Hôpitaux Universitaires Genève

UNIVERSITÉ DE GENÈVE
FACULTÉ DE MÉDECINE

Federal Office of Public Health FOPH
Public Health Directorate Communicable
Diseases Division

Schwarzenburgstrasse 157
3003 Bern
Switzerland

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Swiss national SARS-CoV-2 genomic and variants surveillance program: report of the month of May 2023

Geneva Centre for Emerging Viral Diseases

Division of Infectious Diseases

Department of Medicine

Laboratory of virology

Division of Laboratory Medicine

Diagnostic Department

1. Summary

During the month of May, the number of positive SARS-CoV-2 tests decreased in Switzerland, and the test positivity rate dropped to 15.4% from April's 17.0%. The number of hospitalizations due to COVID-19 is low.

Around 45% of the 2'457 reported positive tests were processed by laboratories participating to the program.

A total of 388 new sequences were submitted to GISAID during the reporting period, covering the month of April (April 24 to May 21), which represents around 15.8% of the positive tests. Note that since the beginning of 2023, the program has been adapted to focus on samples originating from hospitalized patients.

The majority of the sequences in Switzerland belong to the XBB.1.5 or 1.9 sub-lineages. Both have the same Spike mutations and are sublineages of XBB, which results from a recombination between two BA.2 sublineages and additional accumulated mutations. The XBB* variant replaced the previously circulating BQ.1.1 variant (a derivative of BA.5) in Switzerland during February and XBB* continues to dominate in May. The XBB 1.5 variant replaced other circulating variants worldwide but is now sharing the dominate position with the highly similar XBB.1.9 and is facing pressure from the XBB.1.16 variant, which has become dominant in some areas of the world. Current data does not suggest that these subvariants are more severe.

Since January, the currently circulating variants are resistant to all the monoclonal antibody therapies available in Switzerland, which are unable to effectively neutralize circulating SARS-CoV-2 viruses. However, the change in clinical effectiveness is unclear. Of note, hospitalization rates are down due to previous immunity and protection from previous exposure/vaccination.

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. It began in March 2021 and is currently funded through 2023.

Because greater transmissibility and/or immune escape potential of the different VOCs and VOIs can result in new surges in COVID-19 numbers despite the vaccination campaign, this program aims to closely monitor each variant displaying mutations known to be linked with either increased transmissibility or immune escape potential.

As of the beginning of January 2023, the program was adapted and restricted to 7 participating laboratories, comprising the University Hospital Centres in Geneva, Lausanne, Bern, Basel, Zurich, and Ticino), in addition to the cantonal hospital in Valais (Hôpital du Valais – Institut Central), and 1 high-throughput sequencing platform (Health 2030 Genome Centre in Geneva). In addition, since the month of October 2022, sequencing in Geneva has been partially funded by the EU grant for the COVICIS project (https://covicis.eu/).

Processed sequencing data are shared openly 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 Institute of Bioinformatics (SIB).

In order to complement the genomic surveillance based on patient samples, the program includes sequencing of SARS-CoV-2 in wastewater samples. Samples are collected daily in 10 wastewater treatment plants (WWTP), under the coordination of Eawag. 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 six WWTP (https://bsse.ethz.ch/cbg/research/computational-virology/sarscov2-variants-wastewater-surveillance.html). Since the beginning of January 2023, the surveillance in wastewater expanded to 10 facilities and is no longer included in the national surveillance program but benefits from another source of funding.

Immunological characterization of the variants within the surveillance program was included until December 2022 and was coordinated by Professor Trono's team at EPFL.

This report has been produced by Erik Boehm, Pauline Vetter, Marc Friedli, Samuel Cordey, Richard Neher, Christian Althaus, Martina Reichmuth, Cornelius Römer, David Dreifuss, Chaoran Chen, Tanja Stadler, Emma Hodcroft, Erik Studer, 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 April 24 to May 21, 2023 (weeks 17-20). All data presented in this report are based on the sampling date.

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

Five VOCs have been designated by the WHO, B.1.1.7 (Alpha), B.1.351 (Beta), P.1 (Gamma), B.1.617.2 (Delta), and B.1.1.529 (Omicron). Worldwide, all VOCs except Omicron have essentially disappeared from samples collected since the beginning of 2022 (https://www.who.int/publications/m/item/weekly-epidemiological-update-on-covid-19---24-august-2022).

On March 15, 2023, WHO updated its definitions for VOCs and VOIs, mainly consisting in making the VOC definition more specific. Greek letters will thus only be assigned to VOCs.

Omicron

The Omicron VOC (B.1.1.529) is characterized by a high divergence in the spike protein, which has allowed it to substantially escape immunity conferred by vaccination (using the original Wu-1 sequence) and prior infection with pre-Omicron variants. This VOC currently has multiple sublineages. Despite all being considered "Omicron", these sublineages may differ from each other (in terms of mutation counts) more than the earlier VOCs differed from the original Wu-1 strain.

Notably, this is the first VOC to have subvariants causing multiple successive waves. These sublineages have successively replaced each other, with the BA.5 sublineage BQ.1 being dominant in most of January, and then being quickly replaced by the XBB.1.5 variant since mid-February 2023 (see below), which has been seeing competition from XBB.1.9 and XBB.1.16 since April.

XBB* is a highly derived BA.2 sublineage which derives from a recombination event between two sublineages (BJ.1 and BM.1.1.1). Most circulating Omicron subvariants now contain mutations that enable complete escape from monoclonal antibodies available on the market.

In March, 2023, XBB.1.5 was classified as a VOI by WHO. Notably, the XBB.1.5 sublineage seems to have similar immune escape properties to BQ.1.1, but has a higher ACE2 affinity, presumably enhancing its inherent transmissibility. The three most prominent XBB sublineages are currently XBB.1.5/9/16. The XBB.1.9 sublineage has the same spike protein as XBB.1.5 (and is distinguished from XBB.1.5 by non-spike mutations) while the XBB.1.16 spike protein differs from by only a few mutations. Notably XBB.1.9 and XBB.1.16 have overtaken XBB.1.5 in some parts of the world.

Detection

All sub-lineages are still detected by RT-PCR tests There is no evidence that the new subvariants pose any particular detection challenges to these tests. As XBB lineages are currently dominant, S-gene target failure with the Roche PCR assays regularly used in Switzerland is not very informative, and mostly indicates residual BA.5/BQ.1 circulation. Further discrimination between subvariants is not feasible at this time by any method other than genomic sequencing, although variant specific PCRs could be developed.

