LNS
LUXEMBOURG

Respiratory Viruses in Luxembourg (ReViLux)

Report – Sentinel Week 08 and Sequencing Update

Summary

At the end of week **2025/08**, the sentinel network detected a medium epidemic activity with a downward trend, based on **13.7%** 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 **Influenza B** was **33.8%**, **17.3%** for **Human rhinovirus, 12.8 %** for **Influenza A** and **7.5 %** for **RSV**.

During the week 2025/08, Influenza B activity remained above 30% increased, Influenza A decreased to below 15% and RSV activity remained below 10%.

In total, this season (24/25) 2,170 samples were tested with 755 Influenza positive samples (330 Influenza B and 425 Influenza A). Hundred seventy two (44.1%) Influenza A samples have been subtyped as A(H1)pdm09 and 218 (55.9%) as A(H3) virus. Among those RSV subtyped (N=218, 85.5%), there was a mixture of RSV- A (43.6%) and RSV-B (56.4%).

Regarding SARS-CoV-2 genomic surveillance in Luxembourg, since beginning of April 2024, several sub-variants of JN.1 have been circulating in Luxembourg. The estimated distribution for **XEC** was **47.7%** (95%CI: 53.9-74.7%), **22.1%** (95%CI: 11.7-29.1%) for **KP.3, 11.6** (95%CI: 5.7-20.4%) for **LB.1** and **7.0%** for **LP.8.1** during the weeks 2025/03-2025/05.

Currently circulating variants under monitoring

Sub-variant	Genetic features	First detected in Luxembourg	Estimated prevalence (2025/03-2025/05)
JN.1*	BA.2.86 + S:L455S	25.08.2023	7.0%
KP.3	JN.1 + S:F456L, S:Q493E, S:V1104L	03.04.2024	22.1%
KP.2	JN.1 + S:R346T, S:F456L, S:V1104L	08.04.2024	0.0%
JN.1.18	JN.1 + S:R346T	10.01.2024	0.0%
LB.1	JN.1+ S:S31-, S:Q183H, S:R346T, S:F456L	22.05.2024	11.6%
XEC	JN.1 + S:T22N, S:F59S, S:F456L, S:Q493E, S:V1104L	19.07.2024	47.7%
LP.8.1	JN1 + S:S31-, S:F186L, S:R190S, S:R346T, S:V445R, S:F456L, S:Q493E, S:K1086R, S:V1104L	05.11.2024	7.0%

**JN.1 excludes sub-variants listed in table*

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 (**end of week 2025/08**), **13.7%** of the consultations were reported as ILI, representing a medium epidemic activity for Luxembourg, according to ECDC and the Moving Epidemic Method. Over the last two weeks medium ILI rates have been observed, with a decreasing trend. 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.

Table 1. Syndromic surveillance over the last 4 weeks

Week	ARI		ILI		Total consultations
	N	%	N	%	
2025/05	85	15.57	116	21.25	546
2025/06	84	15.36	114	20.84	547
2025/07	102	18.61	87	15.88	548
2025/08	70	19.94	48	13.68	351

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

Laboratory results

Over the last week, the most frequently detected viruses (according to positivity rates) were **Influenzavirus B (33.8%)**, **Human rhinovirus (17.3%)** and **Influenzavirus A (12.8%).** In week 2025/08, **RSV** positivity was **7.5%** and **SARS-CoV-2** positivity was **1.5%** in the sentinel network. Influenzavirus B activity remained high at 33.8% and Influenzavirus A activity decreased from 26.2% to 12.8% compared to week previous week. Overall, 425 Influenza A and 330 Influenza

B cases have been detected during this season. Around 92% of the samples were subtyped with 44.1% A(H1)pdm9 and 55.9% as A(H3).

