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Swiss national SARS-CoV-2 genomic and variants surveillance program: report of the months of May to July 2024

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1. Summary

This report covers the period of 22 April to 30 June 2024 (weeks 17-26), and includes partial data from 1 July to 4 August. All data presented in this report are based on the sampling date. For an overall description of the program, please refer to previous reports or the supplementary annex.

During the months of May and June 2024, the number of positive SARS-CoV-2 tests per week in laboratories participating to the program remained low but increased since the end of April. Similarly, the test **positivity rate remained low, but was higher than the low rate seen at the end of April (11.6% in week 26 vs. 3.3% for week 17).** Partial data for July indicates a 13.6% positivity rate. **The number of hospitalizations due to COVID-19 also remained low**. RNA in the wastewater increased in May and June, but remained well below previous peaks.

The 1'008 positive tests processed by laboratories participating to the program constituted 43.0% of the reported positive tests in Switzerland. A total of 280 new sequences were submitted to GISAID during the May & June 2024 reporting period, mainly originating from hospitalized patients. From 1 July to 4 August an additional 380 positive tests and 135 sequences were obtained.

The **JN.1** sublineage of the BA.2.86 clade **remained dominant** (>95% of wastewater sequences and >95% of clinical samples) **in May, June, and July 2024**, with its KP.3 sublineage becoming dominant at the end of June and July. The "FLiRT" mutations peaked and declined as the new KP.3 sublineage rose in prominence.

Outside of Switzerland no spread of any new highly divergent variant was detected.

New JN.1 sublineages have been appearing, particularly KP.3, that evade antibodies raised following a JN.1 infection. New mutations, such as S:Δ31 have been appearing incrementally, with no highly divergent lineages being spotted.

As the number of cases was low for the months of May and June, sequencing batches have again been deferred. No further sequencing will be processed until a decision regarding the future of respiratory surveillance has been taken by regulatory authorities.

2. Variants of Concern (VOCs), Variants of Interest (VOI), and other surveilled variants: brief summary and special focus

The WHO currently assesses that the currently circulating VOIs are BA.2.86, and JN.1. The current variants under monitoring are: JN.1.7, KP.2, KP.3, KP.3.1.1, JN.1.18, and LB.1

No variants in current circulation have been designated a Variant of Concern. All currently circulating variants are derivatives of JN.1, itself a derivative of the original "Omicron" VOC.

JN.1 and its sublineages accounted for >95% of global sequences collected in May and June 2024 (22 April to 30 June). Two spike mutations in a JN.1 background were showing clear signs of a growth advantage: F456L, and R346T. R346T was previously very common in XBB backgrounds, and was associated with immune escape, but its prevalence has since been declining. Similarly, F456L was also previously identified and was common in XBB.1.9 sublineages. As of the time of this report, R346T is present in approximately 44% of sequences worldwide, and F456L is present in >78% of the sequences worldwide. These two mutations together resulted in what were deemed "FLiRT" variants, which peaked at 66.7% of sequences in week 23 (3 June to 9 June). By week 26, these variants had declined to only 22.5% of the sequences.

A new mutation, S:Δ31 has been increasing in proportion (5% in week 17, and 35% in week 26), and is mostly found alongside F456L, and in the JN.1 sublineages KP.2 and KP.3.

No issues with detection (via PCR or antigenic tests) have been noted for any variants. Nor has increased severity has been noted. While neutralization is relatively poor against all circulating variants (due to antigenic change and immune imprinting), no major reduction similar to that seen when Omicron first appeared has been noted. Neutralization by currently available therapeutic mAbs is extremely low, but there is no loss of efficacy against other antivirals, such as protease inhibitors.

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

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

From 22 April to 30 June, the FOPH reported 2'345 positive tests (including both RT-PCR and antigen-based tests), a substantial increase from the 846 reported from 26 February to 21 April. Positive tests from the labs participating in the national surveillance program produced 43% of these (1'008 of 2'345). The percent of positives sequenced within the program increased: 25.7% in May and June vs 13.1% in March and April. The test positivity rate within the program for May and June was 8.4% an increase compared to March and April's 5.0%. Overall, the percent of sequenced ascertained positive cases was 11.9%, an increase from March and April's 11.3%.