Immune escape

Extensive data demonstrates that Omicron variants are substantially able to evade neutralizing antibodies (nAbs) from non-Omicron infections and after 2-3 doses of vaccine. Current evidence suggests that vaccines updated against BA.4/5 have substantially reduced neutralization of the currently circulating XBB.1.5 and XBB.1.16 lineages. XBB.1.5 and XBB.1.16 only differ antigenically by a few residues, but differ substantially from the BA.5 sublineages that were recently replaced. The latest data suggests that both and vaccines updated against either XBB.1.5 or XBB.1.16 perform similarly against both variants. Therefore, a vaccine update against either sequence would be similarly beneficial.

Escape from monoclonal antibodies is extensive and is covered by the "Therapeutic intervention effectiveness" section.

Severity

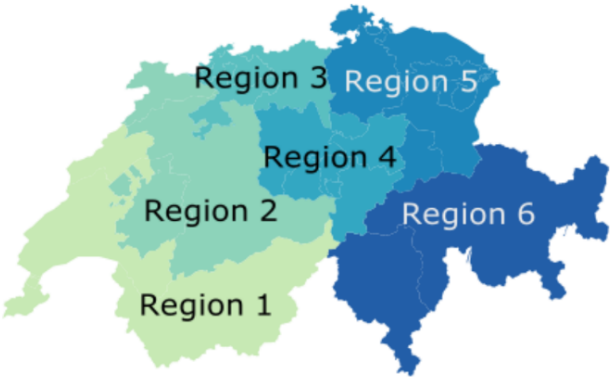
There is currently no evidence that the severity of the new subvariants has significantly changed. Indeed, some studies provide evidence that XBB sublineages are not more severe. There is currently weak evidence that XBB.1.16 may have an increased incidence of non-severe conjunctivitis.

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.

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 May (April 24 to May 21), the FOPH reported a total of 2'457 positive tests (including both RT-PCR and antigen-based tests). Of these, 1'101 (44.8%) were processed by labs participating in the national surveillance program. After the drop in testing observed since the beginning of the year, the number of positive tests decreased Switzerland during the month of May relative to April. Notably, the observed test positivity rate within the program varied from 34.3% to 36.6%, which is consistent with the latter half of April (36.3%). Outside of the program, the rest positivity rate was 15.4%, compared to 17.0% for April. The higher rate within the program may reflect the focus on testing hospitalized patients.

Although case ascertainment rates may be too low to identify meaningful trends, there has not been any sign that the currently low hospitalization rates are rising.

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. 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 supplementary Table 2.

Number of declared SARS-CoV-2 sequences produced through the surveillance program (presented by submission date, further declarations are still ongoing)

A total of 388 SARS-CoV-2 sequences have been declared to have been processed during this period. There are 377 sequences available that were submitted during this period on GISAID (and 372 collected during this period) as of 27 June 2023. This contrast between the numbers of submitted and collected sequences is likely due to reporting delays .

The number of sequences collected and submitted during the reporting period represent around 15.8% of the total of the positive tests.

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 declared and successfully submitted to GISAID during the surveilled period, by all laboratories in the program
17	April 24 - April 30	222
18	May 1 - May 7	
19	May 8 - May 14	166
20	May 15 - May 21	
	Total	388

Table 1: number of sequences submitted to GISAID through the surveillance program. Note these data are not by sampling date but rather by submission to GISAID date.

The total number of SARS-CoV-2 sequences declared and submitted to GISAID by each laboratory during this period 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 declined during the month of May 2023 (Calendar weeks 17 - 20). Since the beginning of this program, almost all of the sequences available, and all of those on which the surveillance is conducted, come from the national surveillance program.

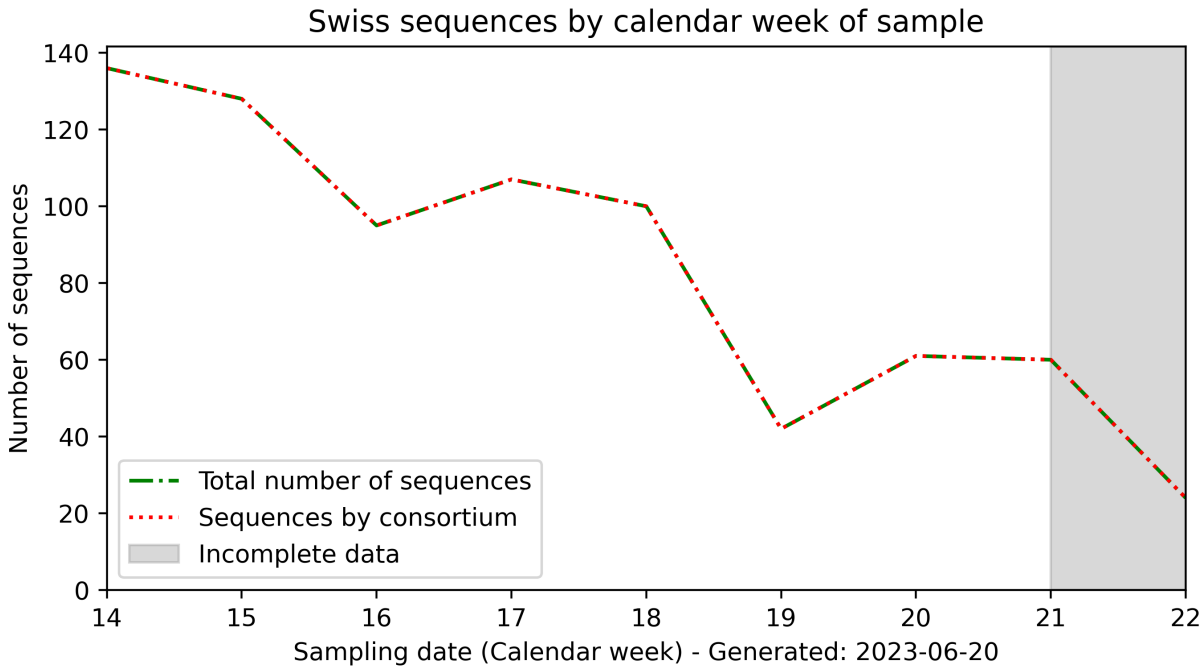


Figure 1: Number of SARS-CoV-2 sequences available for Switzerland (total available Swiss sequences in GISAID in green, Swiss sequences submitted through the program in dotted orange).

Figure 2 displays the number of SARS-CoV-2 cases sequenced for each Swiss region. Notably, region 4 (Luzern, Unterwalden, Uri, Zug and Schwyz) is no longer represented due to the absence of a laboratory participating in the program in this region, after the switch to surveillance of hospitalized cases.

