

Respiratory Viruses in Luxembourg (ReViLux)

Monthly report – August 2023

Executive summary

The sentinel network detected a low/ baseline epidemic activity over the last four weeks, based on 0.0- 3.3 % of consultations being associated with influenza-like illness. Among the specimen collected by the sentinel network over the last four weeks, the percentage of positive tests for Human rhinovirus were 30.8% and 11.8% for SARS-CoV-2, but Influenza activity remained low.

Concerning SARS-CoV-2 genomic surveillance, since late February 2023 recombinant strains that combine characteristics of other variants have been dominant in Luxembourg. During the month of August, the estimated distribution of recombinant EG.5 (descendant of XBB.1.9.2) was 52.7% (95%CI: 45.1-60.2 %), followed by XBB with 15.4 (95%CI: 9.9-20.8%). Proportions of XBB.1.5 and XBB.1.9 (excluding EG.5) have declined over the last few weeks to 10% and 8 % respectively.

BA.2.86- newly designated variant of SARS-CoV-2

BA.2.86 has a high number of mutations within the long branch of the spike protein and is distant from its likely ancestor BA.2 and also from the currently circulating XBB variants. The BA.2.86 has been detected in several countries in different regions, with no known epidemiological link to a common source. No cases have been identified in Luxembourg so far.

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 over 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, one consultation was reported as ILI, which represents a baseline epidemic activity for Luxembourg, according to ECDC and the Moving Epidemic Method. 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 four weeks, the most frequently detected viruses (according to positivity rates) were Human rhinovirus (30.8%), followed closely by SARS-CoV-2 (11.8%). Detected Influenza remains low within the sentinel network. An overview of the viral circulation during the current and previous inter- season is displayed in Figure 2 and Table 2.

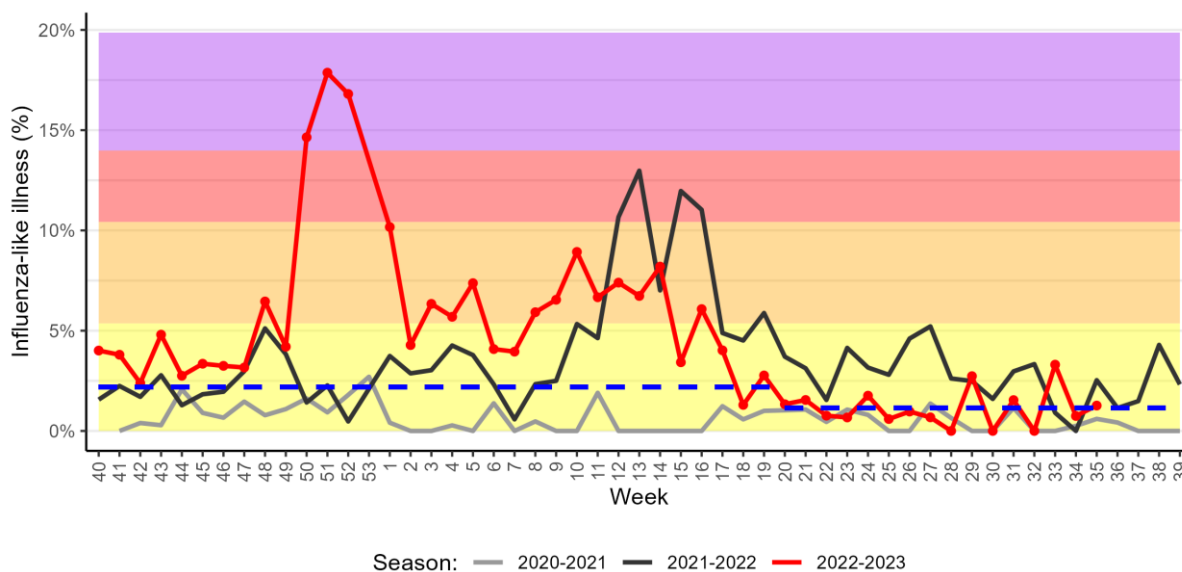


Figure 1. Percentage of patients with influenza-like illness over the last three seasons
Background colours according to intensity of circulation: low, medium, high, very high.

