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Public Health Directorate Communicable Diseases Division

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Geneva, June 02, 2021

Swiss national SARS-CoV-2 genomic and variants surveillance program: first report

1. Introduction: description of the Swiss national SARS-CoV-2 genomic and variants surveillance program.

Geneva Centre for Emerging Viral Diseases

Division of Infectious Diseases

Department of Medicine

Laboratory of virology

Division of Laboratory Medicine

Diagnostic Department

In the midst of the SARS-CoV-2 pandemic, it is crucial to monitor in real time: the relative prevalence of variants of concern, the appearance of new variants, and the risk of escaping immunity conferred by vaccination or previous infection with other variants.

Genetic surveillance of SARS-CoV-2 is essential for COVID-19 outbreak surveillance. While most mutations do not have an epidemiological or clinical impact, when mutations accumulate they may lead to the emergence of a new variants, which may have an increased transmissibility, an increased severity, and/or an ability to escape immunity resulting from previous vaccination or natural infection. Moreover, depending on where mutations arise on the genome, they can also lead to diagnostic test failure, or abolish/diminish the effect of some treatments, such as monoclonal antibodies (mAbs).

The Federal Office of Public Health (FOPH) has decided to fund the Swiss national SARS-CoV-2 genomic and variants surveillance program for SARS-CoV-2 at the suggestion of the Swiss National COVID-19 Science Task Force diagnostics and testing expert group and under the coordination of the Centre for Emerging Viral Diseases and the National Reference Laboratory for Emerging Viral Infections (CRIVE) at the University Hospitals of Geneva. Our country has the resources to conduct this surveillance, has access to a network of unique expertise and has the ability to translate this surveillance in specific public health interventions.

The aim of this program is to assess the impact and to support surveillance of genetic variants of SARS-CoV-2 circulating in Switzerland, in order to rapidly identify and monitor variants of concern (VOCs) or variants of interest (VOIs). The strategy rests on recommendations from the WHO and is supported by the FOPH. Additionally, immunological characterization of VOCs and their potential escape from immunity conferred by previous infection or vaccines will be also performed. Reports will be generated monthly and shared with the FOPH. In addition our group of experts is closely monitoring the situation at the international level and anticipates the need for targeted surveillance.

The program runs from the 1st of March 2021 to the 31st of March 2022 and aims to have at least 10% of SARS-CoV-2 genomes sequenced per week over the 13-months. This should result in

analysis of enough positive samples to have a representative picture of the situation in Switzerland, and will be completed by more systematic approach in dedicated sentinel sites. We aim to cover all geographical areas of Switzerland, and all areas will be sampled to provide an accurate epidemiological picture.

Currently, 8 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, Dianalabs Genève), 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). Additional laboratories will certainly join.

Each laboratory participating in the basic surveillance (EOC-Bellinzona, St-Gallen) will send, depending on the epidemiology, at least 48 samples per week. Centers contributing to "augmented surveillance" will try to provide 96 samples per week (CHUV-Lausanne, IFIK-Bern, IMV-Zurich, Basel, Hôpitaux du Valais, Dianalabs Genève). In addition, 2 centers participate as sentinel surveillance laboratories:

- HUG: the laboratory of virology of University Hospitals of Geneva, which tests 1/4 to 1/3 of the positive cases of the canton of Geneva (samples originating from both symptomatic out- and hospitalized patients, cluster investigation, health care workers as part of hospital surveillance and asymptomatic travelers requiring a screening test) - see weekly report regarding circulation of SARS-CoV-2 in the Geneva area. The laboratory will contribute with up to 350 sequences per week, or as much as possible depending on the number of positive cases each day.
- Viollier/ETHZ: soon after the beginning of the pandemic in Switzerland, the Viollier Laboratories began providing RNA extracts to ETHZ for sequencing. Pr. Stadler's group at ETHZ coordinates the sequencing efforts between the three high-throughput facilities and analyzes the resulting sequences. The bioinformatics is performed in the Computational Biology Group (Pr. Beerenwinkel) at D-BSSE, ETHZ.

Processed sequencing data will be 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 will be 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 Bioinformatic (SIB).

This report has been produced by Marc Friedli, Pauline Vetter, Samuel Cordey, Erik Boehm, Richard Neher, Christian Althaus, Martina Reichmuth, Tanja Stadler, 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 first report covers the period of March 1, 2021, to April 30, 2021.

All data presented in this report are based on the sampling date.

