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Swiss national SARS-CoV-2 genomic and variants surveillance program: report of the month of January 2024

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1. Summary

During the month of January 2024, the number of positive SARS-CoV-2 tests per week decreased significantly within the program. Similarly, the test **positivity rate decreased. The number of hospitalizations due to COVID-19 also steadily decreased**. RNA levels in the wastewater also declined during January 2024.

The 1'914 positive tests processed by laboratories participating to the program constituted about half (47.6%) of the reported positive tests in Switzerland. A total of 807 new sequences were submitted (337 collected during this period) to GISAID during the January 2024 reporting period, mainly originating from hospitalized patients.

The **JN.1** sublineage of the BA.2.86 clade **remained dominant** (>80% of wastewater sequences and >80% of clinical samples) **in January 2024**.

There is no current evidence to suggest that JN.1 is more severe. It's noteworthy that **the neutralizing response against JN.1** and similar variants other BA.2.86 derivatives **induced by the mRNA vaccines is comparable to that against EG.5.**

Outside of Switzerland **a new highly divergent (BA.2.87.1) was detected**, but **its geographic spread is limited and it does not appear to have a growth advantage.**

Recently, a highly divergent variant was spotted in the wastewater surveillance of Lausanne, with no corresponding clinical specimen, and thus no full sequence. **There is no indication of community spread** (see below for more information**).**

This report covers the period of 1 to 28 January 2024 (weeks 1-4). All data presented in this report are based on the sampling date. For an overall description of the program, please see the reports of 2023.

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 XBB.1.5, XBB.1.16, EG.5, BA.2.86, and JN.1. No variants in current circulation have been designated a Variant of Concern. All currently circulating variants are derivatives of the original "Omicron" VOC.

No issues with detection (via PCR or antigenic tests) have been noted for any variants. No increased severity has been noted either. 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 very low, but there is no loss of efficacy against other antivirals, such as protease inhibitors.

The highly divergent BA.2.87.1 (>30 spike mutations and >100 nucleotide mutations) was first detected in South Africa, and has now been detected in low abundance wastewater in South-east Asia as well as a traveler to the USA from the Middle East. Overall abundance is very low and shows no sign of increasing. Preliminary characterization suggests higher ACE2 binding and cell-cell fusion than JN.1, but it is more susceptible to polyclonal sera and available mAbs.

A highly divergent variant was spotted in the wastewater surveillance of Lausanne in August and November 2023, with no corresponding clinical specimen, and thus no full sequence. It likely has very poor ACE2 binding, given the number and the location of mutations. A progenitor sequence was sporadically detected in the same place in 2021 from May to July, and a chronic infection is suspected. There is no indication of community spread.

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 1-28 January, the FOPH reported 4'023 positive tests (including both RT-PCR and antigen-based tests). Positive tests from the labs participating in the national surveillance program produced nearly half this number (1'914 tests). Along with the number of tests performed in the country, the number of positive tests/week decreased in Switzerland during January. Notably, within the program, the percent of positives sequenced within the program remained similar: 22.8% in January 2024 and in December 2023. The test positivity rate within the program for January was 16.0% compared to December 2023's 28.9%. Overall, about 10% of ascertained positive cases were sequenced.

Although case ascertainment rates may be too low to identify meaningful trends, there had been a trend since a peak in late November/early December 2023 towards decreases in the number of cases, hospitalizations, and RNA levels in wastewater. 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 436 SARS-CoV-2 sequences have been declared to have been processed during this period. There are 807 sequences available on GISAID that were submitted during this period (and 337 collected during this period) as of 29 February 2024.

Week	Date	Number of sequences declared and successfully submitted to GISAID, January 2024
1	January 1 to 7	276
2	January 8 to 14	
3	January 15 to 21	160
4	January 22 to 28	
	Total	436

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.

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

As shown in Figure 1, numbers of SARS-CoV-2 sequences submitted each week continued to decrease during the January 2024 reporting period (Calendar weeks 1 - 4).

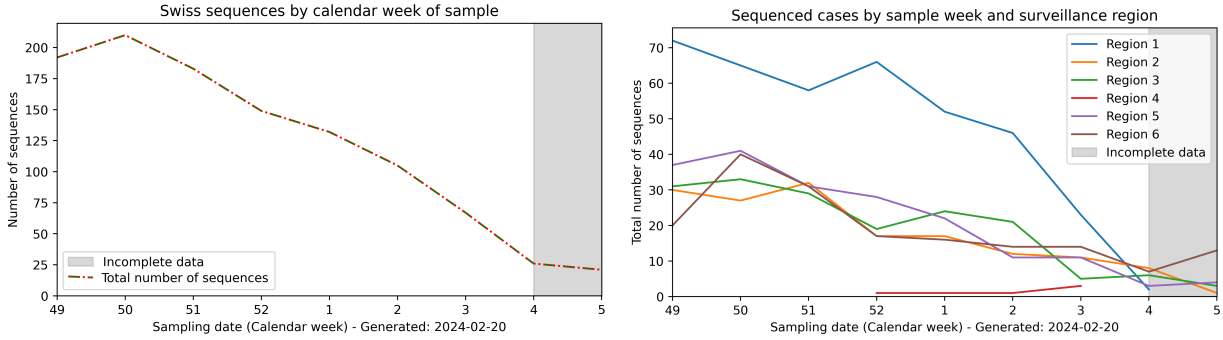

Figure 1: Left: Number of SARS-CoV-2 sequences available for Switzerland (total available Swiss sequences in GISAID in green, Swiss sequences submitted through the program in dotted orange). Right: Sequencing coverage among the different Swiss regions per week, by number of sequences. Note that region 1 is over-represented, with 3/7 sequencing centers.

