Respiratory Viruses in Luxembourg (ReViLux)

Report – Sentinel Week 13 and Sequencing Update

Summary

At the end of week 2024/13, rates of influenza-like illness indicate decreasing trends and the sentinel network detected a baseline epidemic activity, based on 2.9% of consultations being associated with influenza-like illness. Among the specimens collected by the sentinel network over the last week, the percentage of positive tests for Human rhinovirus was 32.4%, 17.6% for Metapneumovirus and 17.6% for Parainfluenzavirus. Positivity for Influenzavirus A was less than 5%, RSV and SARS-CoV-2 positivity remained low over the past few weeks.

This season, 80% of Influenzavirus A strains have been subtyped. Among those A viruses subtyped (N=308) there was a mix of A(H1)pdm09 viruses with 90.6% and A (H3) 9.4% .

Overall during this season (23/24) the sentinel network detected 211 RSV cases with 73% of samples subtyped. Genotyping analyses showed that the most frequent RSV strain during this season is RSV-A (86.2%).

Regarding SARS-CoV-2 genomic surveillance, it is worth noting that since late February 2023 recombinant strains with combined characteristics of other variants have been dominant in Luxembourg. From week 2023/26 to week 2023/41, EG.5 was the most frequent detected variant. Since week 2023/43, the proportions of BA.2.86 and JN.1 (descendent of BA.2.86) have continued to increase and have been dominant since week 2023/47. The estimated distribution for JN.1 was 90.3% (95%CI: 80.1-96.4%), BA.2.86 was 6.5% (95%CI: 1.8-15.7%), and less than 5% for all other circulating variants for weeks 2024/07-2024/09. JN.1 was dominant in the selected community and hospital sample.

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 across 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, 2.9% of the consultations were reported as ILI, representing a baseline epidemic activity for Luxembourg, according to ECDC and the Moving Epidemic Method. Over the past six weeks downward trends in ILI rates have been observed. 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 Human rhinovirus (32.4%), followed by Metapneumovirus (17.6%) and Parainfluenza (17.6%). This season positivity rates of Influenza A peaked in week 2024/06 (52.7%). In week 2024/13 Influenza A positivity was at 2.8%, showing decreasing trends.

Three hundred and eight of 387 (80%) samples have been further characterized with 90.6% as A (H1)pdm09 and 9.4% as A (H3). Thirty samples from the sentinel network were genetically characterised with 13 (H1) samples reported as clade 5a.2a (A/Sydney/5/2021), 13 (H1) samples as subclade 5a.2a.1 (A/Victoria/4897/2022) and 4 (H3) samples as clade 2a.3a.1 (A/Thailand/8/2022). All of the genetically characterised clades belong to clades of the recommended vaccine components.

During week 2024/13, no cases of RSV cases were detected in the sentinel network so far. Overall, this season (23/24), the highest impact of RSV was seen among the 1-4 years age group (Figure3). To date, 153 RSV detections were further subtyped as either RSV A (N=132, 86.8%) or RSV B (N=21, 13.7%).

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SARS-CoV-2 positivity has decreased since the start of 2024, from 14.1% in week 2024/01 to 2.4% in week 2024/07. Over the past few weeks, SARS-CoV-2 activity has been very low within the sentinel network.
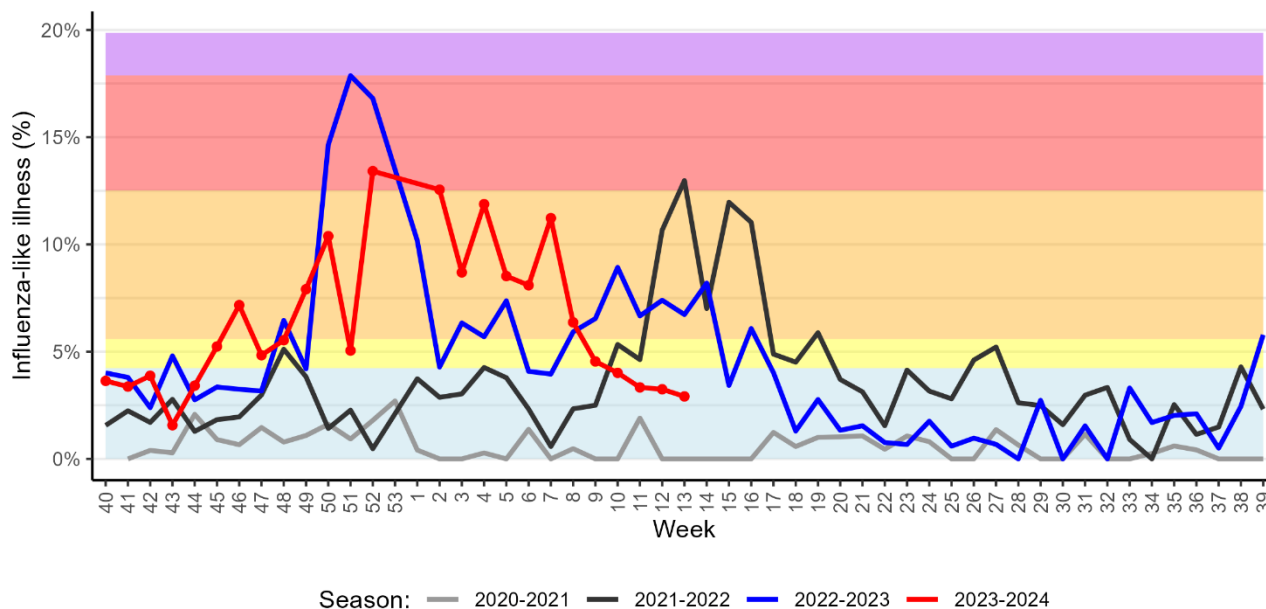

