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

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1. Summary

During the month of July, the number of positive SARS-CoV-2 tests decreased in Switzerland, and the test positivity rate within the program dropped to 7.8% from June's 11.5%. Notably, testing rates are at an all-time low. The number of hospitalizations due to COVID-19 continues to be low.

The 255 positive tests processed by laboratories participating to the program constituted around 38% of the reported positive tests in Switzerland.

A total of 79 new sequences were submitted to GISAID during the reporting period, covering the month of July (July 3 to July 30), which represents around 31% of the program's 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, 1.9, or 1.16, with none of these sublineages exceeding 50%. Circulation of the EG.5 subvariant (now designated as a VOI by the WHO) appears to be increasing in Switzerland, possibly on the way to dominance, comprising 18% of the sequences detected in this reporting period. The new highly divergent BA.2.86 variant was not detected in Switzerland in July, but wastewater data suggests its presence in multiple regions of Switzerland. Current data does not suggest that any of these subvariants are more severe.

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/). Due to reduced numbers of samples available for sequencing, and it being more economical to sequence samples in large batches, the frequency of sequencing has decreased: batches are now sequenced every two weeks, and this has had to be further decreased to once every 4 weeks for July and August 2023.

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 with an update in the present report 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 July 3 to July 30, 2023 (weeks 27-30). 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. Currently, the WHO will only consider a variant as a variant of concern if it "meets at least one of the following criteria when compared with other variants:

- Detrimental change in clinical disease severity; OR
- Change in COVID-19 epidemiology causing substantial impact on the ability of health systems to provide care to patients with COVID-19 or other illnesses and therefore requiring major public health interventions; OR
- Significant decrease in the effectiveness of available vaccines in protecting against severe disease."

Variants under monitoring (VUM) are suspected to have altered characteristics (transmissibility, virulence, antibody evasion, susceptibility to therapeutics or detectability), and signals of a growth advantage, but with a low level of evidential support. Meanwhile, a Variant of Interest is predicted or known to have altered characteristics, and an identified growth advantage in more than one region.

The WHO currently assesses that the currently circulating VOIs are XBB.1.5, XBB.1.16, and EG.5. Currently circulating VUMs consist of BA.2.75, CH.1.1, XBB*, XBB.1.9.1, XBB.1.9.2, XBB.2.3, and BA.2.86.

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).

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.

In August 2023, a sublineage of XBB.1.9.2 with and additional Spike mutation (F456L) called EG.5 was upgraded from a VOM to a VOI. All major XBB sublineages (XBB.1.5/1.9/1.16) show relatively poor neutralization titers following an XBB breakthrough infection, possibly due to previous immune imprinting, indicating that it may be able to cause more frequent cause reinfections.

Also in August, a new sublineage, BA.2.86, was identified and assigned VUM status due to the large number of mutations, with approximately 30 more mutations in the spike protein than the circulating XBB lineages.

In Switzerland, XBB.1.5 was definitively overtaken by XBB.1.9 in week 21, and EG.5 has started overtaking basal XBB.1.9.

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.

The currently dominant XBB lineages do not exhibit ex S-gene target failure (SGTF) with the Roche PCR assays regularly used in Switzerland, and the VUM BA.2.86 does. Therefore, the SGTF assay may be useful for detecting probable BA.2.86 cases. BA.2.86 specific PCRs are being validated to confirm detection of probable BA.2.86 samples identified by SGTF assay. Further discrimination between XBB subvariants is not feasible at this time by any method other than genomic sequencing.

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.

EG.5, BA.2.86, in addition to other XBB* sublineages all show further escape from the already low neutralization. Despite the large number of additional spike mutations, BA.2.86's escape from neutralization appears to be similar to the escape of multiple XBB* sublineages according to multiple preprints using pseudoviruses.

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, including animal studies provide evidence that XBB sublineages including EG.5 are not more severe.

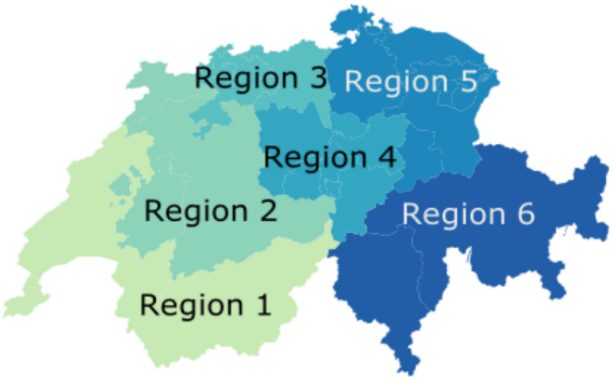
Data on BA.2.86 severity is lacking, but studies with pseudovirus indicate that it is less infective.