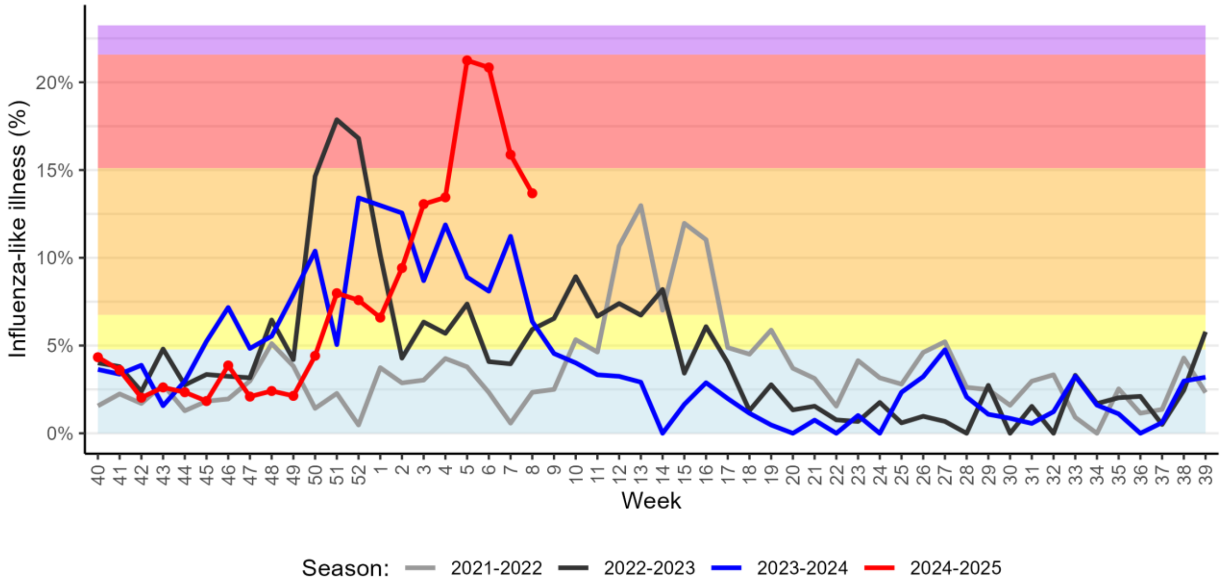


Figure 1. Percentage of patients with influenza-like illness over the last three seasons
Background colours according to intensity of circulation: baseline, low, medium, high, very high.

RSV activity continued to decline slightly from 9.7% (2025/07) to 7.5% (week 2025/08). Over the past 4 weeks RSV activity was below 10%. So far this season (24/25), two hundred and fifty five RSV cases have been detected, including 95 (43.6%) RSV-A and 123 (56.4%) RSV-B. Approximately 71% (N=181) of cases were under 5 years old (Figure 2).

In total, 2,170 sentinel samples have been analysed with about 60% of samples belonging to age-group below 18 years (Figure 3) and with 52% of female cases. Over the last 2 weeks, Human rhinovirus, Influenza A and Influenza B were detected in all age-groups, whereas Adenovirus and Parainfluenza viruses have been primarily detected in children under the age of 5. Human metapneumovirus continues to circulate at low levels (below 5%), primarily in children.

Over the last 2 weeks, approximately 70% (N=28) of all co-infections (N=40) were detected primarily in children below 5 years. The most commonly identified combination was Adenovirus and Human rhinovirus, followed by Human rhinovirus and Influenzavirus B.

An overview of the circulating viral pathogens during the current and previous inter- season is displayed in Figure 5 and Table 2.

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

Virus	Season 2024/25					Season 2023/24	
	Positivity Rate in %						
	W05	**W06**	**W07**	**W08**	**Total N (%)**	**W08**	**Total N (%)**
Influenzavirus B	29.3	31.6	30.6	33.8	330 (15.2)	0.0	12 (0.5)
Human rhinovirus	11.5	13.3	12.6	17.3	521 (24.2)	18.3	572 (24.9)
Influenzavirus A	35.1	23.1	26.2	12.8	425 (19.6)	25.3	388 (16.5)
Respiratory syncytial virus	7.7	6.7	9.7	7.5	255 (11.8)	2.4	212 (9.2)
Adenovirus	2.4	3.6	4.9	6.8	132 (6.1)	8.5	125 (5.4)
Metapneumovirus	6.3	4.9	3.7	3.0	65 (3.0)	8.5	125 (5.4)
SARS-CoV-2	1.9	1.3	0.8	1.5	68 (2.9)	0.0	227 (9.7)
Parainfluenzavirus	0.0	0.9	0.4	0.8	62 (2.9)	1.2	77 (3.4)

