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Geneva, March 31, 2021

N/réf : LK/MS/PV

Geneva Centre for Emerging Viral Diseases

Division of Infectious Diseases

Department of Medicine

Laboratory of virology

Division of Laboratory Medicine

Diagnostic Department

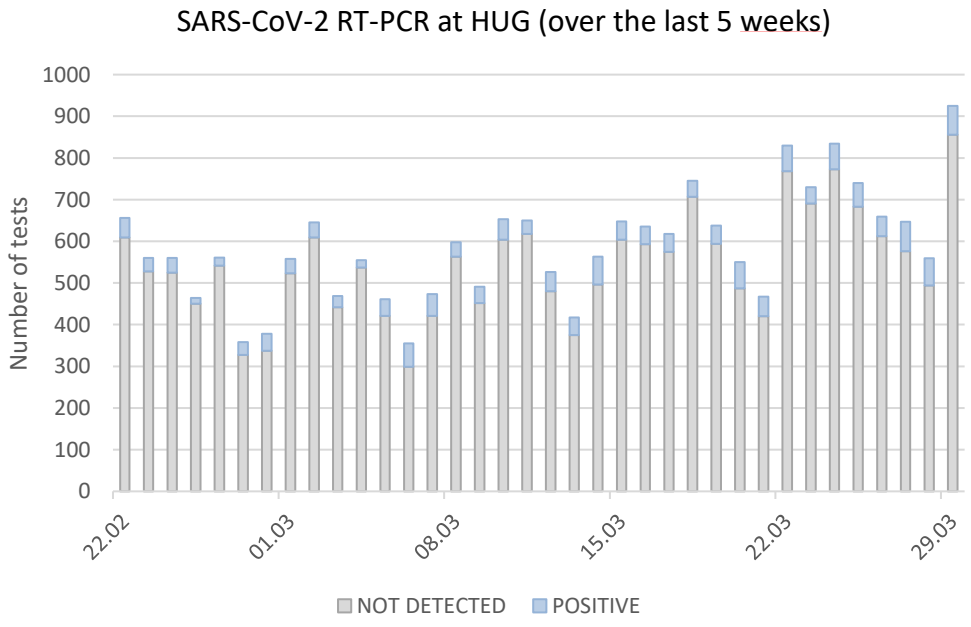
SARS-CoV-2 genomic and variants surveillance in Geneva: weekly update

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 ≤ 32 are subsequently screened for the 501Y and 484K mutations by specific RT-PCR assays. Specimens carrying the 484K mutation 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 is based on a daily random sampling of SARS-CoV-2 positive specimens by RT-PCR with as only selection criterion a Ct value ≤ 32. In some instances, sequencing can be done in specimens sent by other laboratories in Switzerland.