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

From 3 July to 30 July, the FOPH reported 671 positive tests (including both RT-PCR and antigen-based tests). Positive tests from the labs participating in the national surveillance program from overlapping dates produced approximately 38% of this number. From 3 July to 30 July, the labs participating in the national surveillance program produced 255 positive tests. Along with the number of tests performed in the country, the number of positive tests continued to decrease in Switzerland during the month of July relative to June, and since the beginning of the year. Notably, the percent of positives sequenced within the program was 30.98%, which is similar to that of June (31.27%). The test positivity rate within the program for July was 7.8%, compared to 11.5% from 22 May to 2 July was 11.5%.

Although case ascertainment rates may be too low to identify meaningful trends, there has not been any sign that the currently low hospitalization rates (≤5 per week over the last month at the HUG, mostly patients with pauci-symptomatic or mild disease) 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 79 SARS-CoV-2 sequences have been declared to have been processed during this period. There are 65 sequences available on GISAID that were submitted during this period (and 72 collected during this period) as of 5 September 2023.

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
27	July3- July 9	35
28	July 10-July 16	
29	July 17- Ju 23	44
30	July 24-July 30	
	Total	79

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 trend of declining numbers of SARS-CoV-2 sequences submitted each week stopped during the month of July 2023 (Calendar weeks 27 - 30). 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.

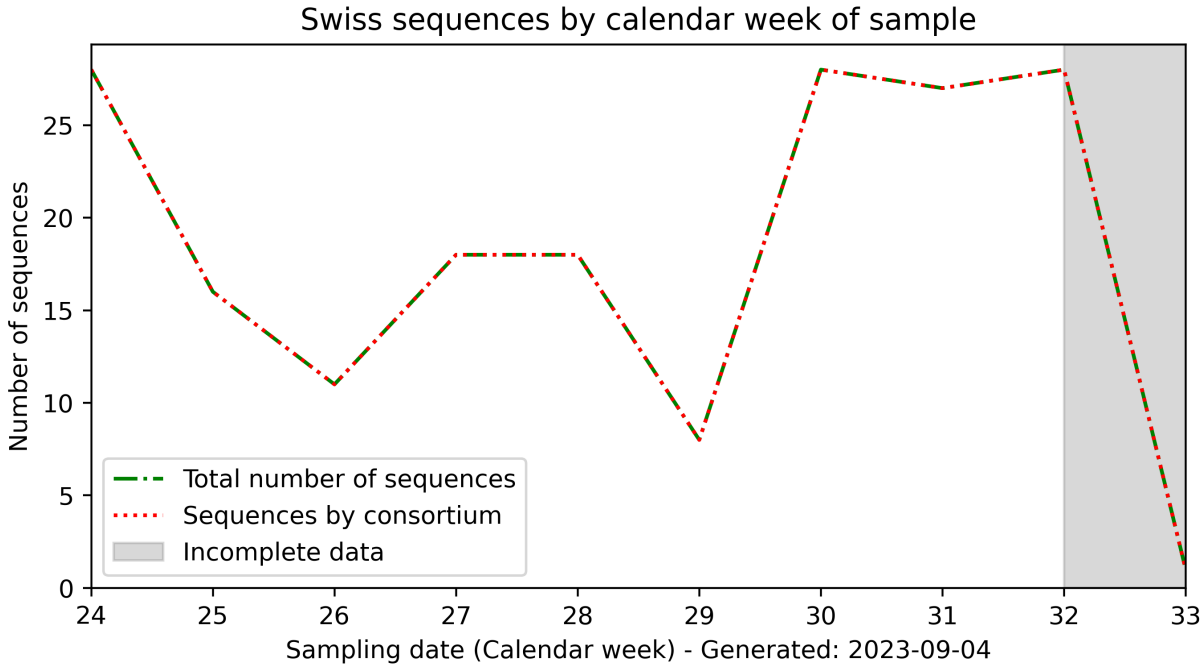


Figure 1: Number of SARS-CoV-2 sequences available for Switzerland (total available Swiss sequences in GISAID in green, Swiss sequences submitted through the program in dotted orange).

Figure 2 displays the number of SARS-CoV-2 cases sequenced for each Swiss region. Sequences remained low in all regions except region 1. The spike in region 1 sequencing was prompted by concern about the BA.2.86 variant, and correspondingly increased detection efforts. Notably, region 4 (Luzern, Unterwalden, Uri, Zug and Schwyz) is no longer effectively represented due to the absence of a laboratory participating in the program in this region, after the switch to surveillance of hospitalized cases.