Figure 1. Percentage of patients with influenza-like illness over the last three seasons
Background colours according to intensity of circulation: baseline, low, medium, high, very high. Data from 2024/01 not presented as low return

Table 1. Syndromic surveillance over the last 4 weeks

Week	ARI		ILI		Total consultations
	N	%	N	%	
2024/10	65	20.06	13	4.01	324
2024/11	69	16.43	14	3.33	420
2024/12	91	19.70	15	3.25	462
2024/13	53	17.15	9	2.91	309

ARI: Acute Respiratory Infections; ILI: Influenza-Like Illness.
Data from 2024/01 not presented as low return

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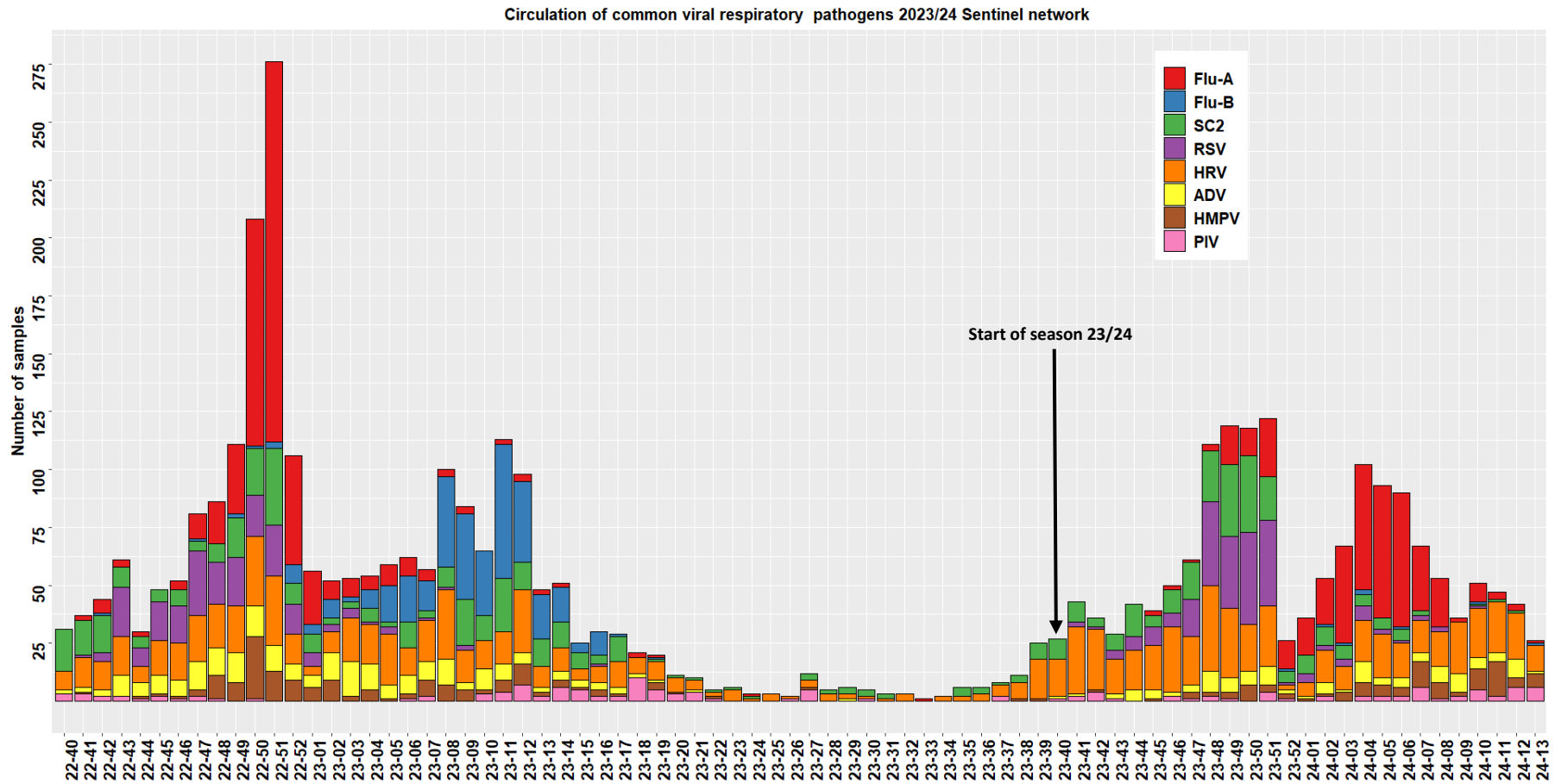
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Figure 2. Distribution of respiratory viruses detected within the Sentinel Network, by calendar week. Results from last weeks are not yet consolidated.
FLU-A: influenzavirus A; FLU-B: influenzavirus B; PIV: parainfluenzavirus; RSV: respiratory syncytial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

