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Swiss national RSV, SARS-CoV-2 and Influenza virus genomic surveillance program: November 2024 – Final report

Geneva Centre for Emerging Viral Diseases

Division of Infectious Diseases

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1. Summary report:

This report covers the samples taken from September to November 2024. Sequencing data was delayed due to manual cross-checking with the SPSP platform as a quality control, and other issues that arose with the first use of this multi-viral panel.

For the first month of this respiratory virus sequencing program, 200 samples of respiratory pathogens were obtained from the IMV in Zurich, the CHUV in Lausanne, the HUG in Geneva, USB in Basel, the ICH in Sion, and the IFIK in Bern.

Between SARS-CoV-2, Influenza virus, and RSV, SARS-CoV-2 was by far the most common virus in these samples (77.5%, n=155), followed by influenza virus (13.5%, n= 27) and then RSV (9%, n= 18). Further data regarding the origin of the sequences are available in the preliminary report dated December, 20, 2024.

The most common for SARS-CoV-2 lineages were XEC (40.7%) and KP3.1.1 (25.9%). For influenza virus, 20% of the sequences were Influenza B and 80% were Influenza A: of the Influenza A sequences, 90% belonged to the H1N1 subtype, while 10% belonged to the H3N2 subtype. For RSV, 58.8% of the sequences were RSV-B, and 41.2% were RSV-B.

No significant sign of additional immune evasion was spotted in SARS-CoV-2. Notably, nearly 59% of RSV sequences contained a mutation weakly associated with Palivizumab resistance.

Acknowledgements:

https://bsse.ethz.ch/cevo/research/sars-cov-2/swiss-sars-cov-2-sequencing-consortium.html
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Table 1: Number of sequenced samples corresponding to each virus and originating lab

Site	SARS-CoV-2	Influenza	RSV
CHUV	8	6 (5A, 1B)	6
HUG	80	11 (8A, 3B)	5
ICH	8	5 (4A, 1B)	7
IFIK	11	4	0
IMV	14	1 (A)	0
USB	34	0	0
Total	155 (77.5%)	27 [18 A, 5B] 13.5%	18 (9%)

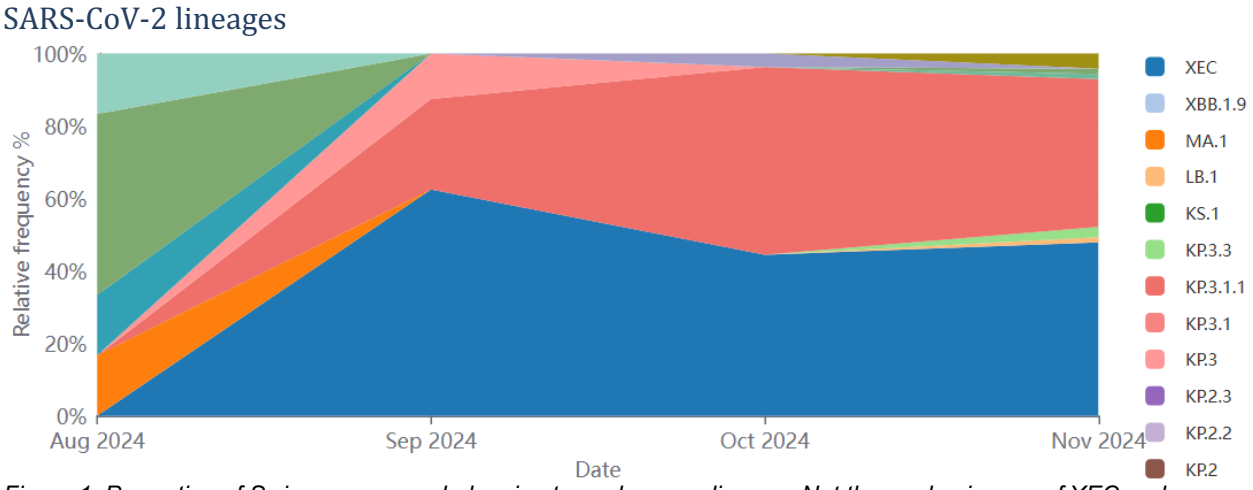

Figure 1: Proportion of Swiss sequences belonging to each pango lineage. Not the co-dominance of XEC and KP.3.1.1

