Respiratory Viruses in Luxembourg (ReViLux)

Report – Sentinel Week 15 and Sequencing Update

Summary

At the conclusion of week 15 of 2025, the sentinel surveillance network reported baseline epidemic activity, with 2.2% of consultations linked to influenza-like illness (ILI). Analysis of specimens collected over the past week indicates positivity rates of 5.4% for Influenza A, 8.1% for RSV, and 2.7% for SARS-CoV-2 where as there was no positive sample for Influenza B. During the 2024/25 season, a total of 2,750 samples have been processed, of which 897 tested positive for Influenza, including 397 cases of Influenza B and 500 cases of Influenza A. Among the Influenza A cases, 476 samples (95.2%) have undergone subtyping, identifying 195 cases (39.0%) as A(H1)pdm09 and 281 cases (56.2%) as A(H3). Additionally, RSV continues to circulate at a rate of 9.7%, with three confirmed samples detected.

Since November 2024, For SARS-CoV-2 multiple sub-variants of JN.1 have been circulating in Luxembourg. The proportion of the detected variants through genomic surveillance was as follows: XEC accounted for 293 cases (57.7%), followed by KP3 with 97 cases (19.1%), BA.2.86 with 74 cases (14.6%), and LP.8.1 with 44 cases (8.7%).

Including Plots

Syndromic surveillance over the last 4 Weeks (Table 1)

Week	ARI		ILI		Total consultations
	N	%	N	%	
2025/12	70	16.3	22	5.1	430
2025/13	51	15.5	18	5.5	328
2025/14	56	15.0	13	3.5	373
2025/15	36	15.9	5	2.2	226

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

At the end of the week 15, only **2.2%** of the consultations were reported as ILI, representing a baseline level 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.

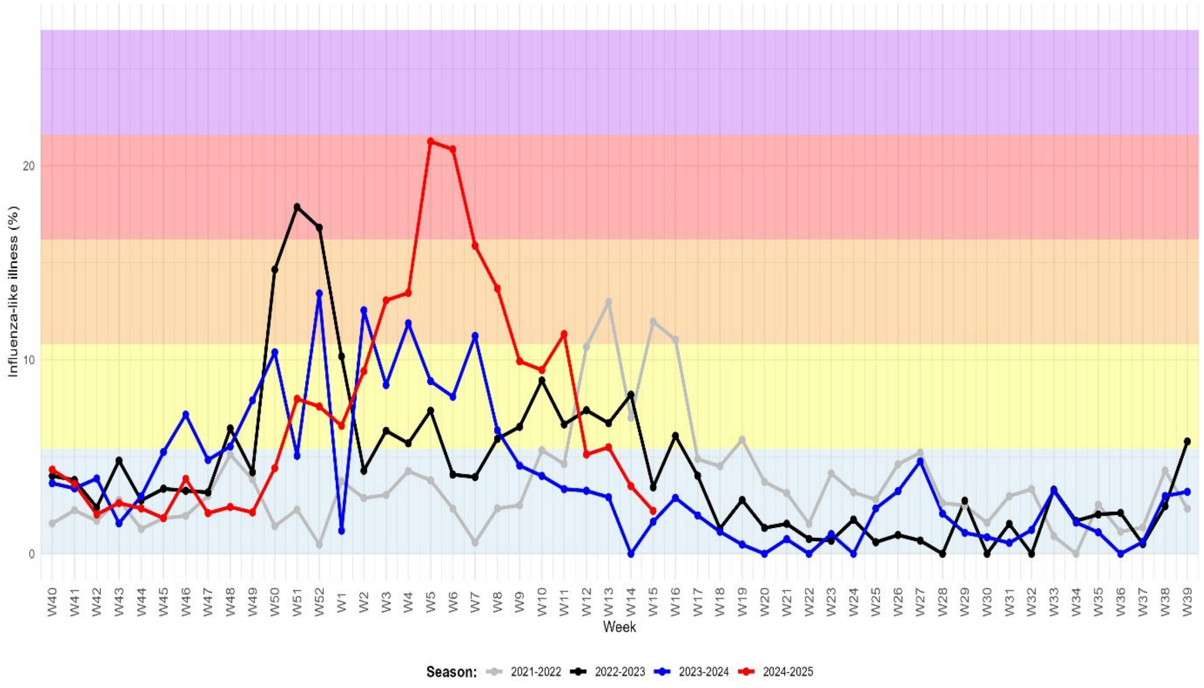

Figure 1. Percentage of patients with influenza-like illness over the last three seasons
Background colours according to intensity of circulation: baseline, low, medium, high, very high.