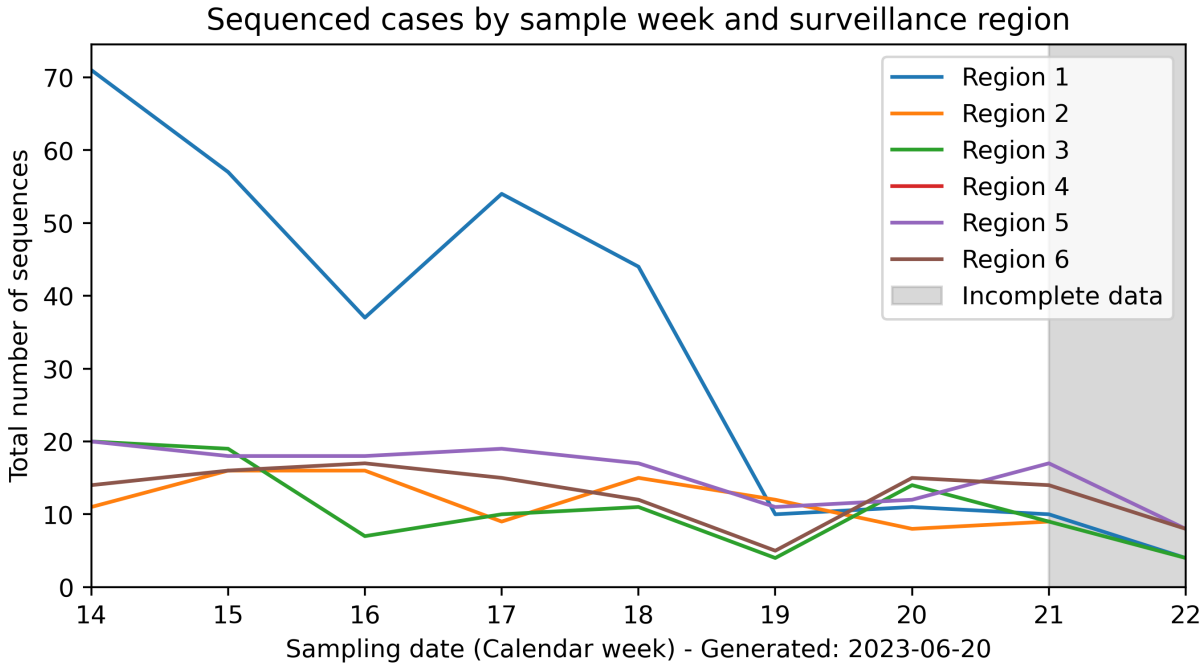


Figure 2: Sequencing coverage among the different Swiss regions per week, by number of sequences.

4. Recently circulating variants in Switzerland

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).

XBB.1.5 and XBB.1.9 continue to vie for dominance. An estimate of the total number of VOCs circulating in Switzerland, corrected by taking in account the fraction of sequencing in Switzerland is available through the covSPECTRUM program, developed at ETHZ, at https://cov-spectrum.ethz.ch/explore/Switzerland.

Region	BA.2.75*	BA.5*	XBB*	XBB.1.16*	XBB.1.5*	XBB.1.9*	XBB.2.3*	Others	Recombinant	sequences
All	2	5	5	19	140	126	10	2	1	310
1	1	1	0	1	56	58	2	0	0	119
2	0	0	1	1	28	9	2	2	1	44
3	1	0	1	6	22	8	1	0	0	39
4	0	0	0	0	0	0	0	0	0	0
5	0	4	3	5	20	26	1	0	0	59
6	0	0	0	6	13	24	4	0	0	47

Table 2: number of sequences corresponding to selected variants in each region of Switzerland from April 24 to May 21, according to data received by 21 June, 2023.

