Respiratory Viruses in Luxembourg (ReViLux)

Report – Sentinel Week 24 and Sequencing Update

Summary

Over the past three weeks (2025/22-24), the sentinel network detected a baseline activity, based on **less than 2%** of consultations being associated with influenza-like illness. Among the specimens collected by the sentinel network over the past two weeks, the percentage of positive tests for **Human rhinovirus** was **36.0%**, **16.0%** for **Parainfluenza** and **12.0%** for **Adenovirus**, while **SARS-CoV-2** activity increased to **9.8%**.

Regarding SARS-CoV-2 genomic surveillance, several sub-lineages and recombinant lineages of JN.1 circulate in Luxembourg and globally.
The estimated distribution for **LP.8.1** was **23.4%** (95%CI: 13.9 – 32.8%), **16.9%** (95%CI: 8.5 – 25.3%) for **NB.1.8.1** and **3.9%** (95%CI: 0.0 – 8.2%) for **XEC**. Other sub-lineages not classified as variant under monitoring have emerged with **19.5%** (95%CI: 10.6– 28.3%) for **LF.7.9** and **7.8**% (95%CI: 1.8– 13.8%) for **XFG**.

Currently circulating variants under monitoring

Sub-variant	Genetic features	First detected in Luxembourg	Estimated prevalence (2025/19-2025/22)
JN.1*	BA.2.86 + S:L455S	25.08.2023	0
KP.3	JN.1 + S:F456L, S:Q493E, S:V1104L	03.04.2024	1.3%
LB.1	JN.1+ S:S31-, S:Q183H, S:R346T, S:F456L	22.05.2024	1.3%
XEC	JN.1 + S:T22N, S:F59S, S:F456L, S:Q493E, S:V1104L	19.07.2024	3.9%
LP.8.1	JN.1 + S:S31-, S:F186L, S:R190S, S:R346T, S:V445R, S:F456L, S:Q493E, S:K1086R, S:V1104L	05.11.2024	23.4%
NB.1.8.1	JN.1 + S:T22N, S:F59S, S:G184S,S:A435S, S:F456L, S:T478I, S:Q493E	07.04.2025	16.9%

**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 called inter-season.

Clinical results

Last week **(end of week 2025/24)**, **1.2%** of the consultations were reported as ILI, representing a baseline activity for Luxembourg, according to ECDC and the Moving Epidemic Method. During week 2025/21 ILI rates increased to 5.5%, indicating low activity, but have since then returned to baseline. 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	%	
2025/21	14	9.66	8	5.52	145
2025/22	19	20.65	0	0.00	92
2025/23	15	10.42	3	2.08	144
2025/24	12	14.81	1	1.23	81

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

Laboratory results

From week 2025/23 to week 2025/24, respiratory viruses were identified in a total of 49 samples (80.3%) of the 61 sentinel samples sent to LNS. **Human rhinovirus (36.0%)** was the most prevalent virus circulating, followed by **Parainfluenza (16.0%)** and **Adenovirus (12.0%)**.

In the last two weeks (2025/23-24), SARS-CoV-2 activity increased from 6.6 % to just below 10% compared to weeks 2025/21-22, indicating increased activity in the network. The majority of cases (66.7%) were detected in patients aged between the ages of 18 and 64.

Overall, during the inter-season no new RSV cases were detected in the network, but low influenza A activity was observed (2%; weeks 2025/23-24). An overview of the submitted samples, circulating viral pathogens during the inter-season and previous inter-season can be found in table 2, figure 2 and figure 3.

