# Respiratory Viruses in Luxembourg (ReViLux)

## Report – Sentinel Week 02 and Sequencing Update


## Summary

The sentinel network detected a high epidemic activity over the last week, based on 12.6 % 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 21.2% and 7.1% for SARS-CoV-2.

Influenza A positivity rates in sentinel data peaked during the week (2023/51) at 33.5% and decreased over the past two weeks to 21.2%, with 85% characterised as A(H1)pdm09 viruses and 15% 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 trending downwards with very low proportions currently circulating. Since week 2023/43, the proportions of BA.2.86 and JN.1 (descendent of BA.2.86) have continued to increase. The estimated distribution for JN.1 was 72.0% (95%CI: 64.1-79.9%), BA.2.86 was 16.8% (95%CI: 10.3-23.3%), and XBB.1.9 was 8.0% (95%CI: 3.2-12.8%) for weeks 2023/50-52. 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, 12.6% 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 for week 2024/01 are not presented. 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 (21.2%), followed by Human rhinovirus (18.6) and SARS-CoV-2(7.1%). Positivity rates of Influenza A decreased from 35.3% (2023/52) to 21.2% (2024/01). Sixty eight of 108 samples have been further characterized with 85% as A (H1)pdm09 and 15% as A (H3). First and only case of Influenza virus B was detected in week 2023/52. Test positivity for RSV decreased further from 28.5% (2023/51) to 4.7% (2024/02), however not all samples from

week 2024/02 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, 143 RSV detections were further subtyped as either RSV A (N=126, 87.4%) or RSV B (N=17, 11.9%). An overview of the circulating viral pathogens during the current and previous inter- season is displayed in Figure 2 and Table 2.

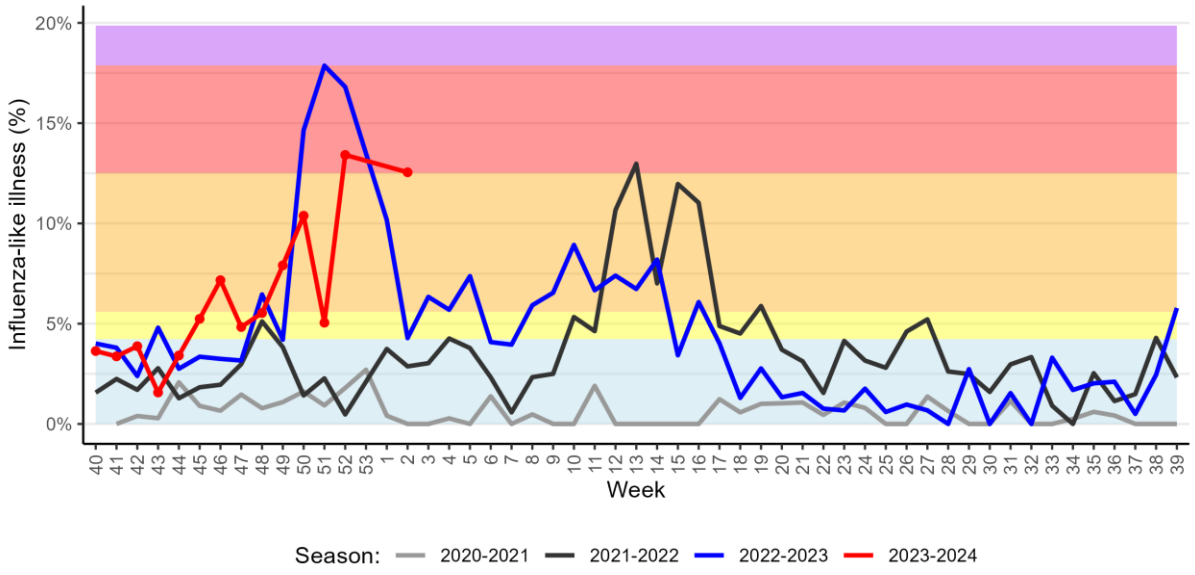


*Figure 1. Percentage of patients with influenza-like illness over the last three seasons*
*Background colours according to intensity of circulation: baseline, low, medium, high, very high. Data from 2024/01 not presented as low return*

*Table 1. Syndromic surveillance over the last 4 weeks*

| Week | ARI | | ILI | | Total consultations |
|---|---|---|---|---|---|
| | N | % | N | % | |
| 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 |
| 2024/02 | 34 | 13.77 | 31 | 12.55 | 247 |