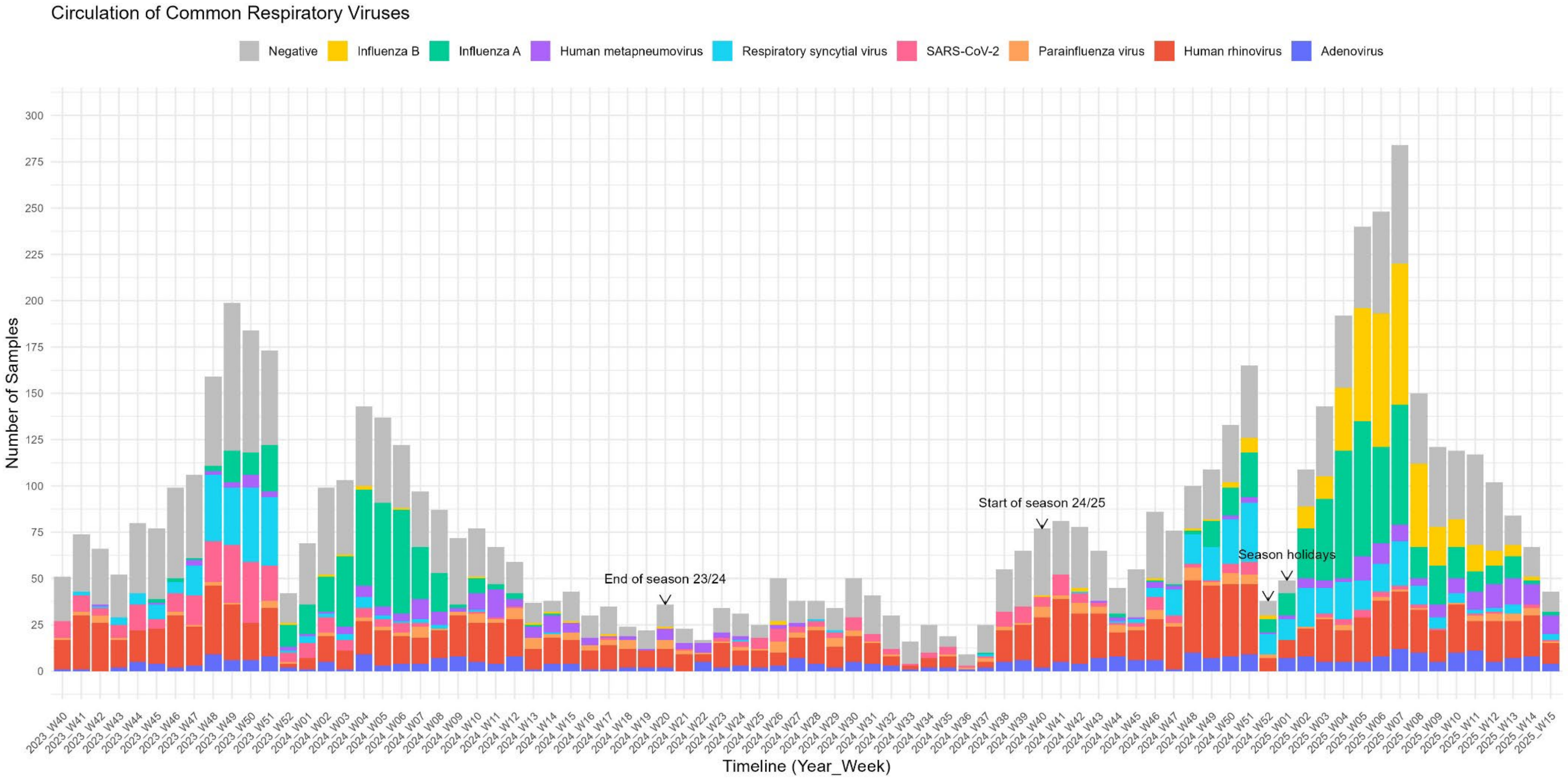

Figure 2. Distribution of respiratory viruses detected within the Sentinel Network, by calendar week. Results from last week are not yet consolidated.

