

Respiratory Viruses in Luxembourg (ReViLux)

Sentinel Network Report -Week 14

Summary of Sentinel Network activities

At the end of week 2024/14, rates of influenza-like illness indicate decreasing trends and the sentinel network detected a baseline epidemic activity, based on 1.3% 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 44.8%, 27.6% for Metapneumovirus and 13.8% for Adenovirus. Influenza A positivity remained below 5% and low circulation of Influenzavirus B and RSV was detected.

This season, 80% of Influenzavirus A strains have been subtyped. Among those A viruses subtyped (N=310), 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 212 RSV cases with 72% of samples subtyped. Genotyping analyses showed that the most frequent RSV strain during this season was RSV-A (86.3%).

Sentinel Surveillance Network

The Sentinel Surveillance aims to monitor 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 (2024/14), 1.3% 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 five weeks baseline 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 (44.8%), followed by Metapneumovirus (27.6%) and Adenovirus (13.8%). This season positivity rates of Influenza A peaked in week 2024/06 (52.7%). In week 2024/14 Influenza A positivity was at 3.3%, showing a stable trend.

Three hundred and ten of 388 (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 2024/14, detection of Influenzavirus B and RSV remained low. 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%).

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.

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

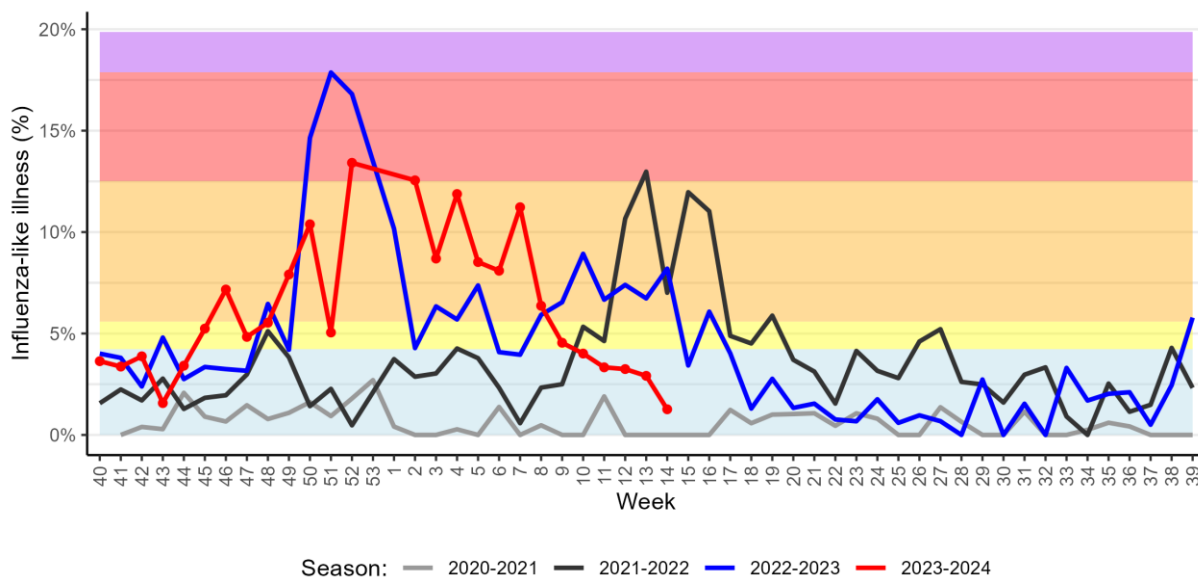


Figure 1. Percentage of patients with influenza-like illness over the last three seasons
Background colours according to intensity of circulation: baseline, low, medium, high, very high. Data from 2024/01 not presented as low return

Table 1. Syndromic surveillance over the last 4 weeks

Week	ARI		ILI		Total consultations
	N	%	N	%	
2024/11	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
2024/14	28	17.72	2	1.27	158

