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Geneva, September 06, 2021

Swiss national SARS-CoV-2 genomic and variants surveillance program: report of the month of July

Geneva Centre for Emerging Viral Diseases

Division of Infectious Diseases

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Laboratory of virology

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1. Summary

Over 30% of the total number of cases identified in Switzerland were sequenced by the Surveillance program, yielding approximately 4500 sequences in July.

In July, COVID-19 cases numbers began to rise again in Switzerland, due almost entirely to the B.1.617.2 (Delta) variant, which completely replaced previously circulating Alpha.

The program confirmed the conserved neutralization capacity of casirivimab and the reduced neutralization capacity of the imdevimab monoclonal antibody against Delta. Of note, the combination of casirivimab + imdevimab available as treatment in Switzerland has been shown to keep neutralizing activity against Delta.

Numerous Delta sub-lineages are now being identified. Those lineages are still new and their definitions are still to be finally determined. However, there is no evidence that any clade within Delta is of greater concern. Similarly, no special issues regarding transmissibility, immune escape, clinical severity or diagnostic failure between Delta and its various sub-lineages have been identified yet. However, data are currently scarce, and more information will follow.

Other VOCs have only rarely been detected during the surveilled period:
- Alpha has been outcompeted by Delta at the end of June, and its detection sharply decreased to almost nothing throughout the surveilled period
- B.1.351 (Beta) circulation has essentially ceased in July
- P.1 (Gamma) continued to circulate at very low levels, although circulation was lower than in June.

Other variants of interest or variants under monitoring were also rarely identified:
- B.1.621 (Mu), which was detected for the first time in June, continued to circulate at very low levels
- B.1.1.318 has been detected in 2 clusters, which are believed to be cause by importation events from South-East Europe. There is currently no sign that it will displace Delta.
- Lastly, C.37 (Lambda), was been detected only once, in July, with no evidence of substantial circulation in the community.

No important geographical breakdown of a particular variant has been noticed.

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2. Description of the Swiss national SARS-CoV-2 genomic and variants surveillance program.

The overall goal of the program is to provide epidemiological trends and to highlight meaningful observations.

Currently, 14 diagnostic laboratories have joined the program, including university hospital centres in Switzerland (Geneva, Lausanne, Bern, Basel, Zurich, St-Gall, Ticino), in addition to private laboratories (Viollier, Medisupport CH Romande including Dianalabs, Bioanalytica), cantonal-based laboratories (Hôpitaux du Valais) and 3 high-throughput sequencing platforms (Health 2030 Genome Centre in Geneva, Functional Genomics Centre Zurich run by ETH Zürich and University of Zürich, Genomics Facility Basel run by ETH Zürich and University of Basel).

In July Synlab Bioggio (TI), Labor Team W (St Gallen, samples across CH), Spital Region Oberaargau (Bern, Solothurn, Aargau, Luzern) and Risch joined the program. Additional laboratories have been requested to join the program in order to fill sequencing gaps in some regions.

Processed sequencing data are shared openly within 14 days from positive PCR result through the GISAID platform (https://www.gisaid.org) and eventually through the Swiss Pathogen Surveillance Platform (SPSP). The centralized analysis of this National Surveillance will be performed by the groups of Pr. Neher, Pr. Stadler and Dr. Althaus, where variants of concern are counted, analyzed and all sequences scanned for new variants with potential changes in antibody-Spike interactions (https://nextstrain.org/groups/swiss, https://covariants.org/per-country, https://cov-spectrum.ethz.ch). This work is done in close collaboration with the Swiss National COVID-19 Science Task Force and the Swiss Institute of Bioinformatics (SIB).

In order to complement the genomic surveillance based on patient samples, sequencing of SARS-CoV-2 in wastewater samples is also performed, initially funded for 6 months. Samples are collected daily in six wastewater treatment plants (WWTP), under the coordination of Eawag. Up to 50 samples per week over the first 26 weeks have been performed. The sequencing and analysis of these samples, including detection of variants, is done under the coordination of Prof Niko Beerenwinkel. It started in December 2020 for Lausanne and Zurich, and in February 2021 for all six WWTP (https://bsse.ethz.ch/cbg/research/computational-virology/sarscov2-variants-wastewater-surveillance.html). The analysis of wastewater samples is envisaged to run until the end of the surveillance program on 31.3.2022.

Immunological characterization of the variants within the surveillance program is coordinated by Professor Trono's team at EPFL.

This report has been produced by Marc Friedli, Pauline Vetter, Samuel Cordey, Erik Boehm, Richard Neher, Christian Althaus, Martina Reichmuth, Cornelius Römer, Niko Beerenwinkel, Chaoran Chen, Tanja Stadler, Priscilla Turelli, Didier Trono, Emma Hodcroft, Nadja Wipf, Damir Perisa, and Laurent Kaiser. The list of the participants and collaborators of the program can be found at the end of this report in the appendix.

This report covers the period of July 5 to August 1 (weeks 27, 28, 29, 30). All data presented in this report are based on the sampling date.

3. Variants of concern, variant of interest and other surveilled variants: brief summary and special focus

Currently, 4 variants are considered variant of concerns (VOCs) by the WHO, B.1.1.7 (first identified in the UK – VOC Alpha), B.1.351 (first identified in South Africa – VOC Beta), P.1 (first identified in Brazil – VOC Gamma), and B.1.617.2 (first identified in India, Delta – currently dominant in Switzerland), and their sub-lineages.

Vaccines effectiveness

Two doses of the mRNA vaccines available in Switzerland have been shown to keep a good effectiveness in real life observational studies against both symptomatic and severe disease due to the B.1.1.7 (Alpha) variant. Protection against severe disease has been shown to be conserved against the B.1.351 (Beta) and B.1.617.2 (Delta) variants. However, reduced protection against symptomatic disease and infection has been observed against those variants. The impact of the mutations carried by the Gamma variant on mRNA vaccine effectiveness is unclear; only limited data are available. (*https://www.who.int/publications/m/item/weekly-epidemiological-update-on-covid-19---24-august-2021*).

Transmissibility

All variants of concern have demonstrated an increased transmissibility relative to the earliest known strains of SARS-CoV-2. Alpha in particular apparently had the largest transmissibility advantage and became dominant worldwide, until Delta emerged. Delta appears to be the most transmissible variant detected so far, and has displaced Alpha. Since the emergence of Alpha, significant population level immunity has developed, which affects real world transmissibility. As Delta has demonstrated some immune escape, it is unclear how much this explains its current transmissibility advantage.