2. 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, currently dominant in Switzerland), B.1.351 (first identified in South Africa – VOC beta), P.1 (first identified in Brazil – VOC gamma), and most recently B.1.617 (first identified in India, with 3 sub-lineages: B.1.617.1 (VOI kappa), B.1.617.2 (VOC delta), B.1.617.3). These variants were all detected in the context of new surges in infection rates, and are thought to be linked to increased transmissibility. B.1.1.7 in particular has proven to be more transmissible than B.1.351 and P.1, with those other VOCs being unable to displace it under current conditions. The N501Y mutation is present in B.1.1.7 and is thought to play a significant role in its increased transmissibility, but this mutation is also present in B.1.351, P.1, and other variants. The full set of mutations responsible for its particularly increased transmissibility are currently unclear. Preliminary epidemiological data suggest that B.1.617.2 may be even more transmissible and able to displace B.1.1.7. B.1.1.7 has also been reported by some studies to be associated with increased severity, with other studies challenging this conclusion (see https://www.who.int/emergencies/diseases/novel-coronavirus-2019/situation-reports for further information). B.1.1.7 is by far the most dominant strain in Europe and much of the world.

B.1.351, P.1, and B.1.617 all have mutations (E484K or L452R in particular) which lead to elevated concerns of reduced vaccine efficacy. Of these, B.1.351 is associated with the greatest reduction in vaccine efficacy, while B.1.617 is only associated with very modest reductions in vaccine efficacy after complete vaccination. As vaccination proceeds, thereby increasing selection pressure for immune escape, there is a concern that these VOCs may displace B.1.1.7 or develop further immune escape mutations.

Greater transmissibility and/or immune escape potential may lead to a renewed surge in infections despite the vaccination campaign. While we have identified some mutations that lead to greater transmissibility or reduced vaccine efficacy in vitro, there are many more such mutations or combinations of mutations which have not been identified. Therefore any variants displaying mutations known to be linked with either increased transmissibility and/or immune escape potential should be closely monitored, lest they acquire further enhancing mutations and develop into an even worse variant.

Therefore variants presented below will be particularly surveilled:

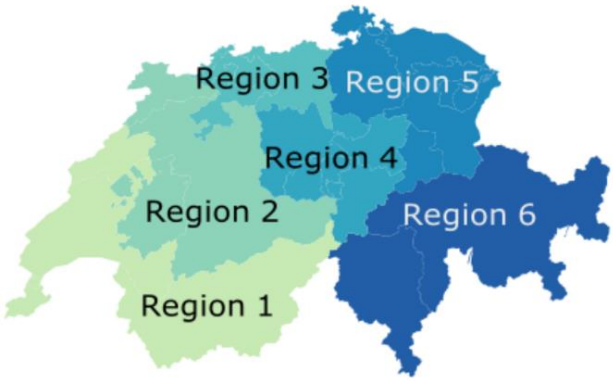
- variants classified as VOCs by the WHO
  - P.1
  - B.1.351
  - B.1.617.2
  - B.1.1.7
- variants that include E484K + N501Y: higher transmissibility, immune escape risk, resistance to mAbs, such as:
  - B.1.621 (N501Y + E484K)
  - B.1.1.7 + E484K in particular
  - P.3
  - B.1.315
- variants that include E484K but not N501Y: immune escape risk, resistance to mAbs, such as:
  - P.2
  - B.1.1.318
  - B.1.525
  - B.1.526: part of the lineage carries E484K, the other S477N
  - B.1.620
  - A.VOI.V2
- variants that include L452R: slightly more transmissible relative to N501, resistance to mAbs, such as:
  - B.1.427/429, C.36, B.1.617.1/3
- variants that include L452R + N501Y, such as A.27 and/or B.1.1.7 + L452R

3. 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. We aim to have a "harmonized" data set in the future with publicly available FOPH data and sequence data from SPSP. The overall goal of the program is to provide epidemiological trends and to highlight meaningful observations.

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 2 months covered by the present report, the FOPH reported a total of 104 235 confirmed SARS-CoV-2 cases in Switzerland, 46 126 in March and 58 109 in April. Supplementary Tables 1 and 2 provide a monthly 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 24 664 positive tests during the surveilled program, 11 906 in March and 12 578 in April, which represent 26 % and 22 % of the total number of cases reported for each month respectively 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 of the surveillance, which applies only to PCR tests.

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

A total number of 11 319 SARS-CoV-2 sequences have been submitted to GISAID during the 2 first months of the program: 5 593 in March and 5 726 in April. This represents between 41 % and 57 % of the total number of the positive cases processed by the laboratories participating in the surveillance program (see Supplementary Table 3 in Appendix for details).

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
9	March 1 to 7	817
10	March 8 to 14	1179
11	March 15 to 21	1230
12	March 22 to 28	989
13	March 29 to April 4	1378
	Total March	5 593
14	April 5 to 11	1330
15	April 12 to 18	1405
16	April 19 to 25	1554
17	April 26 to May 2	1437
	Total April	5 726
	Total March + April	11 319

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 first 2 months of the program is available in Supplementary Table 4 in the appendix.

