Hôpitaux Universitaires Genève

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Geneva Centre for Emerging Viral Diseases

Division of Infectious Diseases

Department of Medicine

Laboratory of virology

Division of Laboratory Medicine

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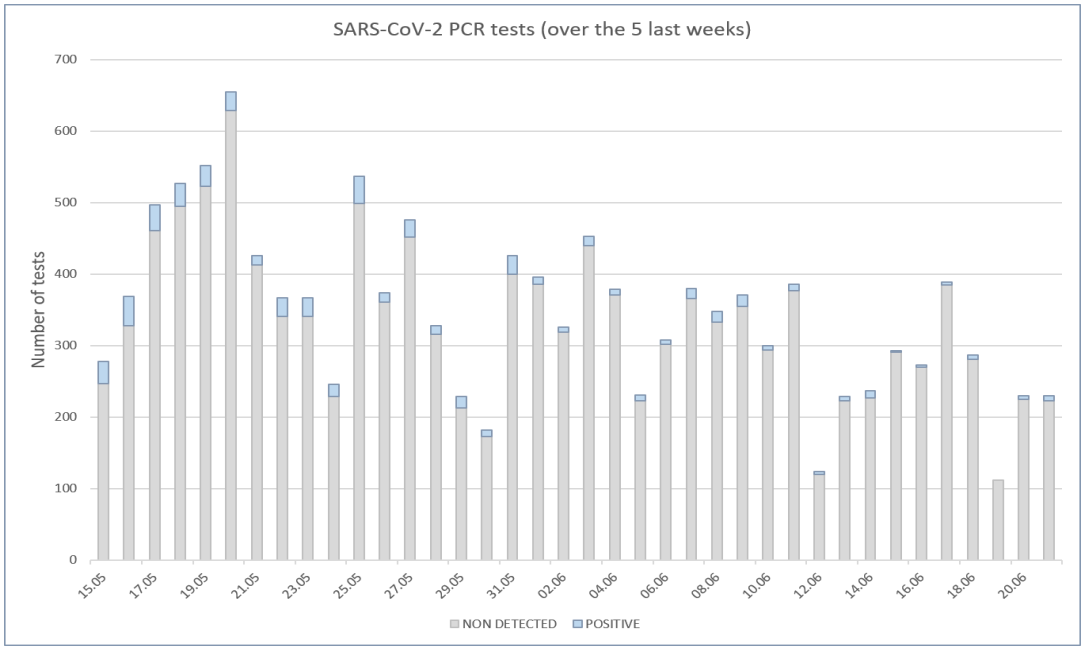
SARS-CoV-2 genomic and variants surveillance in Geneva: weekly update

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 represents around 1/3 of the total number of tests performed in the canton of Geneva during week 24. Specimens analyzed in our laboratory come from the community (the majority: symptomatic patients and asymptomatic contacts), 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.
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 is done within the Swiss national SARS-CoV-2 genomic and variants surveillance program. With the decreased number of SARS-CoV-2 positive cases, all specimens with a Ct value ≤ 32 are sequenced. In some instances, sequencing can be done in 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.



Both the absolute number of positive cases diagnosed at HUG and the positivity rate have continued their progressive decline. The mean daily number of positive tests at HUG was 4 over the last 7 days.

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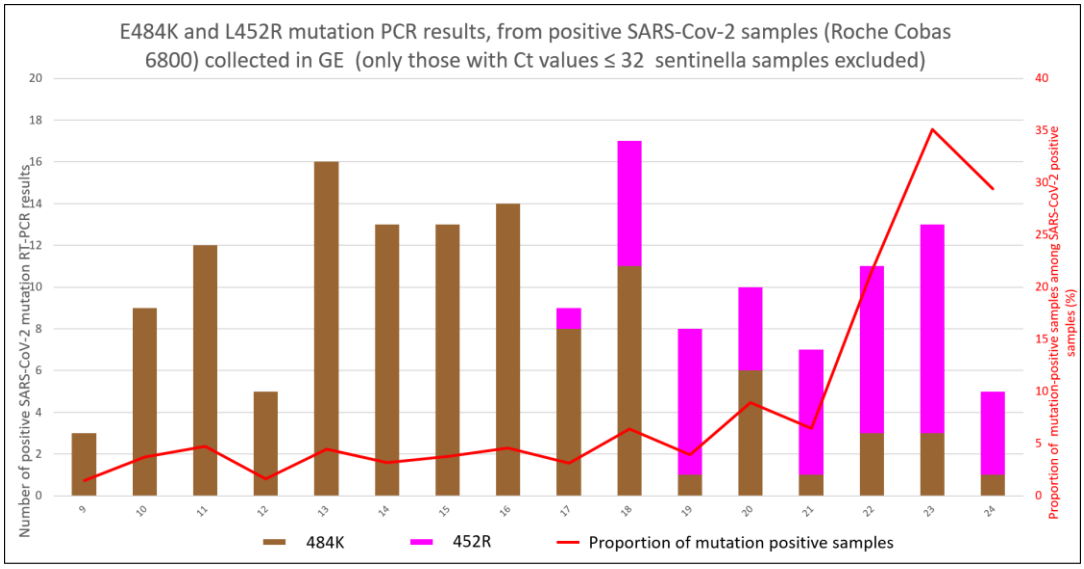
Specific mutations screening by RT-PCR among SARS-CoV-2 positive samples collected in GE and sent to our laboratory for primary diagnosis, according to calendar weeks



Starting date of E484K/Q mutation screening: January, 27, 2021. Starting date of 417N/T mutation screening: March, 3, 2021. This 417N/T screening is done on E484K-positive samples, and presumably allows distinguishing between B.1.351 and P.1 (not depicted on this graph). 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.