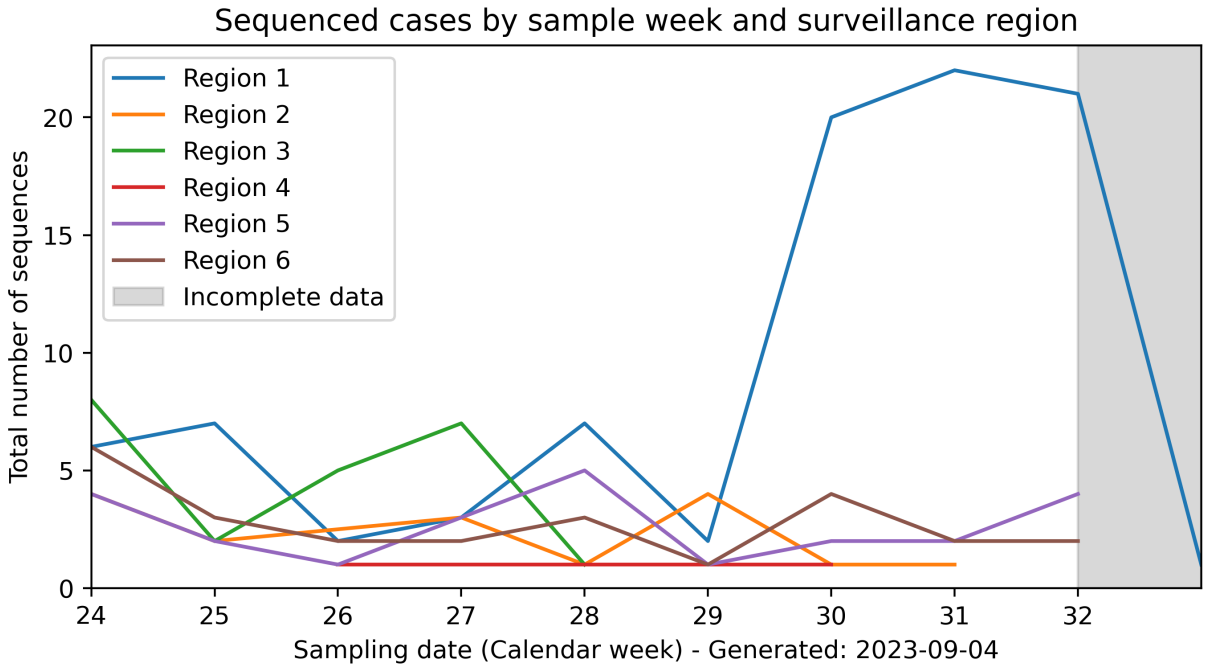


Figure 2: Sequencing coverage among the different Swiss regions per week, by number of sequences.

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).

BA.5 continued to circulate at low levels in July, although the vast majority of circulating viruses are XBB sublineages now. XBB.1.9 continued its dominance over XBB.1.5. XBB.1.9 still does not make up the majority of the sequences in Switzerland due to significant circulation of XBB.1.16 and XBB.2.3, as well as still substantial circulation of XBB.1.5 (Tables 2 and figures 2 and 3). Notably, 13 EG.5 sequences were detected during this period, amounting to 18% of the total sequences, a substantially increased proportion.

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.5*	XBB*	XBB.1.16*	XBB.1.5*	XBB.1.9*	XBB.2.3*	Others	Recombinant	Sequences
All	3	1	14	22	25	4	3	0	72
1	2	0	8	9	11	1	1	0	32
2	0	0	0	0	6	1	2	0	9
3	1	0	2	2	2	1	0	0	8
4	0	0	0	0	2	0	0	0	2
5	0	0	3	4	3	1	0	0	11
6	0	1	1	7	1	0	0	0	10

Table 2: number of sequences corresponding to selected variants in each region of Switzerland from July 3 to July 30, according to data received by 5 September, 2023.

