

Respiratory Viruses in Luxembourg (ReViLux)

Sentinel Network Report - Week 15

Summary of Sentinel Network activities

At the end of week 2024/15, the sentinel network detected a baseline epidemic activity, based on 2.4% 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 36.1%, 13.9% for Metapneumovirus and 11.81% for Adenovirus. Influenza A positivity remained below 5%, but low circulation of Influenzavirus B has been detected over the past three weeks.

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 (2024/15), 2.4% 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 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 (36.1%), followed by Metapneumovirus (13.9%) Adenovirus (11.1%) and Parainfluenza (11.1%). This season positivity rates of Influenza A peaked in week 2024/06 (52.7%). During week 2024/15 no new cases of Influenza A were detected.

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 2024/15, 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 (Figure 3). 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.

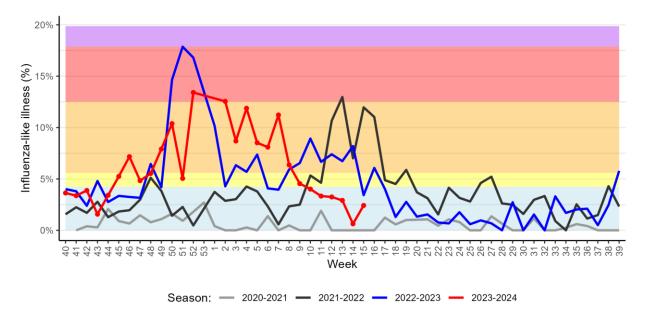
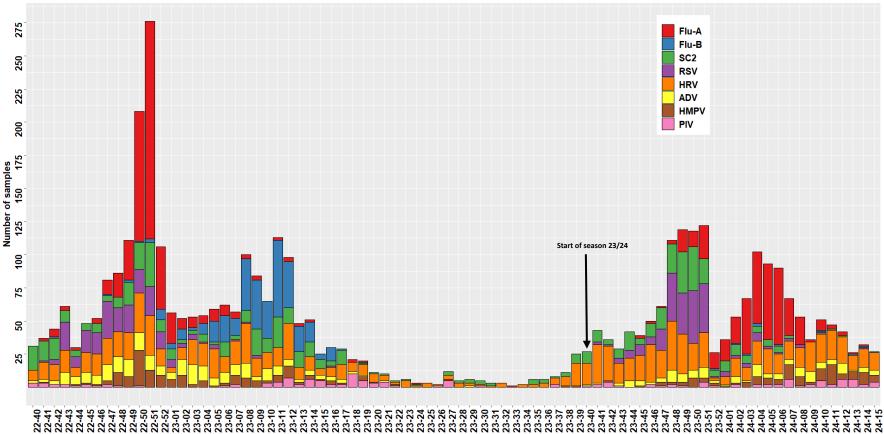


Figure 1. Percentage of patients with influenza-like illness over the last three seasons Background colours according to intensity of circulation: baseline, low, medium, high, very high. Data from 2024/01 not presented as low return

	-				
Week	ARI			ILI	Total
	Ν	%	Ν	%	consultations
2024/12	91	19.70	15	3.25	462
2024/13	53	17.15	9	2.91	309
2024/14	28	17.72	1	0.63	158
2024/15	30	24.19	3	2.42	124

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



Circulation of common viral respiratory pathogens 2023/24 Sentinel network

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.

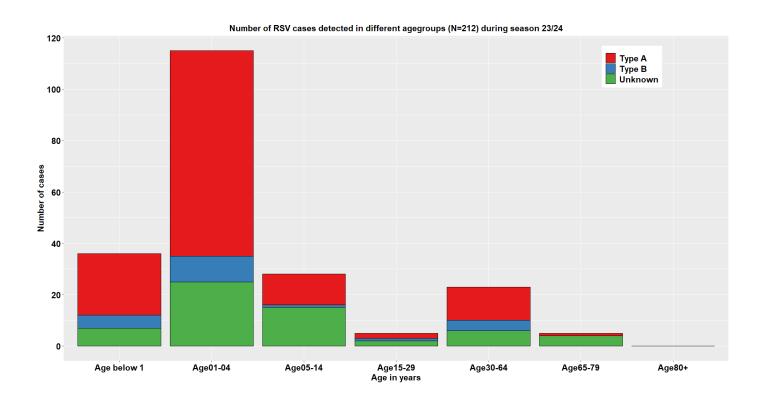
National Reference Laboratory for Acute Respiratory Infections Department of Microbiology - Laboratoire national de santé 1, rue Louis Rech | L-3555 Dudelange T : (+352) 28 100 556 | F : (+352) 28 100 556 | microbiology@lns.etat.lu | www.lns.lu

Virus		Sea	Season 2022/23			
	w12	w13	w14	w15	Trend	w15
Human rhinovirus	41.7	32.4	46.7	36.1	\rightarrow	15.2
Metapneumovirus	8.3	17.6	30.0	13.9	\rightarrow	3.0
Adenovirus	16.7	2.9	13.3	11.1	\uparrow	9.1
Parainfluenzavirus	12.5	17.6	6.7	11.1	\rightarrow	15.2
Influenzavirus B	0.0	2.8	3.3	2.8	\rightarrow	10.8
Respiratory syncytial virus	1.9	0.0	0.0	0.0		0.0
Influenzavirus A	5.6	2.8	3.3	0.0		0.0
SARS-CoV-2	1.9	0.0	0.0	0.0		18.9

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

*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.



National Reference Laboratory for Acute Respiratory Infections Department of Microbiology - Laboratoire national de santé 1, rue Louis Rech | L-3555 Dudelange T : (+352) 28 100 556 | F : (+352) 28 100 556 | microbiology@Ins.etat.lu | www.Ins.lu

References

European Centre for Disease Prevention and Control. SARS-CoV-2 variants of concern. Retrieved 16 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-07-April -13- April 2024-week-15

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 15 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 15 April 2024, from https://www.who.int/activities/tracking-SARS-CoV-2-variants