*ARI: Acute Respiratory Infections; ILI: Influenza-Like Illness.*
*Data from 2024/01 not presented as low return*

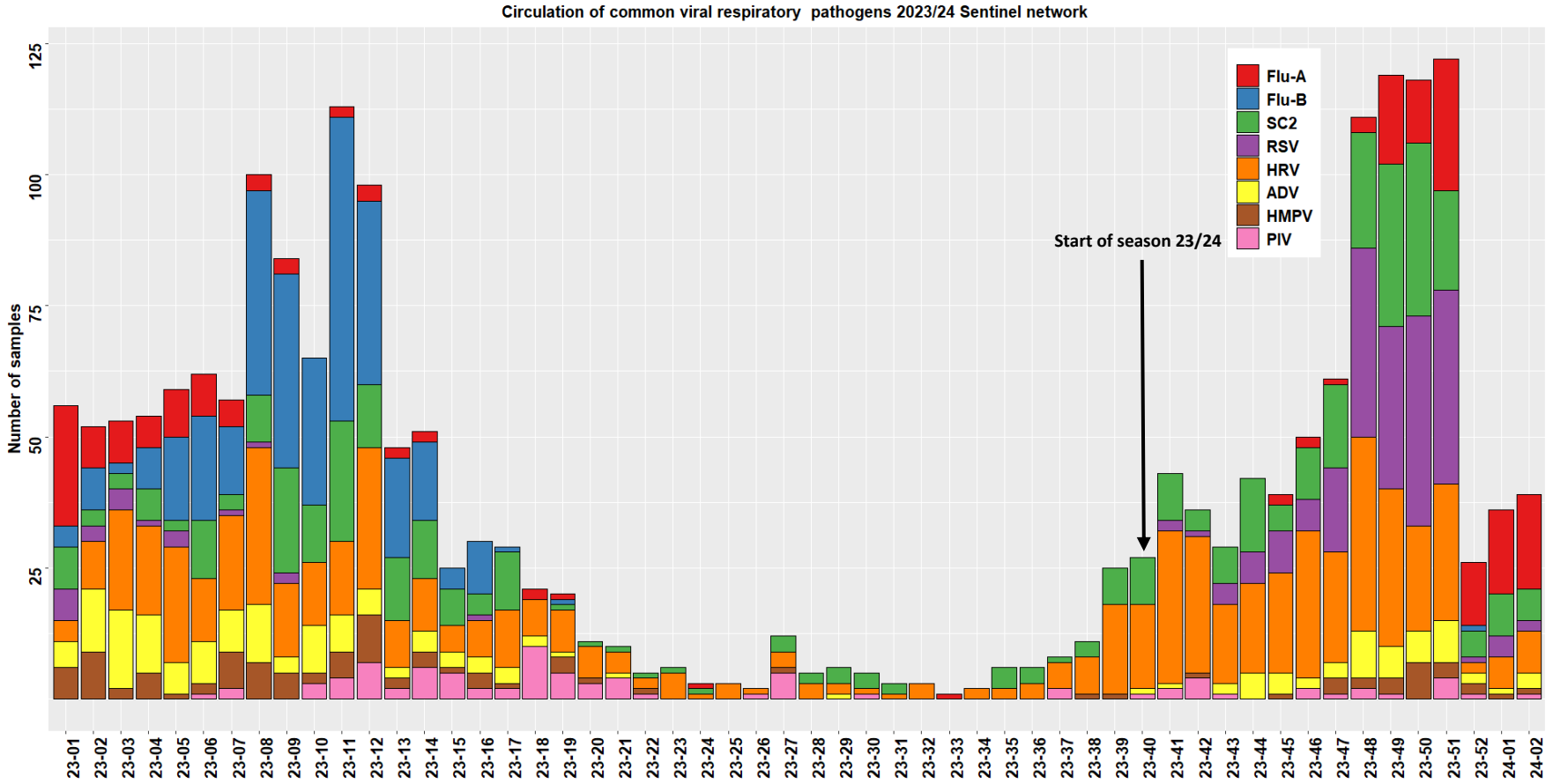


*Figure 2. Distribution of respiratory viruses detected within the Sentinel Network, by calendar week. Results from last weeks are not yet consolidated.*
*FLU-A: influenzavirus A; FLU-B: influenzavirus B; PIV: parainfluenzavirus; RSV: respiratory syncytial virus; ADV: adenovirus; MPV: metapneumovirus; HRV: human rhinovirus; SC2: SARS-CoV-2.*