Data are available for the month of July for the HUG, Valais ICH, and EOC Bellinzona. For July, these three centers sequenced 35.5% of their 380 positive cases (135 sequences).

Although case ascertainment rates may be low, there had been continuing trend since late November/early December 2023 towards decreases in the number of cases, hospitalizations, but not necessarily RNA levels in wastewater. As of the time of this report, there has been an increase in RNA wastewater levels. For more information, please refer to the BAG dashboard (https://idd.bag.admin.ch/). Detailed data regarding the total number of tests performed each week by the laboratories participating in the surveillance program are available in supplementary Table 1.

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

A total of 280 SARS-CoV-2 sequences have been declared to have been processed during this period. There are 112 sequences available on GISAID that were submitted during this period (and 280 collected during this period) as of 23 August 2024.

Week	Date	Number of sequences declared and successfully submitted to GISAID, January 2024
17	April 22-April 28	14
18	April 29 - May 5	
19	May 6 - May 12	38
20	May 13 - May 19	
21	May 20 - May 26	73
22	May 27 to June 2	
23	June 3 - June 9	35
24	June 10 - June 16	
25	June 17 - June 23	120
26	June 24 - June 30	
	Total	280
27-31*	July 1 – August 4	135

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. For a breakdown by laboratory, see the appendix.
** indicates data for only for the HUG, Valais ICH, and EOC Bellinzona.*

Sequencing in Switzerland by the national SARS-CoV-2 surveillance program

Numbers of SARS-CoV-2 sequences submitted and positive tests each week continued to decrease during the March and April 2024 reporting period (weeks 9-16).

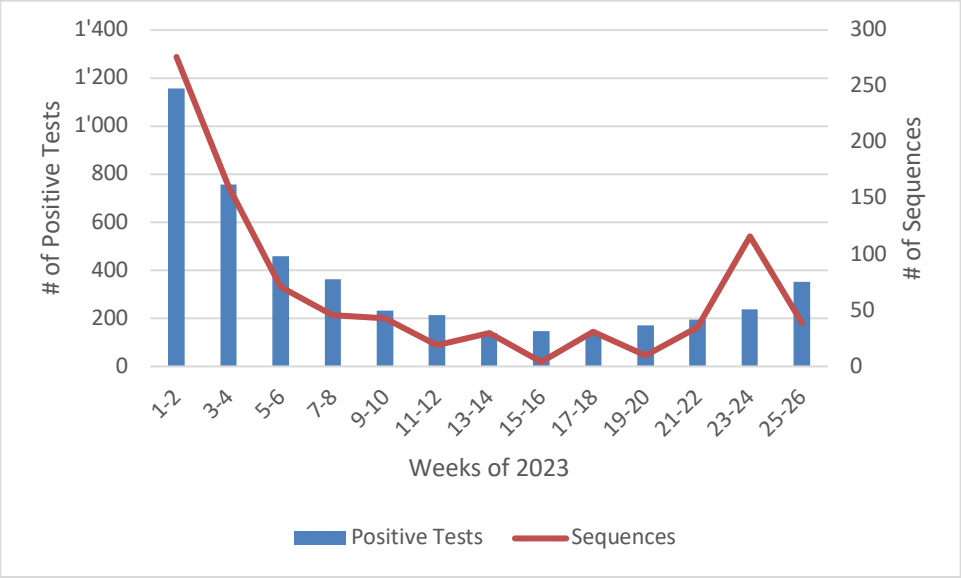

Figure 1: Sequences submitted and positive tests from all regions of the program for 2024, note the declines since the start of the year have stopped and there have since been small increases.

Recently circulating variants in Switzerland

The vast majority of circulating viruses are JN.1 sublineages now, particularly KP.3 as of the time of this report. During the November 2023 reporting period, the XBB.1.9 sublineage lost its dominance as the BA.2.86 sublineage JN.1 rose significantly, and it is still dominant as of the time of this report. Overall and according to GISAID, 2 XBB sequences (1 XBB.2.3.8 and 1 FL.15.1.1) were detected during this period, accounting for 0.71% of the total sequences, in contrast there were 65 BA.2.86 sequences (263 were JN.1*) accounting for 98.5% of May and June's sequences. The XDK recombinant between JN.1 and XBB was detected 8 times. The XDP XDR, and XDY recombinants were each detected once, and the XDV recombinant was detected thrice. No other variant had substantial circulation. For more details, see: https://cov-spectrum.ethz.ch/explore/Switzerland.