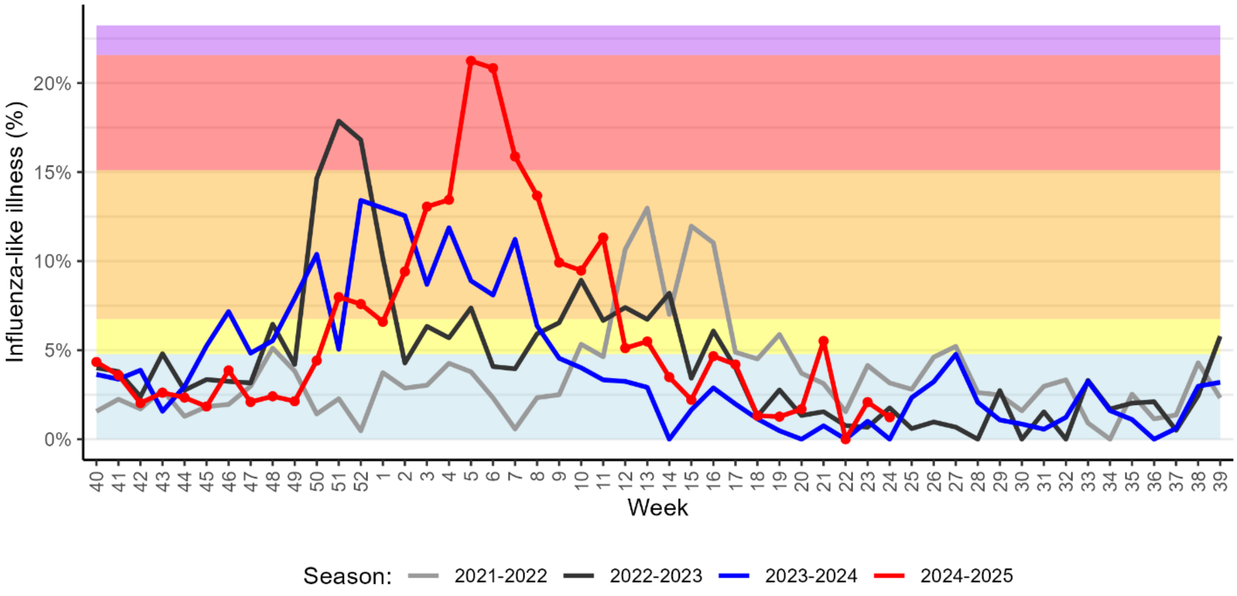


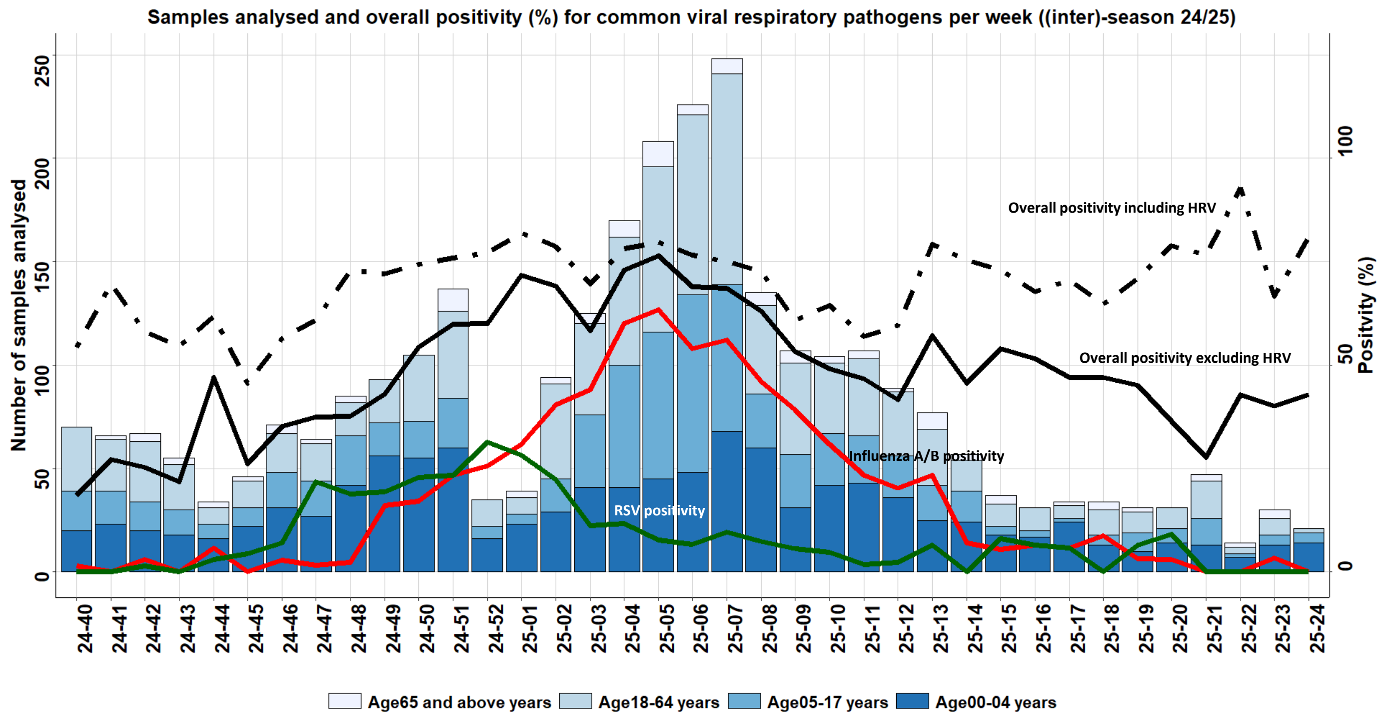
Figure 1. Percentage of patients with influenza-like illness over the last three seasons
Background colours according to intensity of circulation: baseline, low, medium, high, very high.