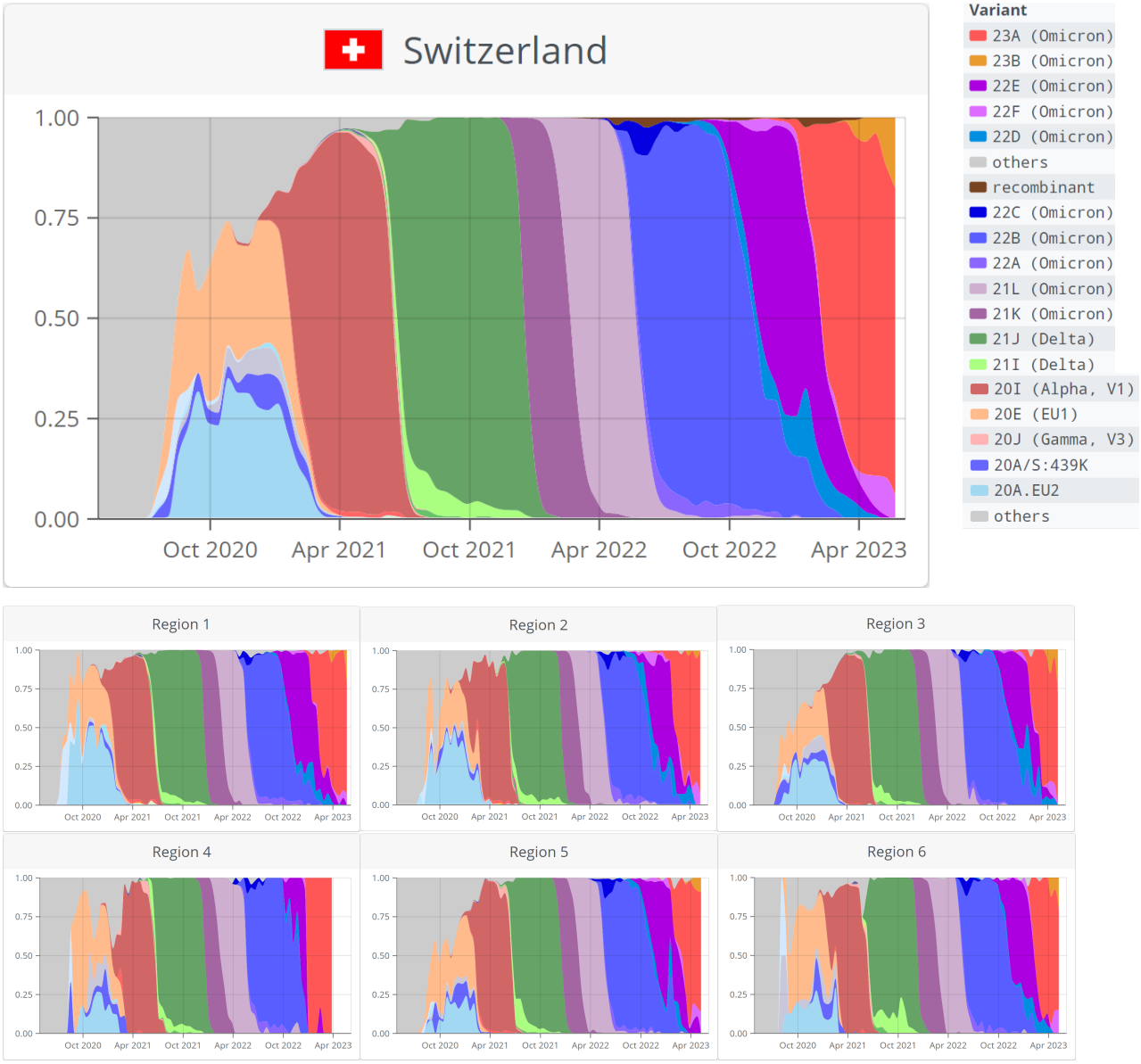


Figure 3: proportion of the total number of sequences (not cases), over time, that fall into defined variant groups, for Switzerland. Screenshot from CoVariants website. Dynamic navigation is available at https://covariants.org/per-country. 21 A/I/J indicates B.1.617.2 (Delta) sub-lineages. 20I indicates B.1.1.7 (Alpha). 21K indicates Omicron BA.1, 21L indicates Omicron BA.2. 22C indicates Omicron BA.2.12.1, while 22B indicates Omicron BA.5 and 22A indicates Omicron BA.4. 22D indicates BA.2.75. 22E indicates BQ.1, 22F indicates the recombinant XBB lineage, and 23A indicates XBB.1.5. 23B indicated XBB.1.16.

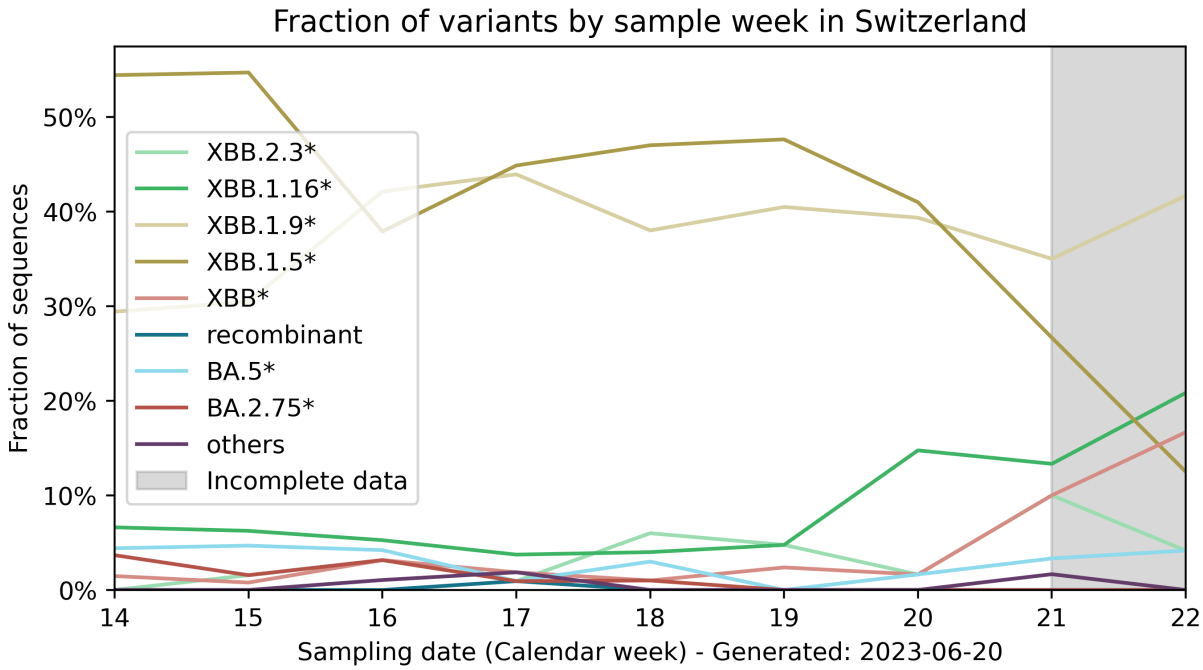


Figure 4: Percentage of circulating VOCs and VOIs in Switzerland by week, up to week 21 of 2023, according to the sequences from Switzerland that were successfully submitted. Note the grey shaded area indicates a period of incomplete data. Note that as of week 16, XBB.1.5 and XBB.1.9 sequences started to be approximately equal, and together were the co-dominant variants.

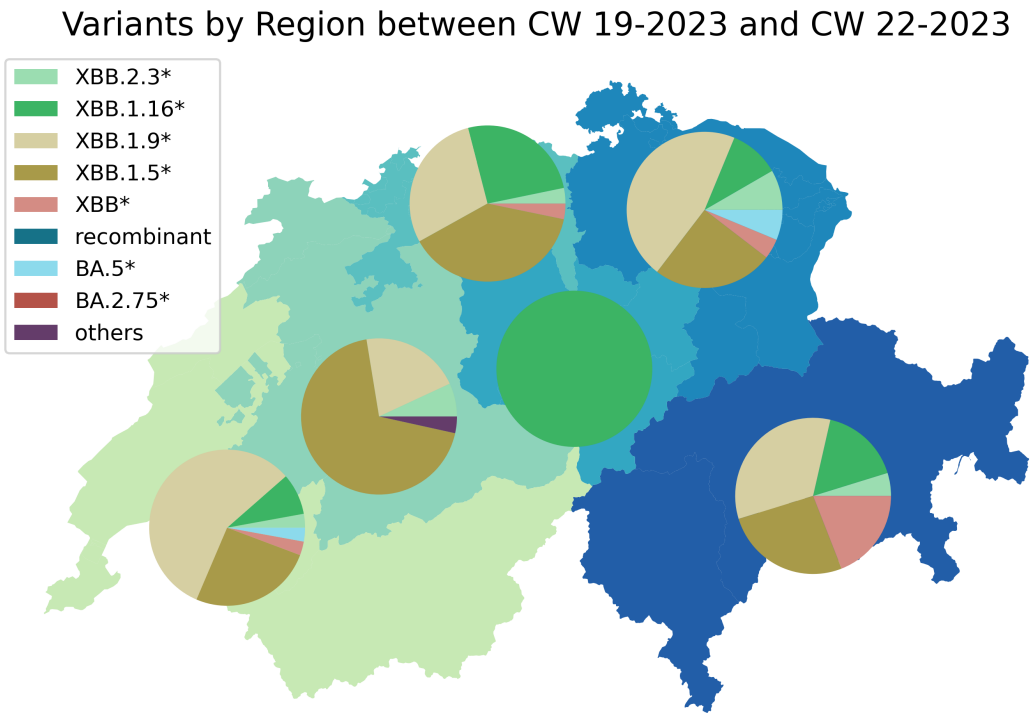


Figure 5: Distribution of variants per region, by Calendar Week (CW), for the end of May 2023. Note the dominance of the XBB.1.5 and XBB.1.9 lineages. Region 4 was underrepresented and had just 1 sample of XBB.1.16.

