Respiratory Viruses in Luxembourg (ReViLux)

Report – Sentinel Week 52 and Sequencing Update

Summary

The sentinel network detected a high epidemic activity over the last week, based on 13.4 % of consultations being associated with influenza-like illness. Out of the specimens collected by the sentinel network over the last week, the percentage of positive tests for Influenza virus A was 33.3% and14.3% for SARS-CoV-2.

Influenza A detections in sentinel data continued to increase from 18.9 (2023/51) to 33.3% (2023/52) with 84% characterised as A(H1)pdm09 viruses and 16% as H3.

Regarding SARS-CoV-2 genomic surveillance, it is worth noting that since late February 2023 recombinant strains with combined characteristics of other variants have been dominant in Luxembourg. From week 2023/26 to week 2023/43, EG.5 was the most frequent detected variant, but showing a decreasing trend. Since week 2023/43, the proportions of BA.2.86 and JN.1 (descendent of BA.2.86) have continuously increased. The estimated distribution for JN.1 was 60.9% (95%CI: 52.0-69.8%), BA.2.86 was 11.3% (95%CI: 5.5-17.1%), and XBB.1.9 was 10.4% (95%CI: 4.9-16.2%) for weeks 2023/48-50. JN.1 was dominant in the selected community and hospital sample.

Introduction

The Laboratoire national de santé, as **National Reference Laboratory for Acute Respiratory Infections** in Luxembourg, performs close surveillance on respiratory viruses, with a special focus on SARS-CoV-2. The main monitoring activities are:

- **The Sentinel Surveillance**. It provides a broad picture of respiratory diseases affecting the Luxembourgish population, based on clinical and laboratory data.

- **The SARS-CoV-2 Genomic Surveillance**. It enables detailed observation of SARS-CoV-2 variants and mutations through time and space, as well as studying specific groups of interest.

The objective of the ReViLux report is to inform public health actions in Luxembourg.

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, 13.4% of the consultations were reported as ILI, representing a high epidemic activity for Luxembourg, according to ECDC and the Moving Epidemic Method. Of note, only a few surgeries participated due to holiday season and therefore, results need to be interpreted with caution. 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 Influenza virus A (33.3%), followed by SARS-CoV-2(14.3%). Positivity rates of Influenza A increased from 18.9% (2023/51) to 33.3% (2023/52). Thirty seven of 63 samples have been further characterized with 84% as A (H1)pdm09 and 16% as A (H3). First case of Influenza virus B was detected in week 2023/52. Test positivity for RSV decreased slightly from 30.1

National Reference Laboratory for Acute Respiratory Infections
Department of Microbiology - **Laboratoire national de santé**
1, rue Louis Rech | L-3555 Dudelange
T : (+352) 28 100 523 | F : (+352) 28 100 512 | microbiology@lns.etat.lu | www.lns.lu

2

(2023/50) to 28.5% (2023/51), however not all samples from week 2023/52 have been tested yet, and results will be displayed next week. Overall, this season (23/24), the highest impact of RSV was seen among the 0-4 years age group (Figure3).

