



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

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N/réf: LK/MS/PV

Geneva Centre for Emerging Viral Diseases

Division of Infectious Diseases

Department of Medicine

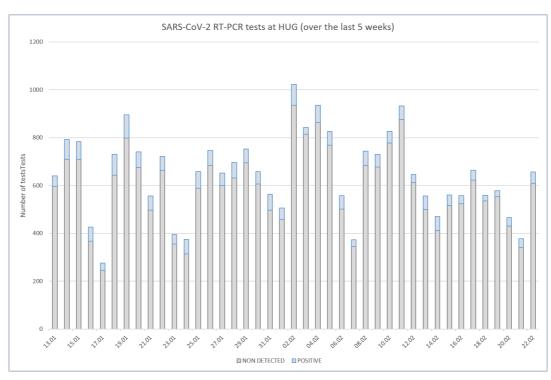
Laboratory of virology

Division of Laboratory Medicine

Diagnostic Department

SARS-CoV-2 variants: follow-up of previous updates in Geneva

SARS-CoV-2 testing at HUG



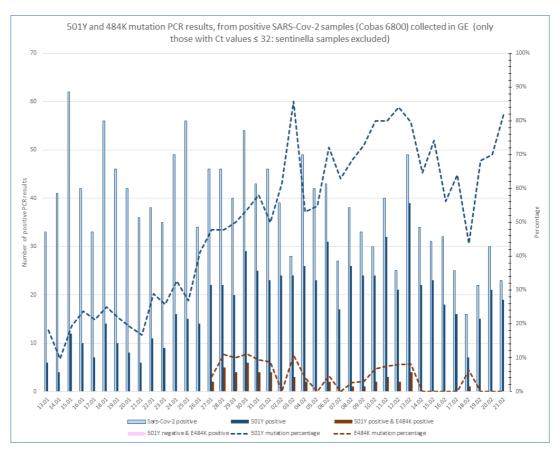
Among all SARS-CoV-2 RT-PCR-positive samples identified in our laboratory, all those with a Ct value \leq 32 are subsequently screened for the 501Y and 484K mutation by specific RT-PCR assays.

Starting date of N501Y mutation screening: January, 5, 2021.

Starting date of E484K mutation screening: January, 27, 2021.

Specimens analyzed in our laboratory come from the community (majority), from hospital workers (systematic screening in case of any symptoms and cluster investigations), from asymptomatic travelers, and from hospitalized patients.

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 proportion of variants carrying the 501Y mutation has recently been fluctuating roughly between 50% and 85%. Over the last week, only one sample carrying the 484K mutation has been identified.

SARS-CoV-2 lineages identified by whole-genome sequencing at HUG from samples (Ct value ≤ 32) collected from Geneva residents 1009 90% 35 80% 30 70% 25 60% 50% 20 40% 15 30% 10 20% 10% 0% 01.02.2021 02.02.2021 03.02.2021 04.02.2021 05.02.2021 06.02.2021 07.02.2021 08.02.2021 09.02.2021 10.02.2021 11.02.2021 ■ B.1.1.7 ■ B.1.351 ■ P.1 ■ P.2 % Others • Number of samples sequenced SARS-CoV-2 lineages identified by whole-genome sequencing at HUG from samples (Ct value \leq 32) collected from any Swiss region and neighbouring France 100% 90% 80% 70% 60% 40% 30% 20% 10 10% 01.02.2021 02.02.2021 03.02.2021 05.02.2021 06.02.2021 07.02.2021 09.02.2021 10.02.2021 11.02.2021 04.02.2021 08.02.2021

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

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 \leq 32. This graph displays the sequences with 95% of positions covered \geq 15x and submitted to GISAID (364 sequences obtained from samples collected from February 1st to February 11, 2021).

■ B.1.1.7 ■ B.1.351 ■ P.1 ■ P.2 ※ Others • Number of samples sequenced

Conclusions

We recently observed a fluctuation of the proportion of variants carrying the N501Y mutation, roughly between 50% and 85%. This fluctuation is probably due a selection bias related to cluster investigations and also may vary according to the number of cases tested (e.g. during the week-end). The identification of only a single sample positive for the E484K mutation during the last week may indicate a reduction in the circulation of variants harboring this mutation (essentially B.1.351). Since February 5, 2021, we have not detected the P.1 variant in the samples analyzed so far. Based on the WGS data showed above and the low number of E484K-positive samples observed in recent days, we can deduce that the B.1.1.7 variant is currently the only variant displaying significant circulation in the Geneva area. Importantly, we observe a trend towards a reduction in the absolute number of daily SARS-CoV-2-positive samples.

Laurent Kaiser

Wrisu

Samuel Cordey

Manuel Schibler

Pauline Vetter