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

As shown in Figure 1, since the beginning of the program (calendar week 9), the total number of SARS-CoV-2 sequences submitted per week has progressively increased, reflecting the fact that new laboratories have joined the program. The vast majority of the sequences available in GISAID (blue curve) and those on which the surveillance is conducted, come from the national surveillance program (orange curve). Between 10 % and 15 % of the total number of cases each week are submitted to GISAID (green curve). Sequences produced at the beginning of 2021 (weeks 1 to 8), before the funding of the program, came mostly from the Viollier/ETHZ and HUG laboratories and were representative sampling from Switzerland and the Geneva area, respectively (See supplementary table 5).

Figure 2 displays the fraction of SARS-CoV-2 cases sequenced for each Swiss region. The highest fraction of the sequences originated from region 3 (AR, BS, BL, SO), followed by region 1 (GE, VD, NE, VS). Those two regions also provided the highest number of sequences per week. Less sequencing was observed in regions 2 and 4 (6.7 % and 3.7 % respectively vs. 12.5 % in Switzerland overall). Within region 3, there was an overrepresentation of the canton of Basel Land and Solothurn, for which respectively 49 % and 32 % of confirmed cases have been sequenced (see supplementary Table 2). The black curve shows the coverage of sequencing among the total number of reported cases in Switzerland, by calendar week.

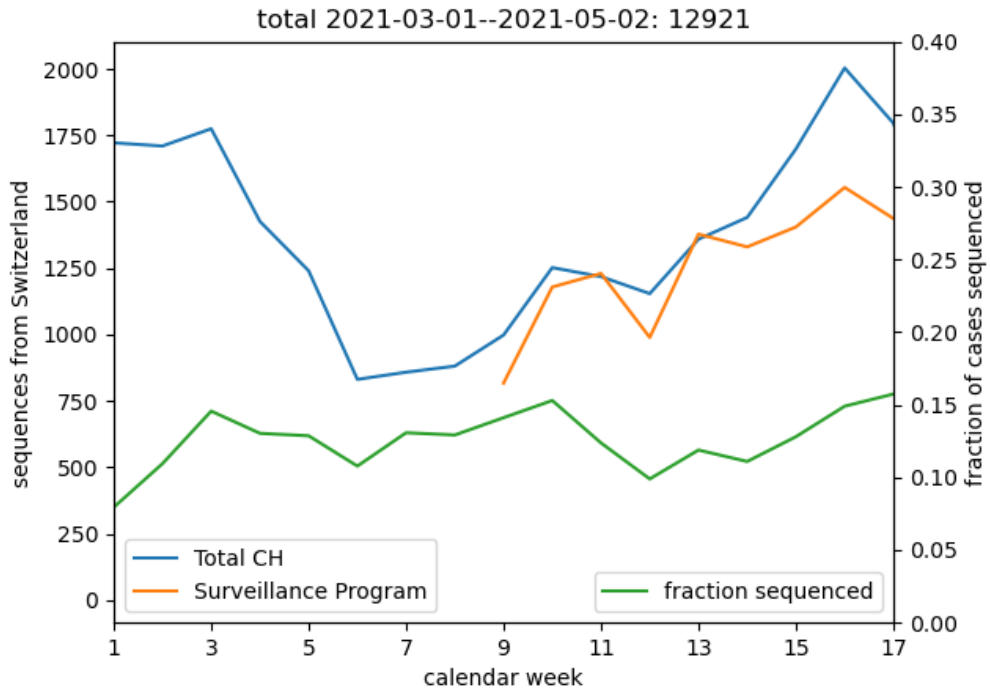


Figure 1: Number of SARS-CoV-2 sequences available for Switzerland (total available Swiss sequences in GISAID in blue, Swiss sequences submitted through the program in orange) and fraction of the total number of positive cases declared to the FOPH that have been sequenced

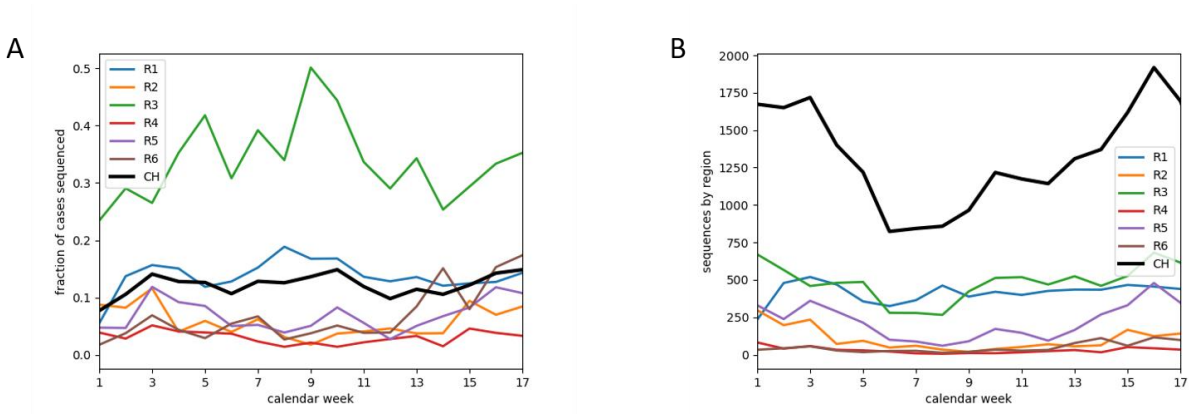


Figure 2: Covering of sequencing among the different Swiss regions per week, presented by fraction of cases sequenced (A) and by number of sequences (B)

4. 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).