To date, 129 RSV detections were further subtyped as either RSV A (N=112, 86.8%) or RSV B (N=17, 13.2%). An overview of the circulating viral pathogens during the current and previous inter- season is displayed in Figure 2 and Table 2.
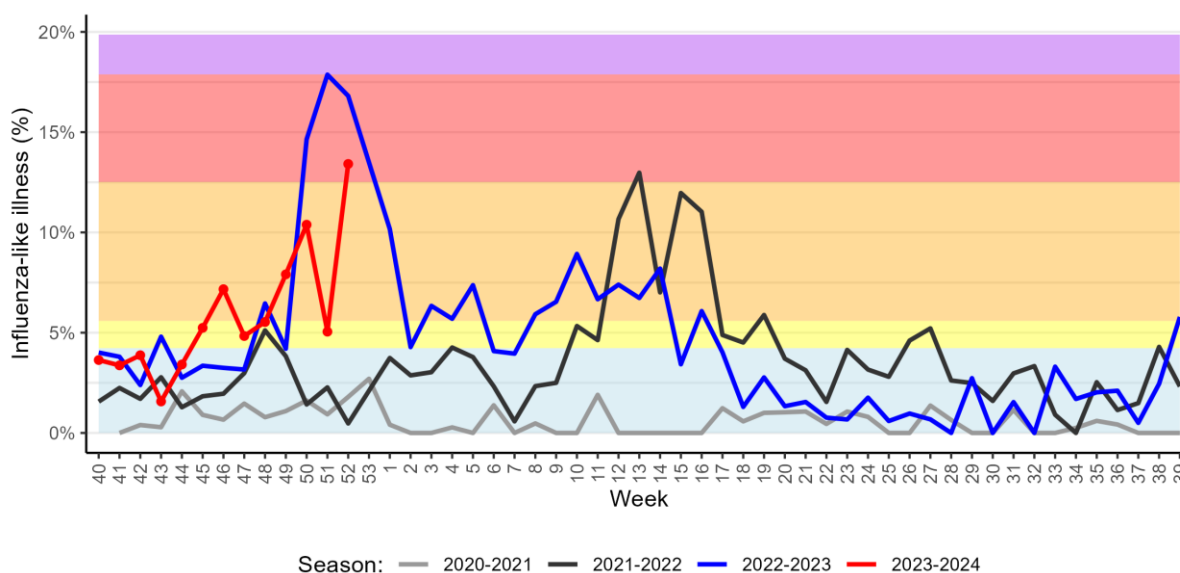

Figure 1. Percentage of patients with influenza-like illness over the last three seasons
Background colours according to intensity of circulation: baseline, low, medium, high, very high.

Table 1. Syndromic surveillance over the last 4 weeks

Week	ARI		ILI		Total consultations
	N	%	N	%	
2023/49	146	27.50	42	7.91	531
2023/50	111	21.35	54	10.38	520
2023/51	86	28.96	15	5.05	297
2023/52	28	34.15	11	13.41	82

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

National Reference Laboratory for Acute Respiratory Infections
Department of Microbiology - **Laboratoire national de santé**
1, rue Louis Rech **|** L-3555 Dudelange
T : (+352) 28 100 523 **|** F : (+352) 28 100 512 **|** microbiology@lns.etat.lu **|** www.lns.lu
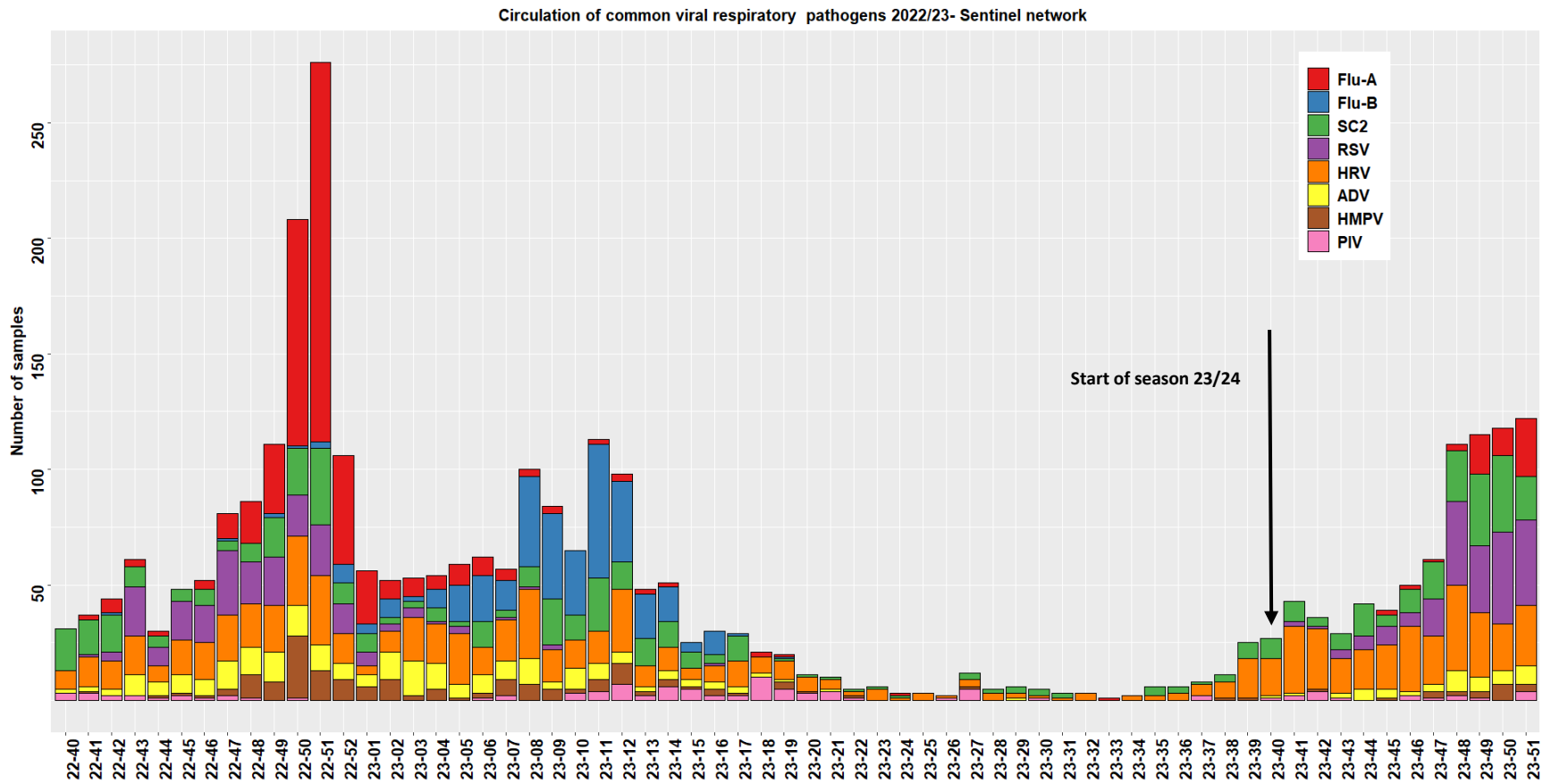
3

