

Respiratory Viruses in Luxembourg (ReViLux)

Report – Sentinel Week 49 and Sequencing Update

Summary

The sentinel network detected a medium epidemic activity over the last week, based on 7.9 % of consultations being associated with influenza-like illness. Among the specimen collected by the sentinel network over the last week, the percentage of positive tests for SARS-CoV-2 was 20.9%, 17.0% for RSV and 11.7 % for Influenza A.

Influenza A detections in sentinel data continued to increase from 2.5 (2023/48) to 11.7% (2023/49) with eight samples characterised as A(H1)pdm09 viruses.

Concerning SARS-CoV-2 genomic surveillance, since late February 2023 recombinant strains that combine characteristics of other variants have been dominant in Luxembourg. From week 2023/26 to week 2023/43, EG.5 was the most frequent detected variant, but showing a decreasing trend. Since week 2023/43, the proportion of BA.2.86 has continuously increased. The estimated distribution for BA.2.86 was 43.9% (95%CI: 34.8-53.0%), XBB.1.9 was 29.8% (95%CI: 21.4-38.2%), and XBB.1.5 was 10.5% (95%CI: 4.9-16.1%) for weeks 2023/46-48. BA.2.86 was dominant in the selected community and hospital sample.

Introduction

The Laboratoire national de santé, as **National Reference Laboratory for Acute Respiratory Infections** in Luxembourg, performs close surveillance on respiratory viruses, with a special focus on SARS-CoV-2. The main monitoring activities are:

- **The Sentinel Surveillance.** It provides a broad picture of respiratory diseases affecting the Luxembourgish population, based on clinical and laboratory data.
- **The SARS-CoV-2 Genomic Surveillance.** It enables detailed observation of SARS-CoV-2 variants and mutations through time and space, as well as studying specific groups of interest.

The objective of the ReViLux report is to inform public health actions in Luxembourg.

Sentinel Surveillance Network

The Sentinel Surveillance aims at monitoring the circulating respiratory viruses, from traditional ones like Influenza to more recent ones like SARS-CoV-2, and hence underpin public health actions. The Sentinel Network is a group of general practitioners and paediatricians spread over the country. They report the weekly number of patients showing symptoms suggestive of acute respiratory infection (ARI) and influenza-like illness (ILI), and those patients are then sampled and tested for a panel of respiratory viruses. The circulation of respiratory viruses in the north hemisphere is generally monitored by seasons that go from week 40 to week 20. The period between weeks 20 and 40 is usually called inter-season.

Clinical results

Last week, 7.9% of the consultations were reported as ILI, which represents a medium epidemic activity for Luxembourg, according to ECDC and the Moving Epidemic Method. ILI rates have increased since week 2023/43 with drop in week 2023/46, but then increased steadily to 7.9% in week 2023/49. The history of ILI consultations is displayed in Figure 1, and a detailed summary of the number of ARI and ILI cases during the last four weeks is included in Table 1.

Laboratory results

Over the last week, the most frequently detected viruses (according to positivity rates) were SARS-CoV-2(20.9%), followed by RSV (17.0%) and Human rhinovirus (18.1%). Positivity rates of Influenza A increased from 2.5% (2023/48) to 11.7% (2023/49). Eight of 23 samples have been characterized as A(H1N1)pdm09. Test positivity for RSV decreased sharply from 30.8

(2023/48) to 17.0 (2023/49), however not all samples have been tested yet. Overall, this season (23/24), the highest impact was seen among the 0-4 years age group (Figure3).

To date, 67 RSV detections were further subtyped as either RSV A (N=61, 91%) or RSV B (N=6, 9.0%). An overview of the circulating viral pathogens during the current and previous inter-season is displayed in Figure 2 and Table 2.