Transmissibility in vaccinated populations

Multiple studies report that breakthrough infections of Delta result in the same peak viral load, as measured by RNA levels, which suggested that vaccinated people could still be transmissible. Additional details have since emerged that make it clear that vaccination is still very effective at reducing transmission: 1) viral loads decline faster, resulting in a shorter transmissibility window; 2) the chance of being infected at all is substantially reduced; 3) peak infectious viral load (which differs from viral load as measured by RNA levels) is substantially reduced, this may be a result of viral particles in vaccinated hosts being effectively coated in antibodies.

Impact on diagnostic tests

Mutations in the virus may affect the sensitivity of diagnostic tests. Nucleic acid detection may be affected by mutations in the RNA sequence of target regions. S-gene dropout, as seen with variant Alpha, is an example of this. Another significant example is the lower sensitivity of the Genexpert® (Cepheid) for the N2 target for the Delta variant (*https://www.fda.gov/medical-devices/coronavirus-covid-19-and-medical-devices/sars-cov-2-viral-mutations-impact-covid-19-tests*). However, as RT-PCR tests use multiple targets, those mutations have not been reported yet to cause diagnostic failure.

Similarly, rapid antigen tests, which primarily detect the presence of the N protein, may be affected by mutations in the N protein. However, diagnostic efficacy of antigenic tests appears to be relatively unaffected thus far (*Bekliz et al. Lancet Microbe. 2021*). As the potential exists, this will continue to be monitored. Of note, no impact on antigenic test sensitivity has yet been reported for Delta.

Greater transmissibility and/or immune escape potential can result in new surges in infections despite the vaccination campaign. Therefore any variants displaying mutations known to be linked with either increased transmissibility and/or immune escape potential should be closely monitored.

Considering the above transmissibility, immune escape, and diagnostic issues, the variants presented below will be particularly surveilled:

- variants classified as VOCs by the WHO: B.1.1.7 (Alpha), B.1.351 (Beta), P.1 (Gamma), B.1.617.2 (Delta) – and their sub-lineages
- new variants (until sufficient monitoring suggests they do not have a replicative/escape advantage) that include E484K + N501Y: higher transmissibility, immune escape risk, resistance to mAbs, such as: B.1.621 Mu (N501Y + E484K), B.1.1.318, and the recently identified C.1.2.
- variants that include E484K alone due to immune escape risk and resistance to mAbs, such as: B.1.525 (Eta), B.1.526 (part of the lineage carries E484K, the other S477N (Iota)), B.1.620.
- variants that include L452R: slightly more transmissible relative to N501, resistance to mAbs, such as: C.36 and C.37 (Lambda)
- variants that include L452R + N501Y, such as A.27

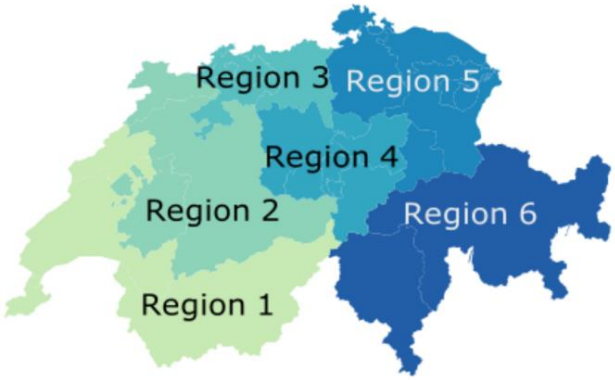
4. Epidemiology in Switzerland and number and origin of sequences produced through the program during the surveilled period

Data in this report comes from 3 sources: 1) The publicly available data on COVID-19 as reported by the FOPH (https://www.covid19.admin.ch), including data that is declared to the FOPH by the different laboratories in Switzerland; 2) data originating from laboratories participating in the surveillance program; and 3) sequences submitted to GISAID, for which the corresponding infected person was in Switzerland (resident or recent travel history to Switzerland).

General caveat: the numbers and denominators are fluid and variable over time; and are subject to change depending notably on the different databases used, and variable declaration delays. All data generated by this program is also submitted to SPSP.

The number and origin of sequences submitted to GISAID by each laboratory during January and February, 2021, prior to the start of the surveillance program can be found in the first report covering the months of March and April 2021.

Data will be presented here by regions, using the same region definitions that are used for the influenza sentinel surveillance system in Switzerland. Data are presented according to residency post-code.



Region 1 includes the cantons of Geneva, Neuchatel, Vaud and Wallis

Region 2 includes the cantons of Bern, Fribourg and Jura

Region 3 includes the cantons of Aargau, Basel (Basel-Stadt and Basel-Land) and Solothurn

Region 4 includes the cantons of Luzern, Unterwalden (Obwalden and Niedwalden), Schwitz, Uri and Zug

Region 5 includes the cantons of Appenzell (Appenzell Ausserrhoden and Appenzell Innerrhoden), Glarus, Sankt Gallen, Schaffhausen, Thurgau and Zurich.

Region 6 includes the cantons of Graubünden and Ticino.

Divisions of the different regions, from https://covariants.org/per-country

Number of cases processed by the laboratories participating in the surveillance program

During the period covered by the present report, the FOPH reported a total of just over 16,000 confirmed SARS-CoV-2 cases in Switzerland, indicating a substantial rise in the number of infections. Supplementary Table 1 provides an overview of the number and incidence of confirmed cases, the effective reproduction number R_e, the number and incidence of tests, test positivity, the number and proportion of sequenced samples, and the number and proportion of VOCs by canton, region and for Switzerland overall.

The laboratories participating in this program reported 4711 positive tests during the surveilled program, which represents about 29% of the total number of cases reported in Switzerland (including both PCR and antigen-based tests). Detailed data regarding the total number of tests performed each week by the laboratories participating in the surveillance program (including negative and positive tests numbers, and the number of the positive tests that have been sequenced) are available in appendix Table 3. Of note, antigen-based tests are by definition excluded from the surveillance, which applies only to PCR tests (although antigen positive cases may be asked to be re-tested by RT-PCR).

Number of SARS-CoV-2 sequences produced through the surveillance program

A total number of 4422 SARS-CoV-2 sequences have been submitted to GISAID during this period. This represents around 28% of all cases detected in Switzerland during the surveilled period (see Supplementary Table 2 and 3 in Appendix for details). Of note, this number includes sequences from samples received from other laboratories in order to ensure sequencing of post-vaccination infections.

Table 1 shows the number of sequences successfully submitted to GISAID through the surveillance program during the surveilled period by calendar week.