Table 1. Syndromic surveillance over the last 4 weeks

Week	ARI		ILI		Total consultations
	N	%	N	%	
2023/32	26	13.13	0	0.00	198
2023/33	12	9.92	4	3.31	121
2023/34	16	11.94	1	0.75	134
2023/35	6	7.59	1	1.27	79

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

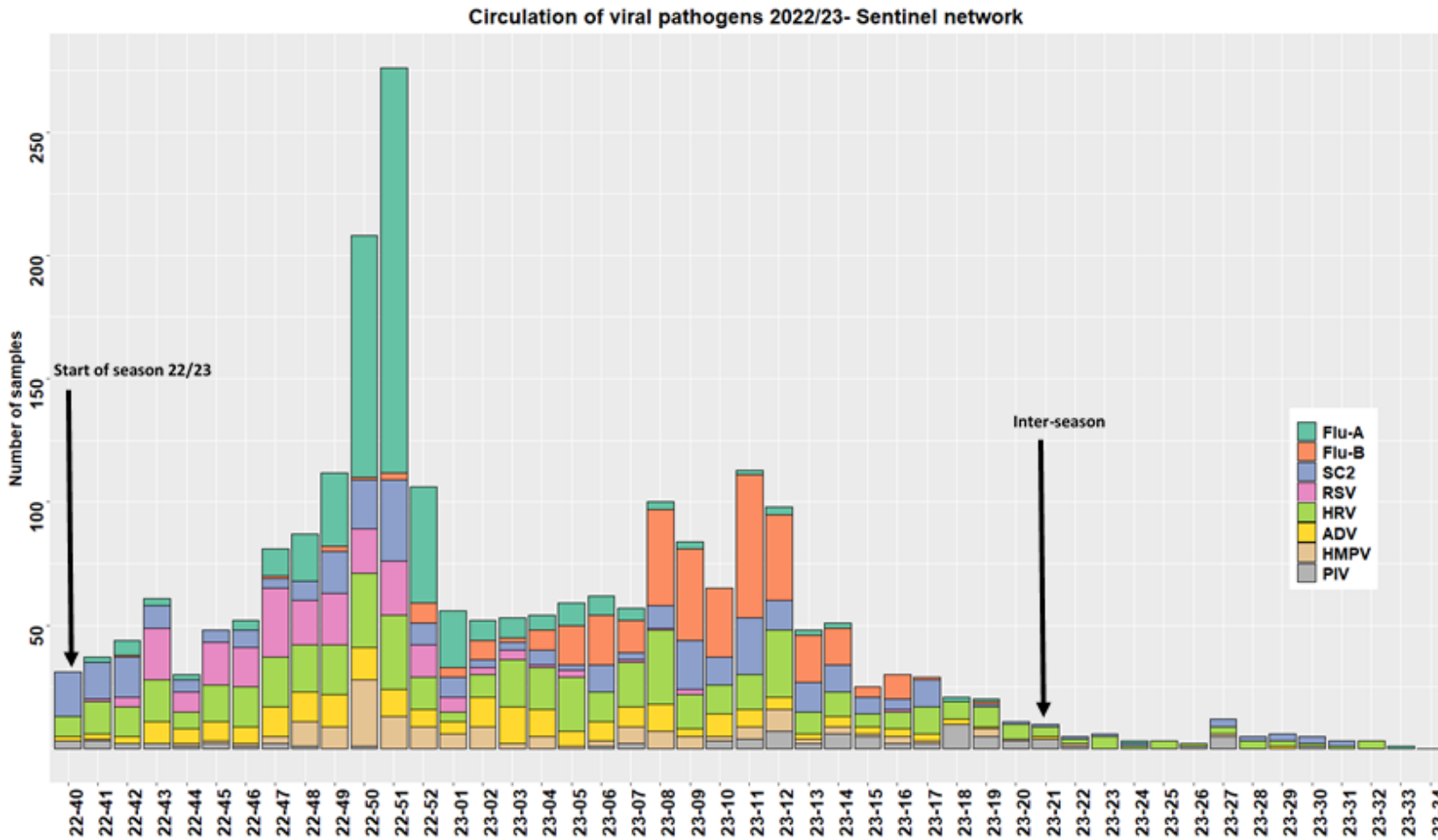


Figure 2. Distribution of respiratory viruses detected within the Sentinel Network, by calendar week. Results from last weeks are not yet consolidated. FLU-A: influenza virus A; FLU-B: influenza virus B; PIV: parainfluenza virus; RSV: respiratory syncytial virus; ADV: adenovirus; MPV: metapneumovirus;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

Table 2. Distribution of respiratory viruses detected within the Sentinel Network during weeks 31-34 compared to previous inter-season.

Virus	Inter-season 22/23 (w31-w34)		Inter-season 21/22 (w31-w34)	
	N*	Positivity rate (%)	N*	Positivity rate (%)
Human rhinovirus	4	30.8	7	30.4
SARS-CoV-2	2	11.8	8	24.2
Influenzavirus A	1	5.6	3	7.5
Respiratory syncytial virus	0	0.0	1	3.3
Influenzavirus B	0	0.0	0	0.0
Adenovirus	0	0.0	0	0.0
Parainfluenzavirus	0	0.0	0	0.0
Metapneumovirus	0	0.0	0	0.0
Total	7		19	

*Co-infection cases counted once for each virus detected.

Genotyping analyses