**Co-detection counted once for each virus detected. All data is provisional as possibility of reporting delays.*

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

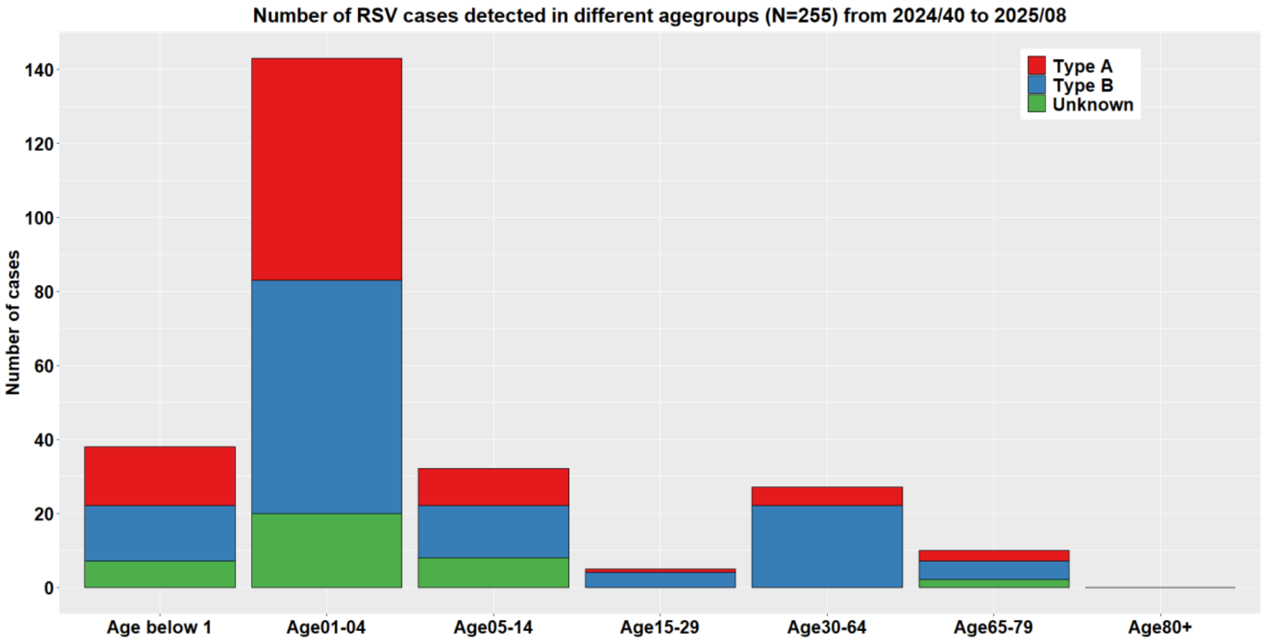


Figure 3. Displays number of sentinel samples received per week by age-group including overall sample positivity including Human rhinovirus (HRV, dotted line), excluding HRV (black line) and Influenza (red). Secondary axis corresponds to positivity