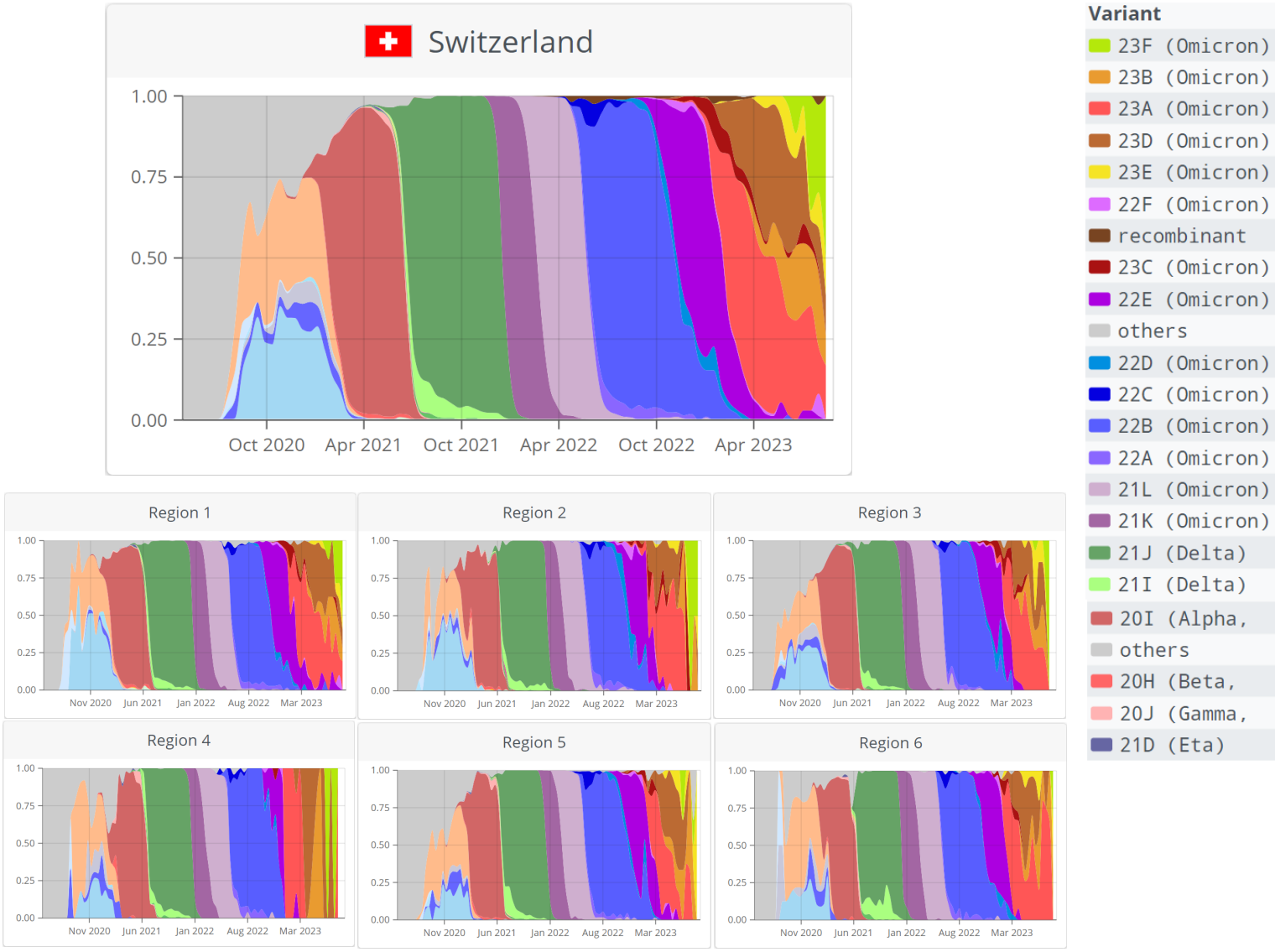


Figure 3: proportion of the total number of sequences (not cases), over time, that fall into defined variant groups, for Switzerland. Screenshot from CoVariants website. Dynamic navigation is available at https://covariants.org/per-country. Nexstrain lineage correspondence with pango lineages are as follows: 21 A/I/J- B.1.617.2 (Delta); 20I- B.1.1.7 (Alpha); 21K- BA.1 (Omicron, as are all the following lineages); 21L- BA.2; 22C- BA.2.12.1; 22A- BA.4; 22B- BA.5; 22C- BA.2.12.2; 22D- BA.2.75; 22E- BQ.1 (a BA.5 sublineage); 22F- XBB (Omicron recombinant); 23A- XBB.1.5; 23B- XBB.1.16; 23C- CH.1.1 (a BA.2.75 sublineage); 23D- XBB.1.9; 22E- XBB.2.3; and 23F- EG.5.1 (an XBB sublineage).