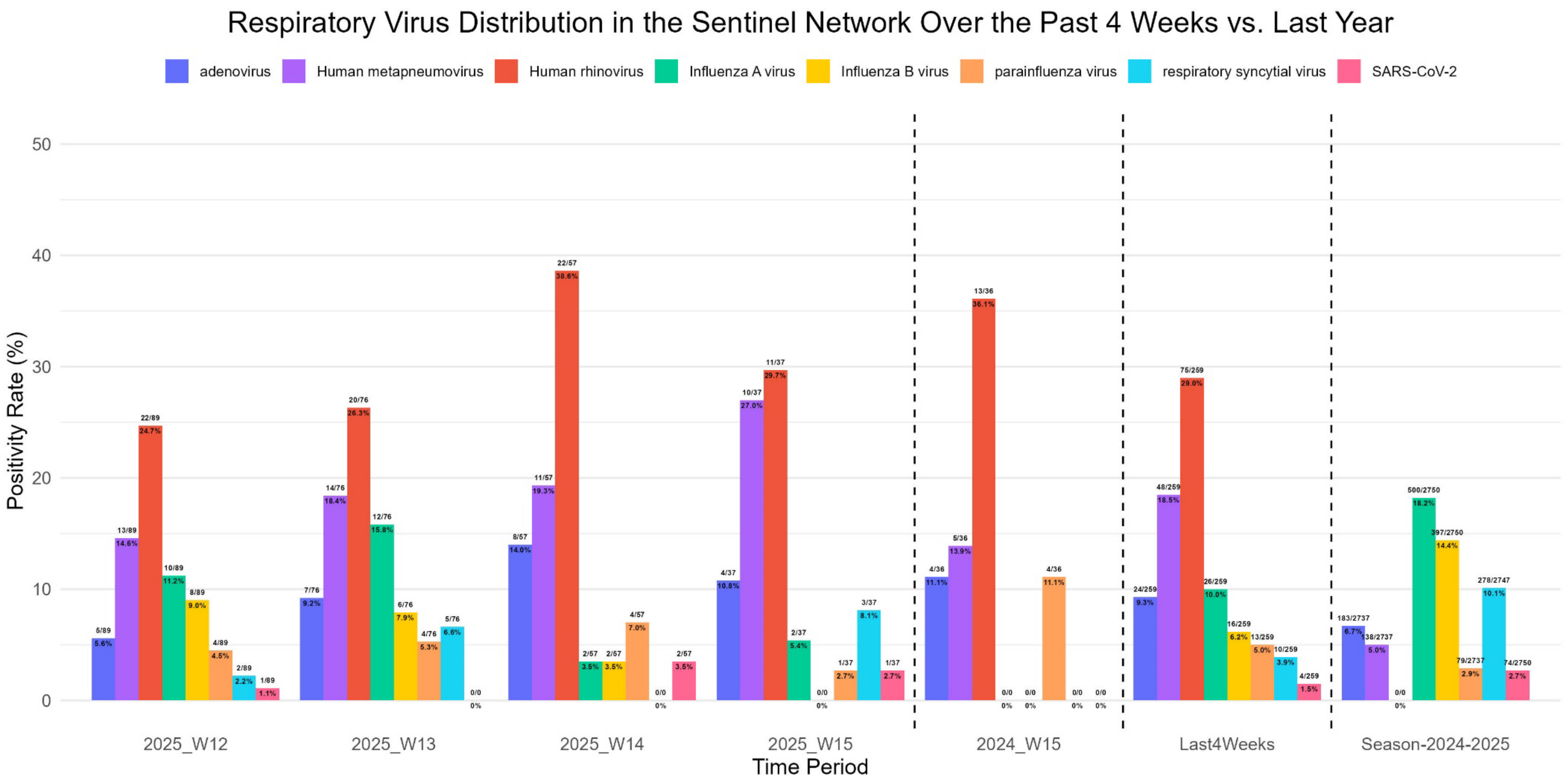

Figure 3. Distribution of respiratory viruses detected within the Sentinel Network over the last 4 weeks compared to previous year.

**Co-detection counted once for each virus detected.*

Laboratory Results

Over the week 15, the most frequently detected viruses (according to positivity rates) were **Human rhinovirus (29.0%)**, **Human metapneumovirus (25.8%)** and **adenovirus (9.7%) & Respiratory Syncytial Virus** was at **(8.1%)** and **Influenzavirus A (5.4%)** and **Parainfluenza Virus (3.2%).** In week 2025/15, **SARS-CoV-2** positivity was **2.7%** in the sentinel network. Influenzavirus activity remained low. Overall, 500 Influenza A and 397 Influenza B cases have been detected during this season. Among the Influenza A cases, 476 samples (95.2%) have undergone subtyping, identifying 195 cases (39.0%) as A(H1)pdm09 and 281 cases (56.2%) as A(H3). Positivity rate plot in Figure 4. Shows decreasing detections over the recent weeks.