Table 2. Distribution of respiratory viruses detected in the Sentinel Network over the last 8 weeks compared to the previous year.

Virus	(Inter) Season 2024/25				Inter-season 2023/24	
	Positivity Rate in %					
	W17/18	**W19/20**	**W21/22**	**W23/24**	**W21/22**	**W23/24**
Human rhinovirus	30.9	46.9	52.5	36.0	38.2	39.6
Parainfluenzavirus	11.8	10.9	9.8	16.0	8.8	5.7
Adenovirus	13.2	7.8	1.6	12.0	14.7	9.4
SARS-CoV-2	4.4	4.7	6.6	9.8	2.9	9.1
Metapneumovirus	11.8	10.9	14.8	2.0	23.5	9.4
Influenzavirus A	2.9	0.0	0.0	2.0	0.0	0.0
Respiratory syncytial virus	2.9	7.8	0.0	0.0	0.0	1.9
Influenzavirus B	4.4	3.1	0.0	0.0	0.0	0.0

**Co-detection is counted once for each virus detected. Data is displayed in two-week intervals due to low case count during inter-season. All data is provisional, taking into account possible*

Figure 2. Displays number of sentinel samples received weekly by age-group, including overall positivity of the samples: including Human rhinovirus (HRV, dotted line), excluding HRV (black line), Influenza (red) and RSV (green). Secondary axis corresponds to positivity