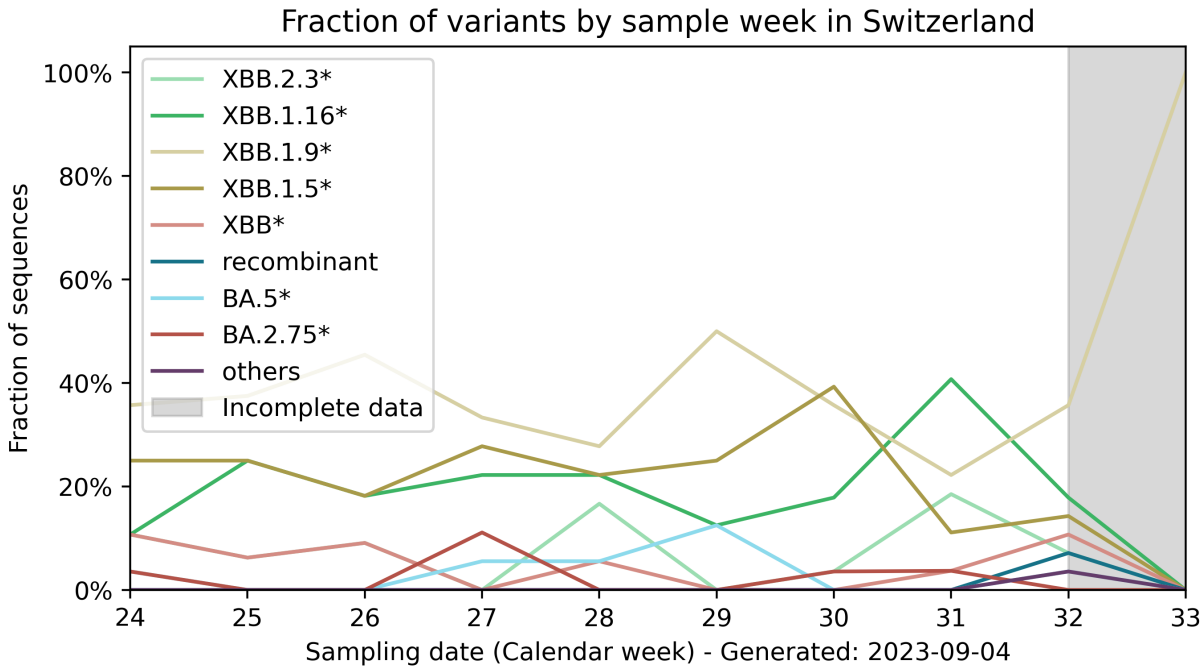


Figure 4: Percentage of circulating VOCs and VOIs in Switzerland by week, up to week 32 of 2023, according to the sequences from Switzerland that were successfully submitted. Note XBB.1.9 was the most common variant but did not account for more than half of the sequences.