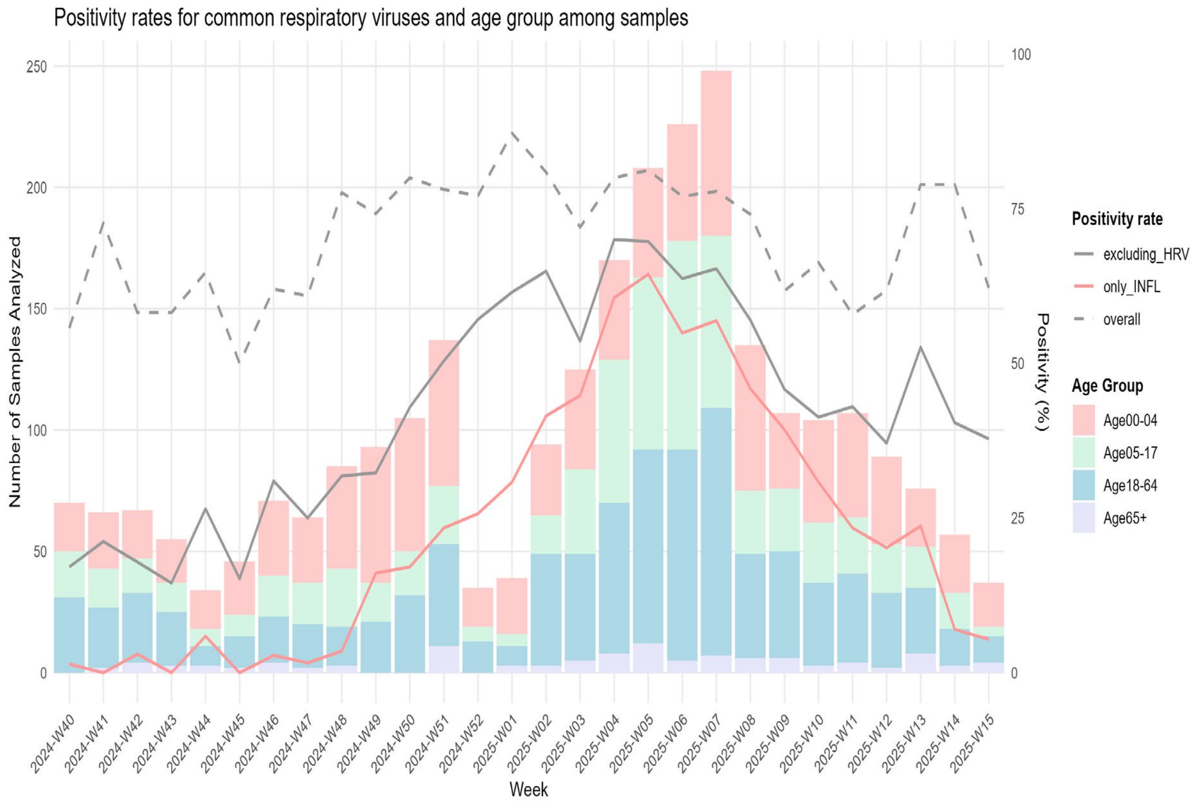

Figure 4. Displays number of sentinel samples received per week by age-group including overall sample positivity including Human rhinovirus (HRV, dotted line), excluding HRV (black line) and Influenza (red). Secondary axis corresponds to positivity

Overall positivity rates are shown with dashed line, continuous gray colored trendline is representing positivityrates after removal of Human Rhinovirus positivity rates and pink line is of positivity rates for Influenzavirus.

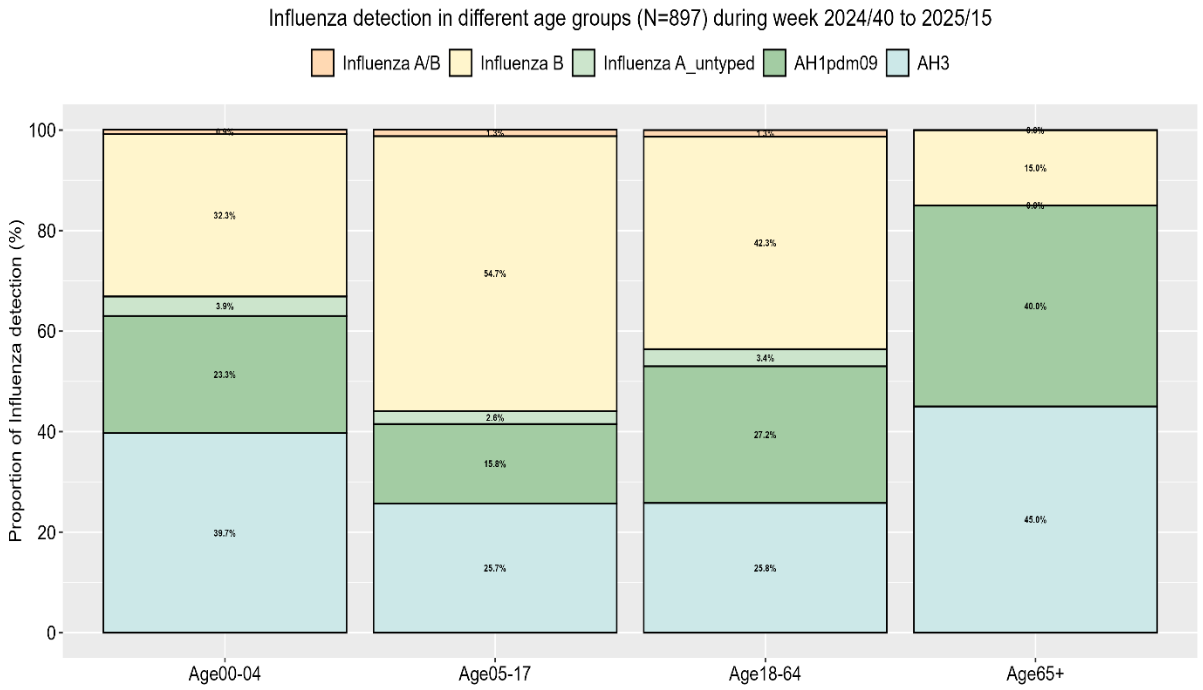

Figure 5. Displays detection of Influenza subtypes by age-group. Data for week 2025/15 not yet completely consolidated.