By the end of February, B.1.1.7 had already become dominant and replaced previously circulating variants all over Switzerland.

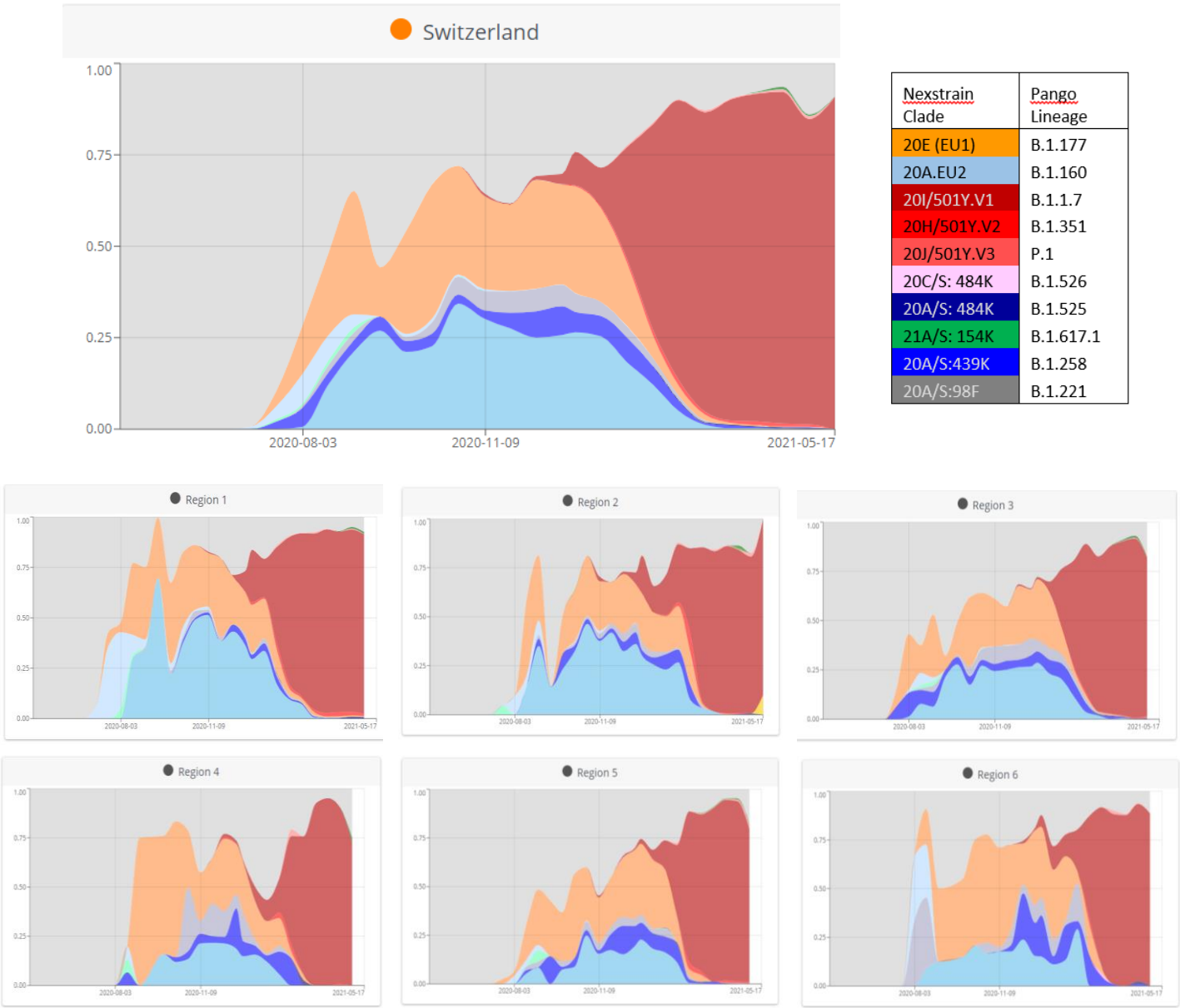


Figure 3: proportion of total number of sequences (not cases), over time, that fall into defined variant groups, for Switzerland and by regions. Screenshot from CoVariant website. Dynamic navigation is available at https://covariants.org/per-country. Dark red indicates lineage B.1.1.7. Note the rapid increase in prevalence and rise to dominance. Light red indicates B.1.351. Green indicates lineage B.1.617, detected since mid-April in Switzerland. Note that for Region 2, the last data point has only 10 sequences so far, so the last point should not be considered as representative of circulating variants.

