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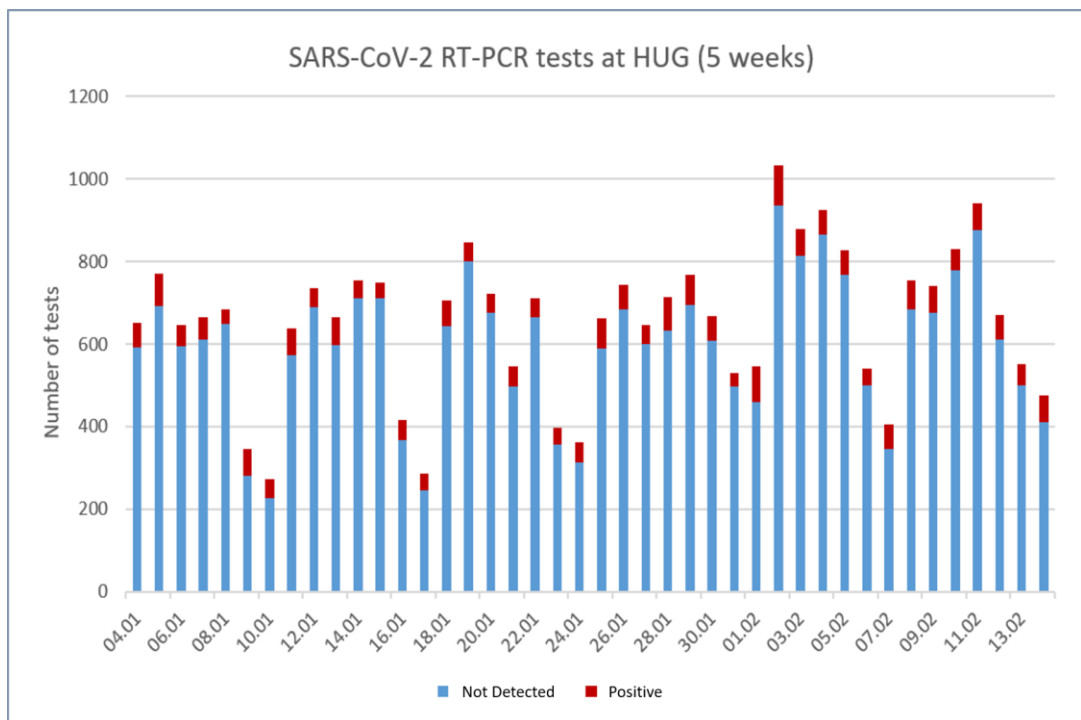
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Division of Laboratory
Medicine

Diagnostic Department

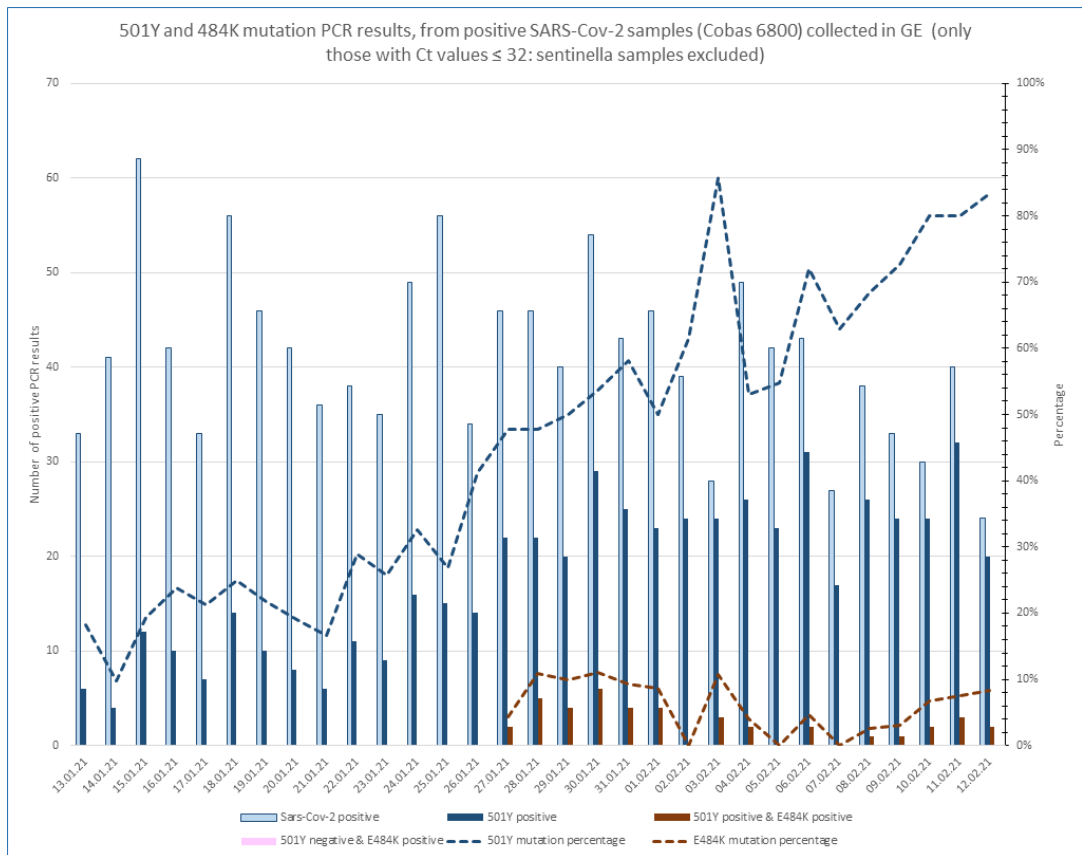
SARS-CoV-2 variants: follow-up of previous updates in Geneva

SARS-CoV-2 testing at HUG



Among the Cobas 6800 RT-PCR positive samples, those with a Ct value ≤ 32 are used for 501Y and 484K mutation screenings by specific RT-PCR assays.