5. 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 current estimate suggests that while the XBB.1.5 lineage will not stay dominant, XBB* and its sublineages will still be dominant.

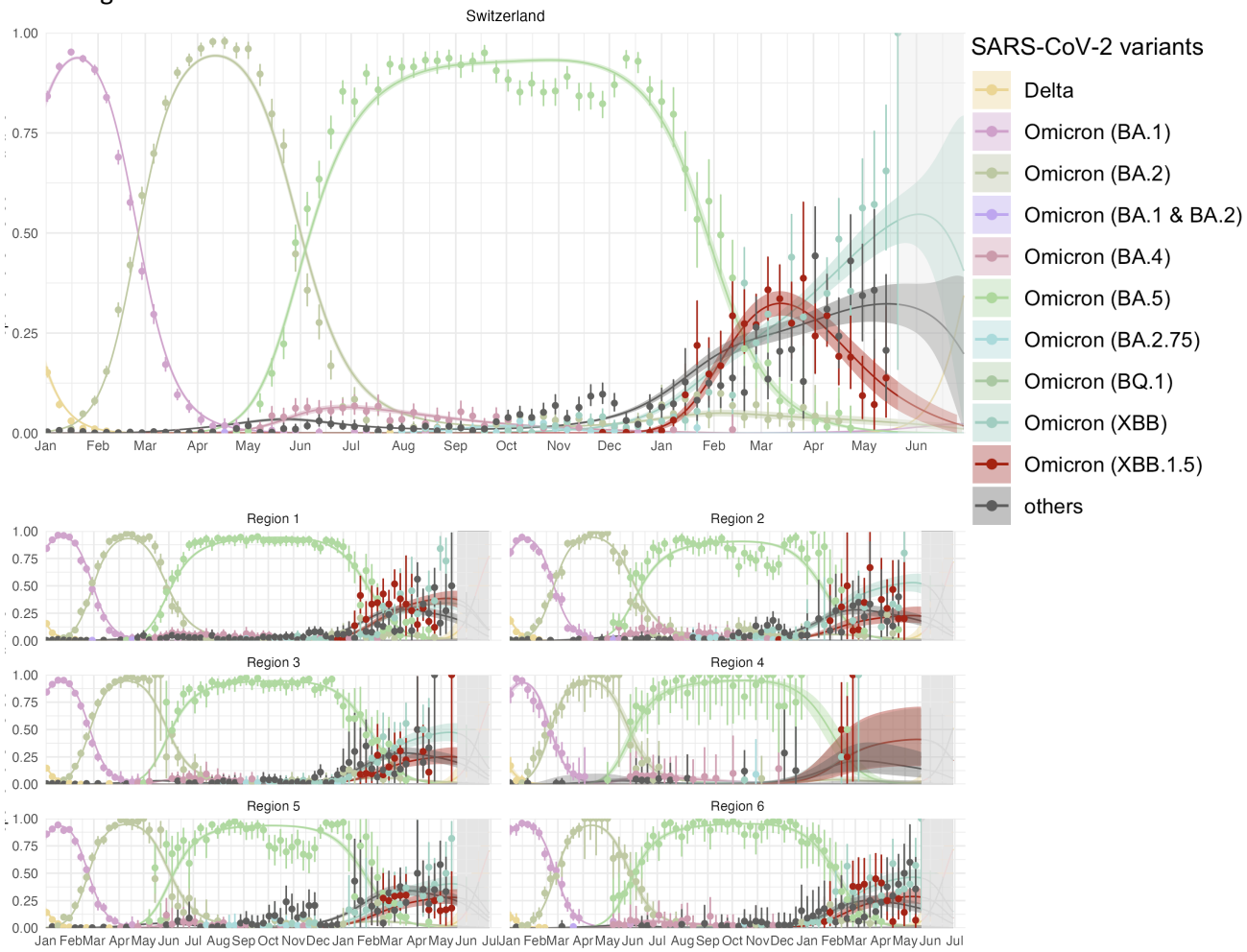


Figure 6: Observed and modeled proportion of SARS-CoV-2 variants over time in Switzerland. Since early 2021, multiple successive variants have been observed to displace all previous variants (often achieving a dominance of >99.9% of the circulation). Alpha was replaced by Delta, followed by Omicron BA.1, then Omicron BA.2, Omicron BA.5, Omicron BQ.1, and now Omicron XBB.1.5. Model fits are based on a multinomial logistic regression with splines.

6. Surveillance of mutations associated with reduced available treatment efficacy

Resistance mutations to available monoclonal antibodies

All sublineages display complete escape from combination of casirivimab/imdevimab.

AA position	World	Europe	Switzerland
Sotrovimab (Spike mutations)			
337	0.08	0.04 (8)	0
340	0.13	0.14	0.65 (2)
356	1.54	0.52	0
371	93.00	91.69	98.39
377	0.05	0	0
449	0.00 (2)	0	0
476	0.03	0.03 (7)	0
494	0.48	0.29	0.32 (1)
Paxlovid® (Nsp5 mutations)			
48	0.06	0	0
49	0.01 (5)	0.00 (1)	0
140	0	0	0
143	0	0	0
144	0	0	0
165	0	0	0
166	0.00 (3)	0.00 (1)	0
167	0	0	0
168	0	0	0
172	0	0	0
186	0.01 (6)	0.01 (2)	0
188	0.00 (2)	0.00 (1)	0
189	0.00 (1)	0.00 (1)	0
192	0.00 (1)	0.00 (1)	0
252	0	0	0

Current data suggests that in vitro neutralization of the currently circulating variants by Sotrovimab is dramatically reduced. Despite this, it may retain some clinical efficacy due to its ability to act as an effector even when it binds to the viral particles without neutralizing them, although this is unclear.
Similarly, *in vitro* data suggests that both antibody components of Evusheld® (tixagevimab and cilgavimab) will have significantly reduced neutralization against the currently circulating variants. Since January 2023, variants with resistance mutations expected to lead to complete escape from both cilgavimab and tixagevimab represented over 95% of the sequences identified in Switzerland.