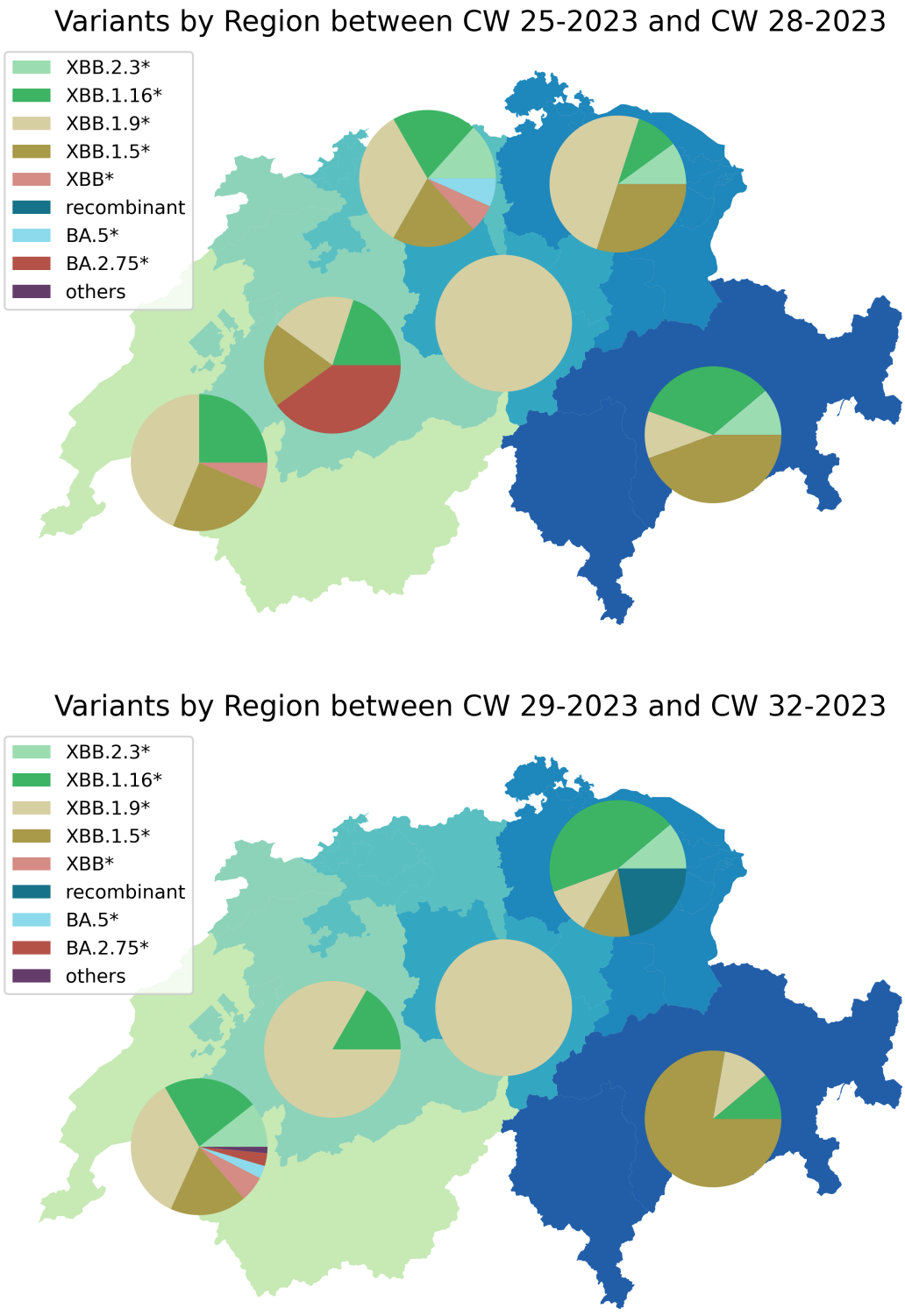


Figure 5: Distribution of variants per region, by Calendar Week (CW), for July 2023. Note the co-dominance of the XBB.1.5, XBB.1.9, and XBB.1.16 lineages. Region 4 was underrepresented and had just 2 samples of XBB.1.9.

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 multiple XBB* sublineages will compete with each other without achieving dominance. At a larger scale, XBB* (including all of its sublineages) will still be dominant. Data for BA.2.86 is unavailable, and represents a considerable unknown.