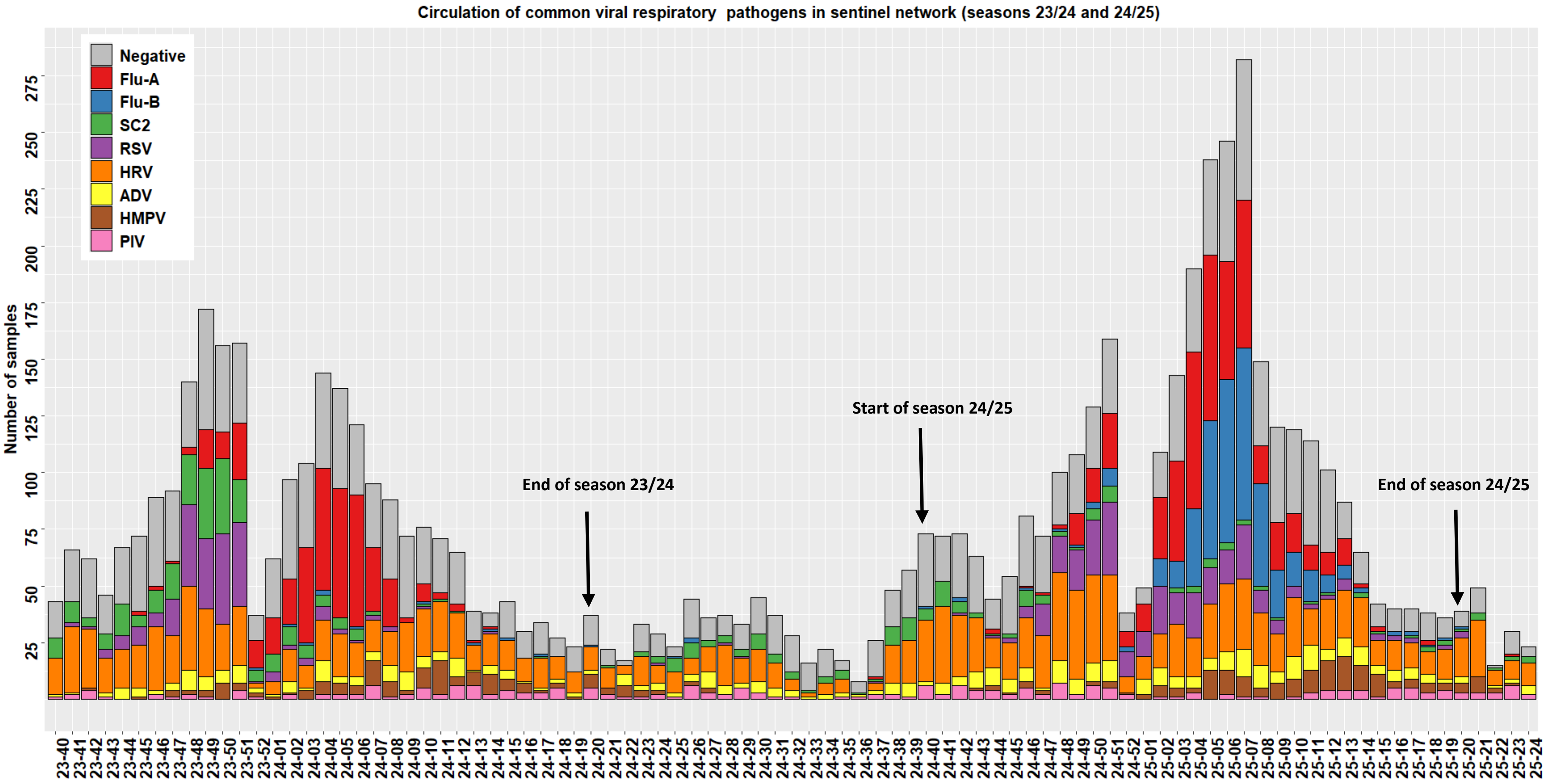


Figure 3. Distribution of respiratory viruses detected within the Sentinel Network, by calendar week. Results from last week are not yet consolidated. FLU-A: influenzavirus A; FLU-B: influenzavirus B; PIV: parainfluenzavirus; RSV: respiratory syncytial virus; ADV: adenovirus; MPV: metapneumovirus; HRV: 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 1.34, mode UShER).

Sequencing activity

77 samples from 197 cases (39.0%) reported in Luxembourg were sequenced with specimen dates between week 2025/19 and 2025/22. About half (48.1%) were hospital samples and the remaining samples were community samples (51.9%). As SARS-CoV-2 activity increased and new variants emerged, we prioritized sequencing the most recent samples. Any low coverage will be addressed in future sequencing runs.