Region 1 continued to have the highest number of sequences. Region 4 (Luzern, Unterwalden, Uri, Zug and Schwyz) is still not 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 1).

3. Recently circulating variants in Switzerland

The vast majority of circulating viruses are JN.1 sublineages now. 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 in January 2024. Overall, 9 EG.5 sequences were detected during this period, amounting to 2.7% of the total sequences, in contrast there were 306 BA.2.86 sequences (304 were JN.1*) accounting for 92.7% of December's sequences (Table 2, Figures 2 & 3). No other variant had substantial circulation. For more details, see: https://cov-spectrum.ethz.ch/explore/Switzerland.

Region	BA.2.86*	EG.5.1*	JN.1*	XBB*	others	Recombinant	Sequences
All	2	9	304	9	0	6	330
1	0	3	116	0	0	4	123
2	1	2	44	1	0	0	48
3	1	1	52	1	0	1	56
4	0	0	4	0	0	0	4
5	0	2	42	2	0	1	47
6	0	1	45	5	0	0	51

Table 2: number of sequences corresponding to selected variants in Switzerland from 1 January to 28 January, by region, according to data received by 28 February 2024

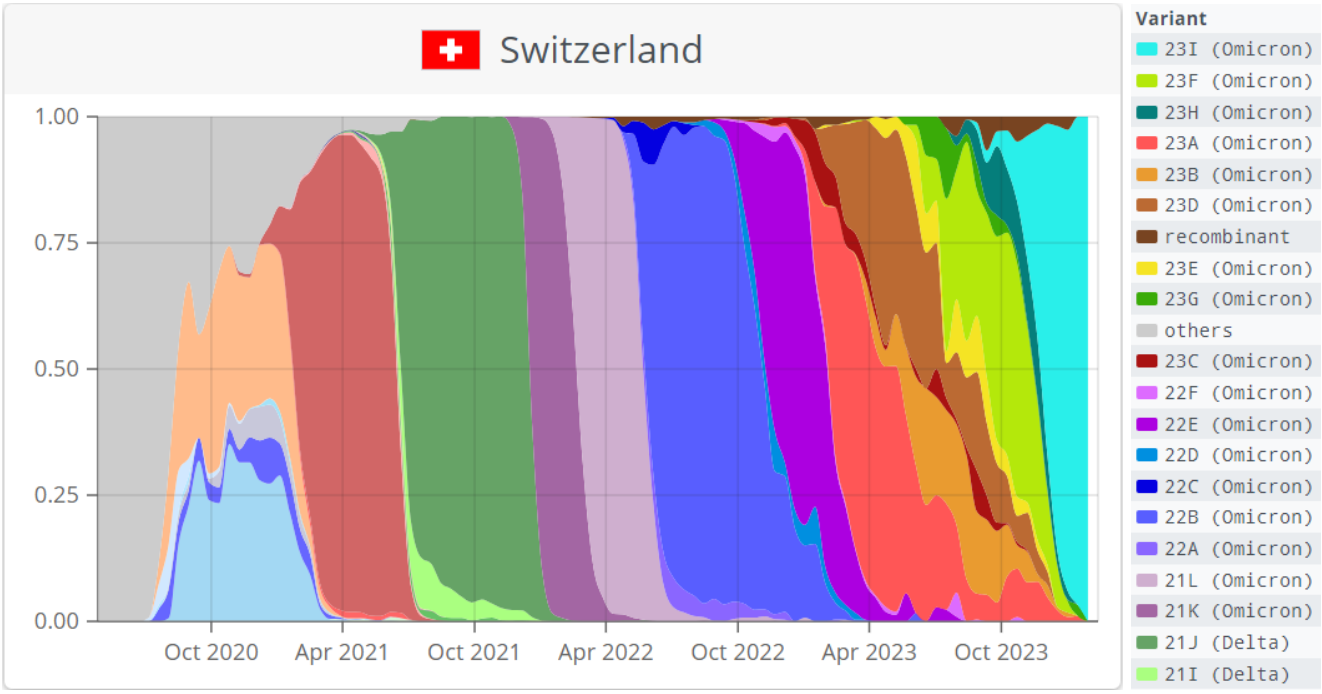

Figure 2: proportion of Swiss sequences over time by variant. For more information, see: https://covariants.org/per-country. Note: 21 J- B.1.617.2 (Delta); 21K- BA.1; 21L- BA.2; 22B- BA.5; 23A- XBB.1.5 (red); and 23I- BA.2.86 (cyan). Also note that the 23I (BA.2.86) includes the JN.1 subvariant