In order to assess the circulation of viral strains, genotyping analyses were also performed for Influenzavirus A and Respiratory syncytial virus (RSV) (Figure 3). During the last season (22/23), the most frequently detected strain for Influenzavirus A was H3 (87.8%), and for RSV it was type B (74.3%). Within the sentinel network RSV activity remains also low.

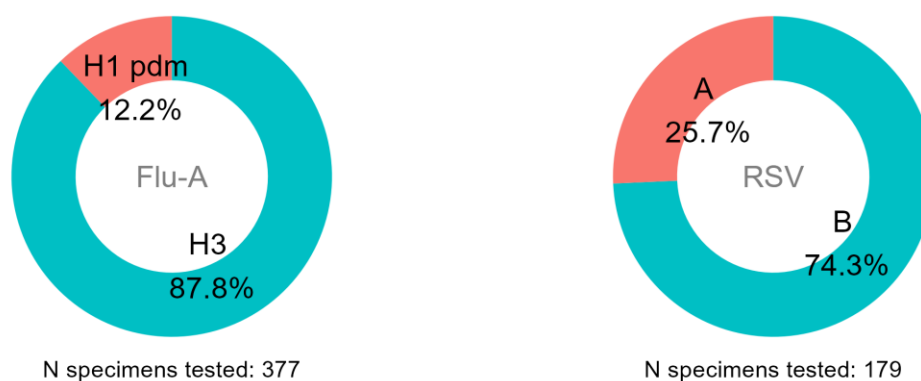


Figure 3. Detection of influenza virus-A (Flu-A) and Respiratory syncytial virus (RSV) strains in sentinel samples during the current season.

SARS-CoV-2 Genomic Surveillance

SARS-CoV-2 has posed a serious threat to the world population since 2020, but over the past 12 months increased immunity and the availability of highly effective vaccines have decreased the pressure on the health system. However, the risk of new variants emerging remains and monitoring on lower scale is still required.

Changes to SARS-CoV-2 testing came into effect at the end of March 2023, with reduction in the use of PCR testing. This will also affect the genomic surveillance and sequencing data will be biased towards hospital admissions and more severe cases. However, LNS continues to monitor, assess risks and prepare the next season.