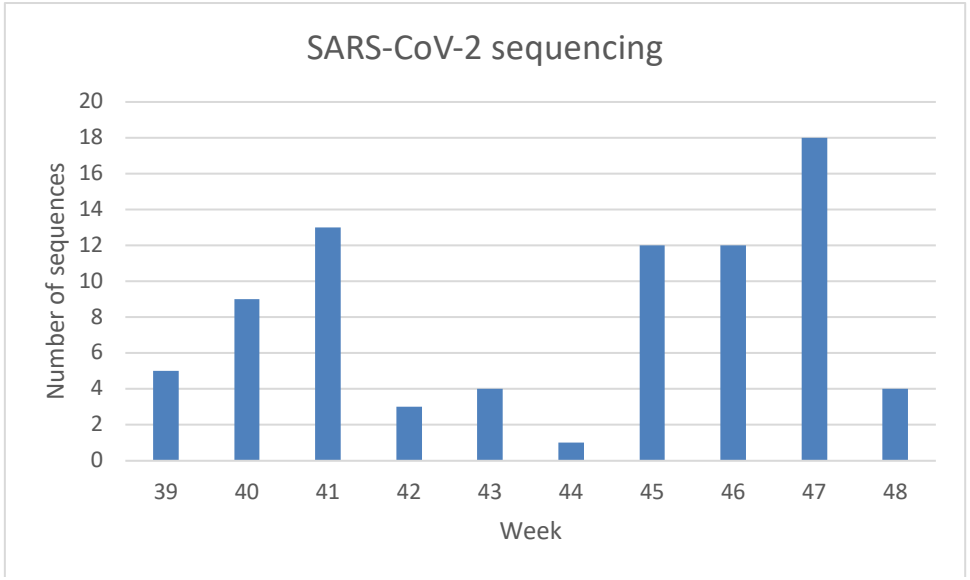

Figure 2: Absolute number Swiss sequences belonging to each pango lineage. Not the co-dominance of XEC and KP.3.1.1

Escape mutation prevalence

Currently, no monoclonal antibodies available in Switzerland are effective at neutralizing the vast majority of the SARS-CoV-2 sub-lineages circulating in Switzerland and the rest of the world. The 3CL protease inhibitor, Paxlovid, remains effective against SARS-CoV-2, and we are monitoring the prevalence of

mutations that have been shown to reduce its efficacy by 5-fold or more (table 2). No resistance mutations were spotted in Switzerland, but 21 such mutations were spotted throughout Europe.

AA position	Switzerland	Europe
Paxlovid®	(Nsp5)	
15	0	6
48	0	7
49	0	0
140	0	0
143	0	0
144	0	0
165	0	0
166	0	1
167	0	0
168	0	1
172	0	0
173	0	0
186	0	1
188	0	0
189	0	0
192	0	0
194	0	0
248	0	0
252	0	1
304	0	4

Table 2: Prevalence NSP5 mutations of SARS-CoV-2 leading to resistance from paxlovid

Influenza lineages

Eighty percent of influenza sequences belonged to Influenza A, and 20% belonged to Influenza B.
Of the Influenza A sequences, 90% were assigned to the H1N1 subtype, while 10% were assigned to the H3N2 subtype. H1N1 was thus responsible for the majority of sampled influenza cases.
All Swiss Influenza sequences available on GISAID originated from samples collected in October (6) or November (19) 2024.

RSV

RSV has two main immunogenic targets, the F-protein and the G- Protein. Currently available monoclonal antibodies target the F-protein. F-protein and G-protein mutations were common.

Escape mutation prevalence

Mutations at positions 209 and 211 mutation has been frequently spotted in Switzerland. Indeed, 58.8% of RSV sequences obtained had the F_S211N mutation (table 3), which have been associated with weak Palivizumab escape (<4 fold reduced neutralization).

Mutation	Gene	Resistance	Mutations at residue in CH
63S	F Protein	Nirsevimab	0
I64M	F Protein	Nirsevimab	0
K65R	F Protein	Nirsevimab	0
66D	F Protein	Nirsevimab	0
67A	F Protein	Nirsevimab	0
68N/R/G	F Protein	Nirsevimab	0
201S/T	F Protein	Nirsevimab (B)	0
206M	F Protein	Nirsevimab / Palivizumab	0
208D	F Protein	Nirsevimab	0
209R/K/L	F Protein	Palivizumab	6
211N/I	F Protein	Palivizumab	10
272K/T	F Protein	Palivizumab	0
275F	F Protein	Palivizumab	0
394R/H	F Protein	fusion inhibimabtors	0

Table 3: Mutation constellations of RSV sequences. Mutations in bold have been shown to have a large effect on neutralization, while other mutations individually have negligible effects.

Mutation Constellations

The following “mutation constellations” were additionally detected during the reporting period:

# of Seqs	Sub-type	F- mutations	G-mutations
2	B	F_S190N, F_S211N, F_S389P	G_A74V, G_I137T, G_I252T, G_I268T, G_K256N, G_P214S, G_P221L, G_S100G, G_S275P, G_T131A, G_Y285H
1	A	F_A518V, F_L119H	G_D284G, G_E295V, G_G224E, G_H90Y, G_I134K, G_I265L, G_K262E, G_L101F, G_L142S, G_L314P, G_P276L, G_P71L, G_S243I, G_T320A, G_V225A, G_Y304H
2	B	F_R209Q, F_S190N, F_S211N	G_A74V, G_I137T, G_I87T, G_K85E, G_P214S, G_P221L, G_P229S, G_R240G, G_S100G, G_S243I, G_T130A, G_T131A, G_T139I, G_Y90H
1	A	F_A23T, F_S377N	G_D284G, G_G224E, G_H90Y, G_I134K, G_I265L, G_K262E, G_L101F, G_L142S, G_P71L, G_S243I, G_T118I, G_T320A, G_V225A, G_Y273H, G_Y304H
1	A	None	G_A122V, G_D284G, G_G224V, G_H90Y, G_I134K, G_I265L, G_K262E, G_L101F, G_L142S, G_L314P, G_N103T, G_P298S, G_P71L, G_S144I, G_S243I, G_T320A, G_V225A, G_Y273H, G_Y304H

Table 4: Mutation constellations of RSV sequences. Mutations co-occurring together in different mutation constellations are highlighted in the same color.