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Geneva, April 19, 2024

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

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1. Summary

This report covers the period of 29 January to 25 February 2024 (weeks 5-8). 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 month of February 2024, the number of positive SARS-CoV-2 tests per week decreased significantly within the program. Similarly, the test **positivity rate decreased significantly. The number of hospitalizations due to COVID-19 also remained low**. RNA levels in the wastewater continued to decline during February 2024.

The 822 positive tests processed by laboratories participating to the program constituted over half (57.4%) of the reported positive tests in Switzerland. A total of 327 new sequences were submitted (127 collected during this period) to GISAID during the February 2024 reporting period, mainly originating from hospitalized patients.

The **JN.1** sublineage of the BA.2.86 clade **remained dominant** (>90% of wastewater sequences and >80% of clinical samples) **in February 2024**.

The highly divergent variant retrieved in Lausanne has not been detected again, although the Lausanne wastewater plant is no longer tested.

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

JN.1 is currently neutralized poorly following the Wu-1 & BA.5 bivalent booster. In contrast, the XBB.1.5 monovalent booster induces significant neutralization of JN.1, with JN.1 neutralization titers being roughly one third to one half of the XBB.1.5 neutralization titers.

A new monoloncal antibody, pemivibart, has been validated by FDA. Data from pseudovirus and authentic virus isolates is conflicting, but live isolates displayed only a 2-fold reduction in neutralization (relative to the ancestral virus), which is overall a very good performance.

As the number of cases has been low for the months of March and continue to decrease in April, sequencing batches will be deferred. Therefore, the production of the sequences and therefore of the report, will be delayed for the months of March and April 2024.

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.

JN.1 and its sublineages accounted for 88% of global sequences collected in February 2024 (29 January to 25 February). Three spike mutations in a JN.1 background are suspected to confer a growth advantage: R346T, F456L and T572I. R346T was previously very common in XBB backgrounds, and was associated with immune escape. Similarly, F456L was also previously identified and was common in XBB.1.9 sublineages, however, T572I has not previously achieved substantial circulation.

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 (with over 30 spike mutations and >100 nucleotide mutations) has not been detected in clinical samples since December 2023, and the last reported wastewater detection was in January 2024 in southeast Asia.

There have been no new reports of the highly divergent variant last spotted in the wastewater surveillance of Lausanne in November 2023. There is no indication of community spread. Note that the wastewater plan that identified it is no longer part of the wastewater surveillance program.

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 29 January to 25 February, the FOPH reported 1'432 positive tests (including both RT-PCR and antigen-based tests). Positive tests from the labs participating in the national surveillance program produced over half this number (822 tests). The percent of positives sequenced within the program decreased: 13.9% in February vs. 22.8% in January. The test positivity rate within the program for February was 8.0% compared to January's 16.0% and December 2023's 28.9%. Overall, the percent of sequenced ascertained positive cases was also about 8%.

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, 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 114 SARS-CoV-2 sequences have been declared to have been processed during this period. There are 320 sequences available on GISAID that were submitted during this period (and 127 collected during this period) as of 29 February 2024.

Week	Date	Number of sequences declared and successfully submitted to GISAID, January 2024
1	January 29 to February 4	70
2	February 5 to 11	
3	February 12 to 18	44
4	February 19 to 25	
	Total	114

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

Numbers of SARS-CoV-2 sequences submitted each week continued to decrease during the February 2024 reporting period.

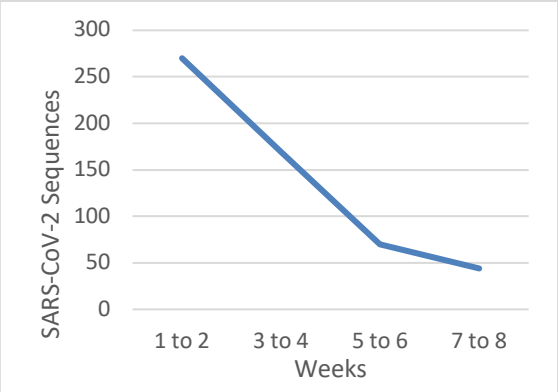

Figure 1: Sequences by two weeks blocks submitted by all regions of the program for 2024, note the continued decline in February's reporting period (weeks 5 to 8)

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 February 2024. Overall, 3 EG.5 sequences were detected during this period, amounting to 2.4% of the total sequences, in contrast there were 119 BA.2.86 sequences (113 were JN.1*) accounting for 93.7% of December's sequences. 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	6	3	113	4	1	0	127

Table 2: number of sequences corresponding to selected variants in Switzerland from 29 January to 25 February, by region, according to data received by 25 March 2024.