Variant circulation

In recent weeks, several SARS-CoV-2 variants have co-circulated in Luxembourg and worldwide. Since May 2025, the number of reported SARS-CoV-2 cases has increased. New variants such as NB.1.8.1, XFG and LF.7.9 have emerged and exhibit a growth advantage over other sub-lineages from JN.1.

NB.1.8.1 (derived from the recombinant variant XDV.1.5.1) is one of the new SARS-CoV-2 variant under monitoring (VUM) by the World Health Organisation with increasing prevalence globally and was first detected in Luxembourg in April 2025. The prevalence of **NB.1.8.1** in Luxembourg increased from **6.9%** (weeks 2025/15-18) to **16.9%** (weeks 2025/19-22) in the selected sample.

Since January 2025, **LP.8.1** has been classified as VUM, but the prevalence declined over the past four weeks from 31.9% (weeks 2025/15-18) to **23.4%** (weeks 2025/19-22). In addition the prevalence of XEC (also VUM) decreased to below 5%.

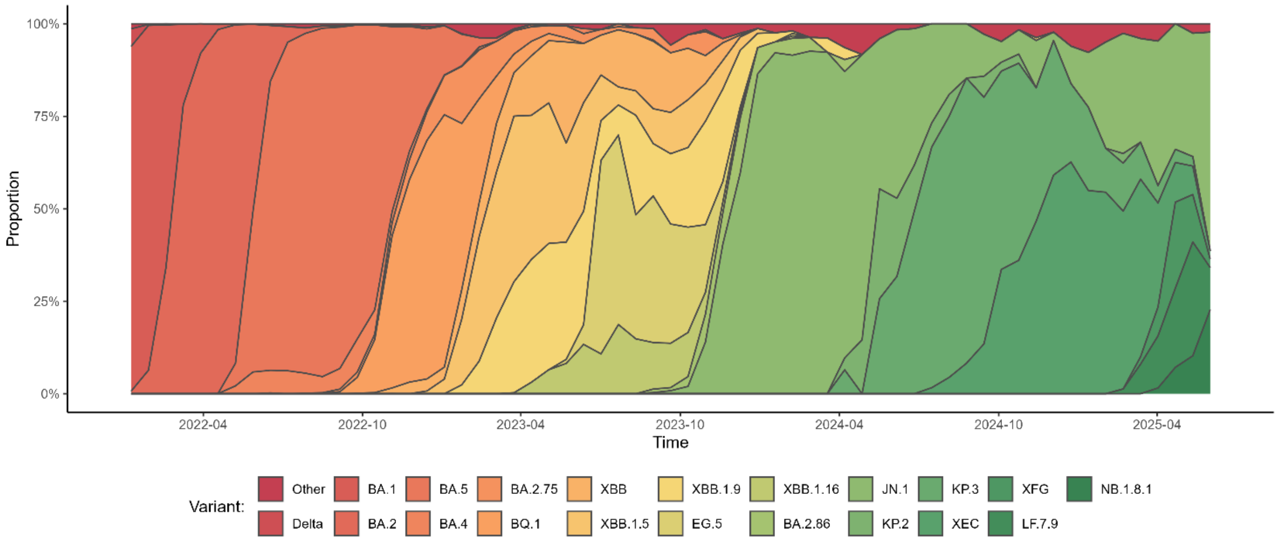
The proportion of **LF.7.9** (spreading in Europe; sub-lineage of JN.1) increased only slightly from **18.1** to **19.1%**. The estimated proportion of XFG was 22.2% in April (weeks 2025/15-18) and decreased to below 10% in recent weeks.

Of note, nearly a quarter (23.4%) of the selected samples belonged to the LF.7.10.1**,** a sub-lineage of JN.1, probably due to a local transmission event and not expected to increase further. The sub-lineage has been detected before in Luxembourg and is not classified as VUM by the World Health Organisation and ECDC.