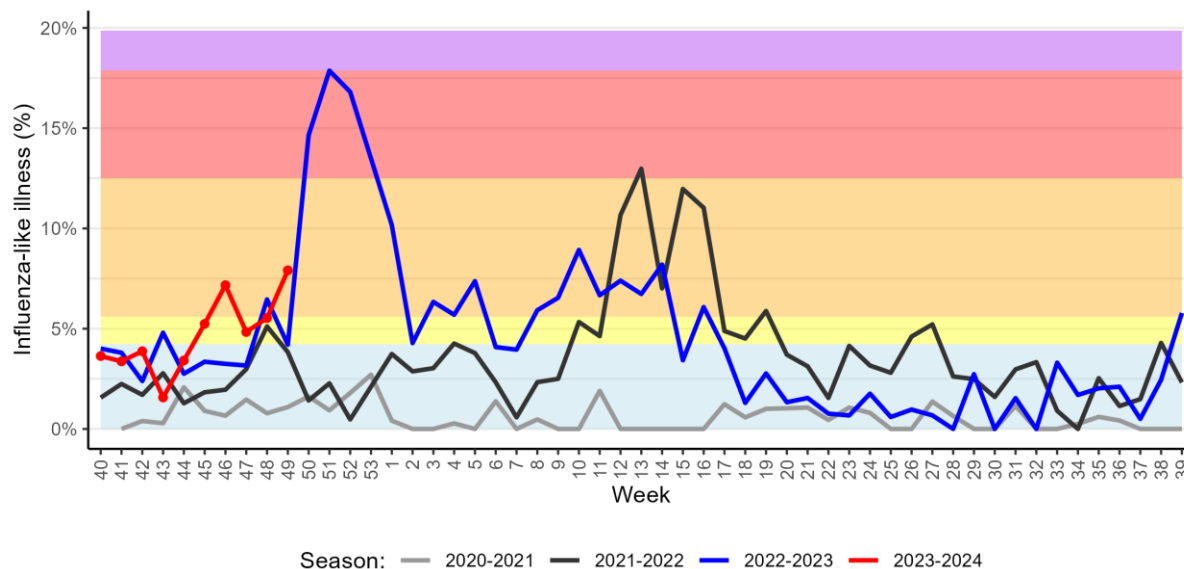


Figure 1. Percentage of patients with influenza-like illness over the last three seasons
Background colours according to intensity of circulation: baseline, low, medium, high, very high.

Table 1. Syndromic surveillance over the last 4 weeks

Week	ARI		ILI		Total consultations
	N	%	N	%	
2023/46	54	19.35	20	7.17	279
2023/47	61	15.52	19	4.83	393
2023/48	123	25.20	27	5.53	488
2023/49	146	27.50	42	7.91	531

ARI: Acute Respiratory Infections; ILI: Influenza-Like Illness.