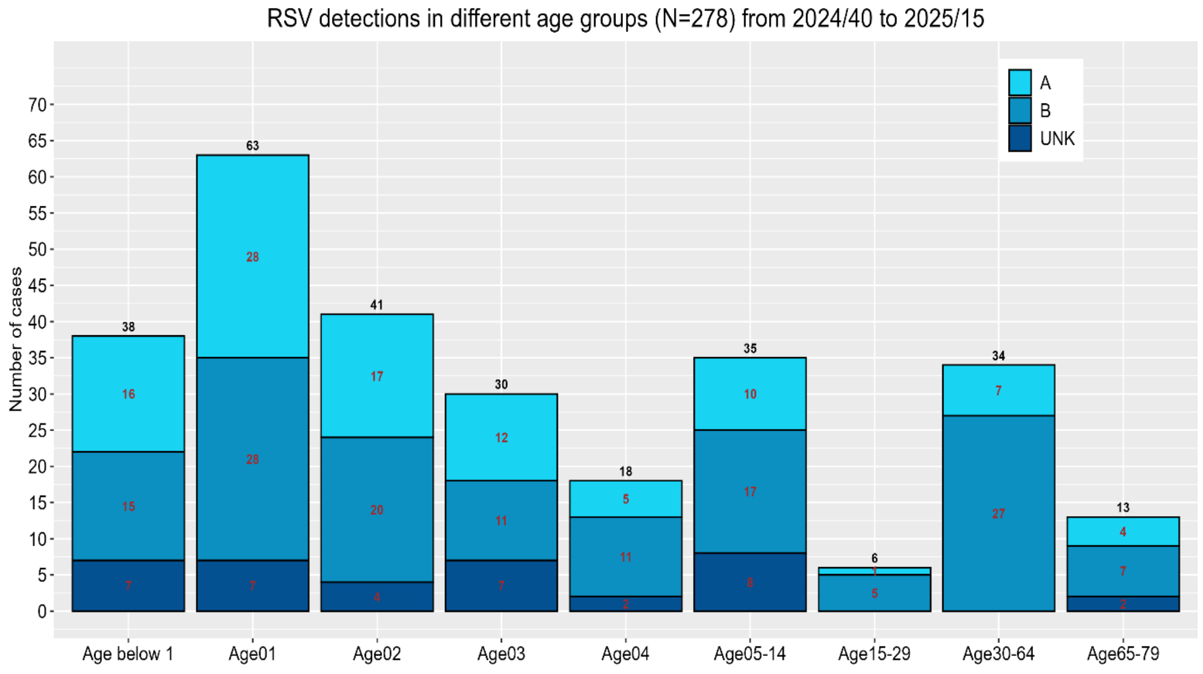

Figure 6. Displays RSV cases according to different age groups with highest impact among the 1-4 years old.

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 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

93 samples were sequenced with specimen dates between week 2025/09 and 2025/14. Approximately 79.6% were community samples and the remaining 20.4% samples were hospital samples.