Mutations causing escape from mAbs are closely followed (Table 3).

Table 3: Frequency (%) of mutations at residues linked (by deep mutations scanning or other experimental results) to escape from sotrovimab, or Paxlovid® (5 fold cutoff), May 2023. Numbers in parentheses denote the total number of sequences detected with a given mutation when it is <10.. Note, both BA.5 and BA.2 (including recombinants such as XBB and XBB 1.5) contain the spike S371F mutation leading to Sotrovimab resistance.*

Resistance mutations associated with resistance to other available antivirals

Other antivirals are available in Switzerland: the 3CL-like protease inhibitor Paxlovid® (PF-07321332, nirmatrelvir/ritonavir) or RNA nucleotide analogues (such as remdesivir).

Preliminary data confirms that Paxlovid® and remdesivir all retain full *in vitro* efficacy against Omicron sub-lineages. Notably all known escape mutations come at a fitness cost (although some are rather small); thus in the absence of any treatment with Paxlovid®, escape mutations are expected to be detrimental and not selected for. These mutations are not linked to general antigenic shift like the escape mutations to the therapeutic mAbs. Importantly, most transmission occurs between hosts that never receive Paxlovid treatment, this likely explains the scarcity of escape mutations against Paxlovid®. While dozens of mutations at sites known to be important for escape from Paxlovid® have been reported worldwide (table 3), only a few that are actually known to cause escape have been sequenced worldwide during May, resulting in a miniscule percentage of total sequences.

7. Wastewater surveillance program

As of 2023, the wastewater surveillance program is no longer funded by the national surveillance program, but it continues using an alternate funding source. Data is presented here to be informative, and not to imply that this program is currently part of the national surveillance program.

In order to complement the genomic surveillance based on patient samples, the program includes sequencing of SARS-CoV-2 in wastewater samples. Notably, wastewater sequencing only recovers fragments of genomes and cannot produce full genome sequences to identify the emergence of a new variant unless that variant is highly divergent. Notably, once a new variant emerges and is identified, wastewater sequencing can be useful to track its spread.

Samples are collected multiple times per week from in total ten wastewater treatment plants (WWTPs), coordinated by Eawag, Microsynth AG, and the canton Basel. The sequencing and analysis of these samples, including detection and quantification of variants, is done under the coordination of Prof. Niko Beerenwinkel, in collaboration with NEXUS Personalized Health Technologies, ETH Zurich. The wastewater sequencing program started in December 2020 for Lausanne and Zurich, and since then has been gradually extended (https://cov-spectrum.org/stories/wastewater-in-switzerland). In February, the wastewater program expanded from 6 sampling centers to 9, in March it increased to 10.

During the Month of May, the quasi-totality of the sequenced SARS-CoV-2 genetic material was estimated to originate from XBB* and its subvariants (Figure 7). At the beginning of the month, the major variant was XBB.1.5 or XBB.1.9 in most localities. The XBB.1.16 variant was growing in relative abundance during the month in most treatment plants.

Modelling of the competition between XBB subvariants (Figure 8) shows for XBB.1.16 a growth advantage of 46.4% (33.5% – 56.7%) relative to XBB.1.5, and an advantage of 34.3% (22.7% – 45.9%) over XBB.1.9. The latter, XBB.1.9, displays an advantage of 9.1% (1.5%, 18.1%) relative to XBB.1.5.

During the month of May, none of the mutations leading to amino acid changes linked with resistance to Remdesivir® were detected in the wastewater samples (Table 4). During that time period, different mutations linked to Paxlovid® resistance were detected in 9 samples of 7 treatment plants. These sporadic detections at a low level could be attributed to artefacts from the protocols.