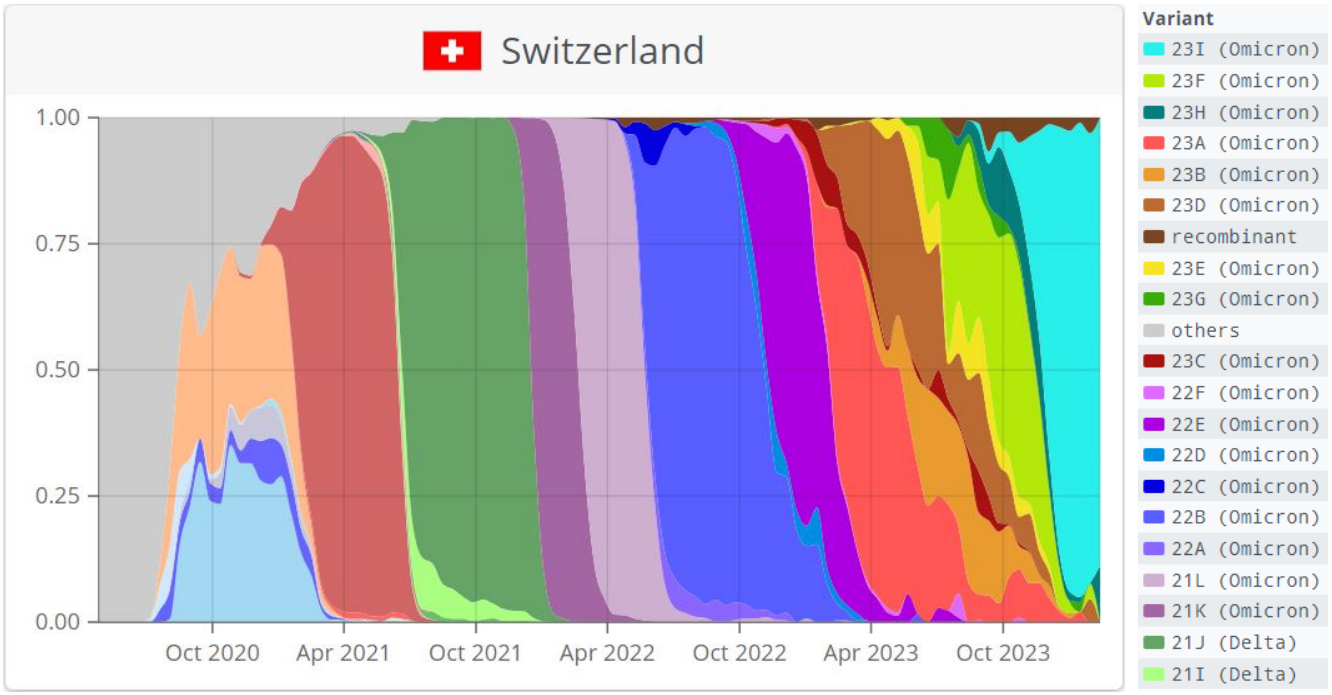

Figure 2: proportion of Swiss sequences over time by variant. For more information, see: https://covariants.org/per-country. Note: 21 J- B.1.617.2 (Delta); 21K- BA.1; 21L- BA.2; 22B- BA.5; 23A- XBB.1.5 (red); and 23I- BA.2.86 (cyan). Also note that the 23I (BA.2.86) includes the JN.1 subvariant