SARS-CoV-2 samples with mutations detected by PCR are now shown according to calendar weeks (including results from Monday to Sunday). Note that the systematic screening of the 452R mutation started only on week 17.
The 452R mutation is mostly, but not exclusively, carried by the delta B.1.617.2 (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).

The absolute number of positive cases of variants carrying one of the screened mutations stayed low over the last week (among positive SARS-CoV-2 samples collected at HUG from persons living in the Geneva area, with Ct values below 32, sentinella samples excluded).
Additional specimens tested positive over the last week for the 452R mutation, and are not depicted on this graph, because they were not collected at HUG but sent to our laboratory for mutation screening, at the request of the cantonal physician team.

This low number of positive cases precludes any firm conclusions regarding variant circulation in the Geneva area. However, the proportion of variants carrying the 452R mutation seems to be increasing over the last 3 weeks. According to the cantonal physician team, all but one cluster of community transmission are linked to imported cases or previously identified clusters.

The 484K mutation detected this week was already known, in an immunosuppressed patient diagnosed with a chronic infection.
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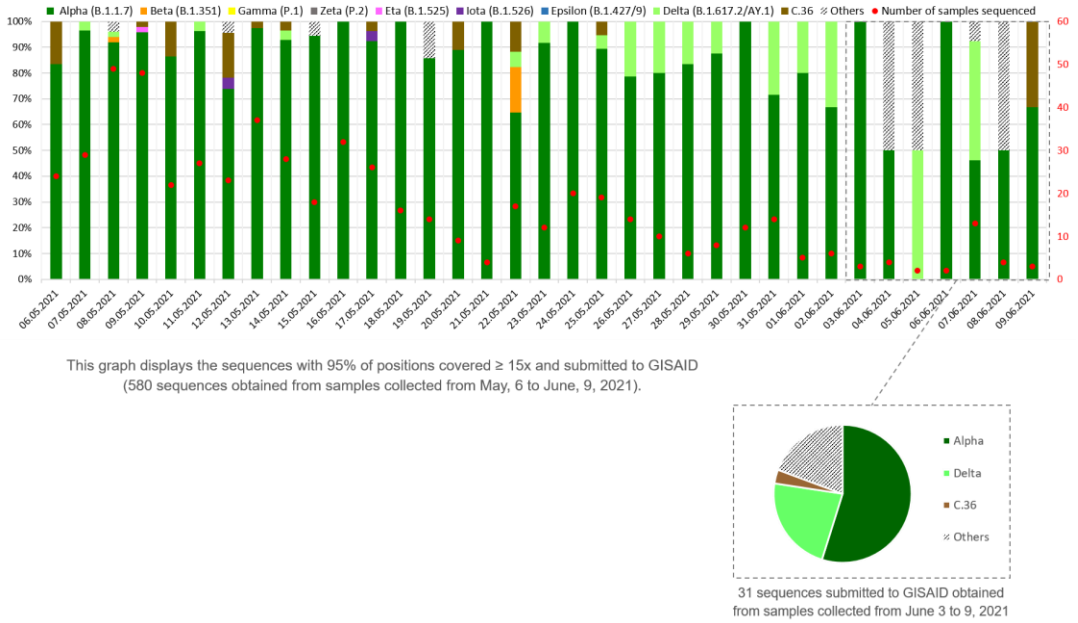
Importantly, mutation-harboring samples are probably overrepresented due to aggressive contact tracing by the cantonal physician team.

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



The number of sequences included in the analysis is sharply decreasing, and only 31 sequences were available for the surveilled period. Until mid-May, up to 200 sequences were analyzed each week. The proportion of the different variants should therefore be carefully interpreted in this context of low numbers.

While alpha was still the variant causing most of the new infections over the surveilled period, the proportion of delta variant is increasing.
Indeed, most (23/24) of the detected variants carrying the 452R mutation between June 3 and June 9 were confirmed by sequencing to be the delta variant B.1.617.2 or AY.1 (corresponding to B.1.617.2 with the additional 417N mutation). In total, 23 more cases of the delta variant have been identified. According to the cantonal physician team, all cases are linked to previously known clusters or to new imported cases.

In Geneva, both B.1.617.2 and AY.1 are circulating. A large AY.1 cluster has been identified and is followed by the cantonal physician team. Most B.1.617.2 identified cases are linked to new importations from abroad.
The last sequence of the variant carrying the 452R was confirmed to be C.36.3.

Among other identified variants circulating in the Geneva area, 4 cases of B.1.621 (considered a VOI by ECDC, but not by WHO and carrying the 484K mutation) have been detected, and linked to an imported case or to known transmission chains according to the cantonal physician team.

Conclusions

- The absolute number of SARS-CoV-2-positive samples and the positivity rate since the end of April, 2021 in the Geneva area continue to decrease.
- The proportion of positive tests carrying the 452R mutation, as well as the proportion of the delta variant among sequenced specimens is progressively increasing over the last weeks. Because of the low number of cases and available sequences, these findings should be interpreted with caution.
- This increase of detection of the delta variant in the Geneva area is not linked to a recrudescence of the new number of cases, nor to a recrudescence of the number of hospitalized patients.
- Most detected cases of variants are either linked to known clusters with identified transmission chains or to new importations with secondary clusters, according to the cantonal physician team.
- Both B.1.617.2 (delta) and AY.1 (delta + 417N) are circulating in the Geneva area.

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