Week	Date	Number of sequences successfully submitted to GISAID
27	July 5to July 11	543
28	July 12 to 18	1079
29	July 19 to 25	1328
30	July 26 to August 1	1472
	Total	4422

Table 1: number of sequences submitted to GISAID through the surveillance program

The total number of SARS-CoV-2 sequences submitted to GISAID by each laboratory during the month of June is available in Supplementary Table 3 in the appendix.

Covering of sequencing in Switzerland and contribution of the national SARS-CoV-2 surveillance sequencing program

As shown in Figure 1, the total number of SARS-CoV-2 sequences submitted per week progressively increased during the month of July (week 27 to 30), reflecting the increase in cases within Switzerland. The vast majority of the sequences available in GISAID (green curve) and those on which the surveillance is conducted, come from the national surveillance program.

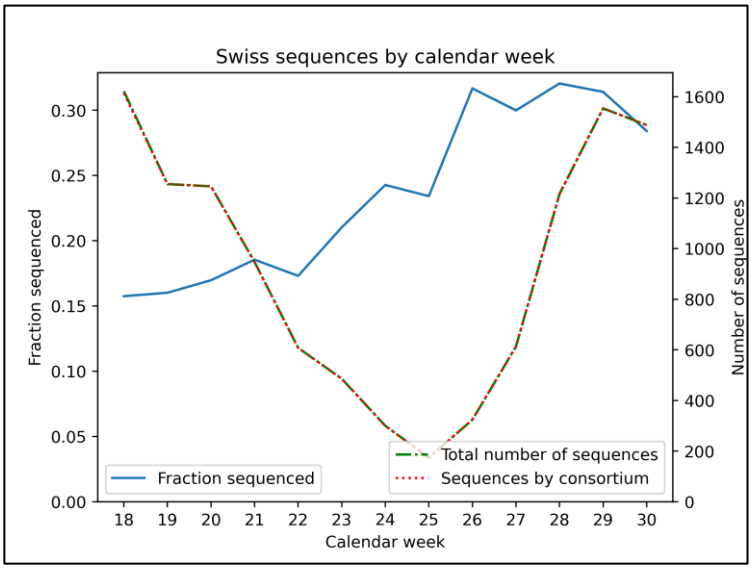


Figure 1: Number of SARS-CoV-2 sequences available for Switzerland (total available Swiss sequences in GISAID in green, Swiss sequences submitted through the program in dotted orange) and fraction of the total number of positive cases declared to the FOPH that have been sequenced (blue curve).

During the surveilled period, the total proportion of positive sequenced cases was on average around 29%, largely above the aim of the program.

Figure 2 displays the fraction of SARS-CoV-2 cases sequenced for each Swiss region. Region 4 continued to have the lowest total number of sequences and the lowest fraction of cases sequenced in Switzerland. However, in this region, the fraction of cases sequenced slightly increased during July, and was just below the 10 % limit. An effort will be made in order to increase the coverage of this area.

Figure 3 shows the sequencing coverage among the different Swiss cantons over the last 3 months, presented by fraction of cases sequenced and the total number of reported cases in the canton. It will be used to guide the contact with new laboratories in order to have a better covering of the country. Appenzell Ausser/Inner rhoden, Fribourg, Glaris, Jura, Lucerna, Neuchâtel, Nidwalden, Obwalden, and Zug in particular had low coverage.

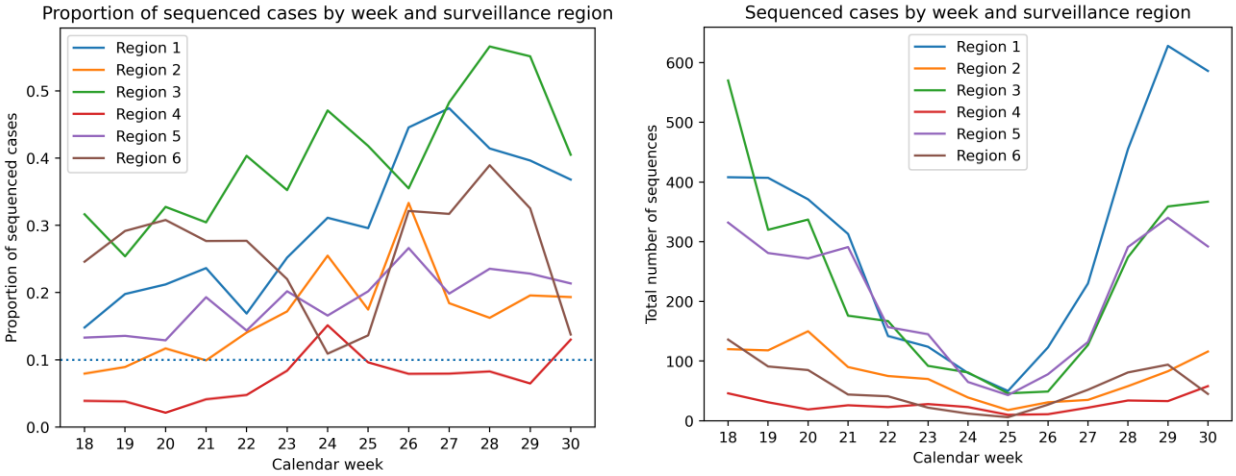


Figure 2: Sequencing coverage among the different Swiss regions per week, presented by fraction of cases sequenced (left) and by number of sequences (right)