Table 3. Distribution of SARS-CoV-2 lineages detected during weeks 2025/15 to 2025/22. Previously reported cases might be updated by retrospective analysis.
**JN.1 excludes sub-variants listed in table. Variants under monitoring in bold letters.*

Lineage	weeks 15-18 (N=72)		weeks 19-22 (N=77)	
	%	CI %	%	CI %
LP.8.1	**31.9**	**21.2 – 42.7**	**23.4**	**13.9 – 32.8**
LF.7.10.1	0.0		23.4	13.9 – 32.8
LF.7.9	18.1	9.2 – 26.9	19.5	10.6 – 28.3
NB.1.8.1	**6.9**	**1.1 – 12.8**	**16.9**	**8.5 – 25.3**
XFG	22.2	12.6 – 31.8	7.8	1.8 – 13.8
Other	5.6	0.2 – 10.6	5.1	0.2 – 10.2
XEC	**11.1**	**3.9 – 18.4**	**3.9**	**0.0 – 8.2**
JN.1*	**4.2**	**0.0 – 8.8**	**0.0**	

Figure 6. Proportion of each variant circulating in Luxembourg since January 2022. All displayed variants include descendant lineages, except those specified on the legend



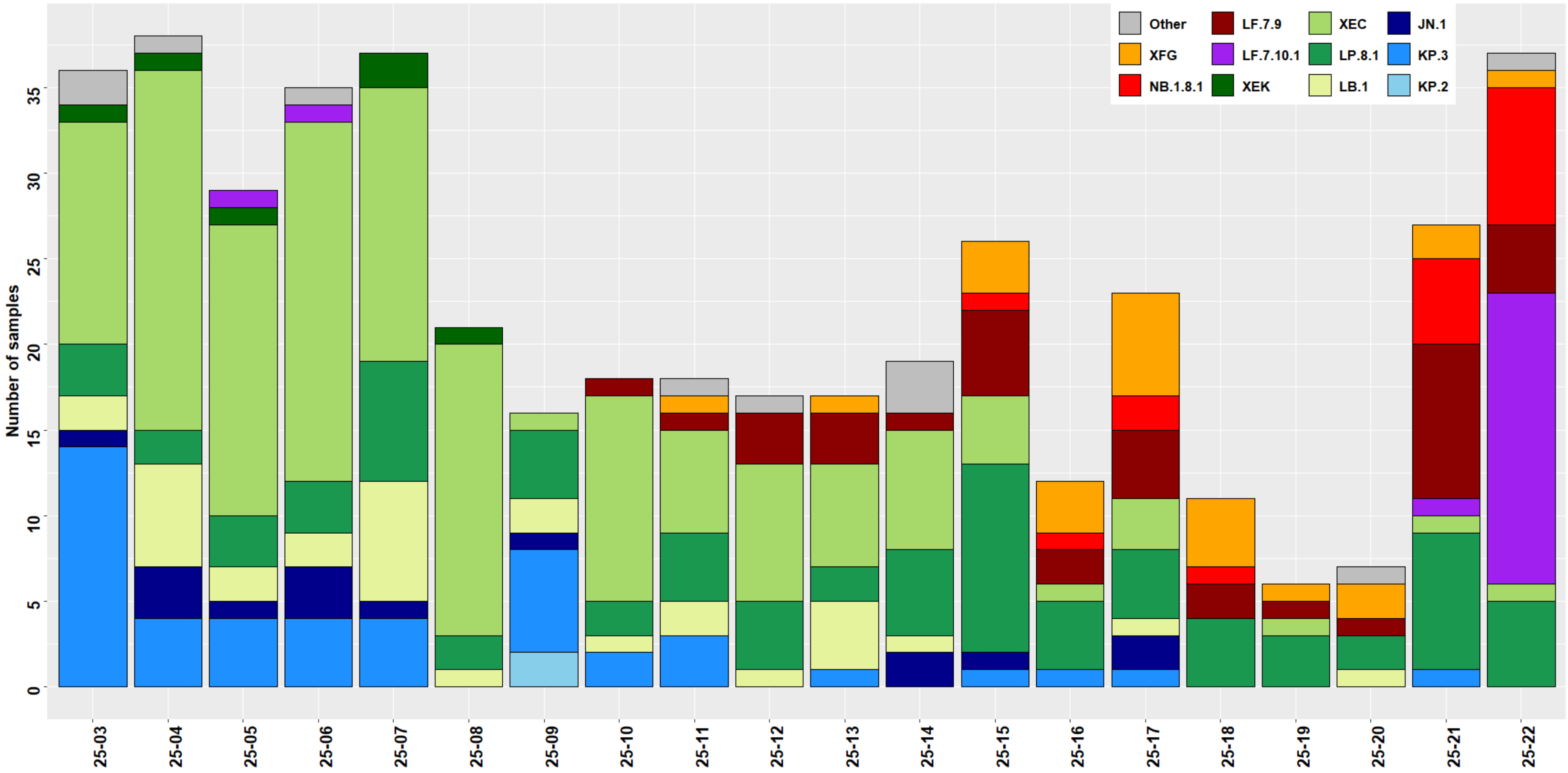


Figure 7. Distribution of lineages since 2025/03 (last 20 weeks).
All displayed variants include descendant lineages, except those specified on the legend, other: recombinant lineages (eg: XFJ, XFB)

References

European Centre for Disease Prevention and Control. SARS-CoV-2 variants of concern. Retrieved 18 June 2025, from https://www.ecdc.europa.eu/en/covid-19/variants-concern

European Centre for Disease Prevention and Control. Communicable Disease Threats Report Week https://www.ecdc.europa.eu/en/publications-data/communicable-disease-threats-report-7-13-june-2025-week-24