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*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 % | | | | | |
| | w51 | w52 | w01 | w02 | Trend | w02 |
| Influenzavirus A | 18.9 | 35.3 | 26.2 | 21.2 | ↓ | 8.9 |
| Human rhinovirus | 20.0 | 5.9 | 9.8 | 18.6 | ↑ | 10.3 |
| SARS-CoV-2 | 14.4 | 14.7 | 13.1 | 7.1 | ↓ | 3.3 |
| Adenovirus | 6.2 | 5.9 | 1.6 | 7.0 | → | 13.8 |
| Respiratory syncytial virus | 28.5 | 2.9 | 6.6 | 4.7 | ↓ | 3.4 |
| Metapneumovirus | 2.3 | 5.9 | 1.6 | 2.3 | → | 10.3 |
| Parainfluenzavirus | 3.1 | 2.9 | 0.0 | 2.3 | → | 0.0 |
| Influenzavirus B | 0.0 | 0.0 | 2.9 | 0.0 | | 8.9 |

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

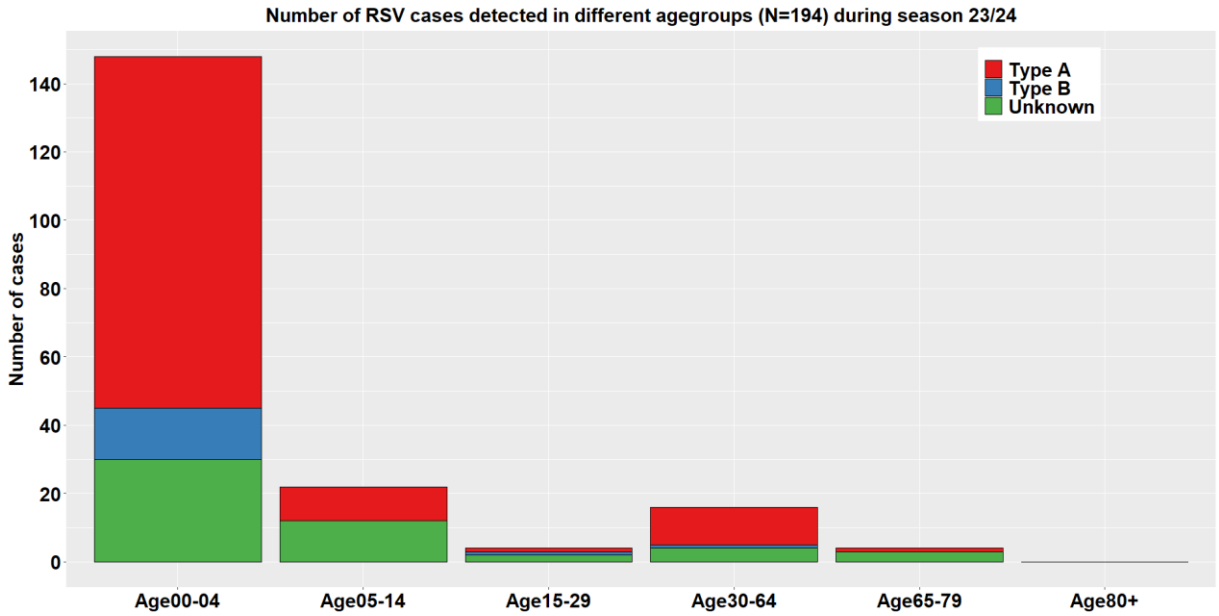


*Figure 3. Displays RSV cases according to different age groups with highest impact among the 0-4 years old.*

## 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.

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

203 samples from 2,551 cases (8.0%) reported in Luxembourg were sequenced with specimen dates between week 2023/49 and 2023/52. Approximately 75% 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 11th and 31st of December 2023 (2023/50-52), the estimated distribution was 72% for JN.1, 16.8% for BA.2.86 and 8.0% for XBB.1.9. JN.1 is closely related to BA.2.86 with only one change in the spike protein, but rapidly growing.