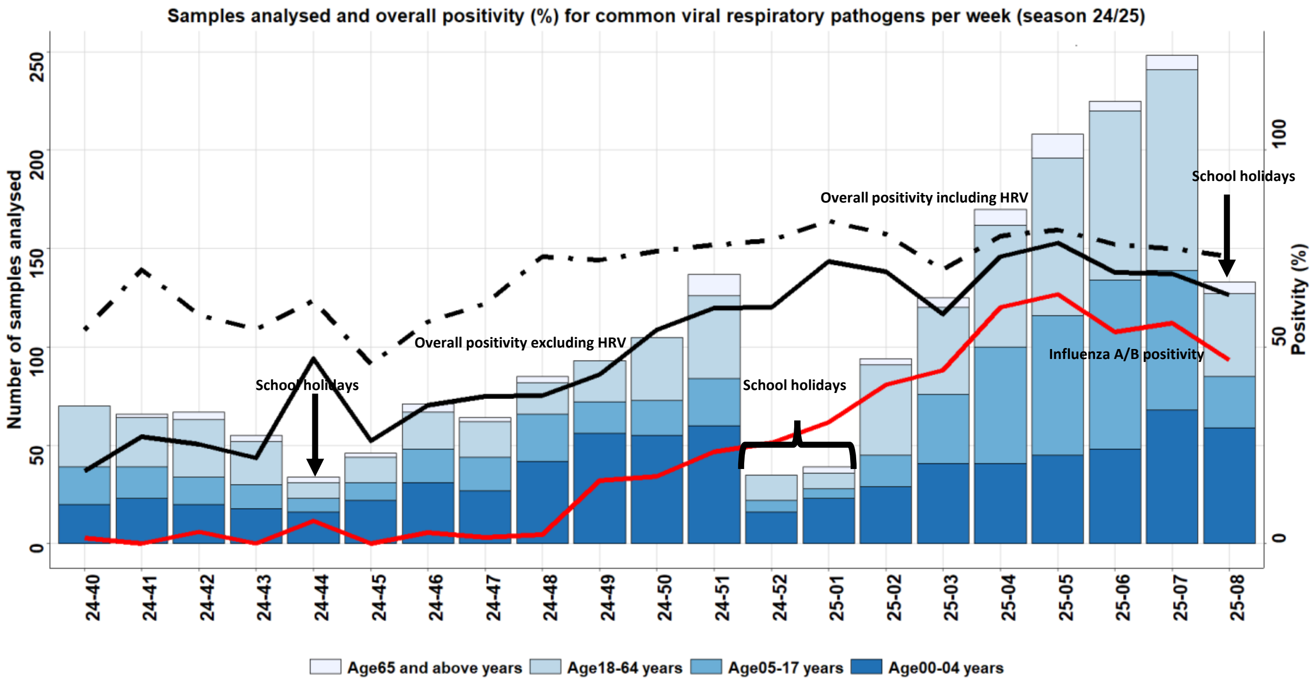
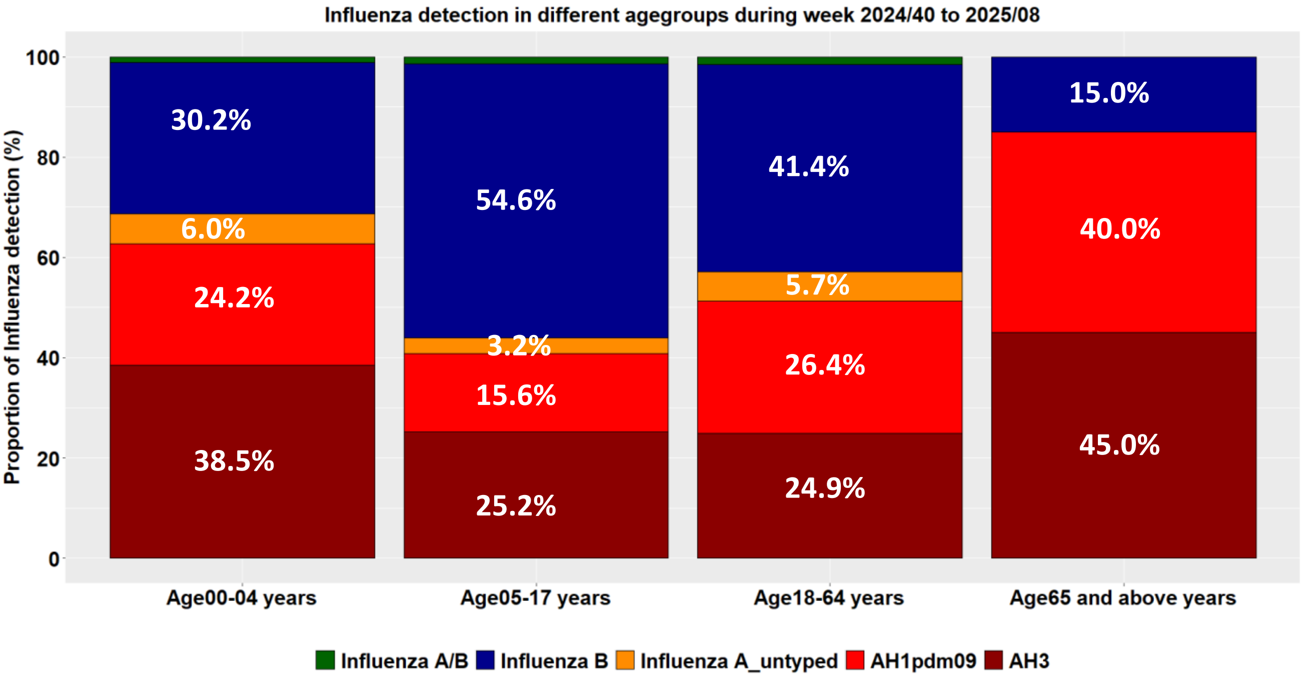


Figure 4. Displays detection of Influenza subtypes by age-group. Data for week 2025/08 not yet completely consolidated.