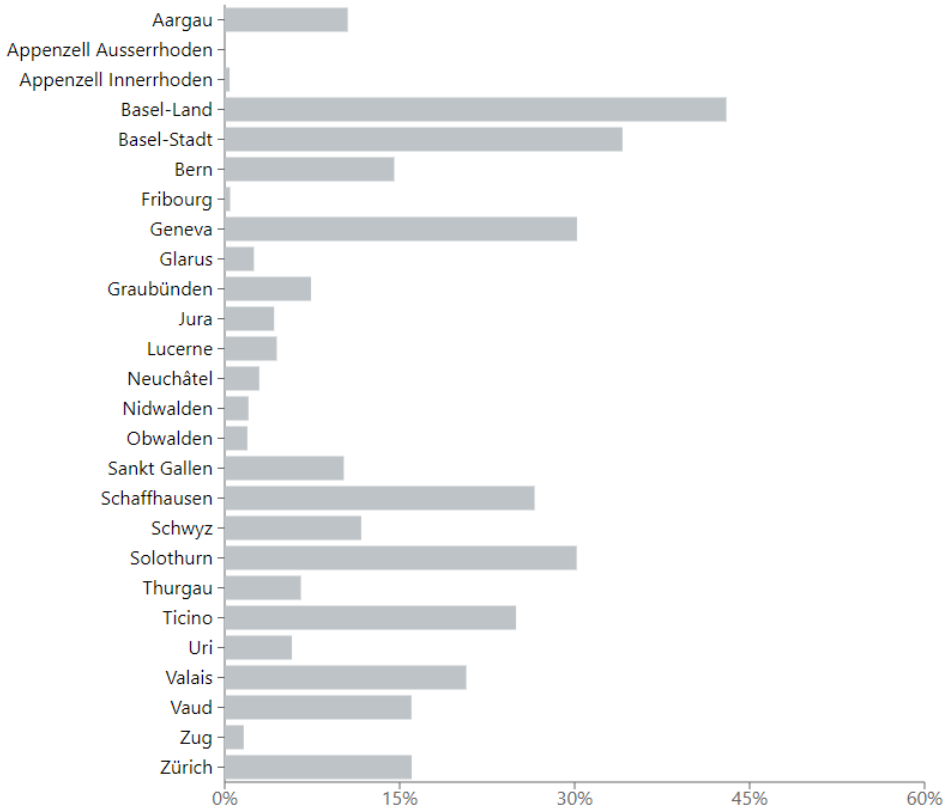


Figure 3: Sequencing coverage among the different Swiss cantons over the last 3 months, presented by fraction of cases sequenced. Screenshot form CoVspectrum website. Online dynamic navigation is available at https://cov-spectrum.ethz.ch/explore/Switzerland/AllSamples/Past3M/sequencing-coverage

5. Variants circulating in Switzerland since January 2021, with a focus on the surveilled period

Determination of the proportion of total number of sequences over time falling into defined variant groups is done by Emma Hodcroft's team and displayed on the CoVariant website (https://covariants.org/per-country). Those results are based on the total number of sequences submitted to GISAID over the time period for Switzerland. Those data mainly, but not exclusively, come from the national genomic surveillance program since its beginning (see Figure 1).

The B.1.617.2 Delta variant (in green in Figure 4) has remained dominant during the month of July all over Switzerland, accounting for almost all the cases in the country at the end of the month (see Figures 5 and 6). See Table 2 below for the number of the main VOCs/VOIs by region

Of note, only 1 case of its sub-lineage AY.1 (Delta + an additional 417N mutation) was detected in Switzerland during week 28, and not retrieved afterwards. Because those AY* lineages (Delta sublineages) are very new, and their definitions are still ongoing, we chose not to elaborate on their proportion and repartition within the country. Indeed, any changes in prevalence should be considered very carefully, as the definition of those sublineages are not clearly assigned.

The B.1.351 (Beta) variant circulation has virtually ceased during the month of July, with only 1 case detected.

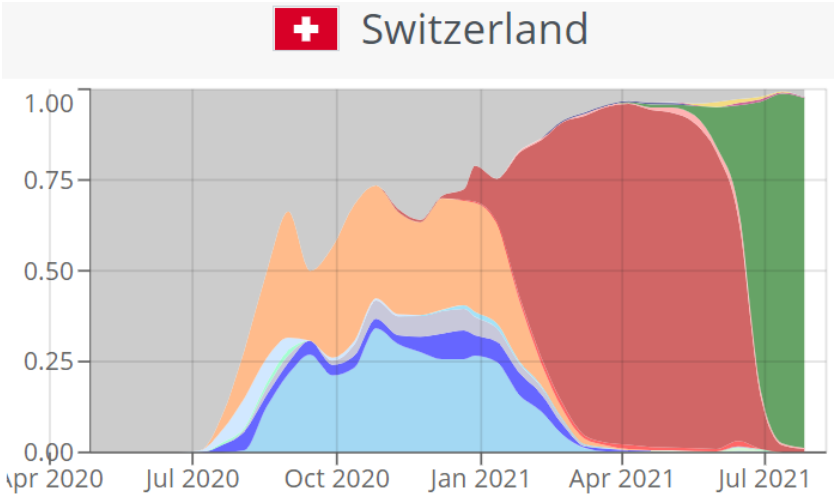
The P.1 (Gamma) variant decreased sharply in proportion in July relative to June, but absolute numbers of cases remained similar. This decrease in proportion is thus due to rising numbers of Delta infections.

Other notable variants were detected in Switzerland over the month of June. One case of the C.37 (Lambda) variant was detected in week 29.

B.1.1.318 was detected in over 30 samples in July, mostly in weeks 29 and 30 from 2 clusters. Phylogenetic analysis suggests importation from Greece, but this is uncertain (Figure 6), there is no discernable trend indicating a competitive advantage.

B.1.621 continued to circulate at very low levels, with less than 10 cases.

An estimate of the total number of VOCs circulating in Switzerland, corrected by taking in account the 12.5 % fraction of sequencing in Switzerland is available through the covSPECTRUM program developed at ETHZ at https://cov-spectrum.ethz.ch/explore/Switzerland.



Nexstrain Clade	Pango Lineage	WHO name
20I/501Y.V1	B.1.1.7	Alpha
20H/501Y.V2	B.1.351	Beta
20J/501Y.V3	P.1	Gamma
21A/S:478K	B.1.617.2	Delta
20C/S.452R	B.1.427/B.1.429	Epsilon
20A/S: 484K	B.1.525	Eta
20C/S: 484K	B.1.526	Iota
21A/S: 154K	B.1.617.1	Kappa
21G	C.37	Lambda
20A/S:439K	B.1.258	
20A/S:98F	B.1.221	
20E (EU1)	B.1.177	
20A.EU2	B.1.160	
21H	B.1.621	