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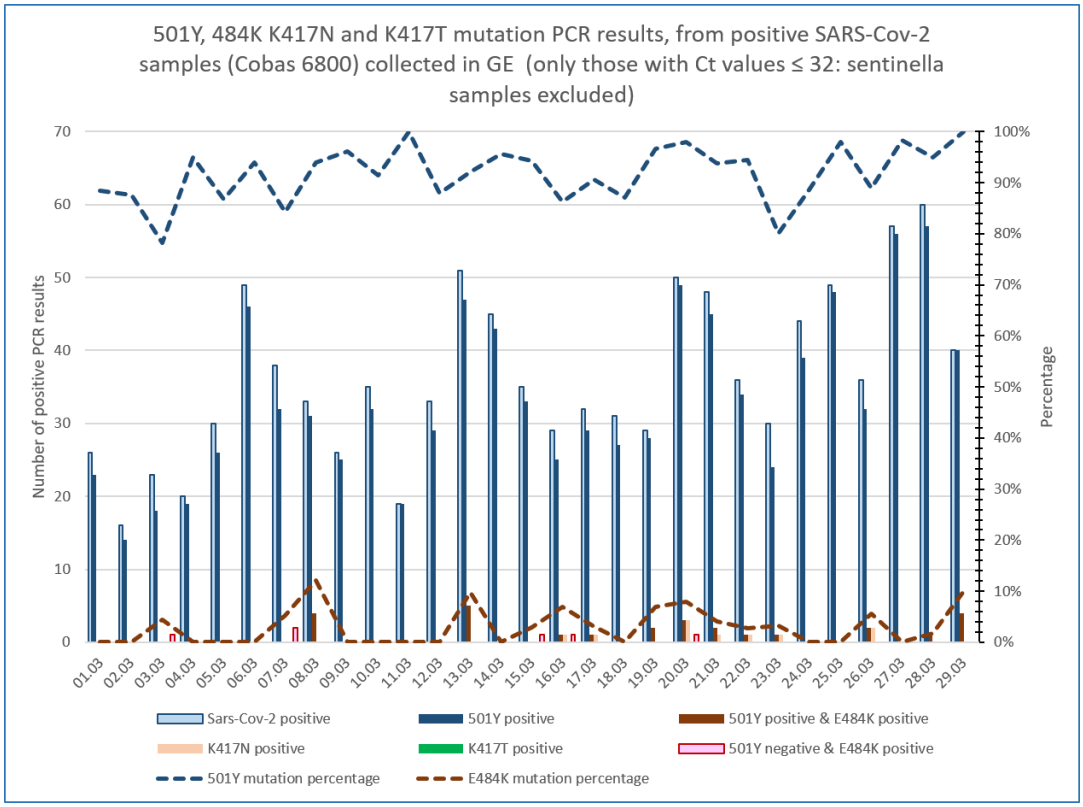
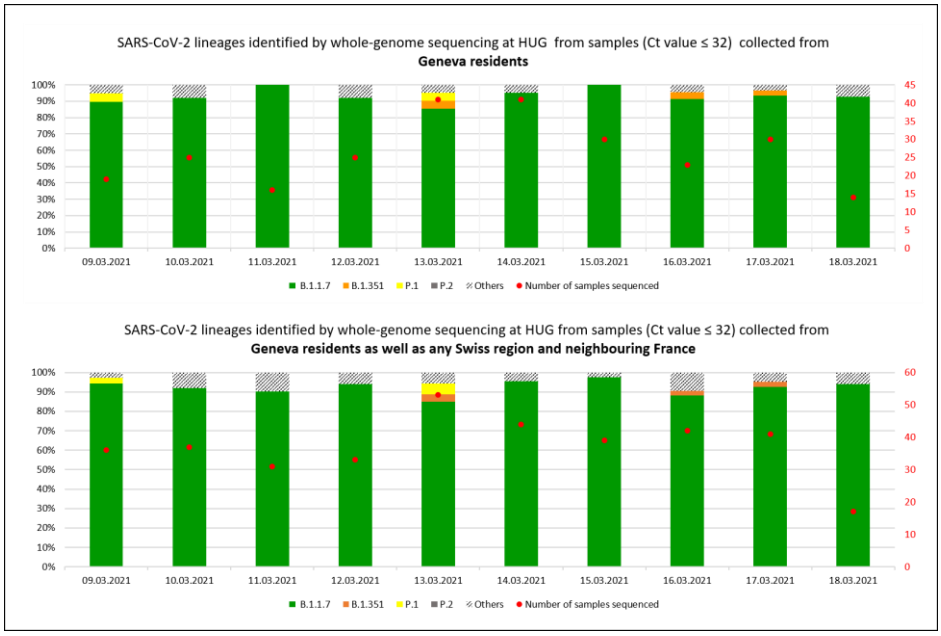
501Y and 484K mutation screening by RT-PCR among SARS-CoV-2 positive samples collected in GE and sent to our laboratory for primary diagnosis



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.

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



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This graph displays the sequences with 95% of positions covered ≥ 15x and submitted to GISAID (373 sequences obtained from samples collected from March, 9 to March 18, 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.
Other variants of interests have been retrieved during the reporting period: one B.1.526.1 sequence, which is 501Y and 484K negative (first detected in New York), but carries the L452R mutation (involved in immune escape). No other variant of concern/interest has been identified over this period.
Low detection of the B.1.214.2 variant (circulating in many European countries, 60% of the reported sequences come from Belgium) has been observed since the beginning of March (7 cases in the last WGS series, samples collected between March 13 and 17). Its phenotypic characteristics are not yet understood.

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.
-Monitoring 484K and avoid its spread is of importance, due to its potential for immune/vaccine escape.
-Genomic surveillance allowed to quickly identify the introduction of the B.1.214.2 in the Geneva area.

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