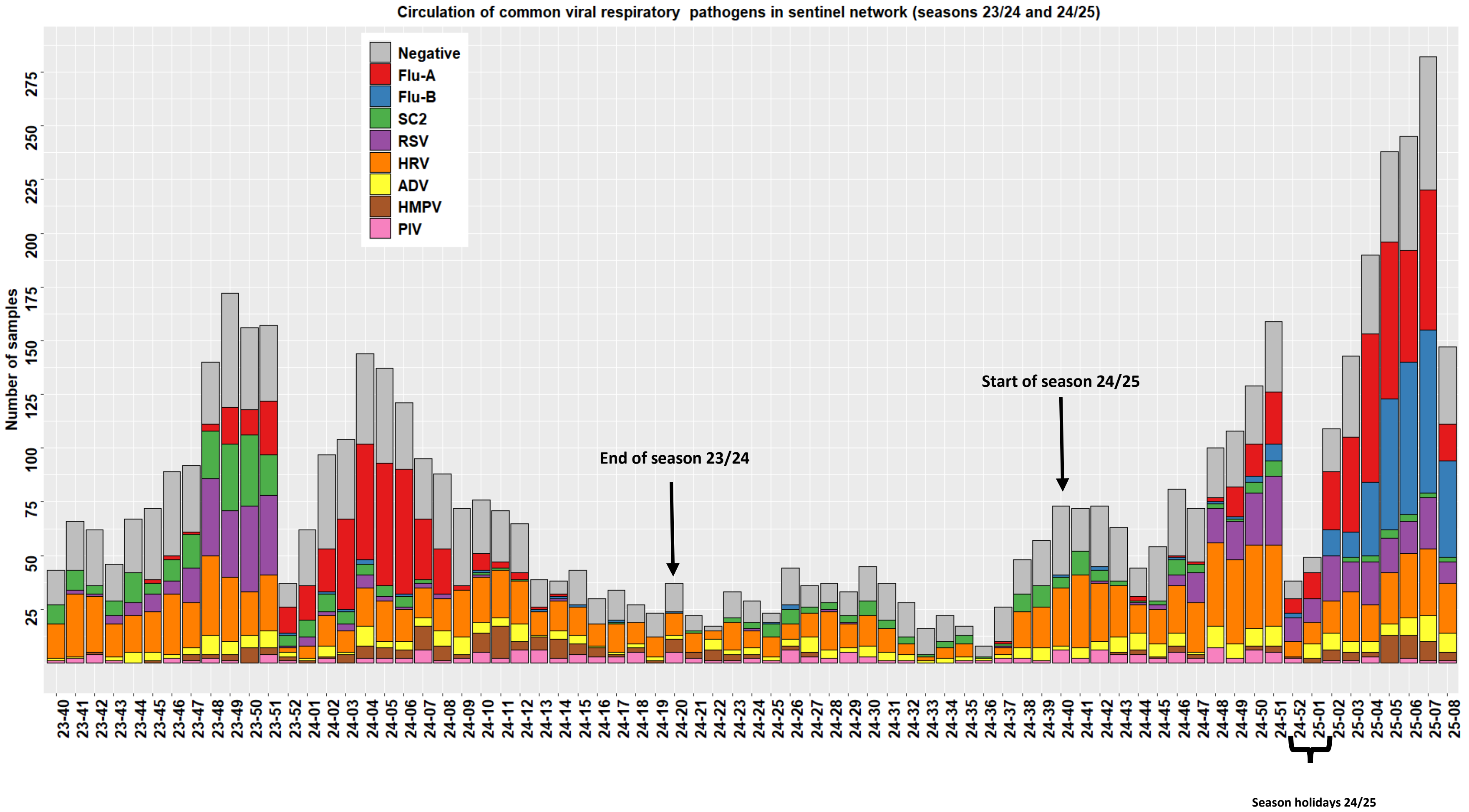


Figure 5. Distribution of respiratory viruses detected within the Sentinel Network, by calendar week. Results from last week are not yet consolidated.
FLU-A: influenzavirus A; FLU-B: influenzavirus B; PIV: parainfluenzavirus; RSV: respiratory syncytial virus; ADV: adenovirus; MPV: metapneumovirus; HRV: human rhinovirus; SC2: SARS-CoV-2

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 devices are used. Bioinformatic analyses are based on a standardised pipeline, and lineage assignment is performed through the Pangolin software (4.3.1, pango-data 1.32, mode UShER).