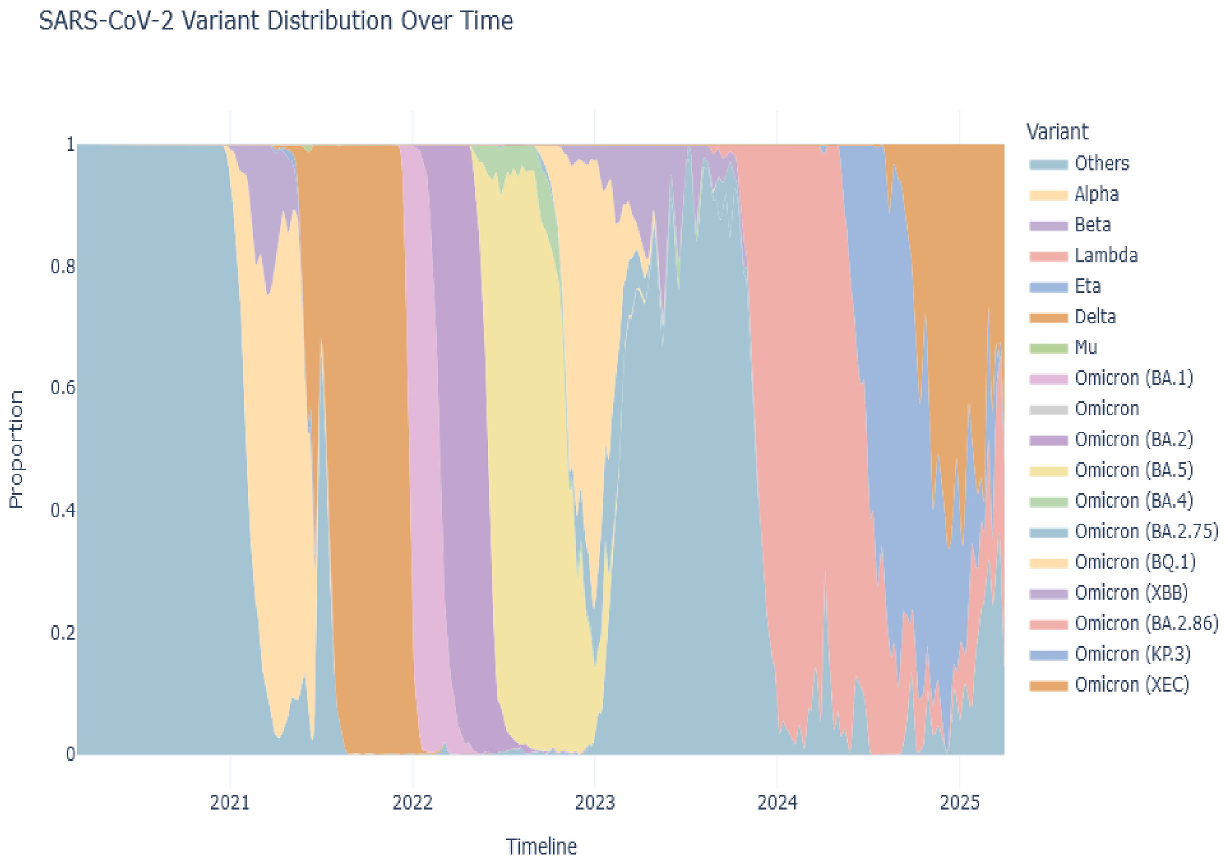

Figure 7. Proportion of variants circulating in Luxembourg since January 2021. The displayed variants include descendant lineages (https://www.ecdc.europa.eu/sites/default/files/documents/PathogenVariant_public_mappings.csv) . All variants shown here are classified by the European Centre for Disease Prevention and Control (ECDC) as de-escalated or active variants of concern (VOC), variants of interest (VOI), or variants under monitoring (VUM).

