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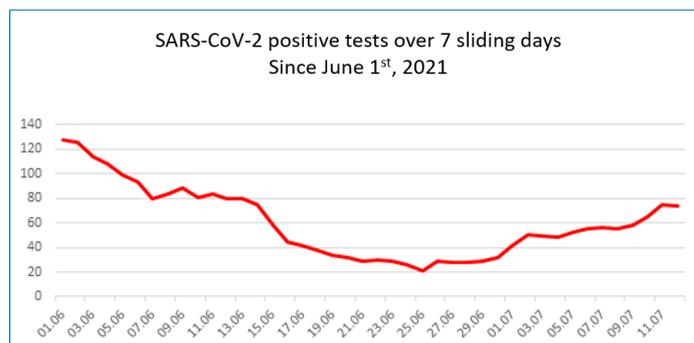
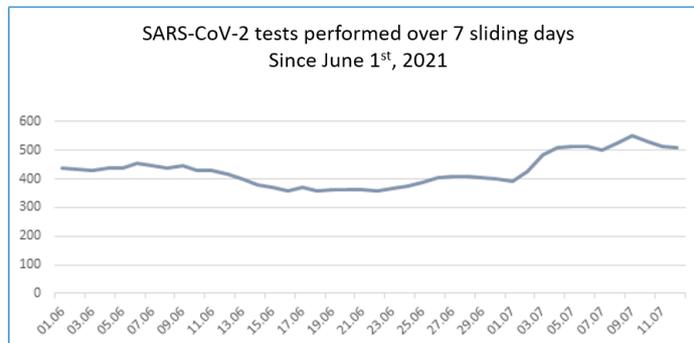
Diagnostic Department

## 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

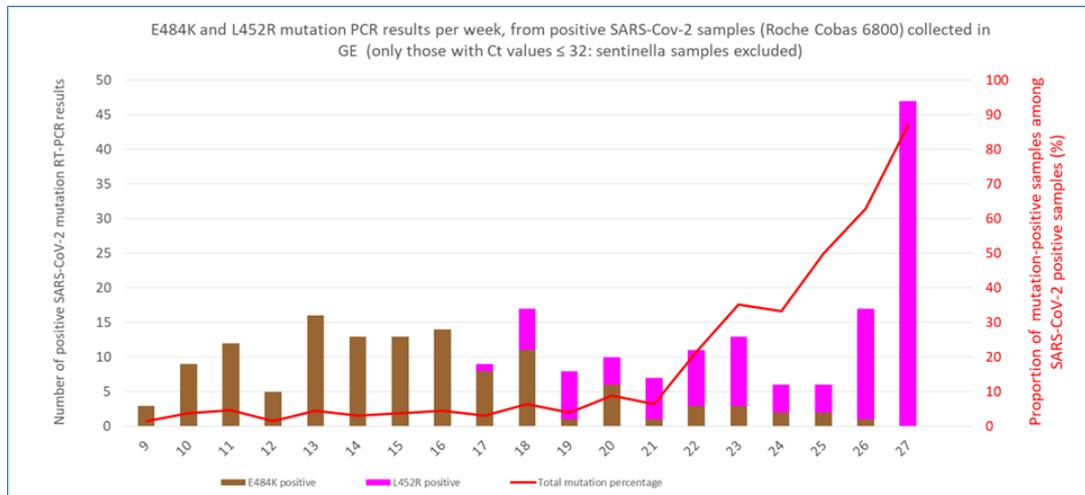
The number of tests (PCR and antigen tests) performed at the laboratory of virology of Geneva University Hospitals represents around 1/4 of the total number of tests performed in the canton of Geneva during week 27 (3613/14'729). Roughly 50% of the positive specimens collected in the Geneva area were processed at HUG for primary diagnosis (N=75). Tests performed at our outpatient testing center (located in the Hospital but open to anyone from the community) are either PCR-based or antigen-based; all positive antigen-based tests are confirmed by PCR, allowing screening for variants.

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. Since March 1, 2021, the sequencing has been done within the Swiss national SARS-CoV-2 genomic and variants surveillance program. All specimens with a Ct value  $\leq 32$  are sequenced. In some instances, sequencing can be done on specimens sent by other laboratories in Switzerland. Phylogenetic analysis data are produced by Nextstrain, in collaboration with Richard Neher's group at the University of Basel.



The number of positive cases diagnosed at HUG and the positivity rate have increased over the last week, and the mean daily number of positive tests at HUG was 11 over the last 7 days (vs 5.5 the week before).

### Specific mutations screening by RT-PCR among SARS-CoV-2 positive samples collected in GE and sent to our laboratory for primary diagnosis, according to calendar weeks



Starting date of E484K/Q mutation screening: January, 27, 2021. Starting date of 417N/T mutation screening: March, 3, 2021. This 417N/T screening was only done on E484K-positive samples until July 5, and presumably allows distinguishing between B.1.351 (Beta) and P.1 (Gamma, not depicted on this graph). Since July 5 (week 27) and the dominance of the Delta variant, the 417N/T screening is done on all positive specimens in order to help differentiate between Delta (452R positive, 417N negative) and its sub-lineage AY.1 (452R positive and 417N positive). Starting date of L452R mutation screening: May, 4, 2021 (week 17). This graph only displays positive results of specific mutations looked for in samples sent for primary diagnostic with Ct values <32, and does not include mutation results obtained in SARS-CoV-2-positive samples sent from other laboratories.