LNS receives positive specimens (nasopharyngeal or oropharyngeal swabs analysed by RT-PCR) from the national network of laboratories. All hospital specimens are sequenced, as well as a representative selection of community specimens. Illumina and Nanopore devices are used. When needed, an additional screening by targeted PCR is also performed to enable earlier evaluation of the spread of newly emerging variants.

Bioinformatic analyses are based on a standardised pipeline, and lineage assignment is performed through the PANGOLin software (4.3, pango-data 1.21, mode UShER). In order to allow easier visualisation, WHO and Nextstrain categorisations are also used.

Sequencing activity

274 samples from cases registered in Luxembourg were sequenced with specimen dates between week 2023/30 and 2023/34. Approximately 33% were samples from the hospital and remaining samples were community samples. Sequencing data probably does not fully represent virus circulation within the population.

Variant circulation

From Luxembourg collected sequences from 7th to 27th of August 2023, 52.7% were classified as EG.5 (descendant of XBB.1.9.2) and 15.4 % of other XBB. The proportion of EG.5 increased slightly from 44.6 % to 52.7% over the last three weeks. Omicron sub-variant BA.2.86 has not yet been identified in Luxembourg. 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 2023/29 to 2023/34. Previously reported cases might be updated by retrospective analysis.

Lineage	weeks 29-31		weeks 32 -34	
	%	CI %	%	CI %
Recomb EG.5	44.6	36.1 – 53.2	52.7	45.1 – 60.2
Recomb XBB*	16.9	10.4 – 23.4	15.4	9.9 – 20.8
Recomb XBB.1.16	22.3	15.2 – 29.5	12.4	7.5 – 17.4
Recomb XBB.1.9*	7.7	3.1 – 12.3	10.1	5.5 – 14.6
Recomb XBB.1.5	6.2	2.0 – 10.3	8.3	4.1 – 12.4
Others	2.3	0.0 – 4.9	1.2	0.0 – 2.8

*XBB excludes EG.5, XBB.1.16, XBB.1.5 and XBB.1.9 and XBB.1.9 excludes EG.5

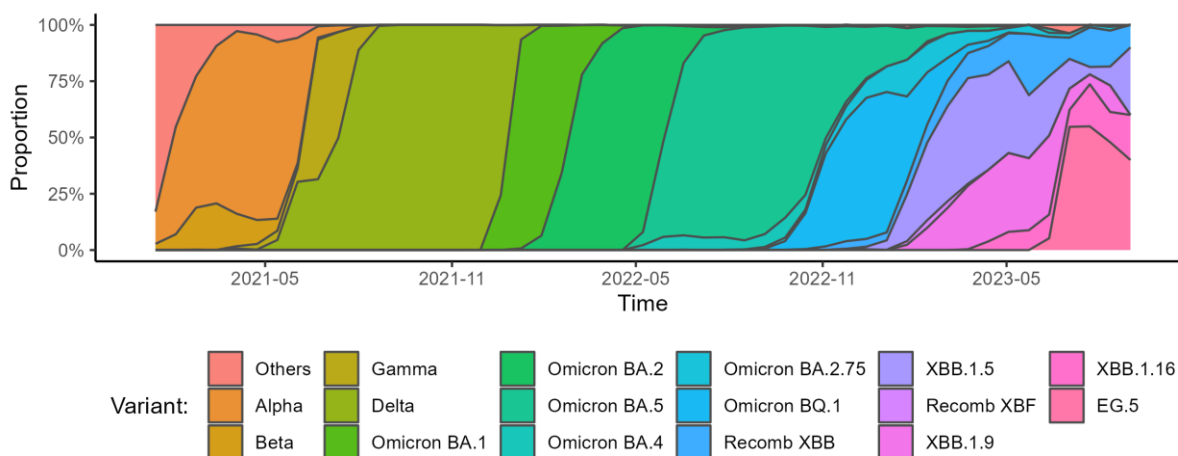


Figure 4. Proportion of each variant circulating in Luxembourg since January 2021.