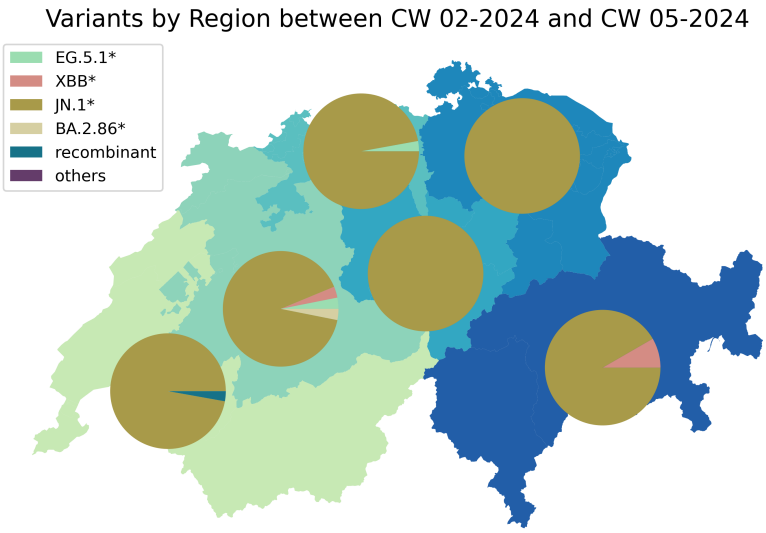

Figure 3: Distribution of variants per region, by Calendar Week (CW), for the start of February 2024 (weeks 2 to 5). Note the JN.1 dominance, in every region.

3. Surveillance of mutations associated with reduced available treatment efficacy

Resistance mutations to available monoclonal antibodies

AA position	World	Europe	Switzerland
Sotrovimab	(Spike mutations)		
337	0.09	0.04 (3)	0
340	0.08	0.06 (5)	0
356	88.9	87.5	94.5
371	93.76	93.84	100
377	0.06	0.05 (4)	0.79 (1)
449	0.01 (6)	0.02 (2)	0
476	0.04	0.04 (3)	0
494	0.06	0.04 (3)	0
Paxlovid®	(Nsp5 mutations)		
15	0	0	0
48	0.03 (11)	0	0
49	0.00 (1)	0	0
140	0	0	0
143	0	0	0
144	0	0	0
165	0	0	0
166	0	0	0
167	0	0	0
168	0	0	0
172	0	0	0
173	0.00 (1)	0	0
186	0.01 (5)	0	0
188	0.00 (2)	0.02 (2)	0
189	0.00 (2)	0.02 (2)	0
192	0.01 (3)	0.04 (3)	0
194	0.03 (11)	0.06 (5)	0.79 (1)
248	0	0	0
252	0.05 (21)	0	0
304	0.00 (1)	0	0

Current data suggests that in vitro neutralization by commercially available monoclonal antibodies, such as sotrovimab, against the currently circulating JN.1 variant is substantially reduced relative to the original virus. The mAb Pemivibart, newly approved by the FDA, currently neutralizes JN.1 with only a 2 fold decrease relative to the ancestral virus, which is very good performance. Escape mutations to Pemivibart have not been evaluated in sufficient detail.

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 at sites known to result in significant escape against Paxlovid remained rare worldwide (all less than 0.1%) in January 2024, with Nsp5:252 mutations being the most common worldwide (0.05%), and Nsp5:194 mutations being the most common in Europe (0.06%, n= 5). **One sequence with a mutation at a known Paxlovid resistance site (Nsp5:194) was detected in Switzerland (Table 3).**

Acknowledgements:

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

This report was primarily prepared by Erik Boehm, Marc Friedli, and Pauline Vetter. Additional acknowledgments are due to: Samuel Cordey, Richard Neher, Christian Althaus, Emma Hodcroft, Tanja Stadler, Philippe Lemercier, Ioannis Xenarios, Lorenzo Cerutti, Louis Du Plessis, Erik Studer, and Laurent Kaiser.

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
5	January 29 to February 4	2'716	231	70	15.3
6	February 5 to 11	2'667	227		
7	February 12 to 18	2'569	197	44	12.1
8	February 19 to 25	2'346	167		
	Total	10'298	822	114	13.9

Supplementary Table 1: Total number of tests performed by the laboratories participating in the surveillance program from 29 January to February 25, 2024.

week	Date	HUG	CHUV	ICH-VS	IFIK	UZH IMV	USB	EOC	All
5	January 29 to February 4	12	8	8	10	8	4	20	70
6	February 5 to 11								
7	February 12 to 18	15	6	4	2	8	4	5	44
8	February 19 to 25								
	Total	27	14	12	12	16	8	25	114

Supplementary Table 2: number of sequences submitted to GISAID by each laboratory during the surveilled period (from 29 January to February 25, 2024).