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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

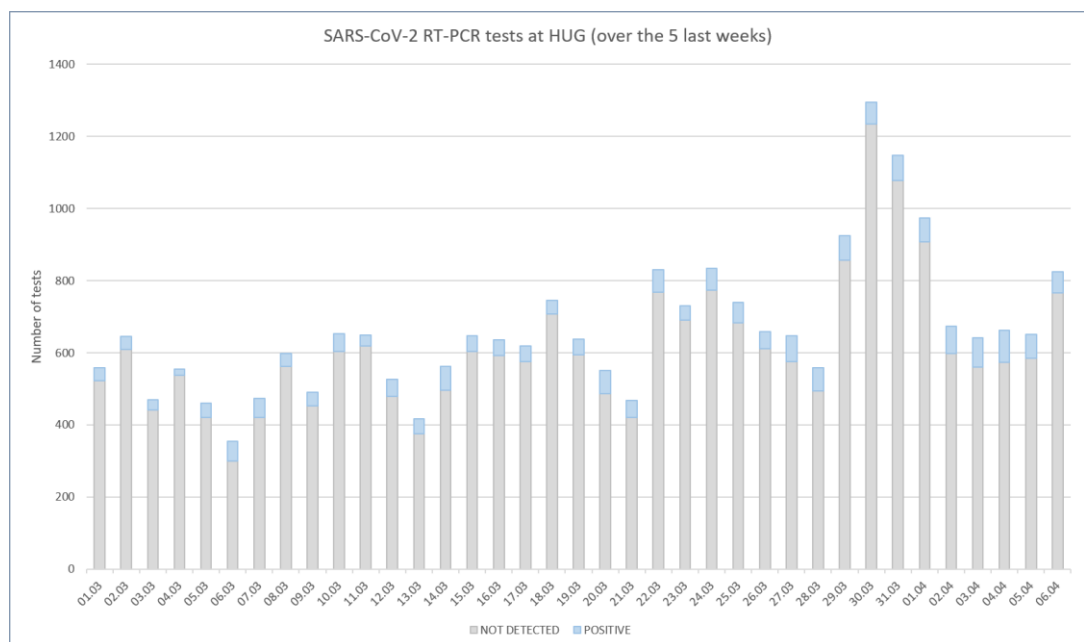
## SARS-CoV-2 genomic and variants surveillance in Geneva: weekly update

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

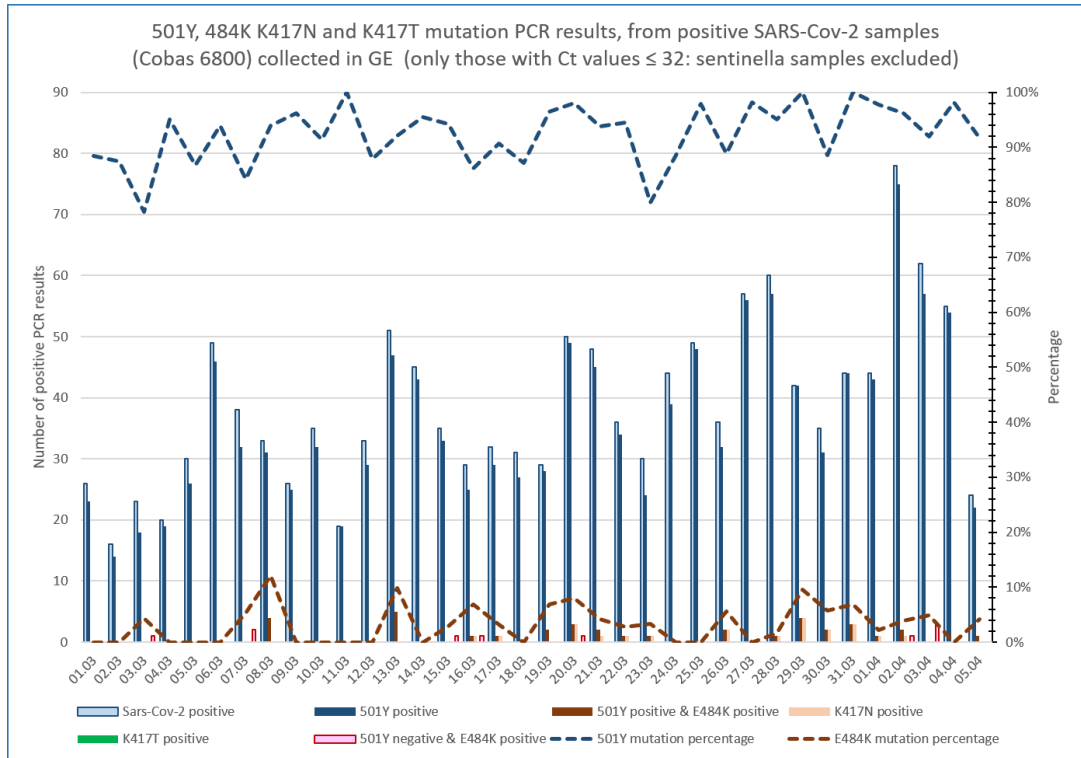
The number of tests performed at the laboratory of virology of Geneva University Hospitals represent around 1/3 of the total number of tests performed in the canton of Geneva. Specimens analyzed in our laboratory come from the community (the majority), from hospital workers (systematic screening in case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

Among all SARS-CoV-2 RT-PCR-positive samples identified in our laboratory, all those with a Ct value  $\leq 32$  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.

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 as only selection criterion a Ct value  $\leq 32$ . In some instances, sequencing can be done in specimens sent by other laboratories in Switzerland.



**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**



The increase in the number of specimens tested at our laboratory between March, 29 and April 1st is mainly due to an increase in the number of asymptomatic subjects that were tested prior to traveling.

Since the end of February, almost all new positive cases are due to variants carrying the 501Y mutation. Variants carrying the 484K mutation (mainly P.1 and B.1.351) are circulating at a low level in the community in the Geneva area since mid-March, and seem to increase in frequency in the last weeks. Several specimen carrying the 484K but without the 501Y mutation have been identified last week. The Geneva cantonal physician team is currently investigating if they are part of a cluster, and sequencing will allow to identify which variant is involved.

**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 (365 sequences obtained from samples collected from March, 16 to March 25, 2021).

B.1.1.7 is generating almost all new SARS-CoV-2 infections since the end of February, as confirmed by whole genome sequencing. B.1.351 and P.1 are still circulating at a low level in the community.

The B.1.214.2 variant, identified in Belgium, is also circulating at low level in Geneva since the beginning of March, mostly in children below 15 years old.

One B.1.526.1 variant (New York variant) has been detected again in Geneva, belonging to the same cluster than the one that was identified last week.

No other variant have been identified so far.

**Conclusions**

-The B.1.1.7 variant is still representing almost all new SARS-CoV-2 contaminations in the Geneva area.

-Variants carrying the 484K mutations (P.1, B.1.351) are circulating at a low level in Geneva and seem to increase in frequency.

-Monitoring 484K and avoid its spread is of importance, due to its potential for immune/vaccine escape.

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