Currently, the dominant lineage in Switzerland remains B.1.1.7. The percentage of VOCs other than B.1.1.7 in Switzerland has been increasing over the last 4 weeks of the surveilled period and represents, at the end of April, around 4 % of the total number of samples sequenced. (Figure 4). This is mainly explained by the detection of B.1.617.2 since mid-April and a low level circulation of B.1.351 (Figure 5). There is still substantial circulation (5-20 cases/week detected for the last 2 weeks) of the E484K containing lineages including P.1, B.1.351, B.1.1.318, and B.1.620. In total, the E484K containing lineages have seen a substantial uptick in the last 2 weeks (Figure 5). 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.

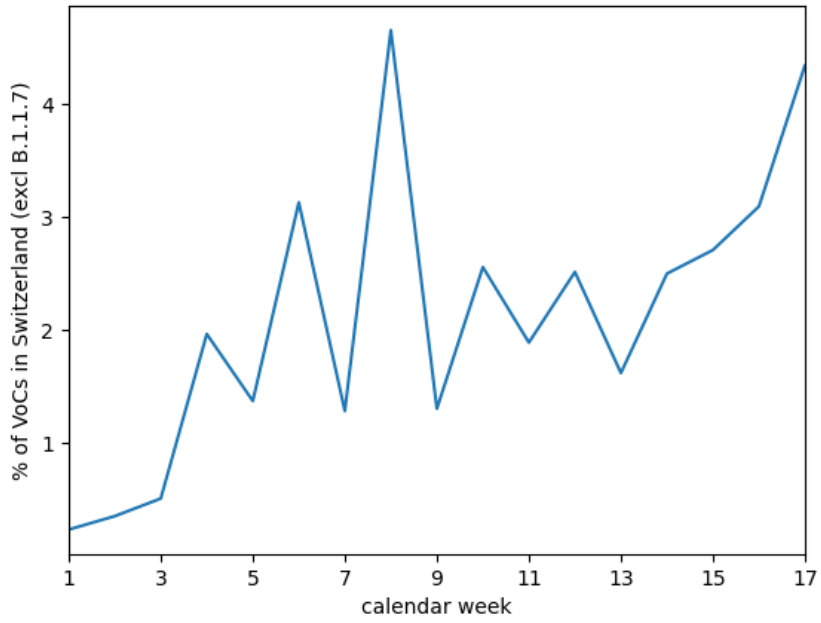


Figure 4: Percentage of circulating VOCs in Switzerland, excluding B.1.1.7, over the 18 first weeks of 2021 (total number of B.1.351, P.1 and B.1.617 sequences from Switzerland and successfully submitted to GISAID are counted here).