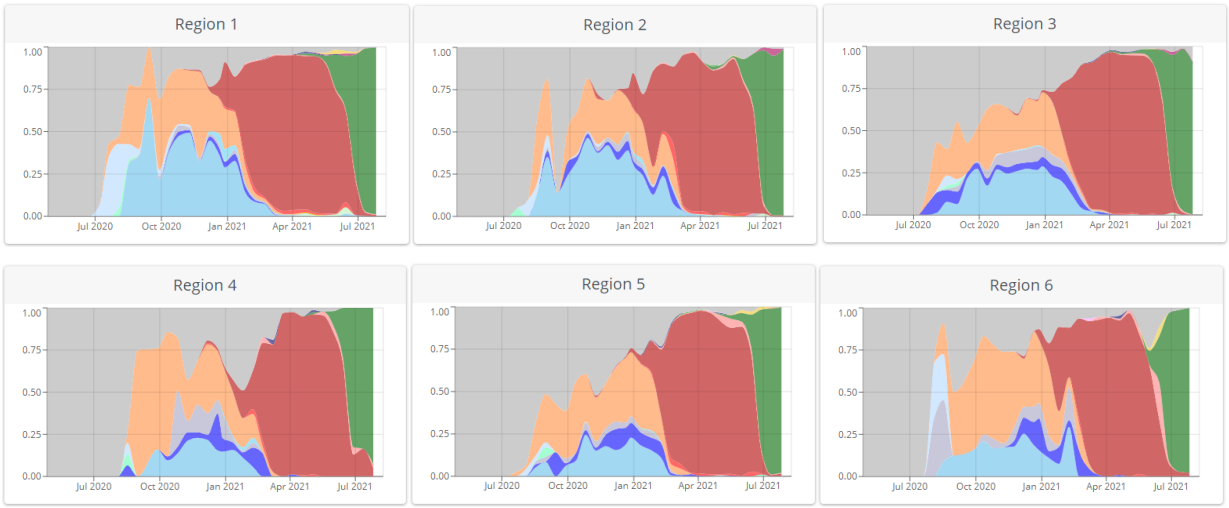


Figure 4: proportion of total number of sequences (not cases), over time, that fall into defined variant groups, for Switzerland. Screenshot from CoVariant website. Dynamic navigation is available at https://covariants.org/per-country. Dark red indicates lineage B.1.1.7 (Alpha). Note the rapid increase in prevalence and rise to dominance. Light red indicates B.1.351 (Beta). Green indicates lineage B.1.617.2 (Delta), detected since mid-April in Switzerland.

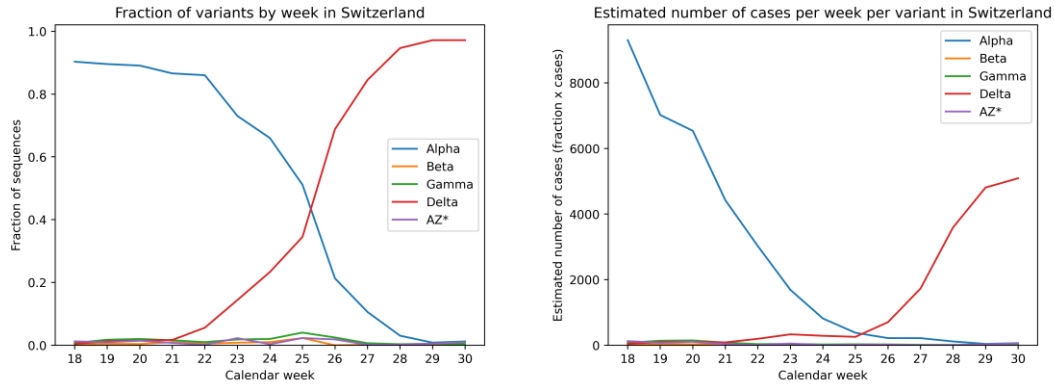


Figure 5: (Left): Percentage of circulating VOCs and VOIs in Switzerland by week, over the 30 first weeks of 2021 (total number of B.1.1.7 (Alpha), B.1.351 (Beta), P.1 (Gamma), B.1.617.2 (Delta) and B.1.1.318 (AZ) sequences from Switzerland and successfully submitted to GISAID are shown here).*

(Right): Estimated number of sequences of the main VOCs/VOIs and variants under monitoring retrieved during the surveilled period.

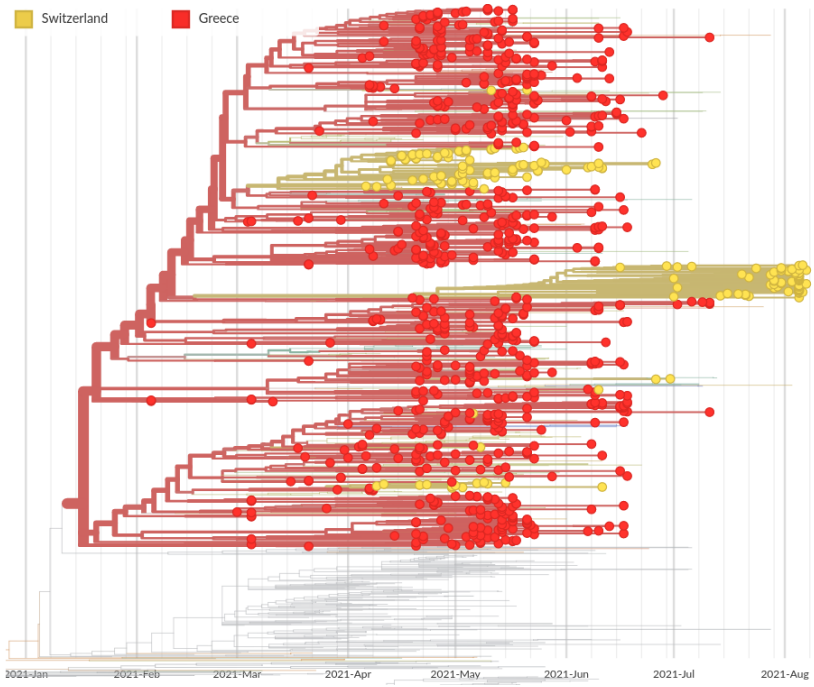


Figure 6: Phylogenetic clustering of B.1.1.318 in Switzerland. Red circles indicate sequences from Greece, Yellow indicates Swiss cases. Note the two Swiss clusters nesting within Greek sequences.