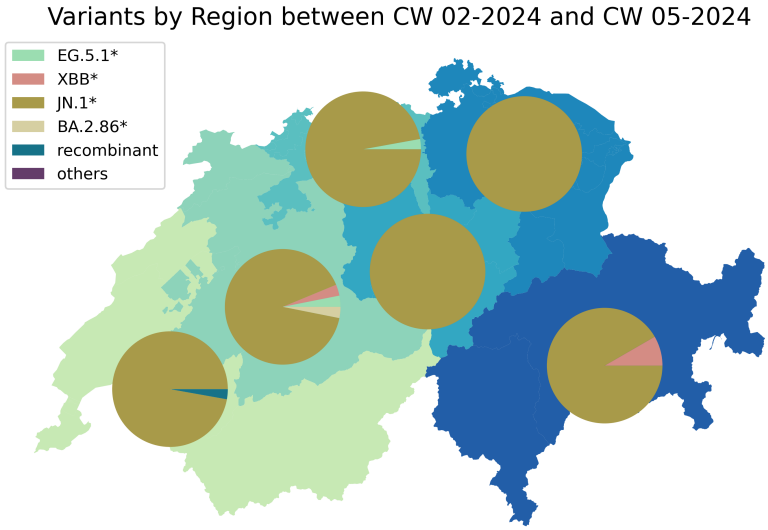

Figure 3: Distribution of variants per region, by Calendar Week (CW), for January 2024 (weeks 2 to 5). Note the JN.1 dominance, in every region.

4. Surveillance of mutations associated with reduced available treatment efficacy

Resistance mutations to available monoclonal antibodies

AA position	World	Europe	Switzerland
Sotrovimab	(Spike mutations)		
337	0.04	0.03 (5)	0
340	0.03	0.04 (7)	0
356	77.8	80.1	85.1
371	92.4	89.8	81.2
377	0.01 (4)	0.01 (2)	0
449	0.02 (9)	0.04 (6)	0
476	0.06	0.04 (6)	0
494	0.12	0.08	0
Paxlovid®	(Nsp5 mutations)		
15	0	0	0
48	0.01 (8)	0	0
49	0.01 (6)	0.01 (1)	0
140	0	0	0
143	0.00 (1)	0	0
144	0.00 (1)	0	0
165	0	0	0
166	0	0	0
167	0	0	0
168	0.00 (1)	0	0
172	0	0	0
173	0.00 (1)	0.01 (1)	0
186	0.02 (9)	0.02 (4)	0
188	0.03 (15)	0.02 (4)	0
189	0.02 (13)	0.01 (1)	0
192	0.02 (12)	0.01 (1)	0
194	0.04 (21)	0.02 (4)	0
248	0.00 (1)	0.01 (1)	0
252	0.00 (3)	0.01 (2)	0
304	0.01 (4)	0.02 (2)	0

Current data suggests that in vitro neutralization by commercially available monoclonal antibodies such as sotrovimab of the currently circulating JN.1 variant is substantially reduced relative to the original virus.

Additional (beyond those found in BA.2.86 and XBB) sotrovimab escape mutations remained rare in Switzerland and worldwide during December 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), January 2024 (according to data as of 29 February, 2024). Numbers in parentheses denote the total number of sequences detected with a given mutation when it is ≤10. Note, BA.2 and its sublineages (including XBB and BA.2.86*) contain the spike S371F mutation leading to partial sotrovimab resistance. Also note: BA.2.86 is mutated at spike position 356.*

Resistance mutations associated with resistance to other available antivirals

Mutations known to result in significant escape against Paxlovid remained rare worldwide (all less than 0.1%) in January 2024, with Nsp5:194 mutations being the most common worldwide (0.04%). **No sequences with a known Paxlovid resistance mutation were detected in Switzerland (Table 3).**

Acknowledgements:

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

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An annex containing supplementary figures, data, and contact list is available at the following url:

https://www.hug.ch/laboratoire-virologie/surveillance-variants-sars-cov-2-geneve-national

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
1	January 1 to 7	3 040	655	276	42.14
2	January 8 to 14	3 049	501		
3	January 15 to 21	3 028	453	160	35.32
4	January 22 to 28	2 841	305		
	Total	11 958	1 914	436	22.78

Supplementary Table 1: Total number of tests performed by the laboratories participating in the surveillance program from 1 to 28 January 2024.

week	Date	HUG	CHUV	ICH-VS	IFIK	UZH IMV	USB	EOC	All
1	January 1 to 7	41	14	21	27	73	54	32	276
2	January 8 to 14		14						
3	January 15 to 21	12	15	22	17	12	38	30	160
4	January 22 to 28		14						
	Total	53	57	43	44	85	92	62	436

Supplementary Table 2: number of sequences submitted to GISAID by each laboratory during the surveilled period (from 1 to 28 January 2024).