Respiratory Viruses in Luxembourg (ReViLux)

Weekly report (9 – 15 May 2022)

Executive summary

The sentinel network reported 5.9% consultations for influenza-like illness, thus exceeding the baseline circulation threshold, according to the European Center for Disease Prevention and Control (ECDC). Within the specimens collected by the sentinel network, SARS-CoV-2 was the most frequently detected virus over the last four weeks (35.6%), followed by Influenzavirus A (29.5%) and Human rhinovirus (15.9%).

Regarding the SARS-CoV-2 genomic surveillance, LNS sequenced 633 specimens from residents in Luxembourg in week 19 (of 2704 total cases in the Grand Duchy of Luxembourg; 23.4%). This meets the ECDC recommendations to detect emerging variants. Including PCR screening results, 865 national specimens were analysed globally (32.0%).

The Omicron variant remains the dominant one in the representative sample. The Omicron BA.2 lineage is the most frequent one (92.7%), followed by Omicron BA.5 (5.5%), which showed a strong increase since last week (0.8%).

All specimens analysed: **926**

National specimens analysed: **865**

National analysis coverage: **32.0%**

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. There are currently two active projects:

- **The Sentinel Surveillance Network**. It provides a broad picture of respiratory diseases affecting the Luxembourgish population, based on its double monitoring system (syndromic and virological).
- **The National SARS-CoV-2 Genomic Surveillance Program**. It enables detailed observation of SARS-CoV-2 mutations and variants through time and space, and also monitoring specific groups of interest.

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

Sentinel Surveillance Network

The **Sentinel Surveillance Network** aims at monitoring the circulating respiratory viruses, including SARS-CoV-2, and hence underpin public health actions. Following the World Health Organization (WHO) and European Centre for Disease Prevention and Control (ECDC) guidance, it focuses on cases of acute respiratory infection (ARI) and influenza-like illness (ILI).

The current influenza season started in week 40/2021, and the history of ILI consultations is displayed in Figure 1. A detailed summary of the number of ARI and ILI cases during the last four weeks is included in Table 1. In the week of study, 5.9% of consultations were reported as ILI, thus exceeding the threshold for baseline circulation, according to ECDC (2.59%).

Table 1. Syndromic surveillance over the last 4 weeks

Week	ARI		ILI		Total consultations
	N	%	N	%	
2022/16	16	11.76	15	11.03	136
2022/17	39	10.03	19	4.88	389
2022/18	42	11.14	17	4.51	377
2022/19	29	13.12	13	5.88	221

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

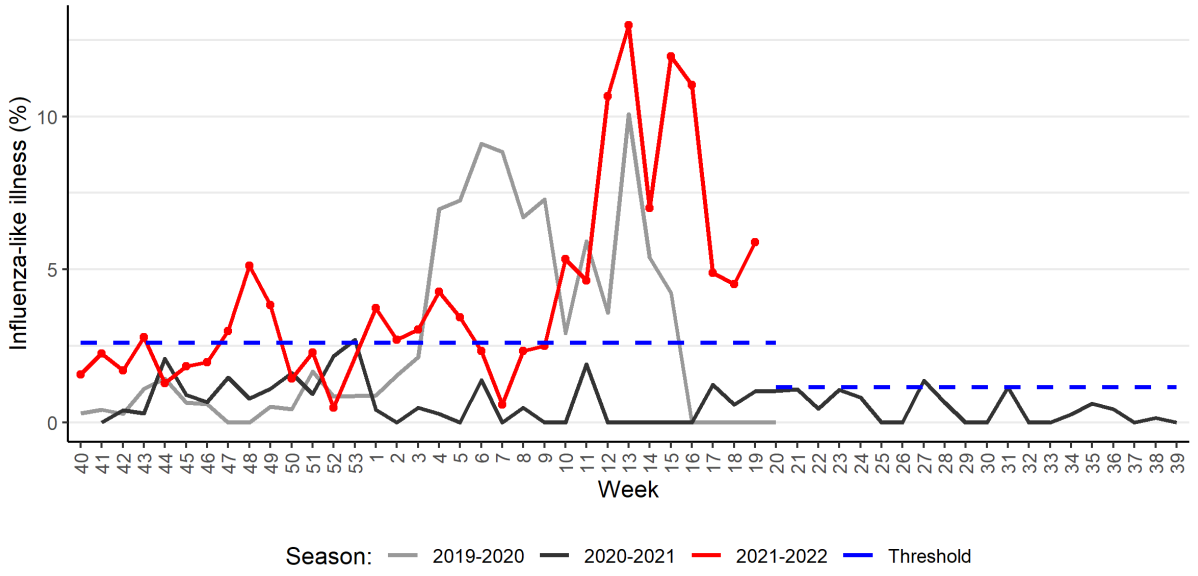

Figure 1. Percentage of patients with influenza-like illness over the last three seasons