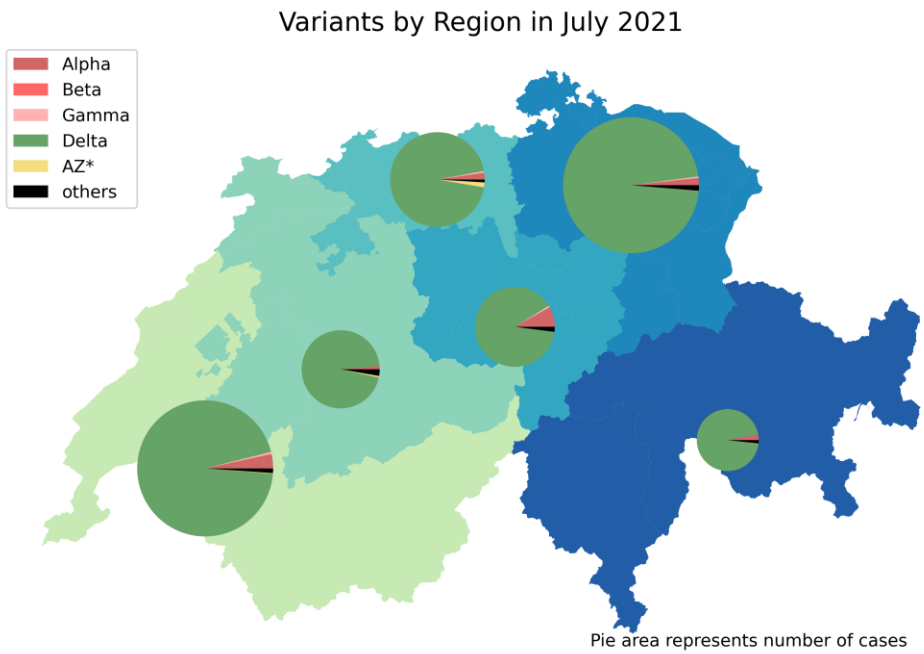


Figure 7: Distribution of variants per region, for July, shown on a map. The total number of sequences in that month, in the region, is shown in parentheses next to each region name. The size of the pie chart corresponds to the total number of sequences. Note the dominance of Delta in all regions.

6. Assessment of the competition between the different variants in Switzerland

The competition between different SARS-CoV-2 variants can be modelled using multinomial logistic regression. The analysis by Dr. Althaus' group is based on sequences retrieved from CovSPECTRUM. The results confirmed that Delta had become the single dominant SARS-CoV-2 variant in Switzerland in July 2021.

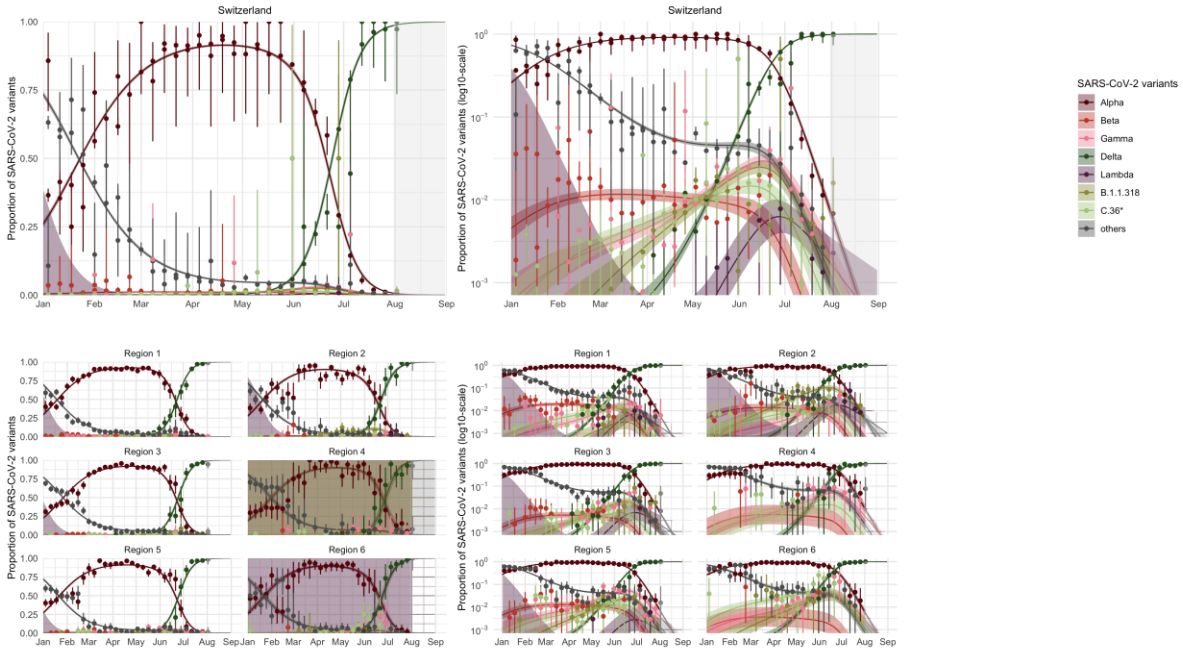


Figure 8: Observed and modeled proportion of SARS-CoV-2 variants over time in Switzerland. The proportion of Alpha and Beta started to grow in Switzerland in December 2020 and January 2021. Beta was subsequently outcompeted by Alpha in February and March 2021. In April and May 2021, Gamma and Delta started to replace Alpha, with Delta now outcompeting all other variants. At the end of July, more than 95% of the retrieved sequences in Switzerland were due to Delta. Model fits are based on a multinomial logistic regression with splines.

7. Wastewater surveillance program

Since February, an increased prevalence of the B.1.1.7 (Alpha) variant has been observed over time in all of the six wastewater treatment plants (WWTPs) that are tested on a daily basis. The B.1.617.2 (Delta) variant started to appear around the beginning of June in all WWTPs. By the end of July it had reached the highest levels in all catchment areas of the respective WWTPs. Notably, detection of variants in wastewater can be challenging if the prevalence is low due to low RNA concentrations, and in this situation, it is difficult to distinguish related lineages that share variant-defining mutations. This is the case, for example, among the sub-clades of B.1.617*.