Figure 2. Distribution of respiratory viruses detected within the Sentinel Network, by calendar week. Results from last weeks 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.

National Reference Laboratory for Acute Respiratory Infections
Department of Microbiology - **Laboratoire national de santé**
1, rue Louis Rech **|** L-3555 Dudelange
T : (+352) 28 100 523 **|** F : (+352) 28 100 512 **|** microbiology@lns.etat.lu **|** www.lns.lu

4

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 %					
	w49	w50	w51	w52	Trend	w52
Influenzavirus A	11.3	8.9	18.9	33.3	↑	37.6
Respiratory syncytial virus	22.7	30.1	28.5			12.0
Human rhinovirus	21.9	15.0	20.0			12.0
SARS-CoV-2	20.7	24.4	14.4	14.3	→	7.2
Metapneumovirus	2.3	5.3	2.3			8.3
Adenovirus	4.7	4.5	6.2			6.5
Parainfluenzavirus	0.8	0.0	3.1			0.0
Influenzavirus B	0.0	0.0	0.0	3.3	↑	6.4

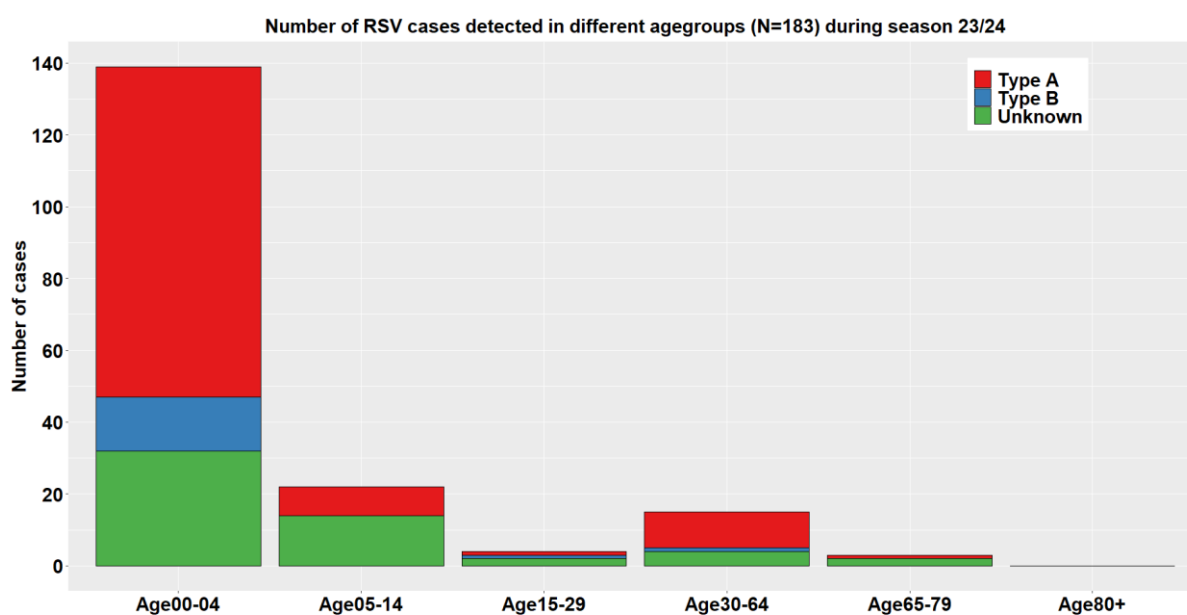**Co-detection counted once for each virus detected.*