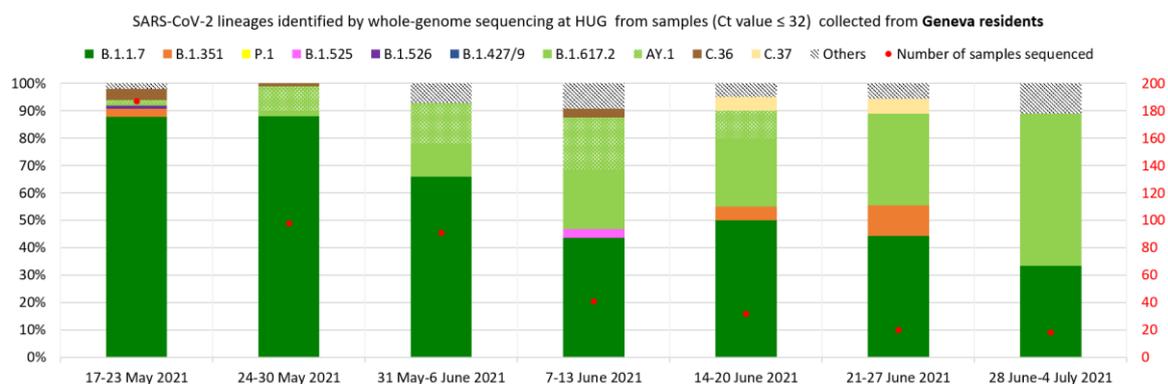
Note:

The 484K mutation is mainly found, but not exclusively, on the B.1.351 (Beta), the P.1 (Gamma) variants, and various variants of interest.

The 452R mutation is mostly, but not exclusively, carried by the B.1.617.2 (Delta) (and AY.1, which is B.1.617.2 with an additional 417N mutation) and the C.36.3 variants (not a VOC but a VOI).

Over the last week, the total number of new cases in the whole canton among persons living in the Geneva area was 149. 58 SARS-CoV-2 PCR-positive specimens with Ct values below 32 were collected at HUG, and 35 from other labs in Geneva over the same period. Among these 93 samples, **82% (N=76) were positive for the 452R mutation**. Of note, the vast majority of 452R positive samples currently represent the delta variant. Indeed, the C.36 is no longer detected. Approximately 50% of these cases derived from importations, and 50% arose through circulation in the community. These data illustrate the progressive delta dominance in the Geneva area.

### SARS-CoV-2 lineages identified by whole-genome sequencing at HUG from samples (Ct value ≤ 32) collected from Geneva residents



Note: AY.1 (dashed light green) is the sublineage of B.1.617.2 (Delta) with the additional 417N mutation.

The WGS data shows that the Delta variant is still progressively increasing in proportion, representing more than half of available sequences collected between June 28 and July 4, 2021.

The AY.1 sublineage has not been detected in the last 2 sequencing batches. According to the cantonal physician team, identified cases were linked together and caused a cluster in the Geneva area.

C.37 (Lambda) sequences are now depicted in the graph. Lambda is not a VOC but a VOI, first detected in Peru, where it rapidly increased in proportion (as well as in neighboring countries, such as Chile), where it is associated with a new surge of cases. Two sequences have already been identified in the Geneva area.

Among other sequences detected in the Geneva area and carrying the 484K mutation (not depicted in this graph), 3 more sequences of the B.1.621 variant originating from 2 patients (not a VOC but a VOI, first identified in Columbia, and carrying a high number of mutations known to reduce neutralization capacity of sera of vaccinees *in vitro*) have been identified. A cluster of 4 sequences were previously identified mid-June and all cases were linked together.

## Conclusions

- The circulation of SARS-CoV-2 in the Geneva area remains low but is increasing
- Since July 5, 2021, all positive SARS-CoV-2 PCR samples processed in the canton of Geneva are sent to the HUG laboratory of virology for specific mutation screening and sequencing at the request of the cantonal physician team. This allows for a more precise representation of the circulating SARS-CoV2 variants in the Geneva area.
- The 452R mutation (currently mostly reflecting Delta variants), was detected in 82% of the specimens tested last week.
- **Both specific mutation screening and sequencing data reflect the replacement of the B.1.1.7 (Alpha) variant by the B.1.617.2 (Delta) variant, which is increasingly circulating in the community.**
- This increase of detection of the Delta variant in the Geneva area is not linked to a recrudescence of the number of hospitalized patients.
- The sublineage AY.1, which caused a cluster in Geneva has not been detected in the last 2 sequencing batches.
- The Lambda variant has been detected in the Geneva area, in few samples.



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