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

Virus	Season 2023/24					Season 2022/23
	Positivity Rate in %					
	w10	w11	w12	w13	Trend	w13
Human rhinovirus	30.9	37.3	41.7	32.4	→	14.5
Parainfluenzavirus	7.4	3.4	12.5	17.6	↑	3.2
Metapneumovirus	13.2	25.4	8.3	17.6	↑	3.2
Adenovirus	7.4	6.8	16.7	2.9	↑	3.2
Influenzavirus A	11.8	4.8	5.6	2.8	→	3.0
Respiratory syncytial virus	0.0	1.5	0.0	0.0		0.0
SARS-CoV-2	1.5	1.6	1.9	0.0		17.9
Influenzavirus B	1.5	0.0	0.0	2.8		28.4

*Co-detection counted once for each virus detected.

Figure 3. Displays RSV cases according to different age groups with highest impact among the 1-4 years old.
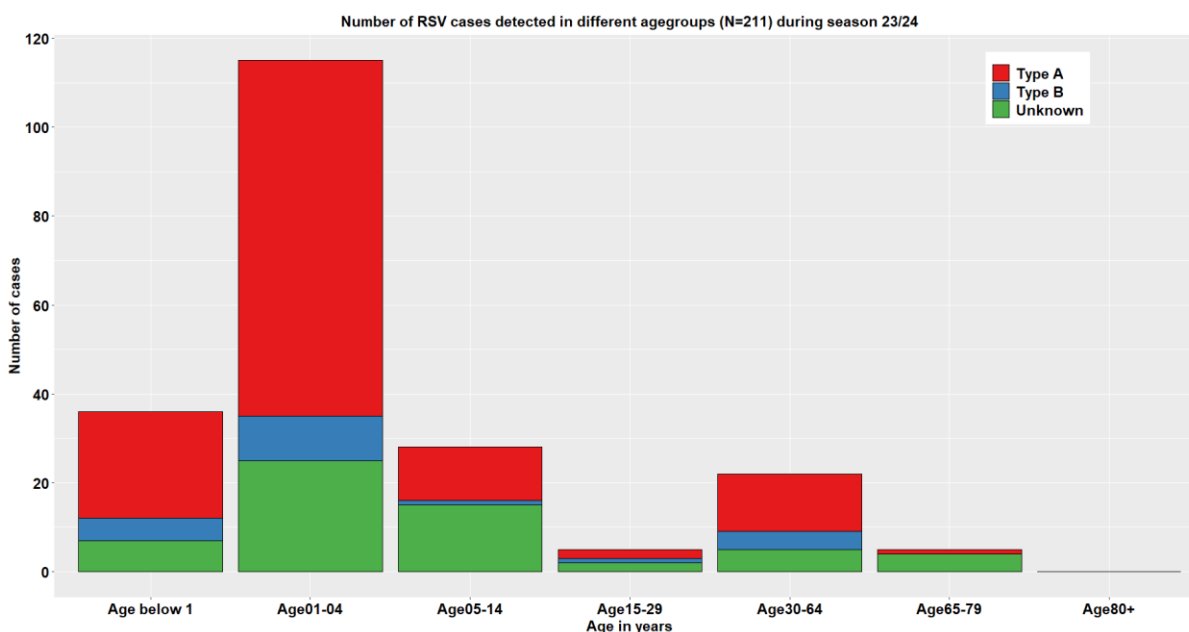
SARS-CoV-2 Genomic Surveillance

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.