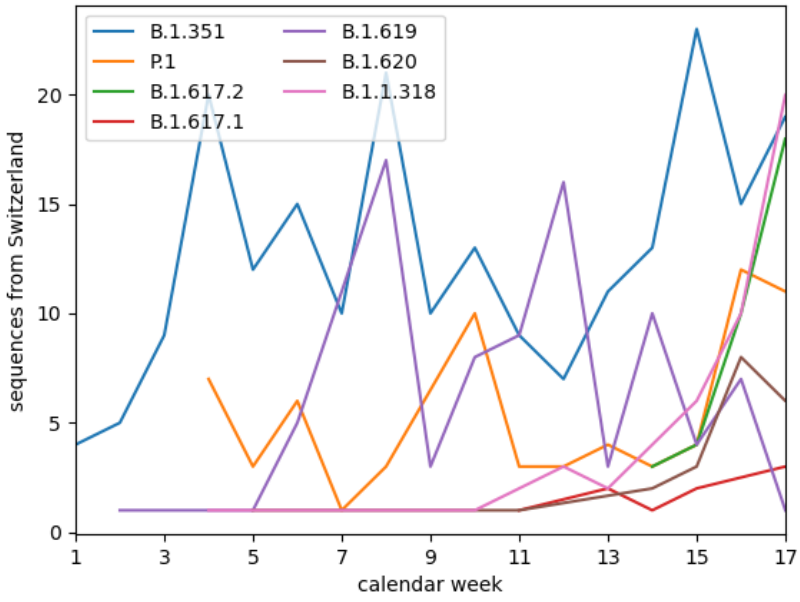
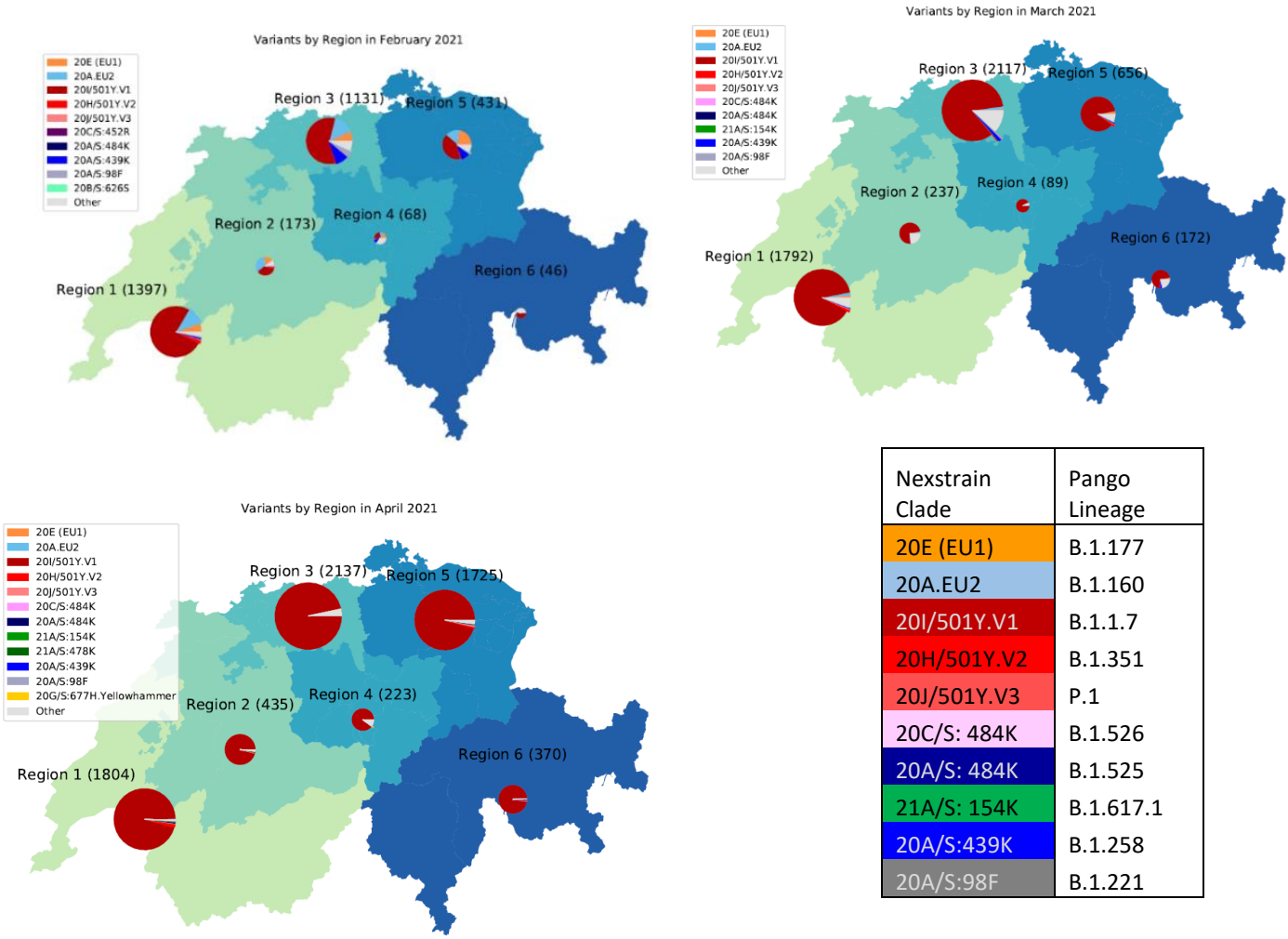


Figure 5: Number of sequences of the main VOCs/VOIs (excluding B.1.1.7) and variants under monitoring retrieved during the surveilled period. Note that 12% of the positive cases in Switzerland were sequenced.



Nexstrain Clade	Pango Lineage
20E (EU1)	B.1.177
20A.EU2	B.1.160
20I/501Y.V1	B.1.1.7
20H/501Y.V2	B.1.351
20J/501Y.V3	P.1
20C/S: 484K	B.1.526
20A/S: 484K	B.1.525
21A/S: 154K	B.1.617.1
20A/S:439K	B.1.258
20A/S:98F	B.1.221

Figure 6: Distribution of variants per region, per month, for February, March, and April, 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.