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

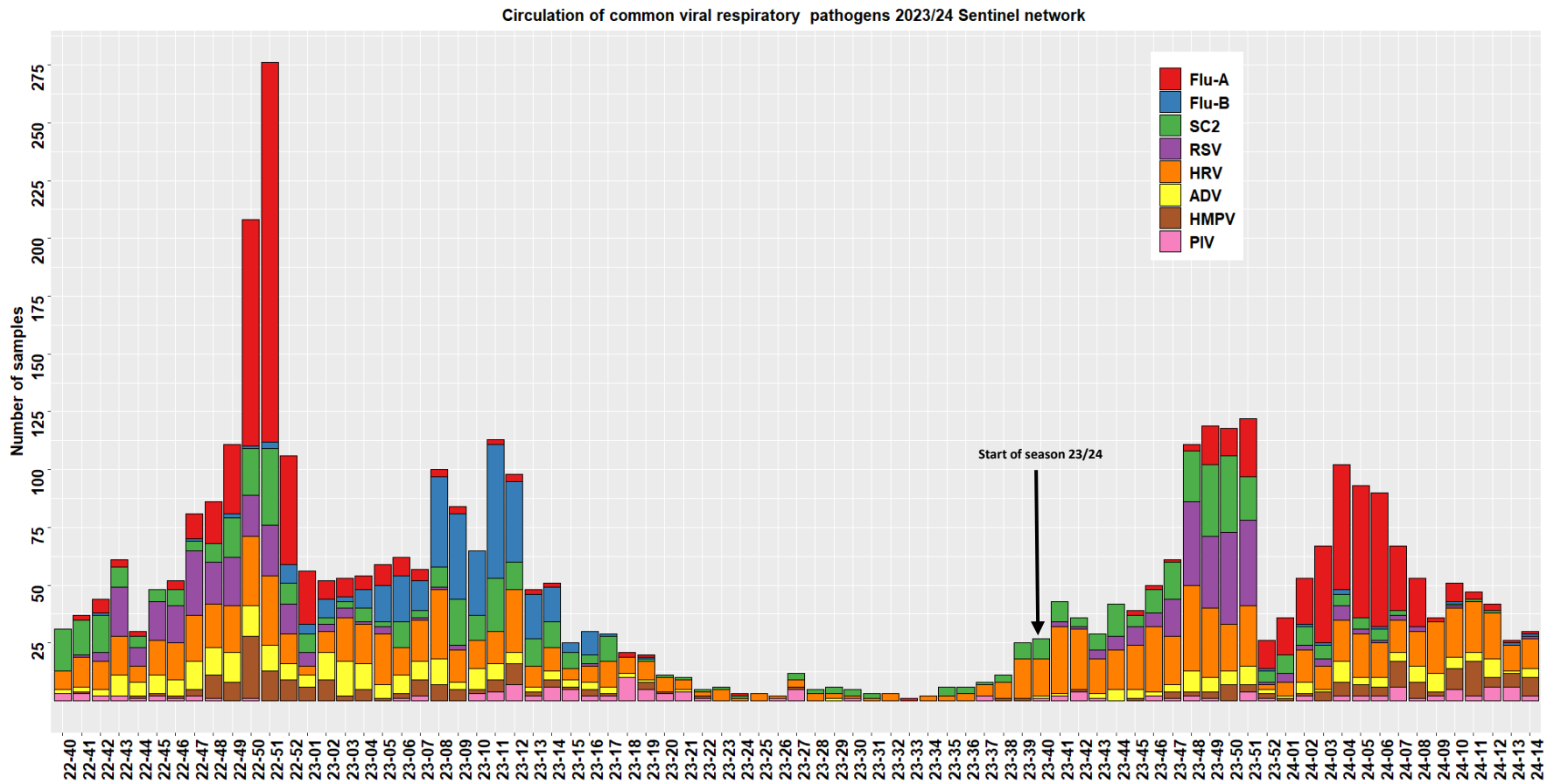


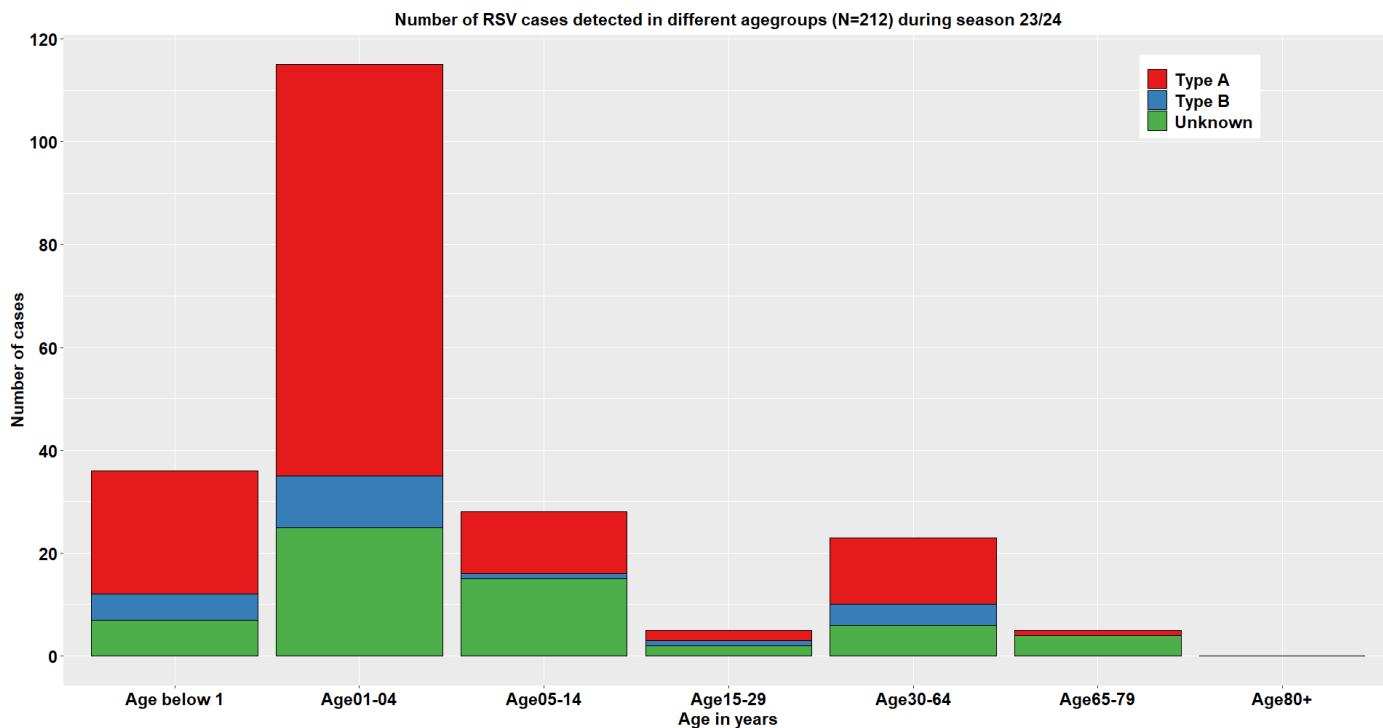
Figure 2. Distribution of respiratory viruses detected within the Sentinel Network, by calendar week. Results from last weeks are not all yet consolidated.
 FLU-A: Influenzavirus A; FLU-B: Influenzavirus B; PIV: Parainfluenzavirus; RSV: Respiratory syncytial virus; ADV: Adenovirus; MPV: Metapneumovirus; HRV: Human rhinovirus; SC2: SARS-CoV-2.

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 %					w14
	w11	w12	w13	w14	Trend	
Human rhinovirus	37.3	41.7	32.4	44.8	↑	15.9
Metapneumovirus	25.4	8.3	17.6	27.6	↑	4.8
Adenovirus	6.8	16.7	2.9	13.8	↑	6.3
Parainfluenzavirus	3.4	12.5	17.6	6.9	↓	9.5
Respiratory syncytial virus	0.0	0.0	0.0	3.4		0.0
Influenzavirus A	4.8	5.6	2.8	3.3	→	2.9
SARS-CoV-2	1.6	1.9	0.0	0.0		15.9
Influenzavirus B	0.0	0.0	2.8	3.3		21.4

*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.



References

European Centre for Disease Prevention and Control. SARS-CoV-2 variants of concern. Retrieved 09 April 2024, 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-31-march -6- April 2024-week-14](https://www.ecdc.europa.eu/en/publications-data/communicable-disease-threats-report-31-march-6-april-2024-week-14)

GISAID. EpiCoV – Pandemic coronavirus causing COVID-19. Retrieved 09 April 2024, from <https://www.gisaid.org>

GitHub - cov-lineages/pangolin: Software package for assigning SARS-CoV-2 genome sequences to global lineages. (2024). Retrieved 09 April 2024, from <https://github.com/cov-lineages/pangolin>

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 09 April 2024, from <https://www.who.int/activities/tracking-SARS-CoV-2-variants>