Additionally, a selection of sentinel cases is further studied, as shown in Figure 2. Over the last 4 weeks, the positivity rate was at 60.6%, and the most frequently detected viruses were: SARS-CoV-2 (35.6%), Influenzavirus A (29.5%) and Human rhinovirus (15.9%). Co-infections were detected in 6 specimens, 1 involving influenza A and 2 involving SARS-CoV-2. These results are displayed more in detail in Table 2.

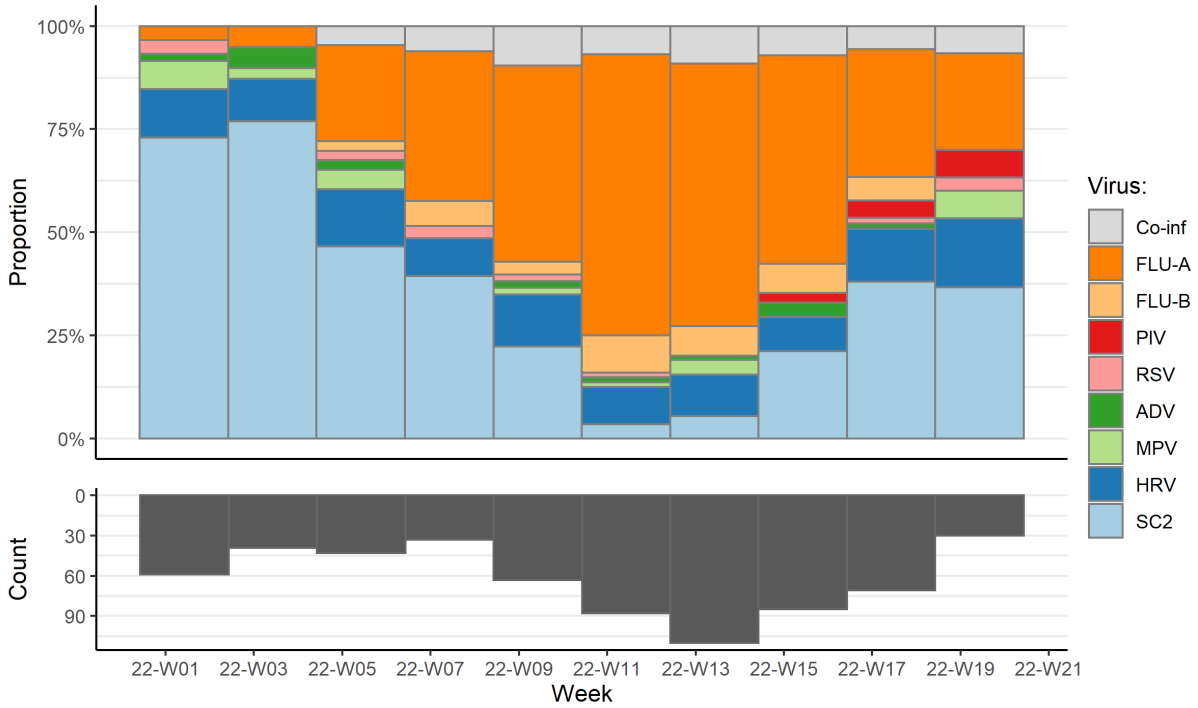

Figure 2. Distribution of respiratory viruses detected within the Sentinel Network, by two-week periods. Results from last weeks are not yet consolidated.

Co-inf: co-infection; FLU-A: influenzavirus A; FLU-B: influenzavirus B; PIV: parapneumovirus; 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 over the last 4 weeks and during the current season.