Region	BA.2.86*	JN.1*	XBB*	others	Recombinant	Sequences
All	1 (0.35%)	263 (93.9%)	2 (0.71%)	1 (0.46%)	14 (5.0%)	280

Table 2: number of sequences corresponding to selected variants in Switzerland from 26 Februar according to data received by 6 June

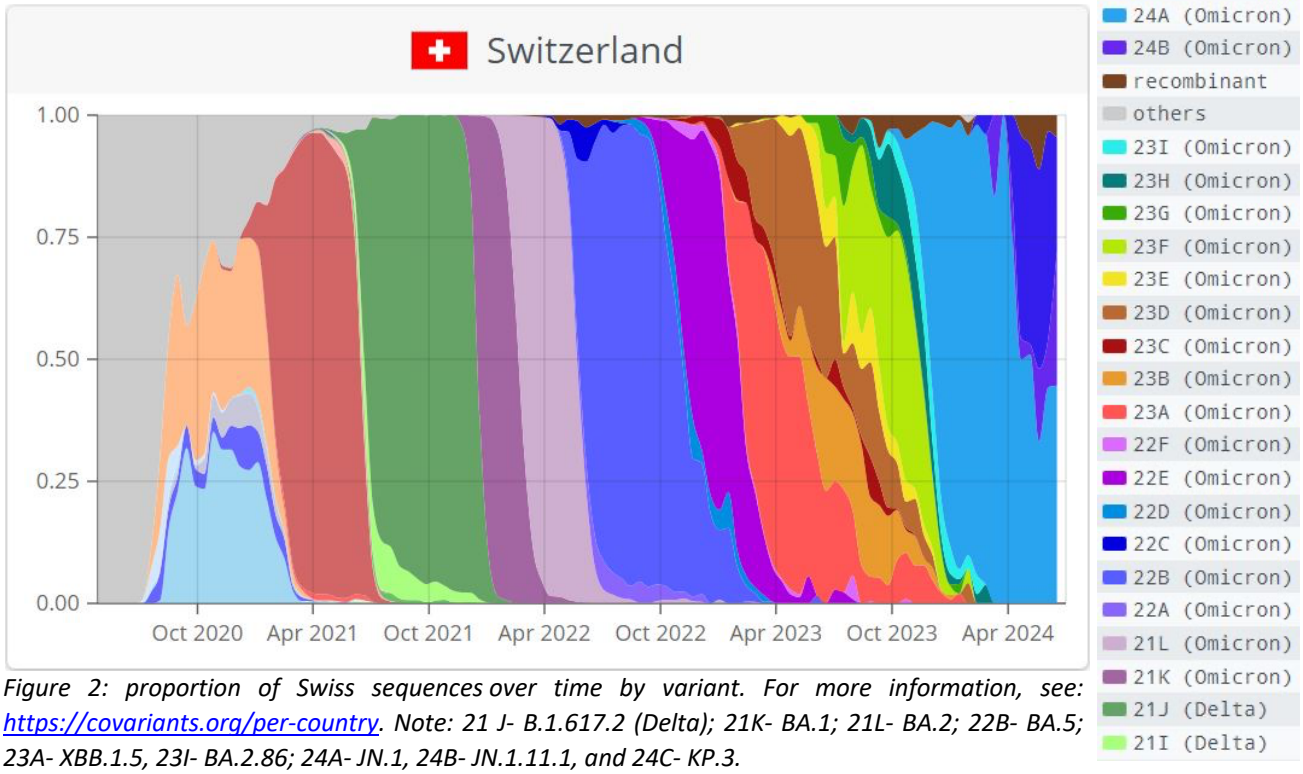

Figure 2: proportion of Swiss sequences over time by variant. For more information, see: https://covariants.org/per-country. Note: 21 J- B.1.617.2 (Delta); 21K- BA.1; 21L- BA.2; 22B- BA.5; 23A- XBB.1.5, 23I- BA.2.86; 24A- JN.1, 24B- JN.1.11.1, and 24C- KP.3.