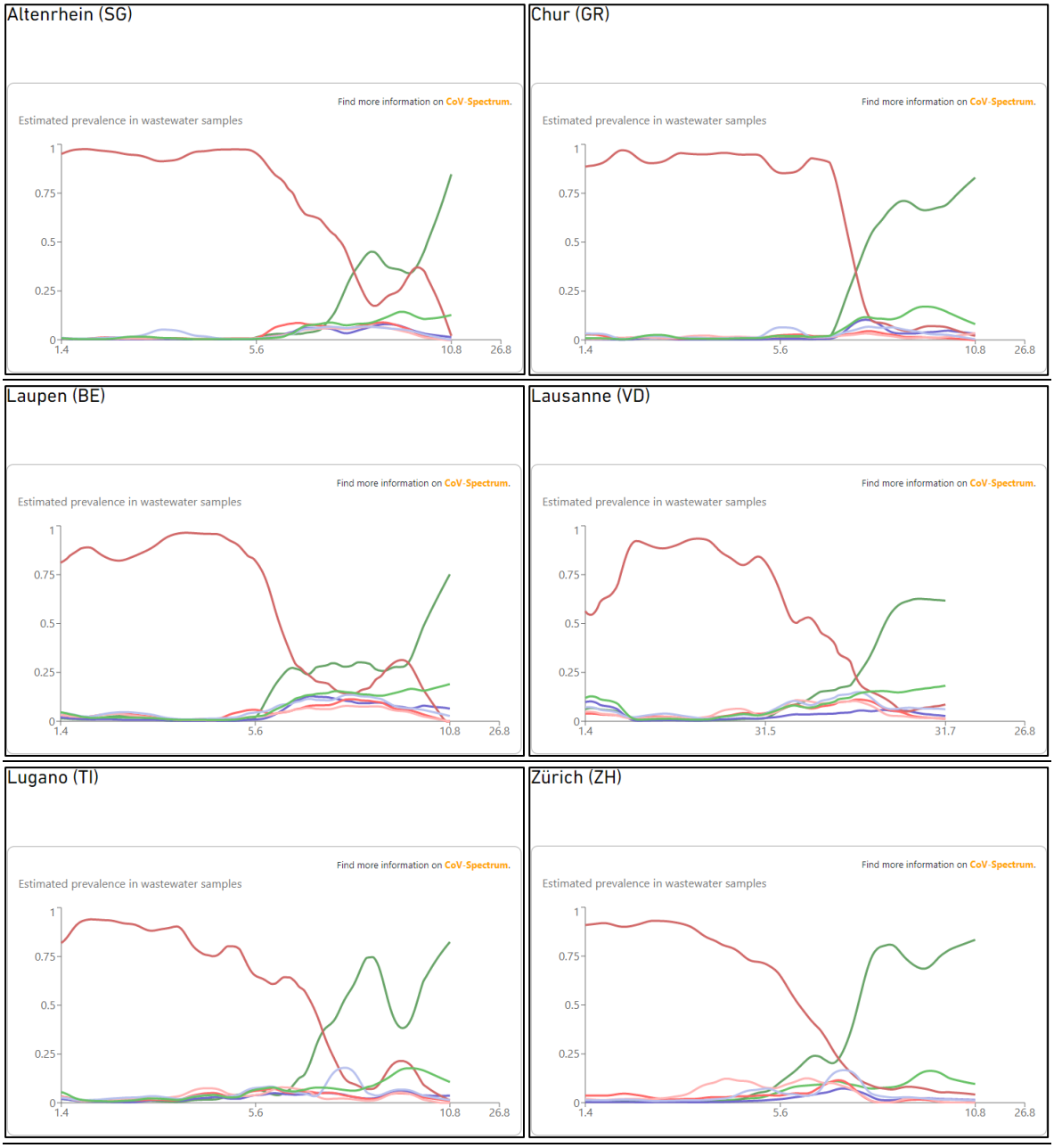


Figure 9 : Prevalence of different genomic variants of SARS-CoV-2 obtained from wastewater samples collected daily until August 10 (except Lausanne: July 31) in WWTPs located in six different Swiss cantons. C.36.3 is represented in light blue, B.1.617.1 in light green (Kappa), B.1.617.2 (Delta) in dark green, B.1.617.3 in purple, B.1.1.7 (Alpha) in dark red, B.1.351 (Beta) in light red, P.1 (Gamma) in pink. Screenshot from the website of ETH Zürich. Online dynamic navigation available at https://bsse.ethz.ch/cbg/research/computational-virology/sarscov2-variants-wastewater-surveillance.html.

8. Immunological characterization of variants

A basic immunological characterization effort is part of the Swiss national SARS-CoV-2 genomic and variants surveillance program. This characterizations involve testing prototypic viral variants (i.e. significant sequence deviation in spike-coding region) for their sensitivity to neutralization by sera from previously infected or vaccinated individuals and by therapeutic / preventive monoclonal antibodies, some already FDA approved and some in development. For this, their spike proteins (the target of antibodies neutralization) is synthesized based on its RNA sequence and analyzed through cell-based or cell-free neutralization assays, i.e. with wild-type replicating isolates, viral pseudotypes or high-throughput surrogate spike-ACE2 (S^3-ACE2) binding assays using a collection of convalescent sera, post-vaccination sera and commercially available or in-house neutralizing monoclonal antibodies. Of note, the cell-free surrogate neutralization assay also provides semi-quantitative information on the relative affinity of each spike variants for the ACE2 viral receptor, which likely plays an important role in viral infectivity and transmission.

In the month of July, the 2 FDA-approved Regeneron® antibodies (RGN10933 and RGN10987) as well as an in house developed monoclonal antibody (P5C3-LS) were tested against the D614G initial variant as well as the Beta, Gamma and Delta VOCs. A cell-based neutralization assay using live replicating isolates shows a highly variable potential of monoclonal antibodies regarding VOCs neutralization, with the P5C3-LS and RGN10987 performing well on Beta and Gamma isolates and P5C3-LS and RGN10933 on Delta isolate.