An overview of the variants and lineages circulating over the past 20 weeks 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 2023/47 to 2023/52. Previously reported cases might be updated by retrospective analysis.*

| Lineage | weeks 47-49 | | weeks 50-52 | |
|---|---|---|---|---|
| | % | CI % | % | CI % |
| **JN.1** | **53.0** | **46.4 – 59.6** | **72.0** | **64.1 – 79.9** |
| BA.2.86 | 11.9 | 7.6 – 16.2 | 16.8 | 10.3 – 23.3 |
| Recomb XBB.1.9 | 17.4 | 12.3 – 22.4 | 8.0 | 3.2 – 12.8 |
| Recomb XBB.1.5 | 5.5 | 2.5 – 8.5 | 1.6 | 0.0 – 3.8 |
| Recomb XBB.1.16 | 3.2 | 0.9 – 5.5 | 0.8 | 0.0 – 2.4 |
| Recomb EG.5 | 4.6 | 1.8 – 7.3 | 0.8 | 0.0 – 2.4 |
| Recomb XBB | 4.1 | 1.5 – 6.7 | 0 | 0.0 – 0.0 |

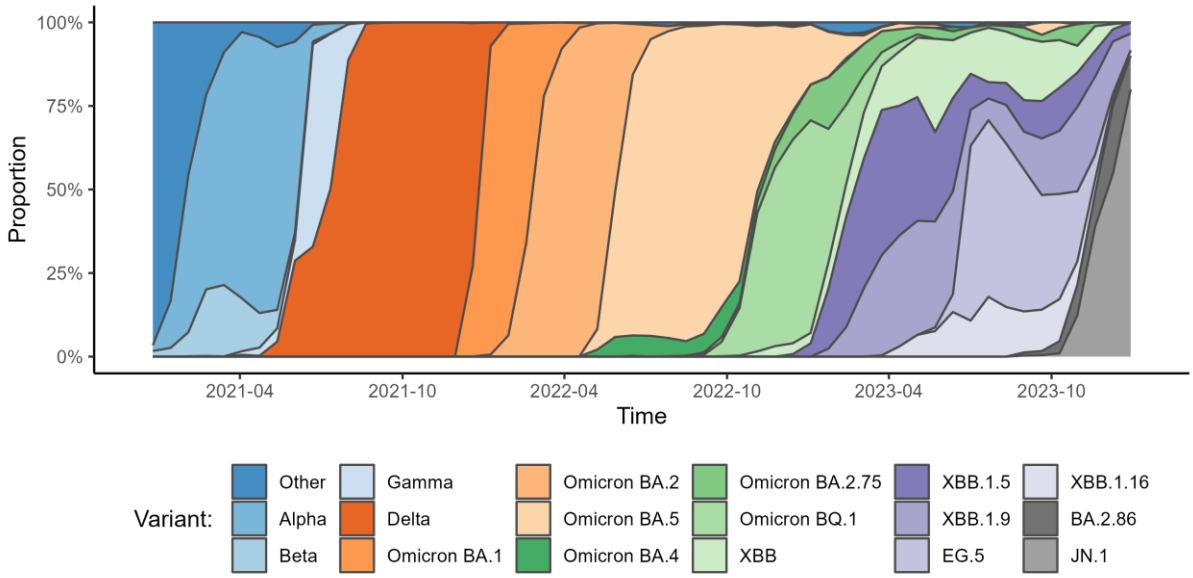


*Figure 4. Proportion of each variant circulating in Luxembourg since January 2021.*
*All displayed variants include descendant lineages, except those specified on the legend. For example, XBB does not include XBB.1.5, XBB.1.16, EG.5 and XBB.1.9*

## Clinical and epidemiological factors

Over the past 4 weeks, 150 (73.9%) samples from hospital laboratories and 53 (26.1%) samples from private laboratories/ sentinel practitioners were sequenced. Table 4 compares sampling setting of JN.1 (descendent lineage of BA.2.86) and BA.2.86 variants.