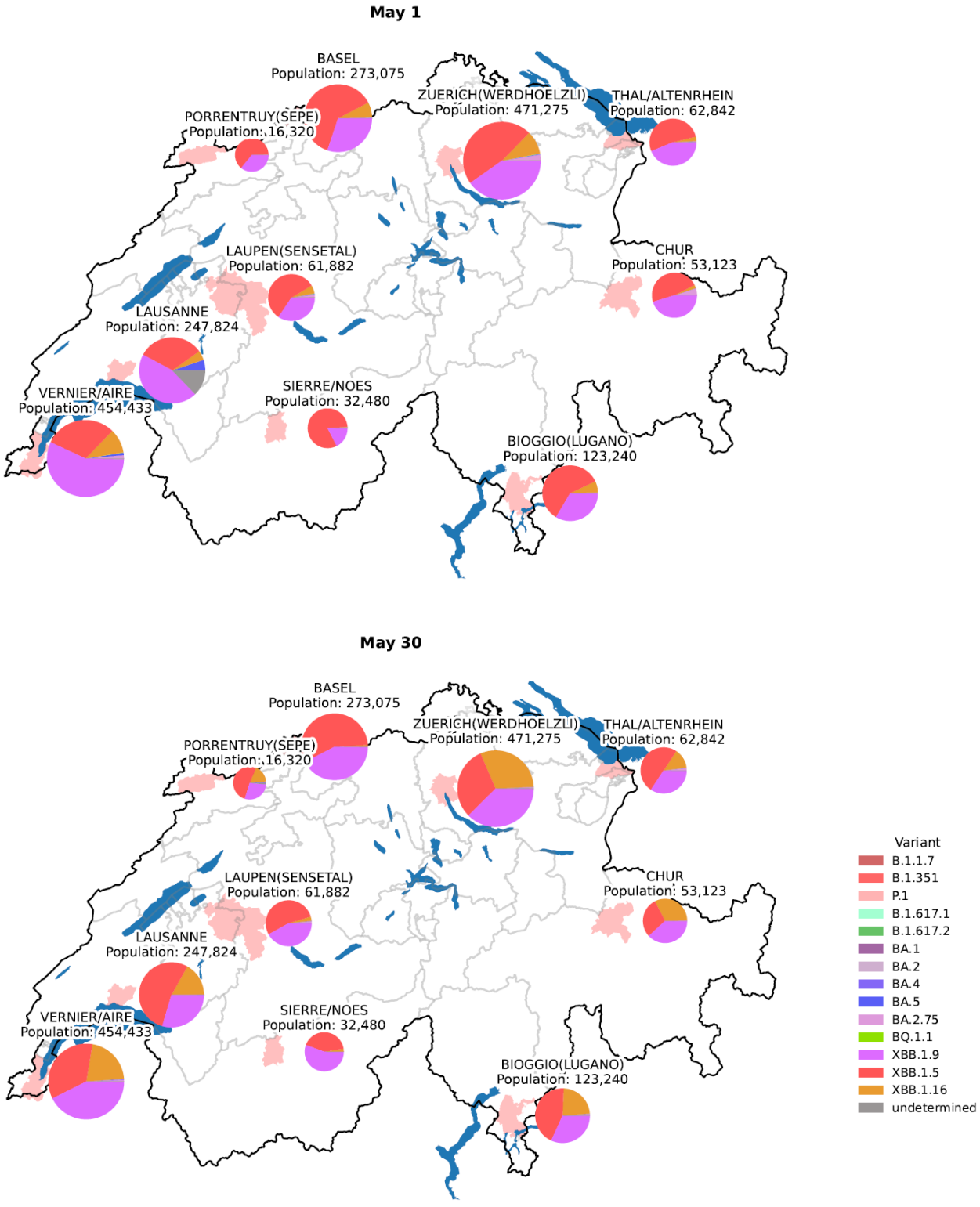


Figure 7: Overview of the relative abundances of variants of SARS-CoV-2 at the beginning and end of May 2023, estimated from wastewater samples collected daily in WWTPs located at 10 different Swiss locations. The size of the pie charts are proportional to the population connected to the wastewater treatment plants. Pink shaded areas represent catchment areas (boundaries from 2017). The population connected to the Vernier (GE) wastewater treatment plant also includes ~44,000 inhabitants from neighbouring French communities

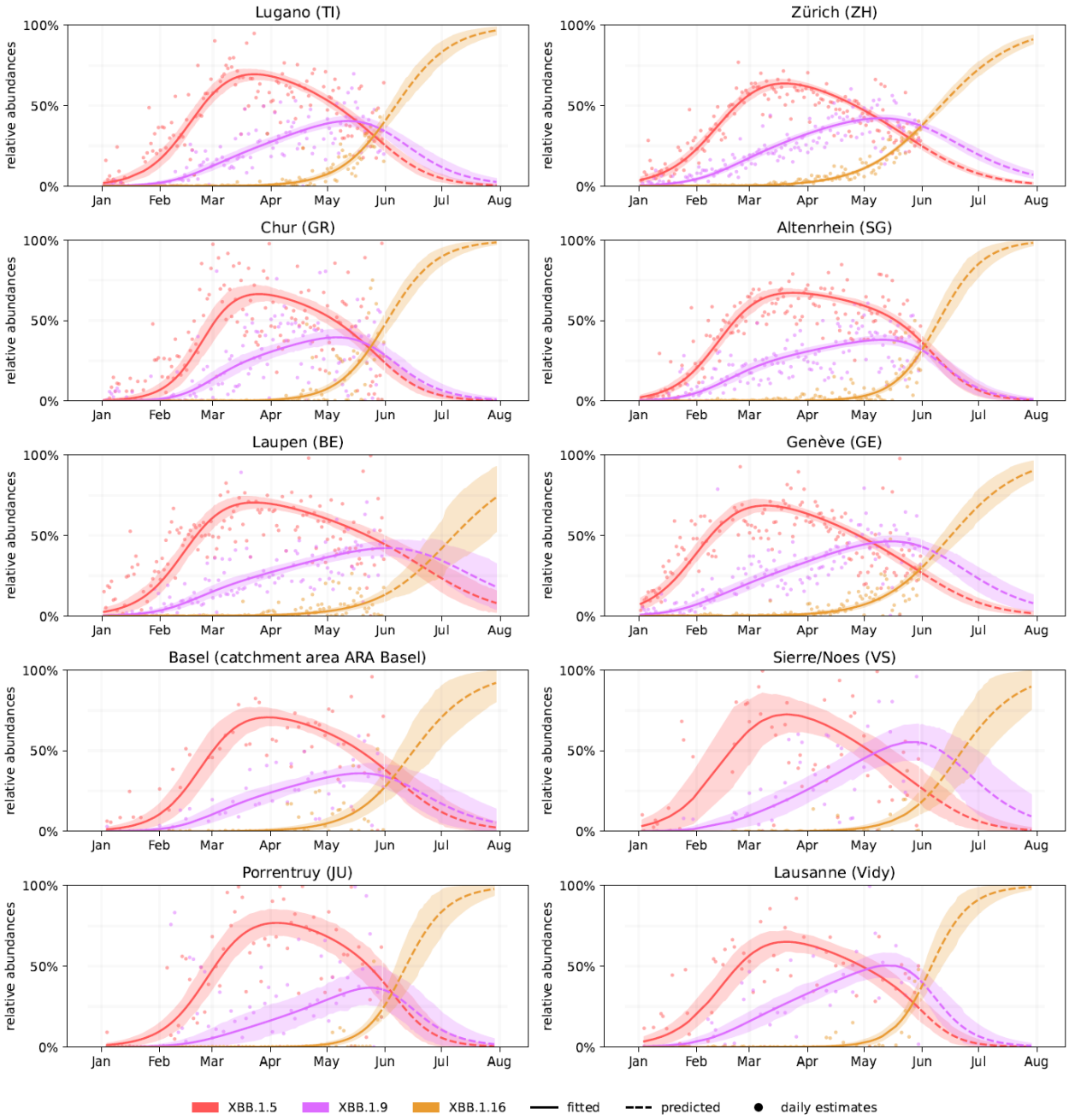


Figure 8: Modelling of the competition XBB subvariants using a hierarchical logistic growth model fitted on the estimated relative abundances of variants. Relative abundances were estimated from wastewater samples collected from January 2023 until the end of May 2023 in WWTPs from 10 different Swiss locations. Plots show fitted models (solid lines) to the daily estimates of variant relative abundances (points), predictions from the models (dashed lines) and 95%HDI for the model fits and predictions (shaded bands). An online dynamic navigation of daily prevalence is available at https://cov-spectrum.org/stories/wastewater-in-switzerland