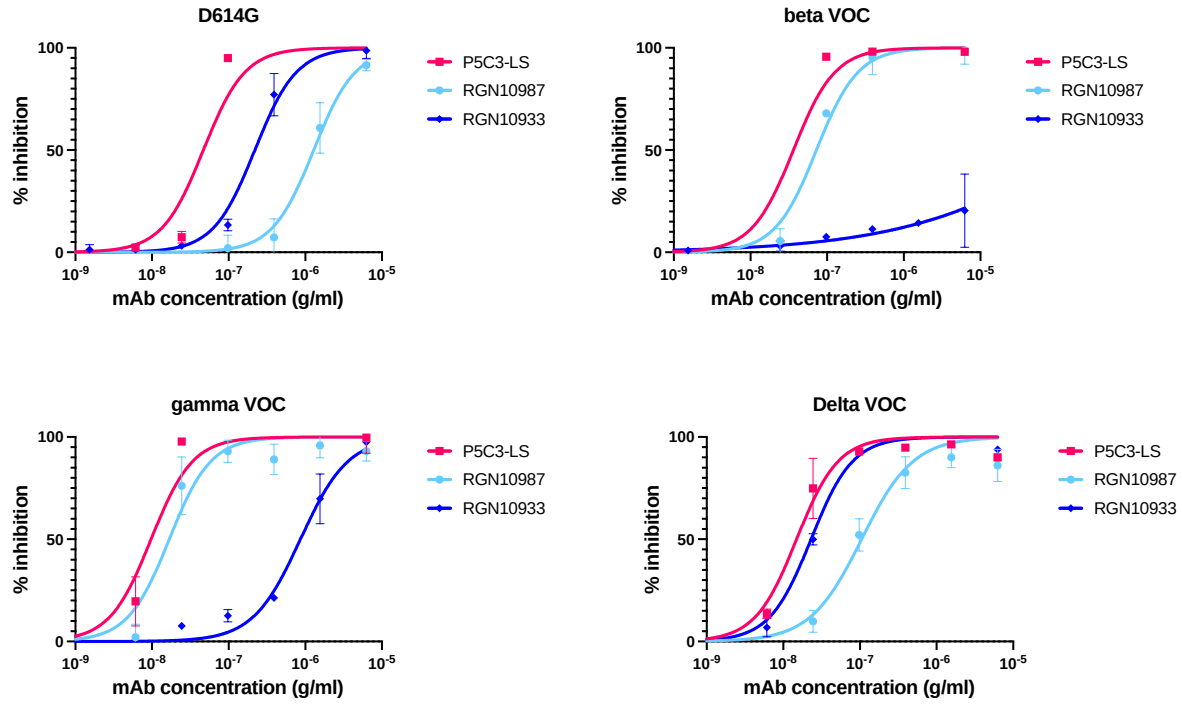


Figure 10: Testing of monoclonal antibodies against replicating VOCs
The neutralization potential of REGEN-CoV-2 (RGN10987 and RGN10933) and in house developed long lasting (P5C3-LS) monoclonal antibodies was evaluated with a cell-based neutralization assay using live replicating VOCs isolates.

In parallel, purified Spike proteins with either each mutation alone or the full combination of mutations found in the Kappa and Delta variants have been produced and will be used in the previously described cell-free neutralization assay with the set of monoclonal antibodies as well as serums from infected or vaccinated people.

Conclusion

In July, approximately 4500 sequences were obtained through this surveillance program. Each week since this surveillance program started, it has contributed almost all of the Swiss SARS-CoV-2 sequences available on GISAID. In July, around 30% of the cases reported in Switzerland were sequenced. Region 4 is still the least represented geographical area. Additional laboratories have been asked to join the program to ensure a substantial coverage, to achieve representative sequencing across the country.

The B.1.617.2 (Delta) variant continues to be the dominant variant, with a relatively homogenous representation over the different Swiss regions; it has completely replaced Alpha and accounted for most cases at the end of the month. Its sub-lineage AY.1 (Delta + 417N) has not been detected after mid-June, and its circulation appears to be limited in Switzerland. Other sub-lineages are increasingly detected, with no particular significance identified so far. Of note, their definitions is still ongoing, and any changes reported of their prevalence should therefore be considered carefully.

While only scarce data are available, preliminary testing – mainly produced by the manufacturers – confirmed the efficacy of the most used antigenic tests in Switzerland to detect Delta.

While the sensitivity of one RT-PCR test (GeneXpert®, Cepheid) has been reported to be decreased for the N2 target because of mutations contained in the Delta variant, no diagnostic failure has yet been reported.

All other variants were only rarely detected, both in clinical samples and in the wastewater surveillance part of the program:

- B.1.351 (Beta) was only detected once in July.
- P.1 (Gamma) circulated at very low levels during July, without increasing trends, and circulation was lower than in June.
- The B.1.621 variant, (considered a VOI), detected for the first time in June, circulated at very low levels in July in Switzerland.
- B.1.1.318, a newly identified "*variant under monitoring*" has been detected and is circulating at a low level, with no evidence to date that it could outcompete Delta.
- C.37 (Lambda), another VOI, has been detected only once, with no evidence of substantial circulation in the community.

No important geographical breakdown of a particular variant has been noticed.

An estimate of the total number of VOCs circulating in Switzerland, corrected by taking in account the fraction of sequencing in Switzerland is available at https://cov-spectrum.ethz.ch/explore/Switzerland.

As the number of cases of SARS-CoV-2 increases due to the Delta variant, and as Delta diversifies, an effort will be made to identify any concerning sub-lineages. Furthermore, an effort will be made to add more laboratories to the program in order to maintain representative sequencing throughout the country.

This revival in the number of new COVID-19 cases raises concerns regarding a new wave of hospitalization especially in unvaccinated population. Vaccination keeps a high effectiveness against severe disease due to the Delta variant and should be promoted.

Acknowledgements:

https://bsse.ethz.ch/cevo/research/sars-cov-2/swiss-sars-cov-2-sequencing-consortium.html

Marc Friedli, Pauline Vetter, Samuel Cordey, Erik Boehm, Richard Neher, Christian Althaus, Emma Hodcroft, Tanja Stadler, Philippe Lemercier, Ioannis Xenarios, Lorenzo Cerutti, Nadja Wipf, Damir Perisa, Laurent Kaiser, for the Swiss national SARS-CoV-2 genomic and variants surveillance program.

Appendix :

SARS-CoV-2 epidemiology in Switzerland:

We used publicly available data on COVID-19 as reported by FOPH (https://www.covid19.admin.ch) and sequence data submitted to GISAID to provide a summary of the SARS-CoV-2 epidemiology in Switzerland.

sup_table_overview_Jul.xlsx

Supplementary Table 1: Epidemiological data for Switzerland, its regions and cantons in July 2021: population, number and incidence of confirmed cases, effective reproduction number R_e, number and incidence of tests, test positivity, number and proportion of sequenced samples, and number and proportion of VOCs. R_e by region is represented as the median and range of the daily R_e values for all cantons within a region.

week	date	Total PCR tests	Positve tests	Sequenced	% positives	% positives sequenced
27	July 5 to July 11	17'855	570	545	3.19%	95.61%
28	July 12 to July 18	18'545	1'043	1088	5.62%	104.31%
29	July 19 to July 25	17'785	1'466	1329	8.24%	90.65%
30	July 26 to August 1	16'285	1'632	1476	10.02%	90.44%
	Total	70'470	4'711	4'438	6.69%	94.21%

Supplementary Table 2: Total number of tests performed by the laboratories participating in the surveillance program from July 5 to August 1, 2021.

Week	Date	Basic Surveillance		Augmented Surveillance						Sentinella laboratories		
		EOC	St-Gallen	USB	IFIK	Dianalabs	CHUV*	UZH*	ICH-VS**	HUG	ETH/Viollier*	All
27	July 5 to July 11	34	15	10	5	33	64	41	29	83	229	543
28	July 12 to July 18	38	24	27	13	81	65	99	72	213	447	1079
29	July 19 to July 25	69	42	71	16	134	52	112	61	263	508	1328
30	July 26 to August 1	80	48	88	29	90	156	200	60	212	509	1472
	Total	221	129	196	63	338	337	452	222	771	1693	4422

*Supplementary Table 3: number of sequences submitted to GISAID by each laboratory during the surveilled period (July 5 to –August 1, 2021). *including sequencing sent to high-throughput platforms ** Samples sent to high throughput platform*

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