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

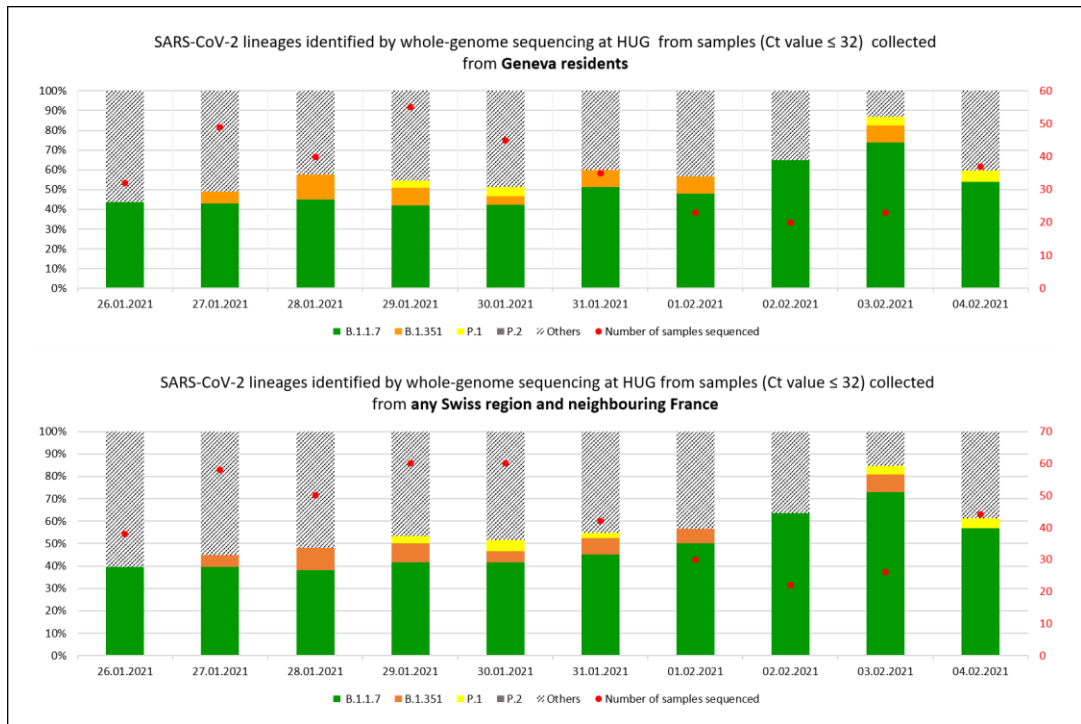


Variants carrying the N501Y mutation now represent more than 80% of the positive samples tested at HUG. The vast majority of those variants belong to the B.1.1.7 lineage, as confirmed by whole genome sequencing (WGS).

The E484K mutation is increasing in frequency, but not in absolute numbers (given the low numbers of positive samples) and is now found in 5 to 10% of the samples tested at HUG. This recent augmentation over the last 7 days is suspected to represent either the B.1.351 (South Africa) variant or P.1, which may be circulating at a low level in the community. The probability is lower that it is the new VOC 202102/02 (the B.1.1.7 lineage that has acquired the E484K mutation), which has not yet been observed in Geneva. The definitive identification and the respective proportion of each of those variants is ongoing by WGS. Nine sequences of the P.1 (Brazil) variant (which also carries the E484K mutation) have been identified by WGS from samples collected between January 29 and February 4, corresponding to 3 identified clusters (originating from an imported case each time according to local health authorities). This includes the 2 cases confirmed last week by Sanger sequencing.

Within the 371 full-SARS-CoV-2 spike sequences retrieved for surveillance in Geneva between January 18 and 28, one specimen collected from a traveler back from Middle East identified a VOC from the A.23.1 lineage, which carries the P681R mutation (but neither 501Y, neither 484K).

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



Conclusions

- We observe a continuous increase in the percentage of the B.1.1.7 variant among SARS-CoV-2 positive samples in the Geneva area, currently around 80%.
- Currently, the E484K mutation is increasing in frequency, but not in absolute numbers (given the low numbers of positive samples) and is now found in 5 to 10% of the samples.
- A total of 9 specimens, within 3 clusters, of the P.1 variant have been identified in Geneva between January 29 and February 4.
- Another variant of concern named A 23.1 (initially detected in Uganda), which carries neither the 501Y nor the E484K mutation, has been identified in a returning traveler at the end of January.
- The detection of other lineages is to be expected with the increased genomic surveillance.

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