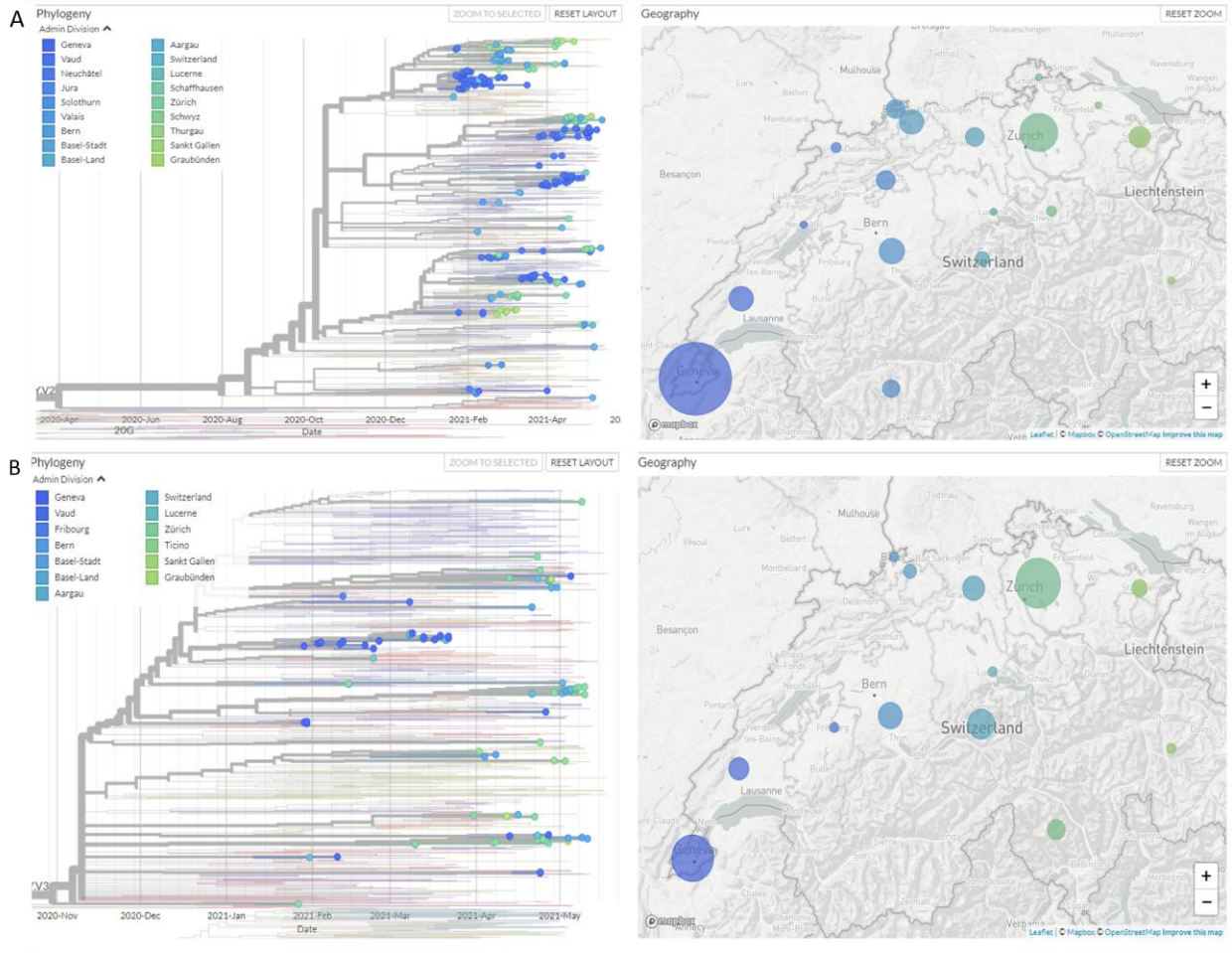


Figure 7: Proportion of sequences and phylogenetic tree from A) B.1.351 B) P.1 in different cantons of Switzerland. Data from A) 222 of 2754 genomes B) 87 of 2722 collected from January 2021 to May 2021. Screenshots from Nextstrain. Dynamic navigation is available online at https://nextstrain.org/groups/swiss/

Conclusion

The national surveillance program started on March 1, 2021, and it is planned to continue until March 31, 2022. Since the beginning of the program, the total number of new sequences deposited to GISAID has been progressively increasing, and new partners have joined the project. In March and April, over 11 000 sequences have been obtained through this surveillance program. Each week since this surveillance program started, it has contributed 80 % or more of the Swiss SARS-CoV-2 sequences available on GISAID. In total, between 10% to 15% of the cases reported in Switzerland were sequenced each week. Currently the least represented geographical areas are regions 2 and 4. Additional laboratories will have to join the program to assure a substantial coverage, especially while the total number of new cases are declining, to achieve representative sequencing across the country. The FOPH may have to require participation of additional hospital-based and/or private laboratories in order to reach at least a 10% of sequence coverage in Switzerland.

During the reporting period, we observed a homogeneous circulation of the different variants through Switzerland.

Despite the occasional detection of other variants, B.1.1.7 is still generating almost all new cases.

B.1.351 continues to circulate at low levels throughout the whole surveilled period, without increasing trends.

P.1 continues to circulate at very low levels, and has been doing so since its first detection during the surveilled period, without increasing trends.

Towards the end of the surveilled period, both B.1.617.1 and B.1.617.2 have been detected in Switzerland. B.1.617.2 has been detected at a very low level in almost all regions, except for region 6. For now, this variant is not considered to pose any particular risk to the efficacy of the ongoing vaccination campaign in patients with a complete mRNA vaccination. Of note, protection against infection is suboptimal after only one dose of vaccine. There is currently too little data to determine if B.1.617 will displace B.1.1.7 in Switzerland.