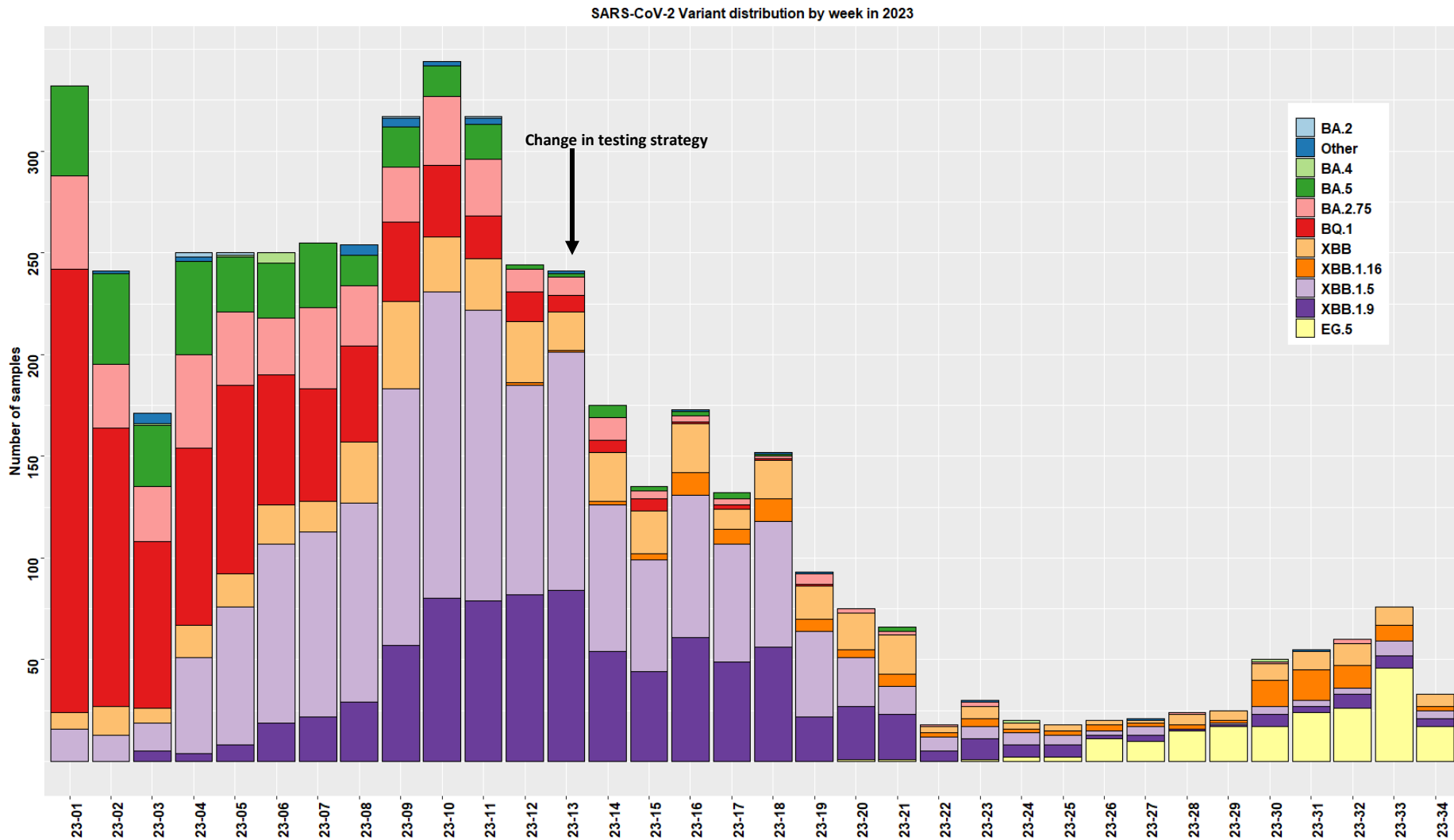


Figure 5. Distribution of lineages since beginning of 2023.