Circulation of common viral respiratory pathogens 2022/23- Sentinel network

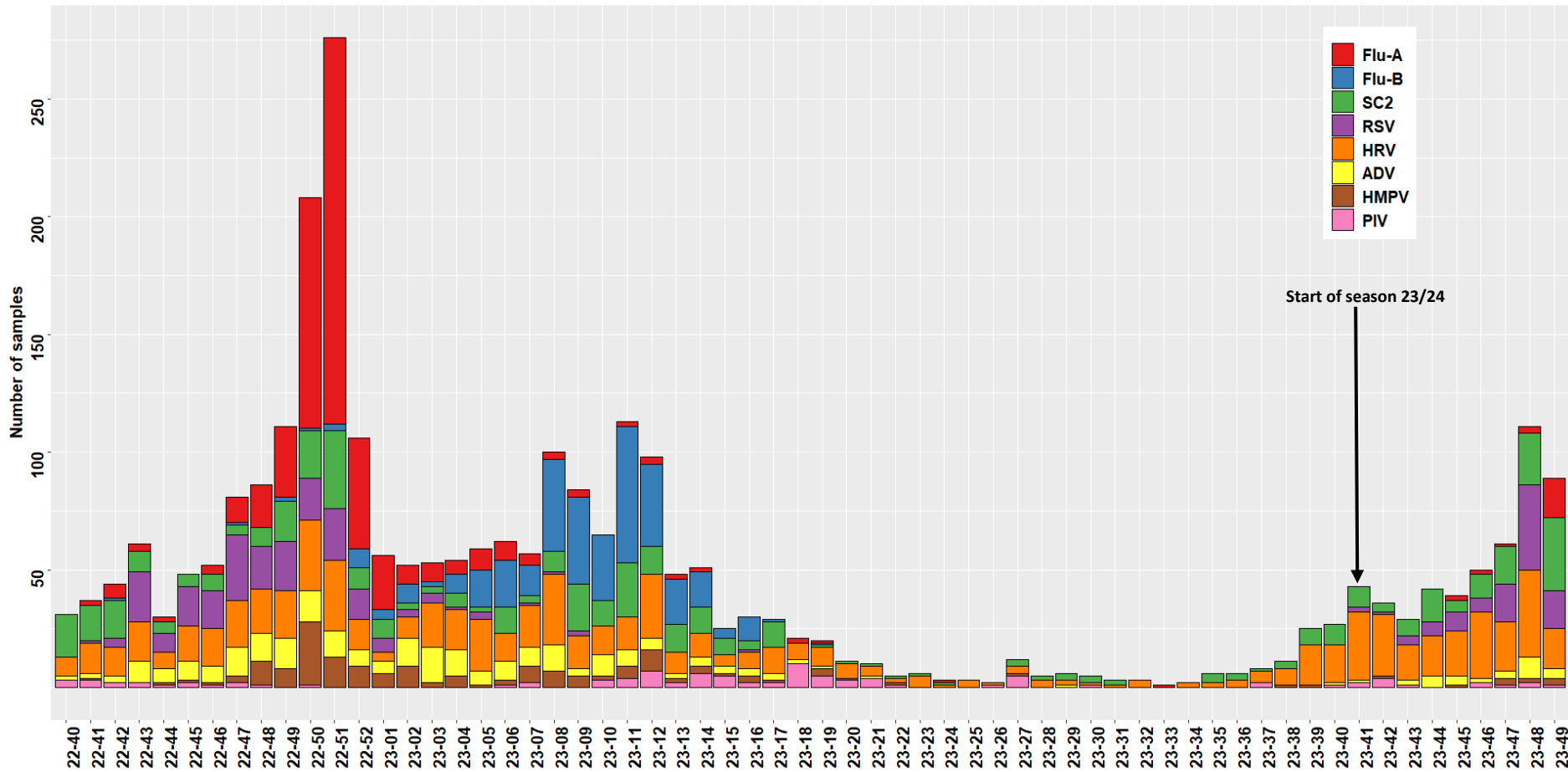


Figure 2. Distribution of respiratory viruses detected within the Sentinel Network, by calendar week. Results from last weeks are not yet consolidated.
 FLU-A: influenza A; FLU-B: influenza B; PIV: parainfluenzavirus; RSV: respiratory syncytial virus; ADV: adenovirus; MPV: metapneumovirus; HRV: human rhinovirus; SC2: SARS-CoV-2.

Table 2. Distribution of respiratory viruses detected within the Sentinel Network previous 4 weeks compared to previous year.

Virus	Season 2023/24				Trend	Season 2022/23
	Positivity Rate in %					w49
	w46	w47	w48	w49		
SARS-CoV-2	11.6	20.3	18.6	20.9	↑	13.2
Respiratory syncytial virus	7.1	20.5	30.8	17.0	→	16.9
Human rhinovirus	32.9	26.9	31.6	18.1	↓	16.1
Influenzavirus A	2.3	1.3	2.5	11.7	↑	23.3
Adenovirus	2.4	3.8	7.7	4.3	→	10.5
Metapneumovirus	0.0	3.8	1.7	3.2	↑	6.5
Parainfluenzavirus	2.4	1.3	1.7	1.1	↓	0.0
Influenzavirus B	0.0	0.0	0.0	0.0	→	1.6

*Co-detection counted once for each virus detected.