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Bioinformatic analyses are based on a standardised pipeline, and lineage assignment is performed through the PANGOLin software (4.3.1, pango-data 1.25, mode UShER). In order to allow easier visualisation, WHO and Nextstrain categorisations are also used.

Sequencing activity

62 samples from 139 cases (44.6%) reported in Luxembourg were sequenced with specimen dates between week 2024/07 and 2024/09. Approximately 16.1% 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 12th February and 2nd of March 2024 (2023/07-2024/09), the estimated distribution was 90.3% (95%CI: 80.1-96.4%) for JN.1, 6.5% for BA.2.86 (95%CI: 1.8-15.7%) and less than 5.0% for all other variants. Since week 2023/48 the most common variant seen in Luxembourg is JN.1, a BA.2.86 sub-variant.

An overview of the variants and lineages circulating over the past 20 weeks 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 2024/04 to 2024/09. Previously reported cases might be updated by retrospective analysis.

Lineage	weeks 04-06		weeks 07-09	
	%	CI %	%	CI %
JN.1	**92.7**	**87.3 – 96.3**	**90.3**	**80.1 – 96.4**
BA.2.86	3.3	1.1 – 7.6	6.5	1.8 – 15.7
Other	2.0	0.0 – 5.7	3.2	0.4 – 11.2
Recomb XBB.1.9	1.3	0.0 – 4.7	0	0.0 – 0.0
Recomb XBB.1.16	0.7	0.0 – 3.6	0	0.0 – 0.0

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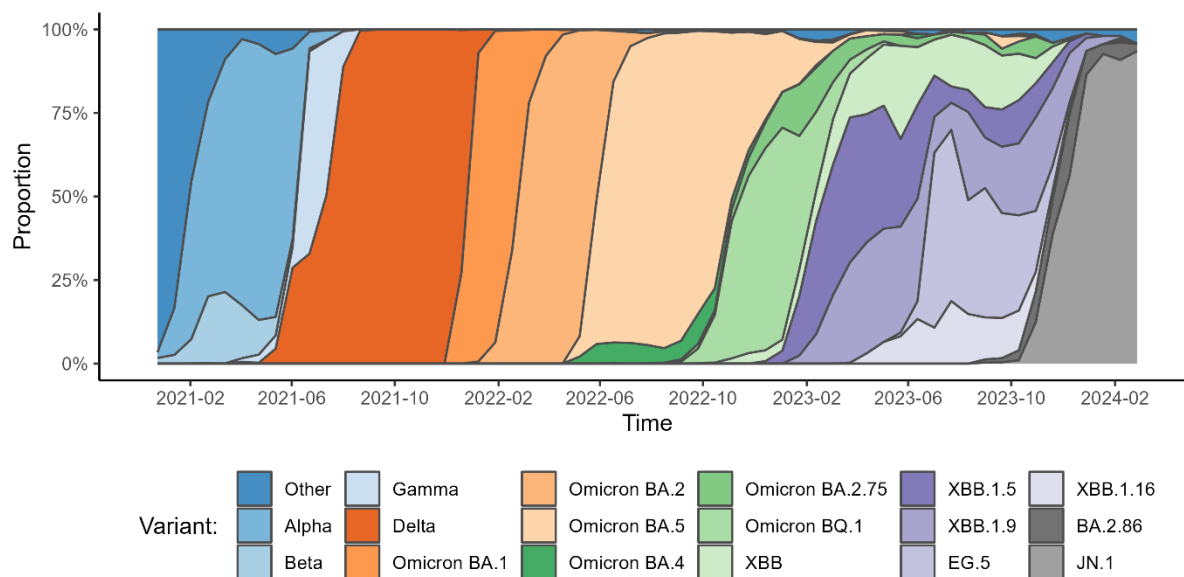
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Figure 4. Proportion of each variant circulating in Luxembourg since January 2021.
All displayed variants include descendant lineages, except those specified on the legend. For example, XBB does not include XBB.1.5, XBB.1.16, EG.5 and XBB.1.9

Clinical and epidemiological factors

Over the past 5 weeks (2024/05-2024/09), 37 (20.3%) samples from hospital laboratories and 145 (79.7%) samples from private laboratories/ sentinel practitioners were sequenced. Table 4 compares sampling setting of JN.1 (descendent lineage of BA.2.86) and BA.2.86 variants.