Virus	Last 4 weeks		Current season	
	N*	%	N*	%
SARS-CoV-2	47	35.6	329	35.7
Influenzavirus A	39	29.5	286	31.1
Human rhinovirus	21	15.9	167	18.1
Influenzavirus B	7	5.3	34	3.7
Metapneumovirus	2	1.5	30	3.3
Parainfluenzavirus	8	6.1	27	2.9
Adenovirus	6	4.5	25	2.7
Respiratory syncytial virus	2	1.5	23	2.5
Total	**132**	**100.0**	**921**	**100.0**

Co-infection cases counted once for each virus detected.

SARS-CoV-2 Genomic Surveillance

The current sequencing strategy

The National Reference Laboratory for Acute Respiratory Infections at LNS receives SARS-CoV-2 positive samples (nasopharyngeal or oropharyngeal swabs analysed by RT-PCR) from the national network of laboratories and proceeds as follows:

1. Sequencing a representative sample of specimens.
2. Sequencing specimens from target groups (i.e. hospital cases and post-vaccination cases).
3. Sequencing specimens from clusters with high transmission.

The representative sample of specimens is a systematic selection from all SARS-CoV-2 positive cases registered in Luxembourg to detect emerging variants and early increases in their incidence and transmission within the community in Luxembourg. This sample is selected according to the ECDC guidelines.

Since the emergence of the Omicron variant of concern, and given the high incidence rates in the European context, targeted PCR tests are carried systematically in order to get an earlier interim evaluation of the variants in circulation. The PCR kits currently used target the following spike mutations: 69/70del, K417N, N501Y.

SARS-CoV-2 lineages have been assigned based on Rambaut et al. using the Phylogenetic Assignment of Named Global Outbreak LINeages (pangolin) software (4.0.6, designation v1.8). The Pango nomenclature is used in addition to the WHO nomenclature to enable easier visualization of links between any evolving variants and their ancestor.

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Screening and sequenced specimens

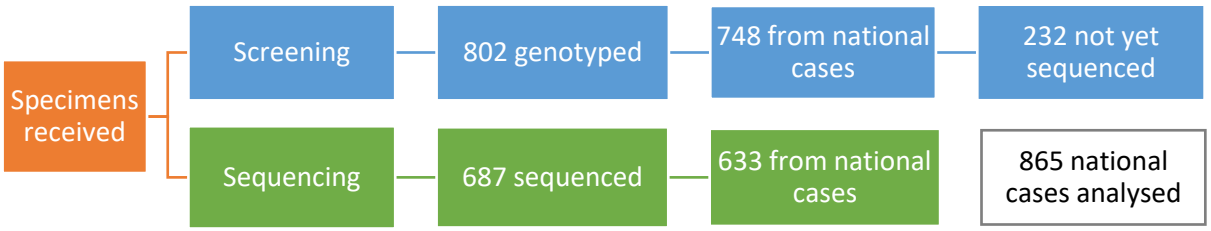

Figure 3. Flowchart of specimens collected during week 19/2022

In week 19, 2704 new cases were registered in Luxembourg; hence, the minimum sample size required to detect emerging variants at a 2.5% incidence is estimated to be 491 specimens (18.2%).

As shown in Figure 3, of all specimens received from the week of study, 802 were screened by targeted PCR for the Omicron variant (including 748 national specimens), in order to enable an earlier detection of potential Omicron cases (see results in the following section). In parallel, the microbial genomics unit at the LNS sequenced 687 specimens, including 633 national ones. The weekly sequencing coverage remains at 23.4% (out of 2704 cases registered in Luxembourg; see coverage trend in Figure 4), which exceeds the recommended sample size. Overall, 865 national specimens were analysed either by sequencing or screening (32.0%).