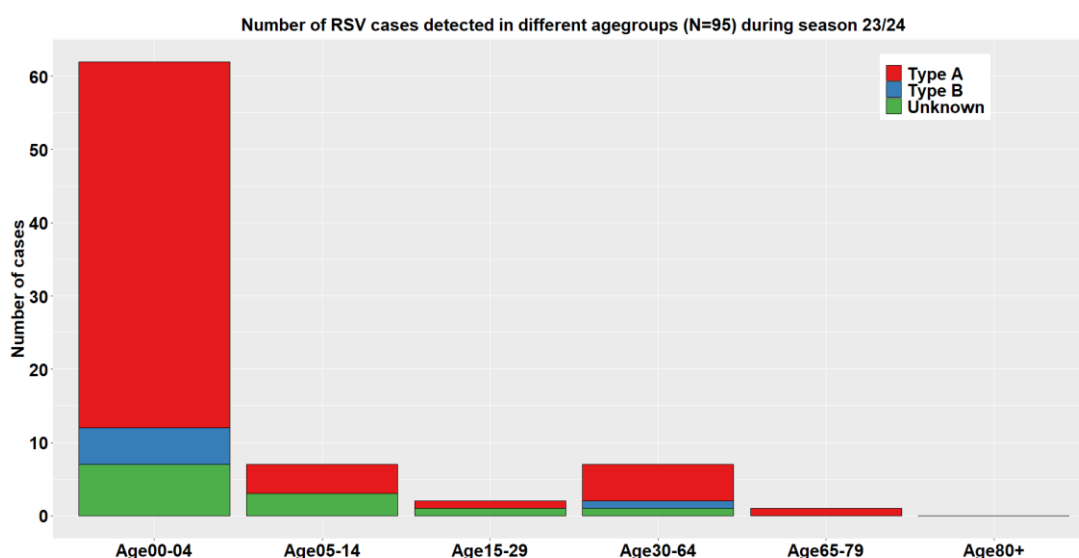


Figure 3. Displays RSV cases according to different age groups with highest impact among the 0-4 years old.

SARS-CoV-2 Genomic Surveillance

LNS receives positive specimens (nasopharyngeal or oropharyngeal swabs analysed by RT-PCR) from the national network of laboratories. A selection of hospital specimens are sequenced, as well as a representative selection of community specimens. Illumina and Nanopore devices are used.

Bioinformatic analyses are based on a standardised pipeline, and lineage assignment is performed through the PANGOLin software (4.3, pango-data 1.23, mode UShER). In order to allow easier visualisation, WHO and Nextstrain categorisations are also used.

Sequencing activity

246 samples from 1,493 cases (16.5%) reported in Luxembourg were sequenced with specimen dates between week 2023/44 and 2023/48. Approximately 66% were hospital samples and the remaining samples were community samples. Sequencing data probably does not fully represent virus circulation within the population.

Variant circulation

For samples sequenced between 13th November to 3rd of December 2023 (2023/46-48), the estimated distribution was 44 % for BA.2.86, 29.8% for XBB.1.9 and 10.5% for XBB.1.5. Since week 46, the most common variant is BA.2.86. Detections of JN.1 are grouped with BA.2.86. JN.1 is closely related to BA.2.86 with only one change in the spike protein, but rapidly growing with 60% of all BA.2.86 belonging to JN.1.

An overview of the variants and lineages circulating since beginning of 2023 is displayed in Figure 5, and further details are shown in Table 3. The history of the circulation of each variant since January 2021 is displayed in Figure 4.

Table 3. Distribution of SARS-CoV-2 lineages detected during weeks 2023/43 to 2023/48. Previously reported cases might be updated by retrospective analysis.