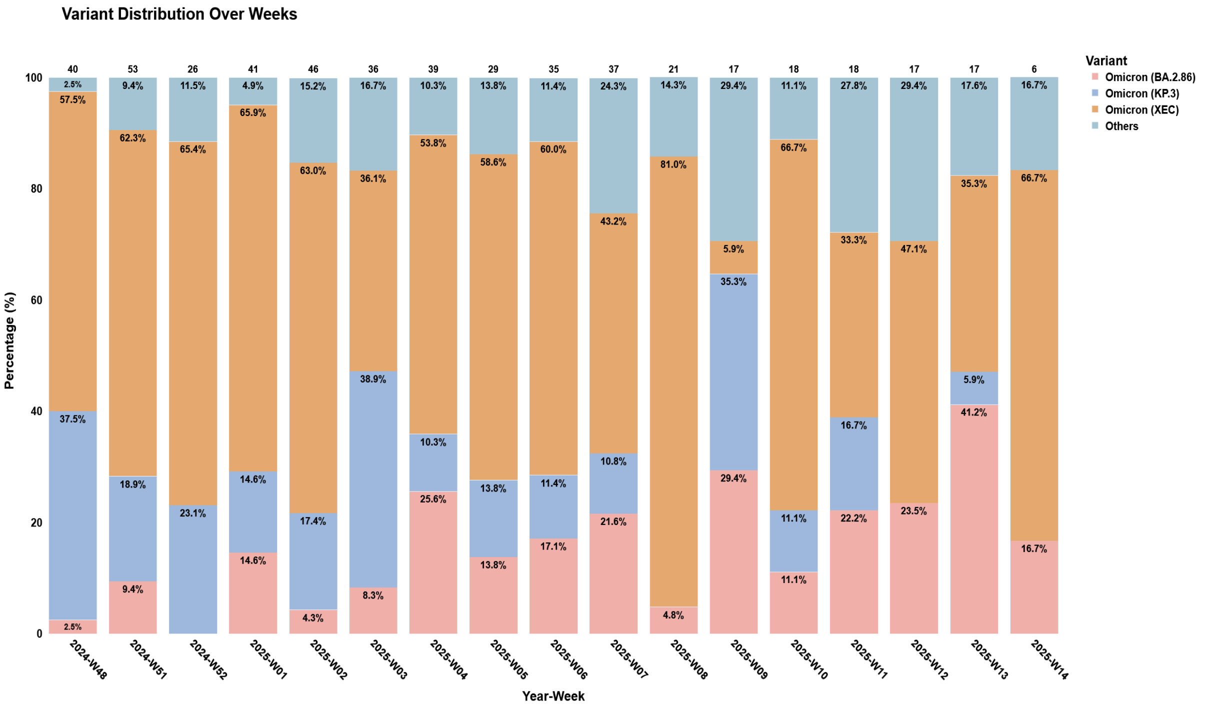

Figure 8. Distribution of lineages since 2024-W48 (last 20 weeks). The displayed variants include descendant lineages (https://www.ecdc.europa.eu/sites/default/files/documents/PathogenVariant_public_mappings.csv). For week 2024/49 and 2024/50 samples were not sequenced as priority was given to more recent samples.

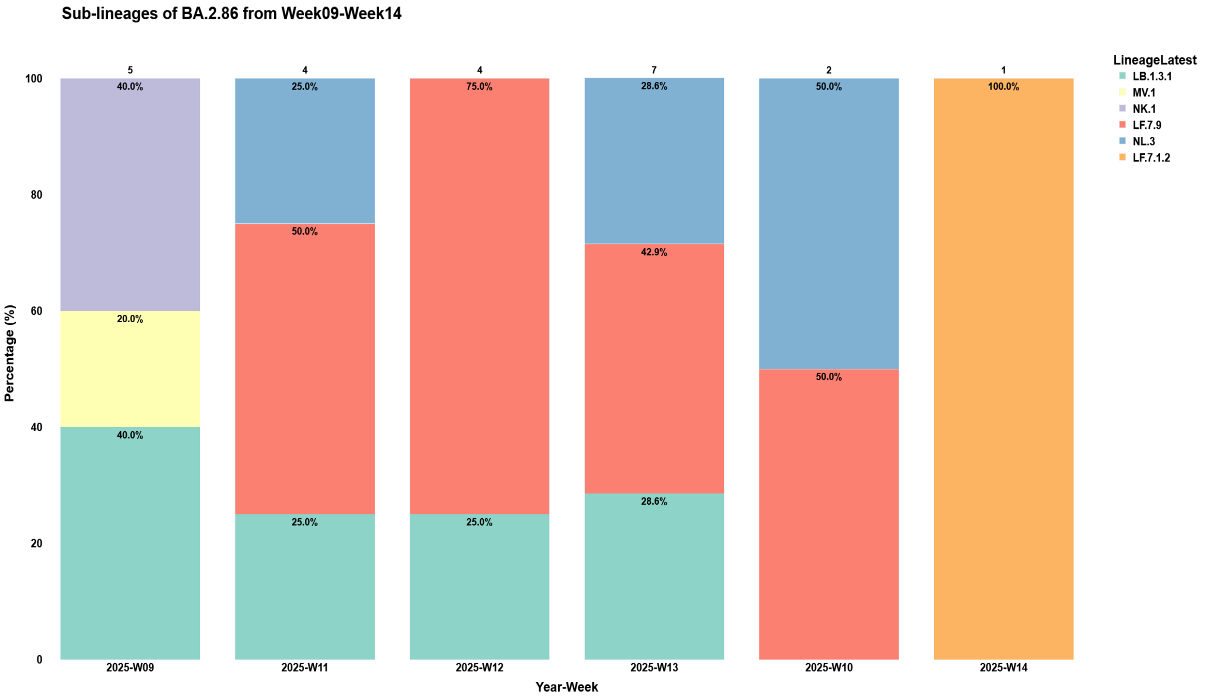

Figure 9. Looking at the last 6 weeks (W09-W14), the sub-lineages under the variant BA.2.86