GISAID. EpiCoV – Pandemic coronavirus causing COVID-19. Retrieved 18 Junel 2025, from https://www.gisaid.org

GitHub - cov-lineages/pangolin: pango-designation/lineage_notes.txt. (2025). Retrieved 18 June 2025, from https://github.com/cov-lineages/pango-designation/blob/master/lineage_notes.txt

Guo C, Yu Y, Liu J, Jian F, Yang S, Song W, et al. Antigenic and virological characteristics of SARS-CoV-2 variants BA.3.2, XFG, and NB.1.8.1. Lancet Infect Dis. 2025 Jun 5 Available at: https://www.ncbi.nlm.nih.gov/pubmed/40484018

Hadfield J., Megill C., Bell S., Huddleston J., Potter B., Callender C. et al. (2018). Nextstrain: real-time tracking of pathogen evolution. Bioinformatics. 34(23). 4121-4123. doi: 10.1093/bioinformatics/bty407

Rambaut A., Holmes E., O'Toole Á., Hill V.,McCrone J.,Ruis C. et al. (2020). A dynamic nomenclature proposal for SARS-CoV-2 lineages to assist genomic epidemiology. Nature Microbiology. 5(11). 1403-1407. doi: 10.1038/s41564-020-0770-5

World Health Organization. Tracking sars-COV-2 variants Retrieved 18 June2025, from https://www.who.int/activities/tracking-SARS-CoV-2-variants

World Health Organization. Risk evaluation for SARS-CoV-2 Variant Under Monitoring: LP.8.1, from https://www.who.int/publications/m/item/risk-evaluation-for-sars-cov-2-variant-under-monitoring-lp81

World Health Organization. Risk evaluation for SARS-CoV-2 Variant Under Monitoring: NB.1.8.1, from https://cdn.who.int/media/docs/default-source/documents/epp/tracking-sars-cov-2/23052025_nb.1.8.1_ire.pdf?sfvrsn=7b14df58_5