*Table 4. Comparison of lineage distribution by sampling setting.*

| Lineage | Community | | | Hospital | | |
|---|---|---|---|---|---|---|
| | Women | Men | **Total** | Women | Men | **Total** |
| JN.1 | 80.0% | 78.3% | **79.1%** | 84.3% | 81.2% | **82.5%** |
| BA.2.86 | 20.0% | 21.7% | **20.9%** | 15.7% | 18.8% | **17.5%** |
| **Total** | **100.0%** | **100.0%** | **100.0%** | **100.0%** | **100.0%** | **100.0%** |


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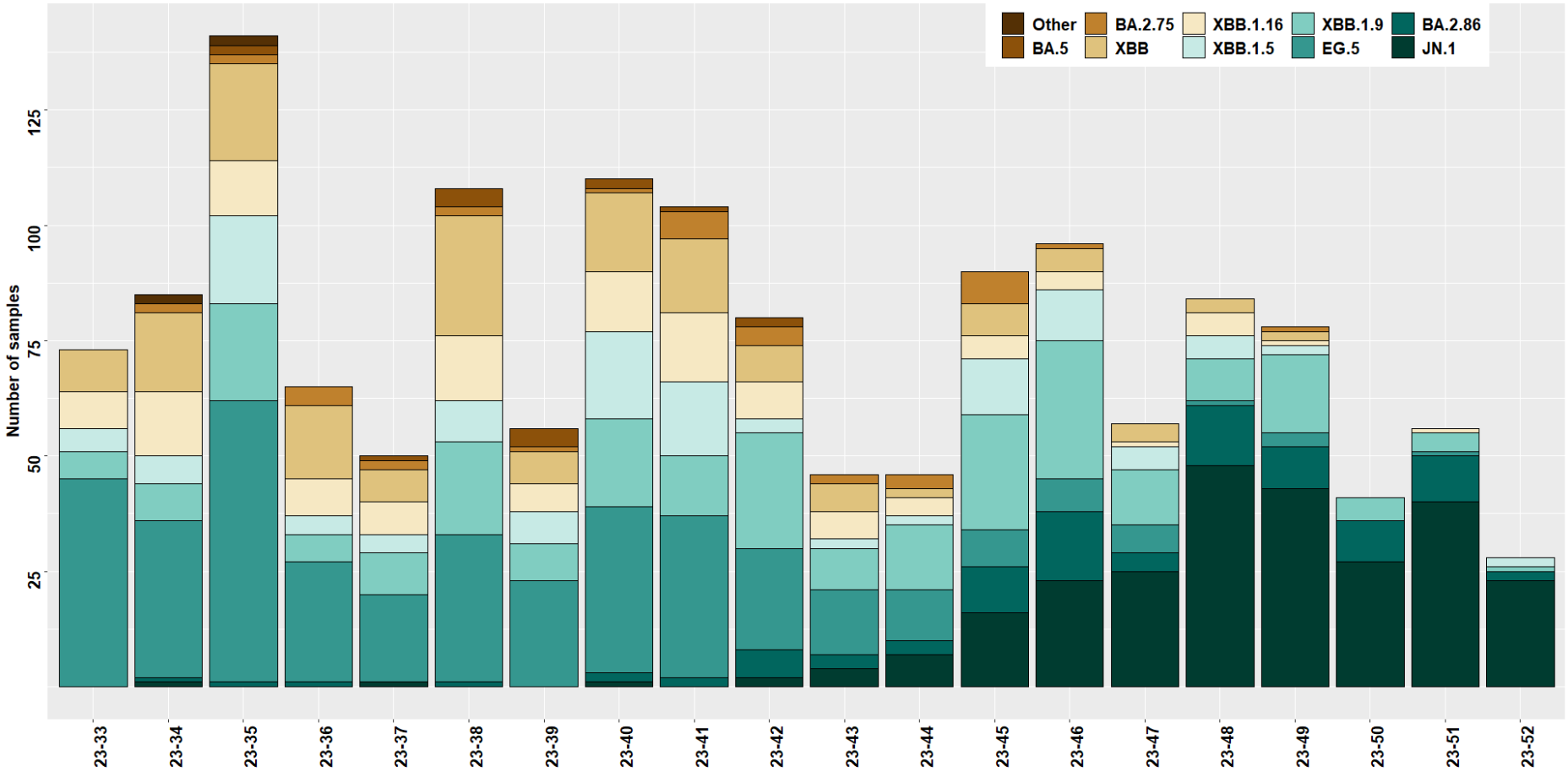


*Figure 5. Distribution of lineages since 2023/33(last 20 weeks).*

** 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*



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# References

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

GISAID. EpiCoV – Pandemic coronavirus causing COVID-19. Retrieved 16 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 16 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 16 January 2024, from https://www.who.int/activities/tracking-SARS-CoV-2-variant



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