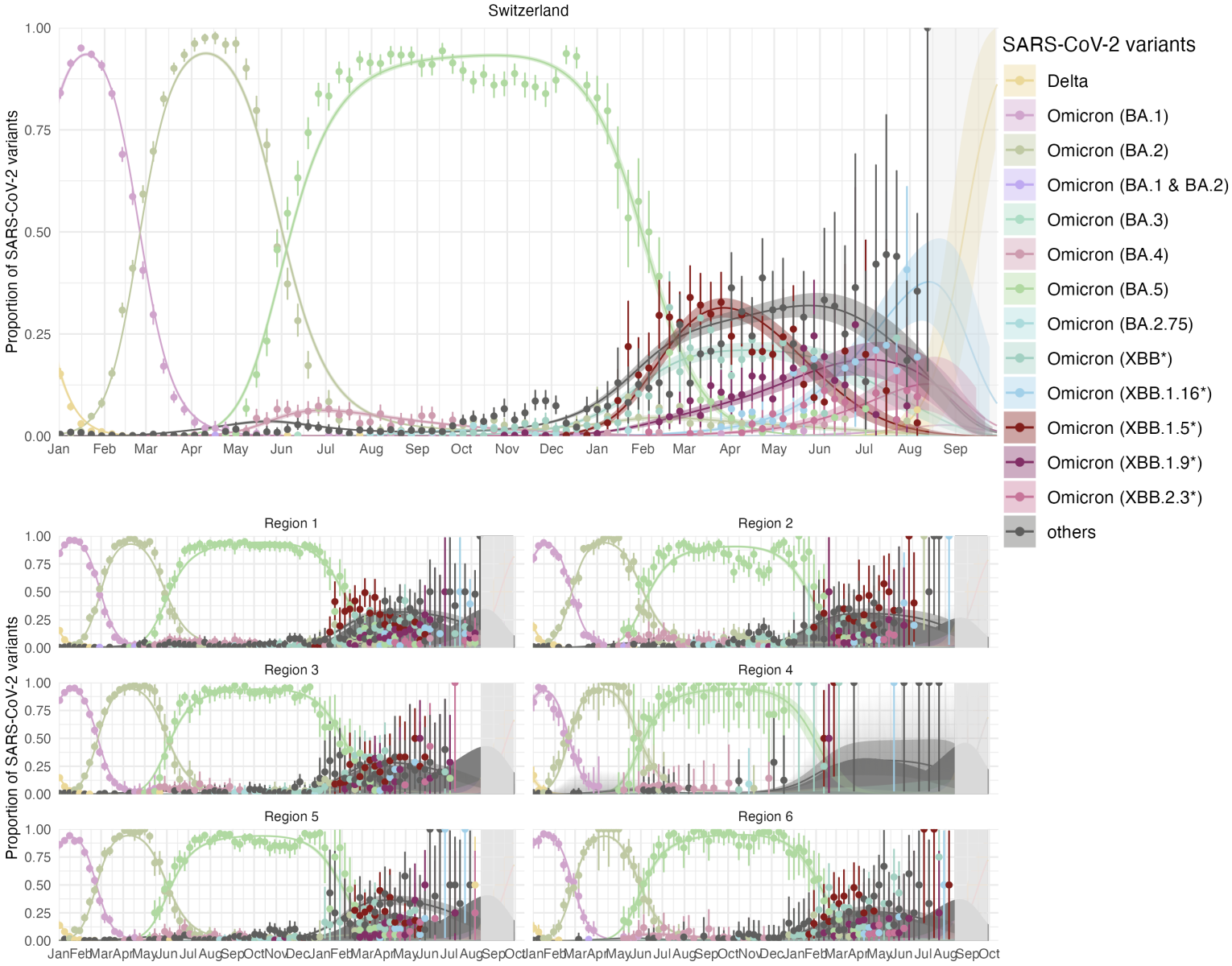


Figure 6: Observed and modeled proportion of SARS-CoV-2 variants over time in Switzerland. Since early 2021, multiple successive variants have been observed to displace all previous variants (often achieving a dominance of >99.9% of the circulation). Alpha was replaced by Delta, followed by Omicron BA.1, then BA.2, BA.5, BQ.1, XBB.1.5. After XBB.1.5, no lineage has been able to achieve strict dominance (>50% of all circulating viruses). 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	0.09	0.06 (4)	0
340	0.11	0.06 (4)	0
356	1.05	0.72 (45)	2.78 (2)
371	92.29	91.26	100
377	0.06	0	0
449	0.01 (2)	0.02 (1)	0
476	0.02 (9)	0.02 (1)	0
494	0.97s	1.49	2.78 (2)
Paxlovid®	(Nsp5 mutations)		
15	0	0	0
48	0.03 (11)	0	0
49	0.02 (6)	0	0
140	0	0	0
143	0	0	0
144	0	0	0
165	0	0	0
166	0.00 (1)	0	0
167	0	0	0
168	0	0	0
172	0	0	0
173	0.02 (7)	0.02 (1)	0
186	0.01 (2)	0	0
188	0.00 (1)	0	0
189	0	0	0
192	0	0	0
194	0.02 (7)	0	0
248	0.00 (1)	0	0
252	0.00 (1)	0	0
304	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.

Since January 2023, variants with resistance mutations expected to lead to complete escape from both cilgavimab and tixagevimab (the components of Evusheld) represented over 95% of the sequences identified in Switzerland.

Additional (beyond those found in BA.2 and BA.5) Sotrovimab escape mutations remained rare in Switzerland and worldwide during July 2023 (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), June 2023 (according to data as of 6 September, 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.

Mutations known to result in significant escape against Paxlovid remained extremely rare in July, both in Switzerland and worldwide (table 3).

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. 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 July, the quasi-totality of the sequenced SARS-CoV-2 genetic material was estimated to originate from XBB* and its subvariants (Figure 7). The viral loads of SARS-CoV-2 in surveyed treatment plants were particularly low during that month, leading to an increase in the noise in the sequencing data, but it was still possible to identify XBB subvariants. At the end of the month, the most abundant variant was EG.5. The rest of the genetic material was a mixture of XBB.1.5, XBB.1.16, XBB.2.3 and non-EG.5 XBB.1.9.

During the month of July, different mutations linked to Paxlovid® resistance were detected in 7 samples of 7 treatment plants (Table 4). These sporadic detections at a low level could be attributed to protocol artefacts.

In the first two weeks of July, due to a restructuring in the WW station monitoring, a decreased number of samples was available for sequencing. This restructuring includes the addition of new treatment plants to the monitoring program: Luzern (LU), Neuchâtel (NE), Schwyz (SZ), Solothurn (SO) and Bern (BE).

The BA.2.86 variant was not detected in samples from the month of July. On 5 and 6 August it was detected in the samples from Laupen (BE). There is also low-confidence evidence of the variant in Basel on August 10. On August 12 the variant was detected in Luzern. On August 13 there was low-confidence evidence of the variant in Chur, and clear detections of BA.2.86 variant were noted in Schwyz on August 13, 14, and 15. By August 22 BA.2.86 had again been detected again in the treatment plants of Luzern, Laupen, Schwyz and Chur, and there were new detections in the treatment plants of Neuchâtel, Altenrhein and Genève.

Despite this widening distribution, the detection remains sporadic and the prevalence of BA.2.86 in the wastewater remains very low, without a sign of increasing proportions.