Table 4. Comparison of lineage distribution by sampling setting.

Lineage	Community			Hospital		
	Women	Men	**Total**	Women	Men	**Total**
JN.1	95.3%	98.2%	**95.7%**	95.2%	93.3%	**94.4%**
BA.2.86	4.7%	1.8%	**4.3%**	4.8%	6.7%	**5.6%**
Total	**100.0%**	**100.0%**	**100.0%**	**100.0%**	**100.0%**	**100.0%**

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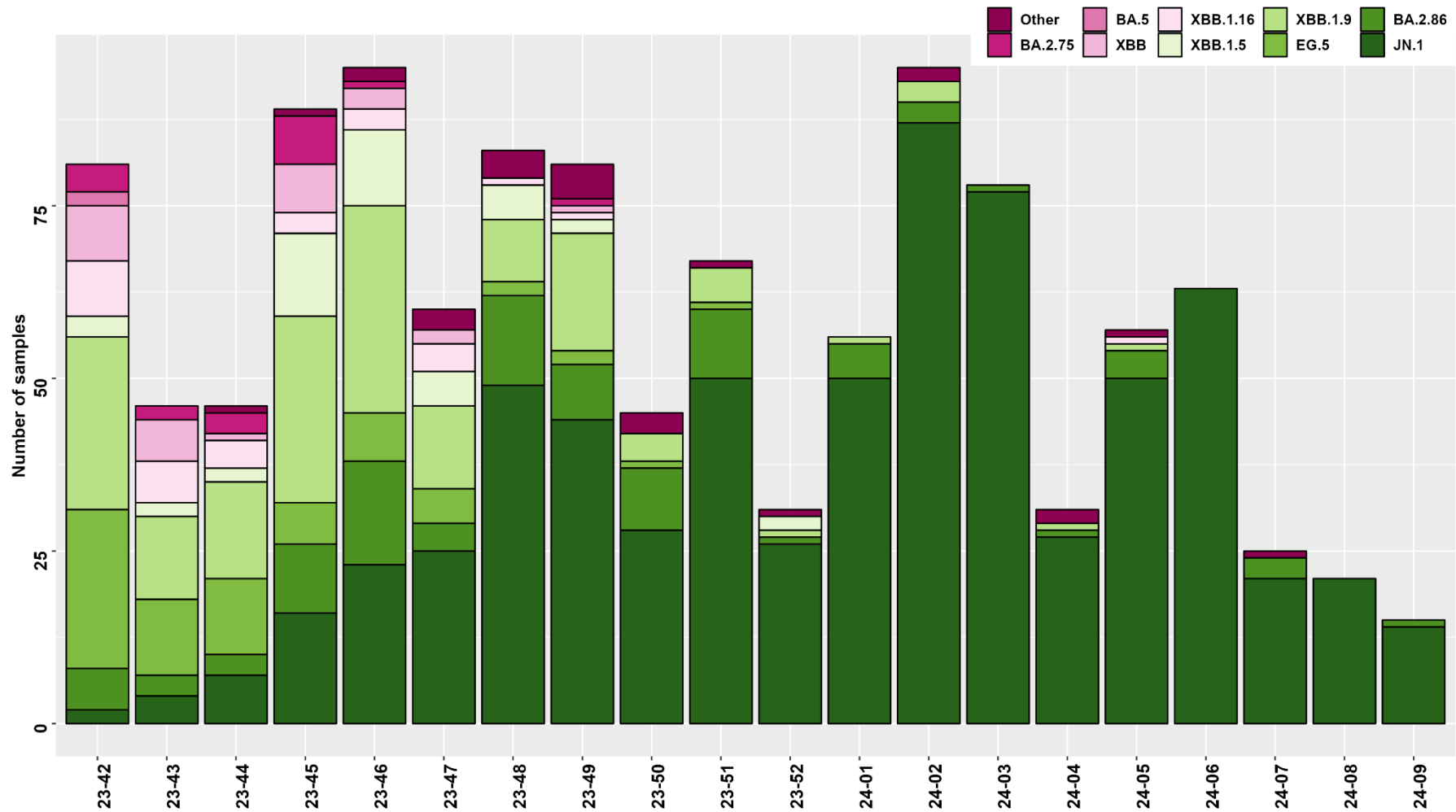
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Figure 5. Distribution of lineages since 2023/42(last 20 weeks).

* All displayed variants include descendant lineages, except those specified on the legend. For example, XBB does not include XBB.1.5, XBB.1.16, EG.5 and XBB.1.9

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