	AA position	Lugano (TI)	Laupen (BE)	Altenrhein (SG)	Chur (GR)	Genève (GE)	Zürich (ZH)	Lausanne (Vidy)	Sierre/Noes (VS)	Porrentruy (JU)	Basel (catchment area ARA
Remdesivir®	157	0	0	0	0	0	0	0	0	0	0
	750	0	0	0	0	0	0	0	0	0	0
	783	0	0	0	0	0	0	0	0	0	0
	793	0	0	0	0	0	0	0	0	0	0
Paxlovid®	50	0	0	0	0	0	1	0	0	0	0
	54	0	0	0	0	0	0	0	0	0	0
	138	0	1	0	0	0	0	0	0	0	0
	166	0	0	0	0	1	0	0	0	0	1
	167	0	0	0	0	0	0	0	0	0	0
	192	0	0	0	0	0	0	0	0	0	1
	194	1	0	0	0	0	0	0	0	1	0
	305	0	1	1	0	0	0	0	0	0	0

Table 4: Overview of the surveillance of potential treatment escape mutations. Entries show for each location the number of samples during the month of May that had a positive detection of mutations leading to amino acid changes linked to resistance to Remdesivir® or Paxlovid®. Mutations to be monitored were selected from https://www.science.org/doi/10.1126/scitranslmed.abo0718, https://journals.asm.org/doi/10.1128/aac.00198-22, https://doi.org/10.1038/s41467-022-29104-y and https://doi.org/10.1101/2022.06.07.495116.

Acknowledgements:

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

We would also like to thank the CoVICIS project (https://covicis.eu/) for supplementary funding for genomic sequencing in Geneva.

Erik Boehm, Marc Friedli, Pauline Vetter, Samuel Cordey, Richard Neher, Christian Althaus, Emma Hodcroft, Tanja Stadler, Philippe Lemercier, Ioannis Xenarios, Lorenzo Cerutti, Louis Du Plessis, Erik Studer, Laurent Kaiser, for the Swiss national SARS-CoV-2 genomic and variants surveillance program coordination committee.

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_May.xlsx

Supplementary Table 1: Epidemiological data for Switzerland, its regions and cantons for May 2023: 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	Positive tests	Sequenced	% positives sequenced
17	April 24 - April 30	1'799	328	166	34.3
18	May 1 - May 7	1'697	319		
19	May 8 - May 14	1'523	238	288	36.6
20	May 15 - May 21	1'401	216		
	Total	6'420	1'101	388	35.2

Supplementary Table 2: Total number of tests performed by the laboratories participating in the surveillance program from 24 April to 21 May 2023.

week	date	HUG	CHUV	ICH-VS	IFIK	UZH IMV	USB	EOC	All
17	April 24 - April 30	45	50	25	20	38	21	23	222
18	May 1 - May 7								
19	May 8 - May 14	31	45	0	22	23	20	25	166
20	May 15 - May 21								
	Total	76	95	25	42	61	41	48	388

Supplementary Table 3: number of sequences submitted to GISAID by each laboratory during the surveilled period (24 April to 21 May 2023).

Contact list as of 24.05.23:

Coordination committee mailing list	
Name	e-mail address
Laurent Kaiser	Laurent.Kaiser@hcuge.ch
Samuel Cordey	Samuel.Cordey@hcuge.ch
Marc Friedli	marc.friedli@epfl.ch
Richard Neher	richard.neher@unibas.ch
Tanja Stadler	tanja.stadler@bsse.ethz.ch
Louis Du Plessis	louis.duplessis@bsse.ethz.ch
Emma Hodcroft	emma.hodcroft@ispm.unibe.ch
Christian Althaus	christian.althaus@ispm.unibe.ch
Ioannis Xenarios	ioannis.xenarios@unil.ch
Philippe Le Mercier	Philippe.Lemercier@sib.swiss
Pauline Vetter	Pauline.Vetter@hcuge.ch
Erik Boehm	Erik.Boehm@hcuge.ch
Lorenzo Cerutti	lorenzo.cerutti@health2030.ch
Erik Studer	Erik.Studer@bag.admin.ch

Laboratories mailing list		
Laboratory	Name	e-mail address
HUG	Laurent Kaiser	Laurent.Kaiser@hcuge.ch
HUG	Samuel Cordey	Samuel.Cordey@hcuge.ch
HUG	Pauline Vetter	Pauline.Vetter@hcuge.ch
HUG	Erik Boehm	Erik.Boehm@hcuge.ch
CHUV	Gilbert Greub	Gilbert.Greub@chuv.ch
CHUV	Claire Bertelli	Claire.Bertelli@chuv.ch
Universtätsspital Basel	Pascal Schlaepfer	Pascal.Schlaepfer@usb.ch
Universtätsspital Basel	Karoline Leuzinger	Karoline.Leuzinger@usb.ch
Universtätsspital Basel	Hans Hirsch	Hans.Hirsch@usb.ch
IFIK UNIBE	Alban Ramette	alban.ramette@ifik.unibe.ch
UZH	Alexandra Trkola	trkola.alexandra@virology.uzh.ch
UZH	Michael Huber	huber.michael@virology.uzh.ch
EOC Bellinzona	Gladys Martinetti Luchini	Gladys.MartinettiLucchini@eoc.ch
Hopitaux du Valais – Institut Central	Alexis Dumoulin	Alexis.Dumoulin@hopitalvs.ch

BAG mailing list:	
Name	e-mail address
Erik Studer	Erik.Studer@bag.admin.ch
Katrin Schneider	katrin.schneider@bag.admin.ch
Anna Fesser	Anna.Fesser@bag.admin.ch
Ursina Roder	ursina.roder@bag.admin.ch
Lionel Rohner	lionel.rohner@bag.admin.ch
Michael Bel	Michael.Bel@bag.admin.ch
Urs Mayr	urs.mayr@bag.admin.ch
Damir Perisa	Damir.Perisa@bag.admin.ch
Martine Bourqui	Martine.Bourqui@bag.admin.ch
Natalia Krempaska	natalia.krempaska@bag.admin.ch
Mirjam Mäusezahl	Mirjam.Mäusezahl@bag.admin.ch
Tobias Schuster	tobias.schuster@bag.admin.ch

Sequencing centers:		
Center	Name	e-mail address
Health 2030 Genome Center	Keith Harshman	keith.harshman@health2030.ch
Health 2030 Genome Center	Ioannis Xenarios	ioannis.xenarios@health2030.ch
Genomics Facility Basel-ETH Zurich	Christian Beisel	christian.beisel@bsse.ethz.ch
The Functional Genomics Center Zurich (FGCZ)- ETHZ and UZH	Ralph Schlapbach	ralph.schlapbach@fgcz.ethz.ch

Wastewater surveillance program mailing list:	
Name	e-mail address
Niko Beerenwinkel	niko.beerenwinkel@bsse.ethz.ch
David Dreifuss	david.dreifuss@bsse.ethz.ch