Figure 3. Displays RSV cases according to different age groups with highest impact among the 0-4 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 and Nanopore devices are used.

National Reference Laboratory for Acute Respiratory Infections
Department of Microbiology - **Laboratoire national de santé**
1, rue Louis Rech **|** L-3555 Dudelange
T : (+352) 28 100 523 **|** F : (+352) 28 100 512 **|** microbiology@lns.etat.lu **|** www.lns.lu

5

Bioinformatic analyses are based on a standardised pipeline, and lineage assignment is performed through the PANGOLin software (4.3, pango-data 1.23, mode UShER). In order to allow easier visualisation, WHO and Nextstrain categorisations are also used.

Sequencing activity

164 samples from 2,227 cases (7.4%) reported in Luxembourg were sequenced with specimen dates between week 2023/47 and 2023/50. Approximately 70% were hospital samples and the remaining samples were community samples. Sequencing data probably does not fully represent virus circulation within the population.

Variant circulation

For samples sequenced between 27th November to 17th of December 2023 (2023/48-50), the estimated distribution was 60.9% for JN.1, 11.3% for BA.2.86 and 10.4% for XBB.1.9. JN.1 is closely related to BA.2.86 with only one change in the spike protein, but rapidly growing with 70% of all BA.2.86 belonging to JN.1.

An overview of the variants and lineages circulating since beginning of 2023 is displayed in Figure 5, and further details are shown in Table 3. The history of the circulation of each variant since January 2021 is displayed in Figure 4.

Table 3. Distribution of SARS-CoV-2 lineages detected during weeks 2023/45 to 2023/50. Previously reported cases might be updated by retrospective analysis.

Lineage	weeks 45-47		weeks 48-50	
	%	CI %	%	CI %
JN.1	**26.0**	**20.5 – 31.6**	**60.9**	**52.0 – 69.8**
BA.2.86	12.0	7.9 – 16.1	11.3	5.5 – 17.1
Recomb XBB.1.9	27.7	22.1 – 33.1	10.4	4.9 – 16.2
Recomb XBB.1.5	11.6	7.5 – 15.6	5.2	1.2 – 9.3
Recomb XBB.1.16	4.1	1.6 – 6.6	5.2	1.2 – 9.3
Recomb XBB	6.6	3.5 – 9.7	4.4	0.6 – 8.1
Recomb EG.5	8.7	5.1 – 12.2	1.7	0.0 – 4.1
BA.2.75	3.3	1.1 – 5.6	0.9	0.0 – 2.6