No specific geographical breakdown has been noticed, and no significant clusters have been identified.

Various E484K containing variants (B.1.1.318 (variant under monitoring), B.1.620 (VOI) continue to be detected at low levels across Switzerland, and there has been an increase in the number of such E484K-containing variants in the last 2 weeks. 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 decline, an effort will be made to add more laboratories to the program in order to keep a representative sequencing over the country.

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.

report_Mar.xlsx

Supplementary Table 1: Epidemiological data for Switzerland, its regions and cantons in March 2021: 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.

report_Apr.xlsx

Supplementary Table 2: Epidemiological data for Switzerland, its regions and cantons in April 2021: 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 RT-PCR tests performed in laboratories participating to the surveillance	Total number of negative tests perfomed in laboratories participating to the surveillance	Total number of positive cases in laboratories participating to the surveillance program	Number of positive tests that have not been sequenced	Number of positive tests that have been sequenced	% postives tests in the laboratories participating to the surveillance program	% total of positives tests that have been sequenced
9	March 1 to 7	29 488	27 800	1688	871	817	5.72%	48.40%
10	March 8 to 14	33 715	31 647	2068	889	1179	6.13%	57.01%
11	March 15 to 21	37 522	35 177	2345	1115	1230	6.25%	52.45%
12	March 22 to 28	40 331	37 684	2647	1658	989	6.56%	37.36%
13	March 29 to Apr 4	48 695	45 537	3158	1780	1378	6.49%	43.64%
	Total March	189 751	177 845	11 906	6 313	5 593	6.27%	46.98%
14	April 5 to 11	31 477	28 679	2798	1468	1330	8.89%	47.53%
15	April 12 to 18	33 799	30 425	3374	1969	1405	9.98%	41.64%
16	April 19 to 25	34 640	31 223	3417	1863	1554	9.86%	45.48%
17	April 26 to May 2	33 104	29 935	3169	1732	1437	9.57%	45.35%
	Total April	133 020	120 262	12 758	7 032	5 726	9.59%	44.88%
	Total March + April	322 771	298107	24664	13 345	11 319	7.64%	45.89%

Supplementary Table 3: Total number of tests performed by the laboratories participating in the surveillance program.

Week	Date	Basic surveillance		Agumented surveillance				Sentinella laboratories	
		EOC	St-Gallen	UBS	IFIK	CHUV	UZH	HUG	ETH/Viollier
9	March 1 to 7	0	14	39	0	47	0	215	502
10	March 8 to 14	0	14	87	0	63	0	256	759
11	March 15 to 21	0	14	42	0	44	0	280	850
12	March 22 to 28	0	22	27	0	23	0	259	658
13	March 29 to Apr 4	46	45	100	0	70	0	351	812
	Total March	46	109	295	0	247	0	1 361	3 581
14	April 5 to 11	47	47	41	0	100	0	253	842
15	April 12 to 18	48	45	17	0	68	43	310	874
16	April 19 to 25	47	46	20	7	66	33	271	1064
17	April 26 to May 2	94	42	3	138	89	37	306	672
	Total April	236	180	81	145	323	113	1 140	3 452
	Total March + April	282	289	376	145	570	113	2 501	7 033

Supplementary Table 4: number of sequences submitted to GISAID by each laboratory during the surveilled period. Due to technical reasons, during the surveilled period, one laboratory participating in the augmented surveillance has only submitted a very small proportion of its sequences to GISAID (as low as 2.9 to 13.9% for 3 weeks in a row), explaining the very low number of sequences produced by this laboratory between week 15 and 17. These sequences are expected to appear later on GISAID.

Institution	Number of sequences
Department of Biosystems Science and Engineering, ETH Zürich	7262
HUG, Laboratory of Virology and the Health2030 Genome Center	2143
University Hospital Basel, Clinical Bacteriology	631
Laboratory of genomics and metagenomics, Institute of Microbiology, University Hospital Centre and University of Lausanne	291
Genomics and Transcriptomics, Philip Morris International	232
Clinical Bacteriology	180
Institute of Medical Virology, University of Zurich	122
Center for Laboratory Medicine St. Gallen	58
Swiss Tropical and Public Health Institute	52
Institute for Infectious Diseases, University of Bern	20
University Hospital Basel	20
HUG, Laboratory of Virology and Universitätsspital Basel	15
Laboratory of genomics and metagenomics	4
Center for Laboratory Medicine	1

Supplementary Table 5: number and origin of sequences submitted to GISAID by each laboratory during January and February, 2021, prior to the start of the surveillance program. The proportion of sequenced cases out of all cases for the Viollier dataset between mid-december 2020 and March 11, 2021 can be found in Table S1 at https://www.medrxiv.org/content/10.1101/2021.03.05.21252520v3.full.pdf

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