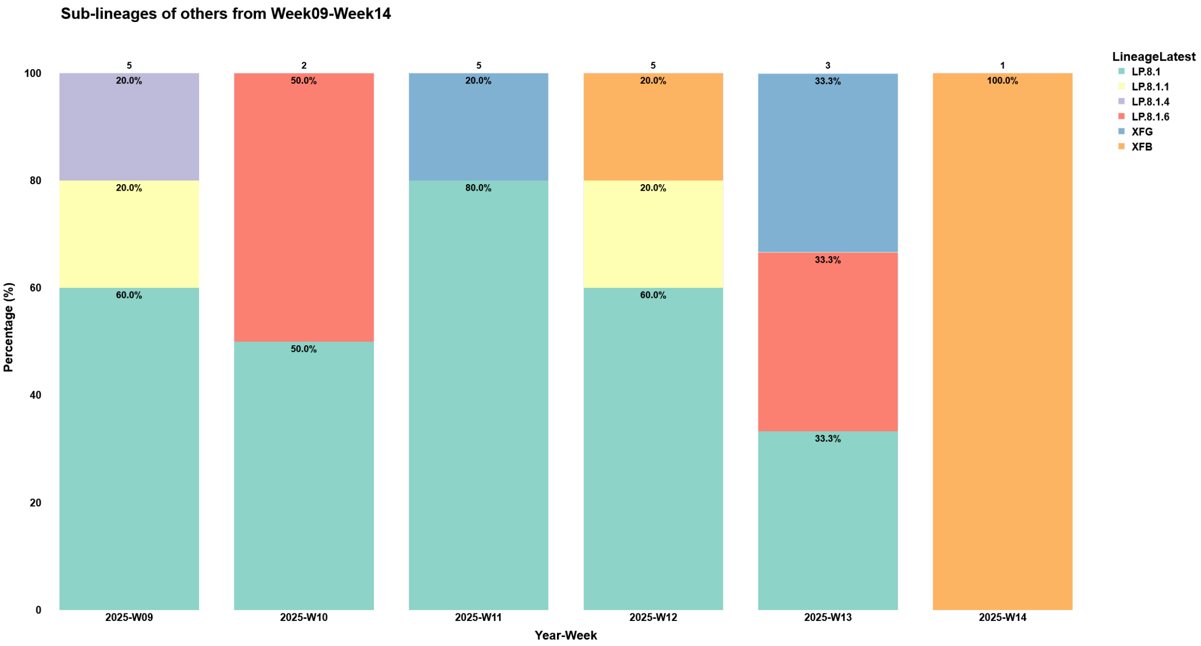

Figure 10. Looking at the last 6 weeks (W09-W14), the sub-lineages under the variant Others

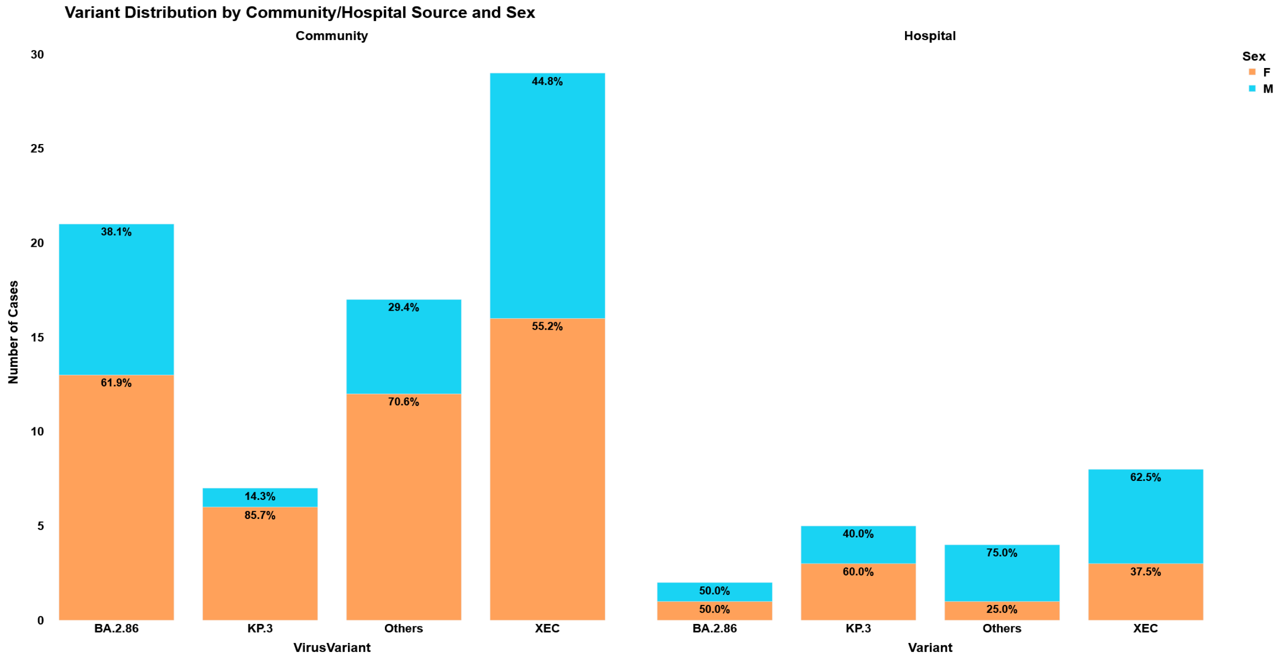

Figure 11. Comparison of lineage distribution by sampling setting from last 6 weeks (W09-W14). The displayed variants include descendant lineages according to (https://www.ecdc.europa.eu/sites/default/files/documents/PathogenVariant_public_mappings.csv).

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