Lineage	weeks 43-45		weeks 46-48	
	%	CI %	%	CI %
BA.2.86	22.9	16.6 – 29.1	43.9	34.8 – 53.0
Recomb XBB.1.9	26.3	19.8 – 32.8	29.8	21.4 – 38.2
Recomb EG.5	18.3	12.6 – 24.0	5.3	1.1 – 9.4
Recomb XBB.1.16	8.6	4.4 – 12.7	3.5	0.1 – 6.7
Recomb XBB.1.5	8.6	4.4 – 12.7	10.5	4.9 – 16.1
Recomb XBB*	8.6	4.4 – 12.7	6.1	1.7 – 10.6
BA.2.75	6.9	3.1 – 10.6	0.9	0.0 – 2.3

**XBB excludes EG.5, XBB.1.16, XBB.1.5, XBB.1.16 and XBB.1.9 and XBB.1.9 excludes EG.5*

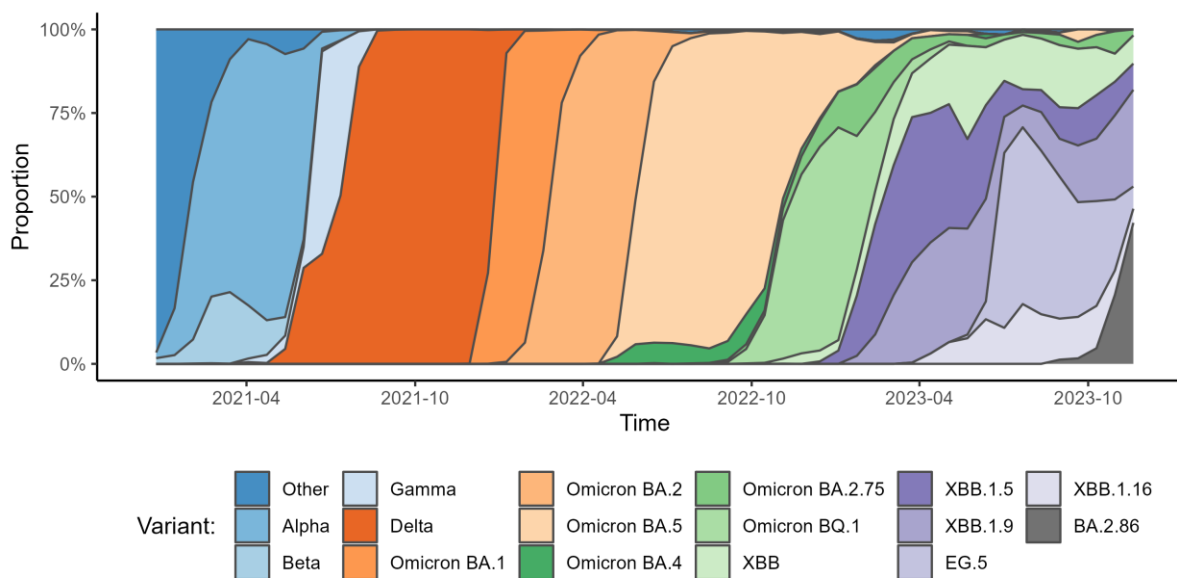


Figure 4. Proportion of each variant circulating in Luxembourg since January 2021. *XBB excludes EG.5, XBB.1.16, XBB.1.5, XBB.1.16 and XBB.1.9 and XBB.1.9 excludes EG.5

Clinical and epidemiological factors

Over the past 4 weeks, 126 (63.0%) samples from hospital laboratories and 74 (37.0%) samples from private laboratories/ sentinel practitioners were sequenced. Table 4 compares sampling setting of BA.2.86 and XBB.1.9 variants.

Table 4. Comparison of lineage distribution by sampling setting.