Sequencing activity

86 samples from 225 cases (38.2%) reported in Luxembourg were sequenced with specimen dates between week 2025/03 and 2025/05. Approximately 33% were hospital samples and the remaining samples were community samples (67%).

Variant circulation

For samples sequenced between 13th January and 2nd of February 2025 (2025/03-2025/05), the estimated distribution was **47.7%** (95%CI: 36.8 – 58.7%) for **XEC** (recombinant of JN.1 sub-variants), **22.1%** for **KP.3** (95%CI: 13.9 - 32.3%), **11.6%** (95%CI: 5.7-20.4%) and **7.0%** (95%CI: 2.6-14.6%) for **LP.8.1**.

LP.8.1 (derived from KP.1.1.3) is one of the new SARS-CoV-2 variant under monitoring by the World Health Organisation with increasing prevalence globally and was first detected in Luxembourg in November 2024.

Low circulation of other recombinant lineages such as XEP and XEK has been detected in recent weeks. An overview of the variants and lineages circulating is displayed in Figure 7. The history of the circulation of each variant since January 2021 is displayed in Figure 6.

During weeks 2025/02 to 2025/05, 36 (27.2%) samples from hospital laboratories and 96 (72.7%) samples from private laboratories/ sentinel practitioners were sequenced. Table 4 compares sampling setting and variants.

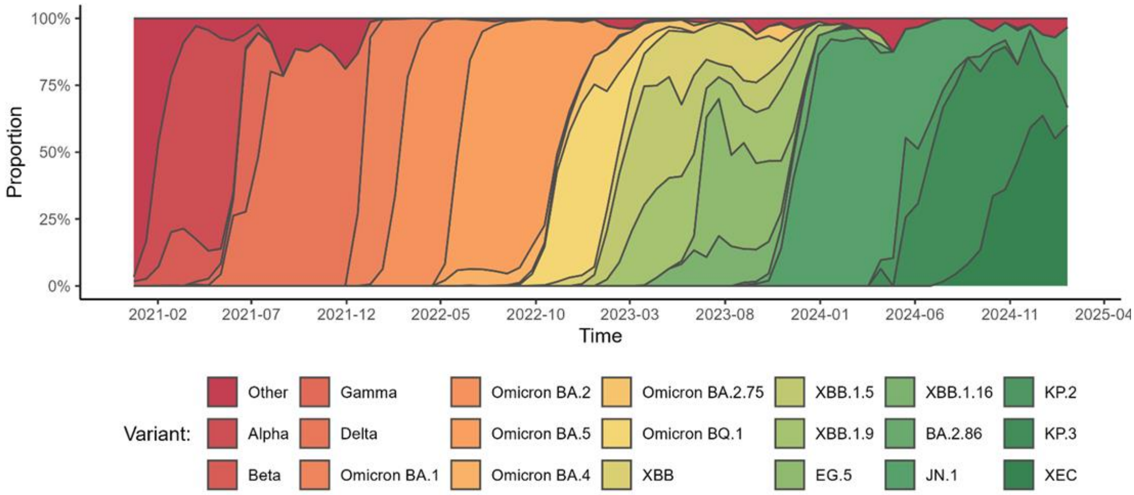
Table 3. Distribution of SARS-CoV-2 lineages detected during weeks 2024/52 to 2025/05. Previously reported cases might be updated by retrospective analysis.

Lineage	weeks 52-02		weeks 03-05	
	%	CI %	%	CI %
XEC	**65.8**	**56.2 – 74.5**	**47.7**	**36.8 – 58.7**
KP.3	17.1	10.6 – 25.4	22.1	13.9 – 32.3
LB.1	2.7	0.6 – 7.7	11.6	5.7 – 20.4
LP.8.1	**3.6**	**0.9 – 9.0**	**7.0**	**2.6 – 14.6**
JN.1	4.5	1.5 – 10.2	7.0	2.6 – 14.6
XEK	6.3	2.6 – 12.6	2.3	0.2 – 8.2
Other	0.0		2.3	0.3 – 8.2

Table 4. Comparison of lineage distribution by sampling setting (weeks 2025/02-2025/04).

