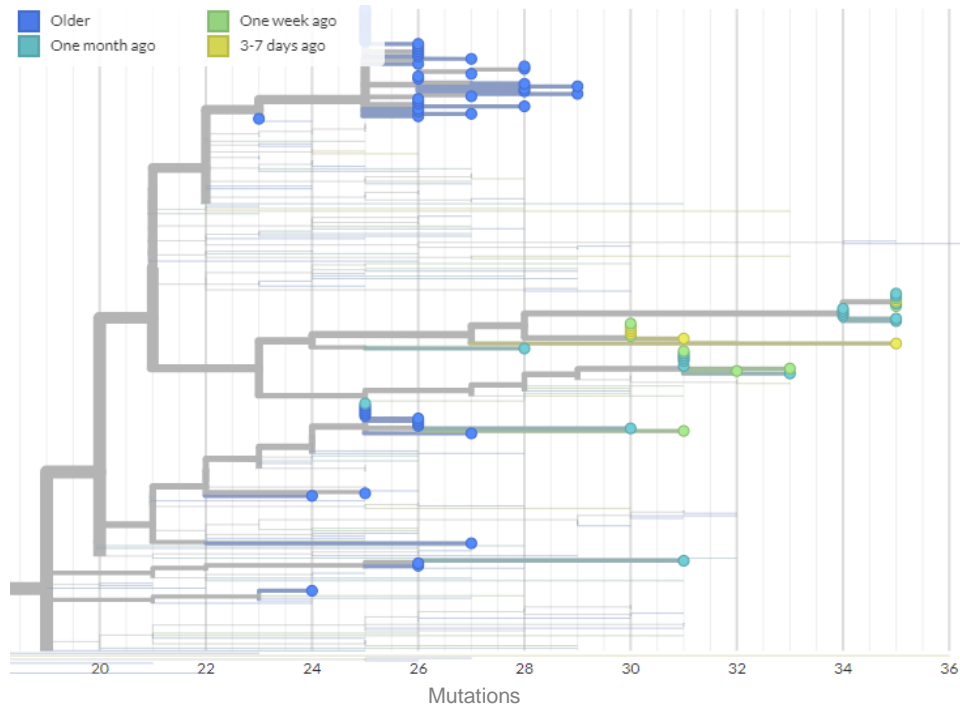
This graph displays the sequences with 95% of positions covered $\geq 15x$ and submitted to GISAID (396 sequences obtained from samples collected from April, 13 to April, 22, 2021).

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.

B.1.351 is still circulating at a low level in the community.

A single P.1 sequence was identified, as well as a B.1.617.2. (one of the variants first detected in India, not harboring the E484Q mutation).

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 SARS-CoV-2 positivity rate seems to slightly decline over the last few days; this trend needs to be confirmed.
- 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 are currently not able to outcompete B.1.1.7.; the isolated finding of a higher proportion of 484K-positive cases observed on May, 3 should not be over interpreted at this time, but warrants close monitoring in the coming days.
- A single P.1, as well as a single B.1.617.2 sequence (one of the variants first detected in India, not harboring the E484Q mutation), have been identified in the Geneva area during the last surveillance period.

Laurent Kaiser

Samuel Cordey

Manuel Schibler

Pauline Vetter