Lineage	Community			Hospital		
	Women	Men	Total	Women	Men	Total
BA.2.86	61.3%	55.0%	58.8%	50.9%	60.7%	54.3%
XBB.1.9	38.7%	45.0%	41.2%	49.1%	39.2%	45.7%
Total	100.0%	100.0%	100.0%	100.0%	100.0%	100.0%

* XBB.1.9 excludes EG.5

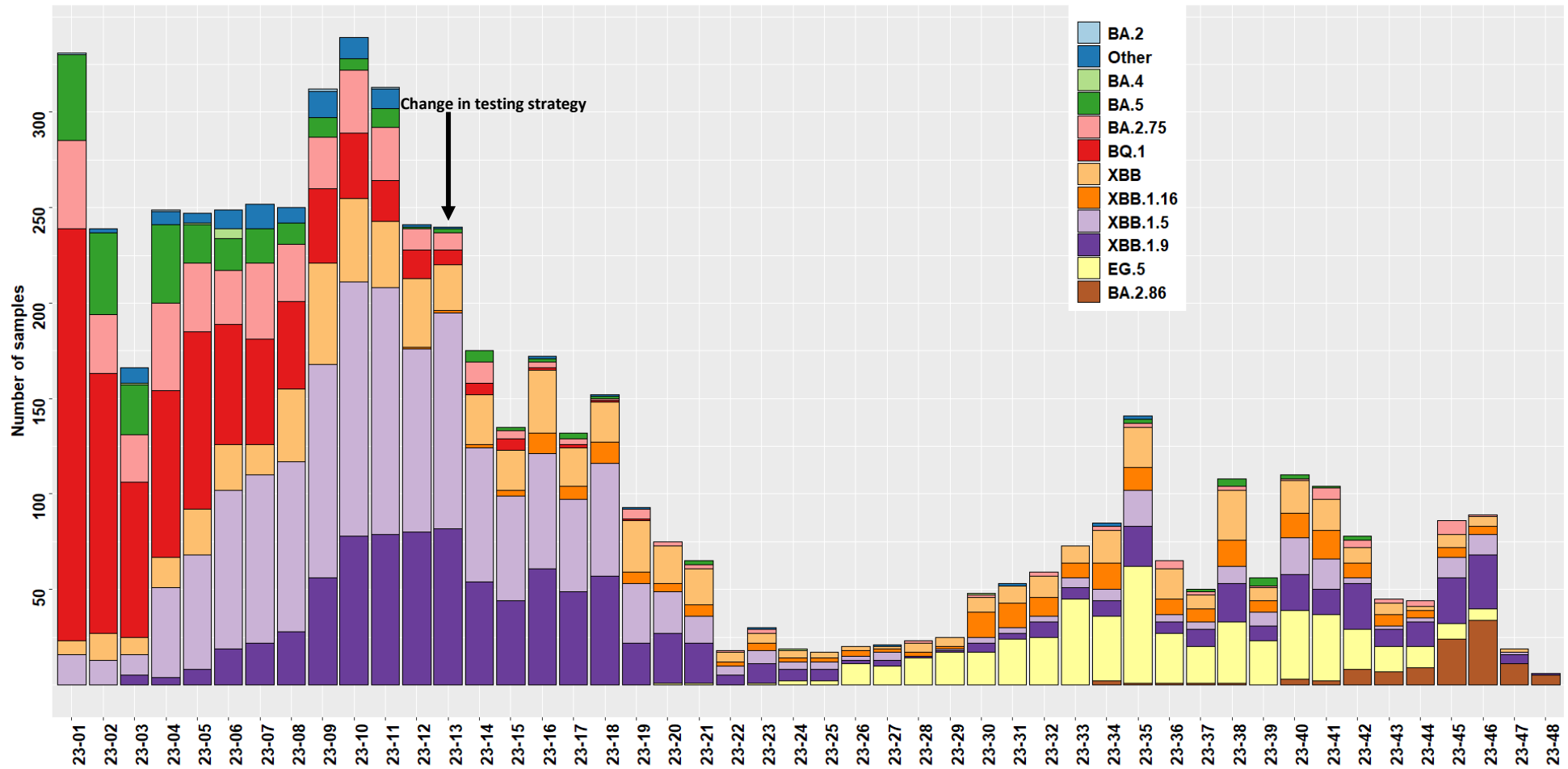


Figure 5. Distribution of lineages since beginning of 2023.
 *XBB excludes EG.5, XBB.1.16, XBB.1.5, XBB.1.16 and XBB.1.9 and XBB.1.9 excludes EG.5

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