Lineage	Community			Hospital		
	Women	Men	**Total**	Women	Men	**Total**
KP.3	17.8%	19.0%	**18.1%**	52.4%	44.4%	**48.4%**
XEC	82.2%	81.0%	**81.8%**	47.6%	55.6%	**51.6%**
Total	**100.0%**	**100.0%**	**100.0%**	**100.0%**	**100.0%**	**100.0%**

Figure 6. Proportion of each variant circulating in Luxembourg since January 2021. All displayed variants include descendant lineages, except those specified on the legend



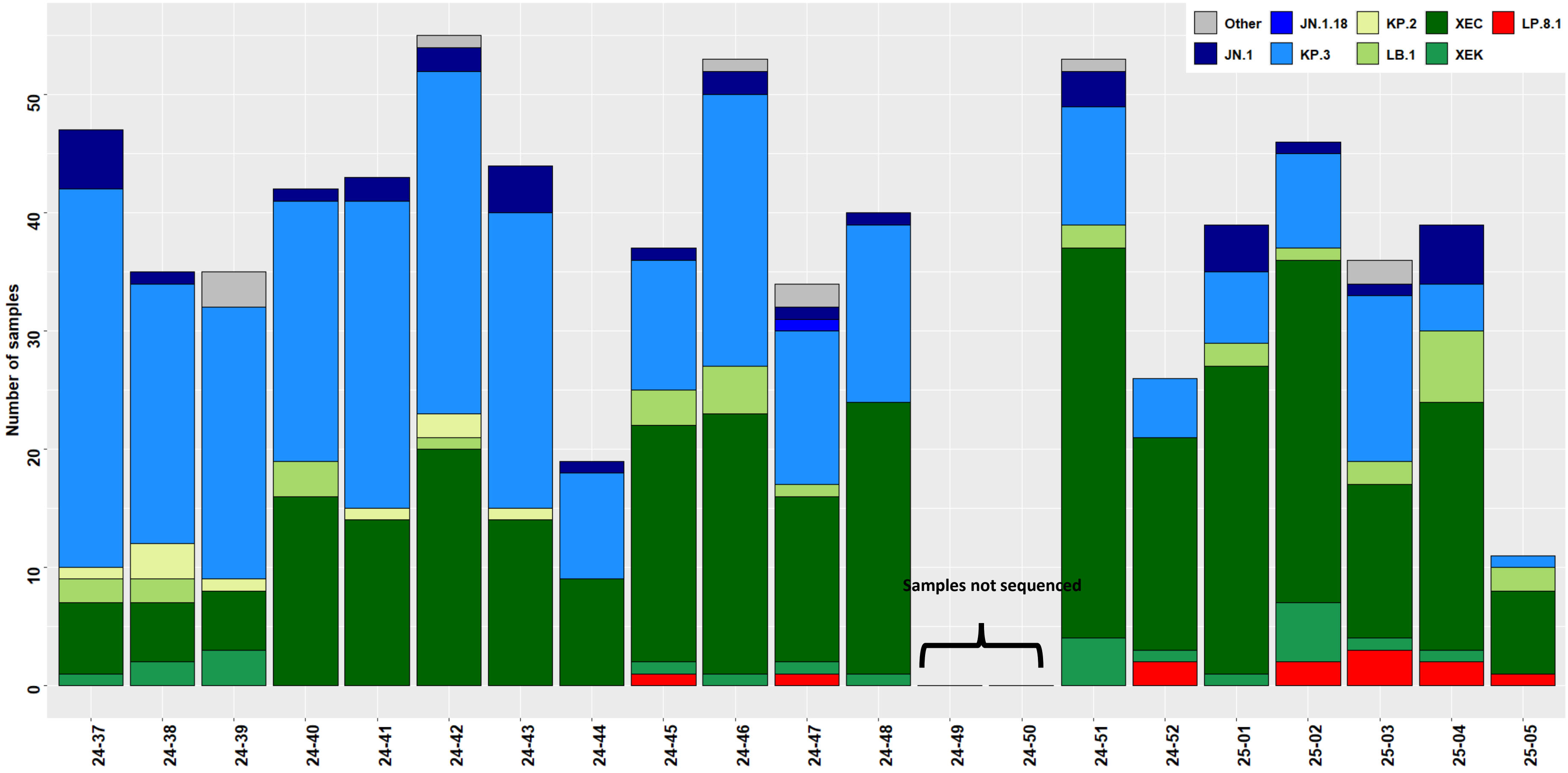


Figure 7. Distribution of lineages since 2024/37 (last 20 weeks).
All displayed variants include descendant lineages, except those specified on the legend, other: recombinant lineages (eg: XEP, XEU), data are not available for weeks 2024/49 and 2024/50 as priority given to sequence more recent samples

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