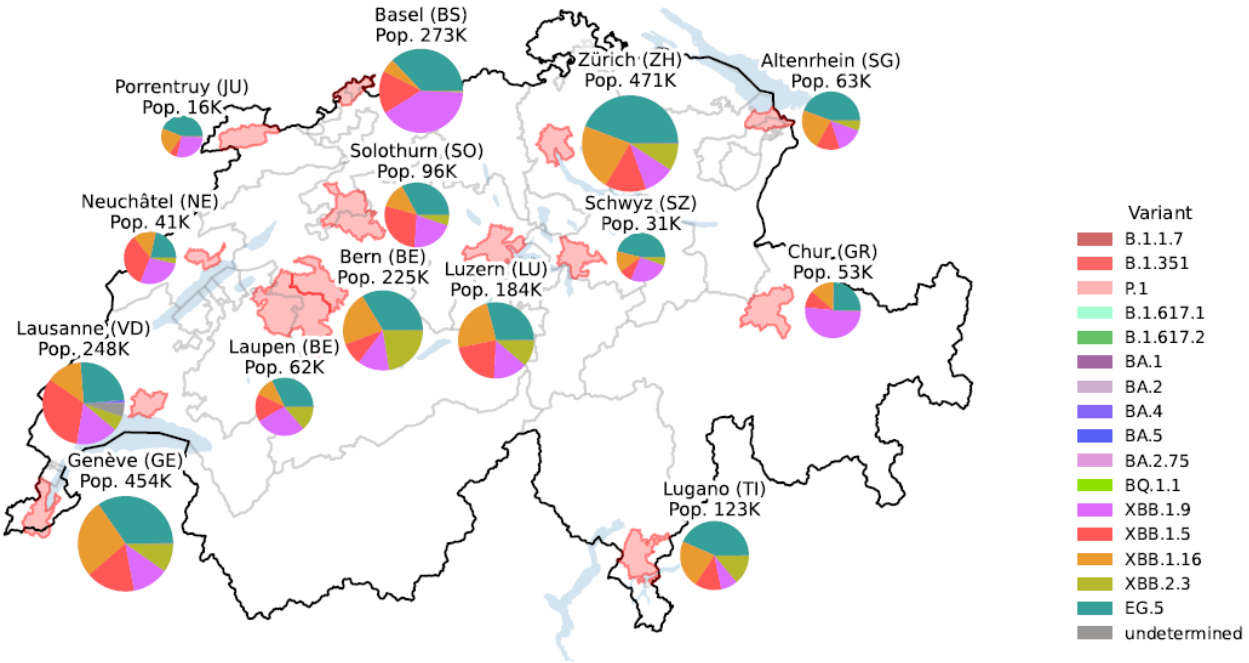


Figure 7: Overview of the relative abundances of variants of SARS-CoV-2 at the beginning and end of May 2023, estimated from wastewater samples collected daily in WWTPs located at 10 different Swiss locations. The size of the pie charts are proportional to the population connected to the wastewater treatment 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

https://cov-spectrum.org/stories/wastewater-in-switzerland

AA position	Lugano (TI)	Zürich (ZH)	Basel (BS)	Chur (GR)	Luzern (LU)	Laupen (BE)	Neuchâtel (NE)	Schwyz (SZ)	Porrentruy (JU)	Lausanne (VD)	Altenrhein (SG)	Genève (GE)	Solothurn (SO)	Bern (BE)
15	0	0	0	0	0	0	0	0	0	1	0	0	0	0
138	1	0	0	0	0	0	0	0	0	0	0	0	0	0
140	0	0	0	0	0	0	0	0	0	0	0	0	0	0
142	0	0	0	0	0	0	0	0	0	0	0	0	0	0
143	0	0	0	0	0	0	0	0	0	0	0	0	0	0
144	0	0	0	0	0	0	0	1	0	0	0	0	0	0
165	0	0	0	0	0	0	0	0	0	0	0	0	0	0
166	0	0	1	0	0	1	0	0	0	0	0	0	0	0
167	0	0	0	0	0	0	0	0	0	0	0	0	0	0
168	0	0	0	0	0	0	0	0	0	0	0	0	0	0
172	0	0	0	0	0	0	0	0	0	0	0	0	0	0
173	0	0	0	1	0	0	1	0	0	0	0	0	0	0
186	0	0	0	0	0	0	0	0	0	0	0	0	0	0
188	0	0	0	0	0	0	0	0	0	0	0	0	0	0
189	0	0	0	0	0	0	0	0	0	0	0	0	0	0
192	0	0	0	0	0	0	0	0	0	0	0	0	0	0
194	0	0	0	0	0	0	0	0	0	0	0	0	0	0
248	0	0	0	0	0	0	0	0	0	0	0	0	0	0
252	0	0	0	0	0	0	0	0	0	0	0	0	0	0
304	0	0	0	0	0	0	0	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 June that had a positive detection of mutations leading to amino acid changes linked to resistance to Paxlovid®. Mutations to be monitored were selected from https://covdb.stanford.edu/drms/3clpro.

Acknowledgements:

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

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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 for June 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
27	3 July - 9 July	799	57	35	27.3
28	10 July - 16 July	825	71		
29	17 July - 23July	782	48	44	34.6
30	24 July - 30 July	846	79		
	Total	3 252	255	79	31.0

Supplementary Table 2: Total number of tests performed by the laboratories participating in the surveillance program from 3 July to 30 July 2023.

week	date	HUG	CHUV	ICH-VS	IFIK	UZH IMV	USB	EOC	All
27	3 July - 9 July	4	7	0	4	0	15	5	35
28	10 July - 16 July								
29	17 July - 23July	10	15	0	3	11	0	5	44
30	24 July - 30 July								
	Total	14	22	0	7	11	15	10	79

Supplementary Table 3: number of sequences submitted to GISAID by each laboratory during the surveilled period (3 July to 30 July 2023).

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