Clinical and epidemiological factors

In this section, the lineage distribution of all specimens sequenced over the last month is assessed by demographics (sex and age group, Figure 6) and sampling setting (community vs. hospital, Table 4).

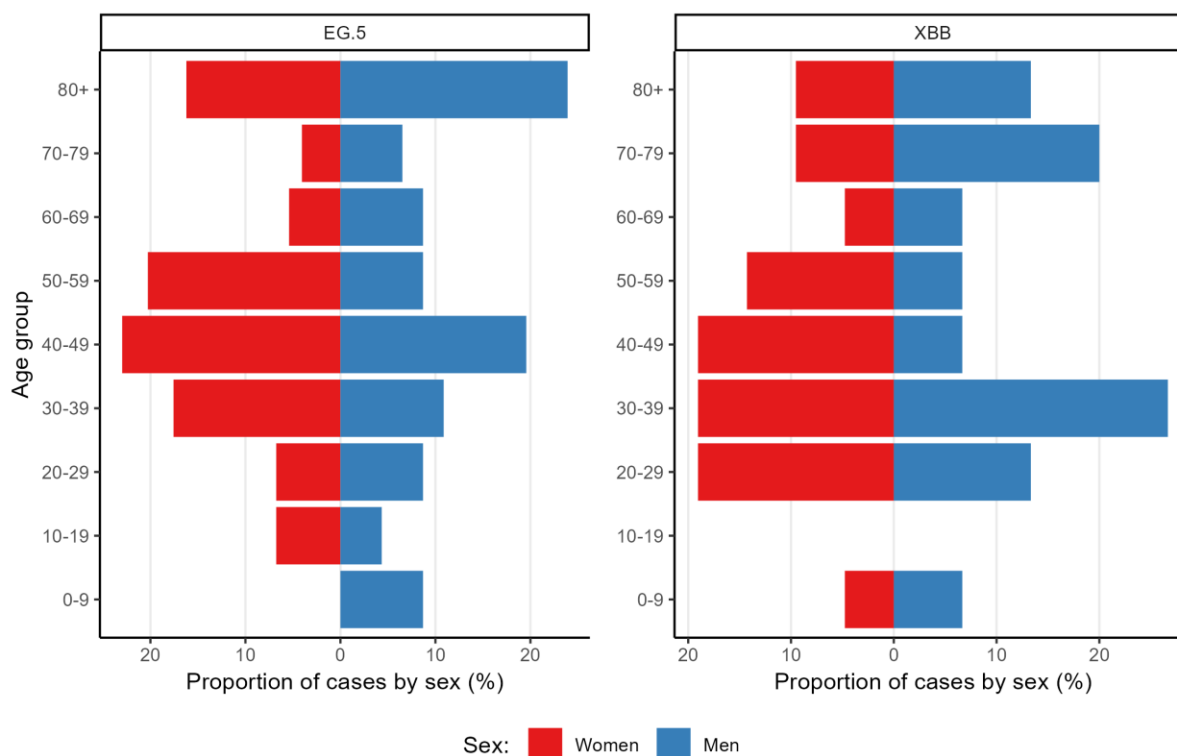


Figure 6. Age group and sex distribution of specimens sequenced over the last 4 weeks, by lineage.

Table 4. Comparison of lineage distribution by sampling setting.

Lineage	Community			Hospital		
	Women	Men	Total	Women	Men	Total
Recomb EG.5	74.6%	81.1%	77.0%	84.4%	66.7%	76.8%
Recomb XBB	25.4%	18.9%	23.0%	15.6%	33.3%	23.2%
Total	100.0%	100.0%	100.0%	100.0%	100.0%	100.0%

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