National Reference Laboratory for Acute Respiratory Infections
Department of Microbiology - **Laboratoire national de santé**
1, rue Louis Rech **|** L-3555 Dudelange
T : (+352) 28 100 523 **|** F : (+352) 28 100 512 **|** microbiology@lns.etat.lu **|** www.lns.lu
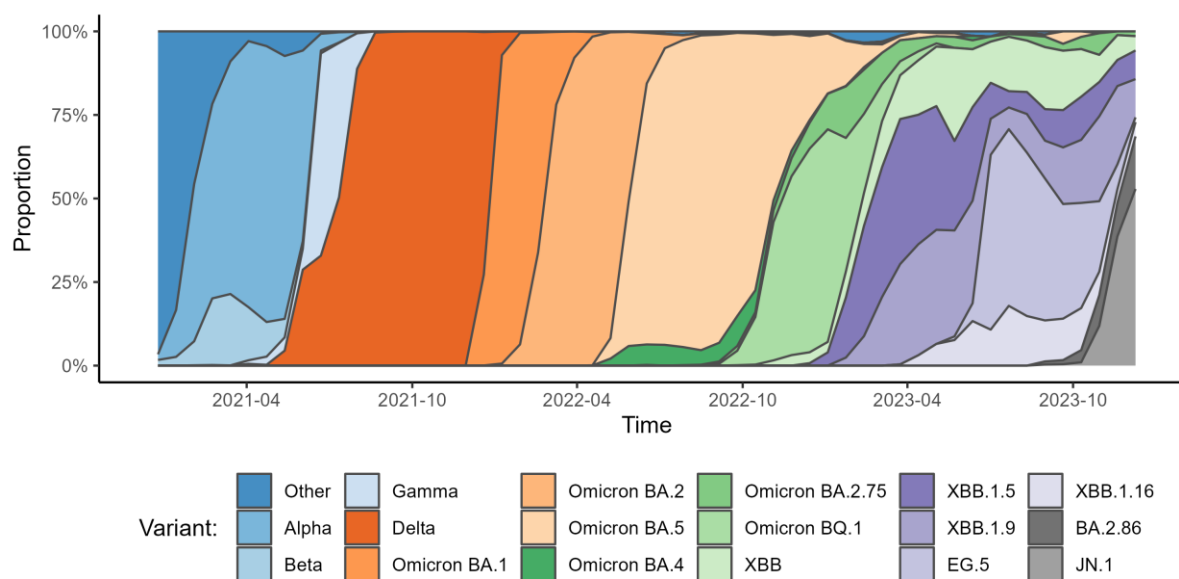
6

Figure 4. Proportion of each variant circulating in Luxembourg since January 2021.
All displayed variants include descendant lineages, except those specified on the legend. For example, XBB does not include XBB.1.5, XBB.1.16, EG.5 and XBB.1.9

Clinical and epidemiological factors

Over the past 4 weeks, 119 (69.2%) samples from hospital laboratories and 53 (30.8%) samples from private laboratories/ sentinel practitioners were sequenced. Table 4 compares sampling setting of JN.1 (descendent lineage of BA.2.86) and XBB.1.9 variants.

Table 4. Comparison of lineage distribution by sampling setting.

Lineage	Community			Hospital		
	Women	Men	**Total**	Women	Men	**Total**
JN.1	77.3%	89.5%	**82.9%**	76.9%	79.5%	**78.2%**
XBB.1.9	22.7%	10.5%	**17.1%**	23.1%	20.5%	**21.8%**
Total	**100.0%**	**100.0%**	**100.0%**	**100.0%**	**100.0%**	**100.0%**