4. Surveillance of mutations associated with reduced available treatment efficacy

Resistance mutations to available antivirals

AA position	World	Europe	Switzerland
Paxlovid®	(Nsp5 mutations)		
15	0	0	0
48	0.03 (21)	0.01 (4)	0
49	0.01 (6)	0.00 (1)	0
140	0.00 (1)	0	0
143	0	0	0
144	0	0	0
165	0.01 (4)	0.00 (1)	0
166	0.00 (2)	0	0
167	0	0	0
168	0	0	0
172	0	0	0
173	0.00 (1)	0	0
186	0.01 (9)	0.01 (4)	0
188	0.00 (1)	0	0
189	0.00 (3)	0.00 (1)	0
192	0.00 (1)	0	0
194	0.03 (25)	0.01 (4)	0
248	0	0	0
252	0.00 (2)	0.00 (1)	0
304	0.01 (4)	0.01 (3)	

Table 3: Frequency (%) of mutations at residues linked (by deep mutations scanning or other experimental results) to escape from Paxlovid® (5-fold cutoff), May and June 2024 (according to data as of 23 August, 2024). Numbers in parentheses denote the total number of sequences detected with a given mutation when it is ≤10.

Current data suggests that all monoclonal antibodies commercially available in Switzerland, such as sotrovimab, are unable to effectively neutralize JN.1 and its subvariants. The mAb Pemivibart, approved by the FDA but not available Switzerland currently neutralizes JN.1 with only a 2-fold decrease relative to the ancestral virus, however, multiple JN.1 sublineages (in particular KP.3.1.1) have substantially reduced neutralization. Escape mutations to Pemivibart have not been evaluated in sufficient detail to follow.

Paxlovid remains effective against all circulating variants, and escape mutations remained rare in Switzerland and worldwide (all less than 0.04%) in May and June 2024 (Table 3), with Nsp5:48 and 194 mutations being the most common worldwide (0.03%). No sequence with a mutation at an identified Paxlovid resistance site was detected in Switzerland.

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://idd.bag.admin.ch/) and sequence data submitted to GISAID to provide a summary of the SARS-CoV-2 epidemiology in Switzerland.

week	date	Total PCR tests	Positive tests	Sequenced	% positives sequenced
17	April 22-April 28	1 367	61	14	10.7
18	April 29 - May 5	1 255	70		
19	May 6 - May 12	1 292	79	38	22.1
20	May 13 - May 19	1 355	93		
21	May 20 - May 26	1 179	81	73	37.2
22	May 27 to June 2	1 239	115		
23	June 3 - June 9	1 213	105	35	14.7
24	June 10 - June 16	1 288	133		
25	June 17 - June 23	1 379	182	120	34.2
26	June 24 - June 30	1 347	169		
	Total	12 914	1 088	280	25.7
27-31	July 1 – August 4	2 801	380	135	35.6

Supplementary Table 1: Total number of tests performed by the laboratories participating in the surveillance program from 22 April to 30 June, 2024, and from 1 July to 4 August only for the HUG, Valais ICH, and EOC Bellinzona .

week	Date	HUG	CHUV	ICH-VS	IFIK	UZH IMV	USB	EOC	All
17	April 22-April 28	8	0	0		18	5	0	14
18	April 29 - May 5	8	1	10	10		0		
19	May 6 - May 12		10				0	0	38
20	May 13 - May 19		20				0		
21	May 20 - May 26	8	2				5	0	73
22	May 27 to June 2		10				10		
23	June 3 - June 9	34	15	0	20	27	10	0	35
24	June 10 - June 16		10	0			0		
25	June 17 - June 23		19	0			0	0	120
26	June 24 - June 30		20	0			0	0	
	Total	58	107	10	30	45	30	0	280
27	July 1 - July 7	78		9					
28	July 8 - July 14			19					
29	July 15 - July 21			19					
30	July 22 - July 28			10					
	Total	78		57					

Supplementary Table 2: number of sequences submitted to GISAID by each laboratory during the surveilled period (from 22 April to 30 June, 2024). Note the dates of the sequencing blocks differ significantly between centers, primarily due to low sample numbers.