* XBB.1.9 excludes EG.5

National Reference Laboratory for Acute Respiratory Infections
Department of Microbiology - **Laboratoire national de santé**
1, rue Louis Rech **|** L-3555 Dudelange
T : (+352) 28 100 523 **|** F : (+352) 28 100 512 **|** microbiology@lns.etat.lu **|** www.lns.lu
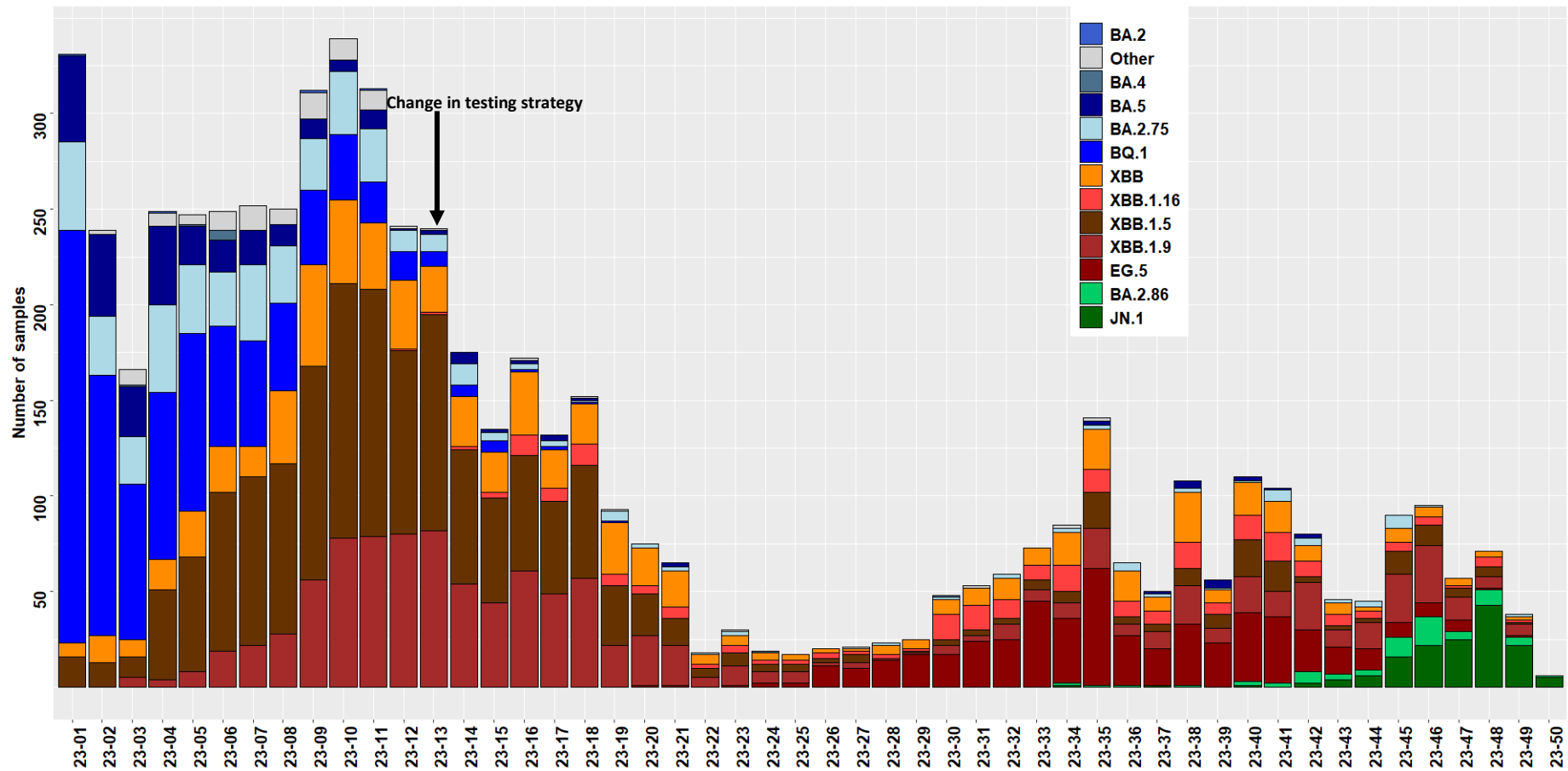
7

Figure 5. Distribution of lineages since beginning of 2023.

* All displayed variants include descendant lineages, except those specified on the legend. For example, XBB does not include XBB.1.5, XBB.1.16, EG.5 and XBB.1.9

National Reference Laboratory for Acute Respiratory Infections
Department of Microbiology - **Laboratoire national de santé**
1, rue Louis Rech | L-3555 Dudelange
T : (+352) 28 100 523 | F : (+352) 28 100 512 | microbiology@lns.etat.lu | www.lns.lu

8

References

European Centre for Disease Prevention and Control. SARS-CoV-2 variants of concern. Retrieved 02 January 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-17 -23 December 2023-week-51

GISAID. EpiCoV – Pandemic coronavirus causing COVID-19. Retrieved 02 January 2024, from https://www.gisaid.org

GitHub - cov-lineages/pangolin: Software package for assigning SARS-CoV-2 genome sequences to global lineages. (2023). Retrieved 02 January 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 02 January 2024, from https://www.who.int/activities/tracking-SARS-CoV-2-variant

National Reference Laboratory for Acute Respiratory Infections
Department of Microbiology - **Laboratoire national de santé**
1, rue Louis Rech **|** L-3555 Dudelange
T : (+352) 28 100 523 **|** F : (+352) 28 100 512 **|** microbiology@lns.etat.lu **|** www.lns.lu

9