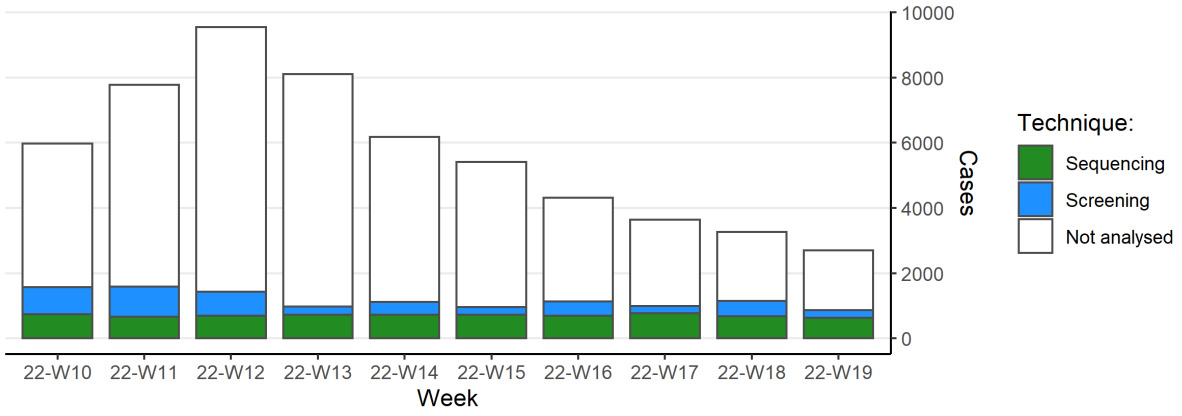

Figure 4. National coverage based on weekly number of positive cases in Luxembourg. The coverage from the latest weeks might not be consolidated yet.

Screening results

As shown in Figure 5, the PCR screening suggests that Omicron BA.2 will continue to be the dominant lineage, while a different Omicron lineage keeps increasing its circulation.

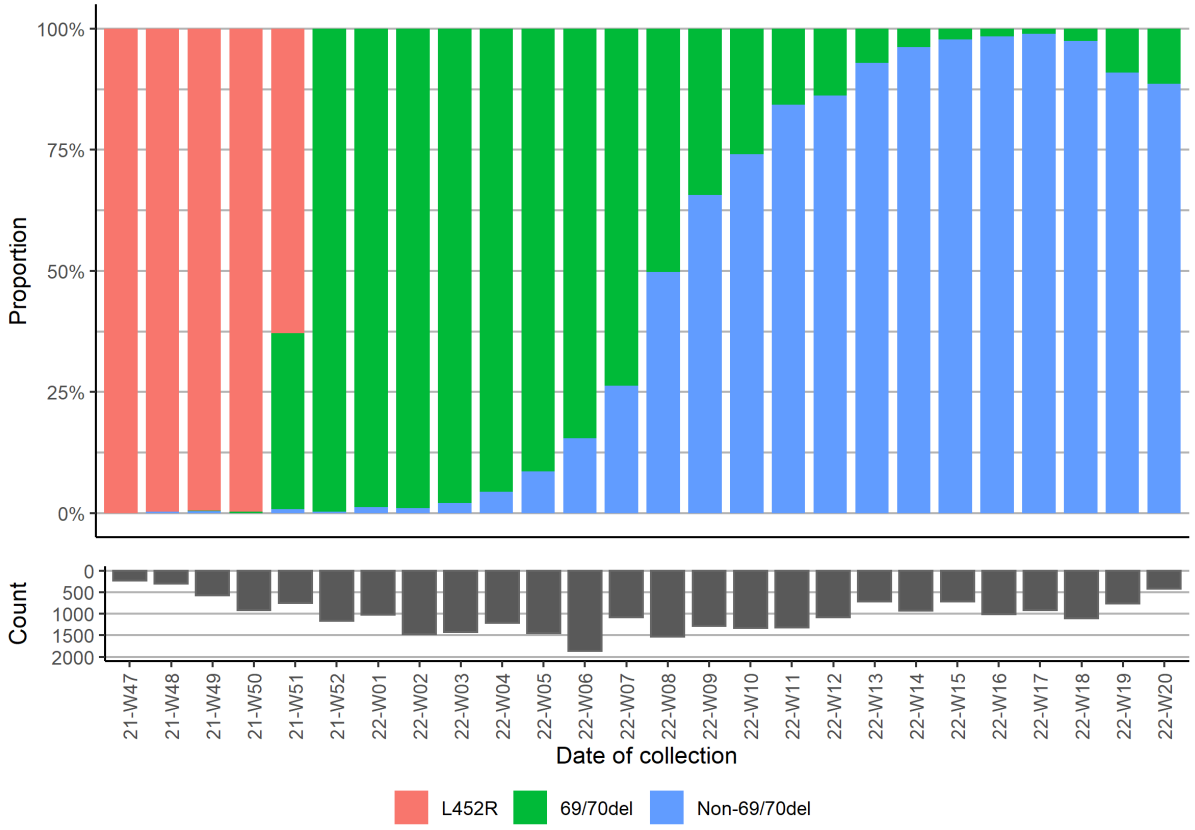

Figure 5. Distribution of specimens included in the screening for the Omicron variant by date of collection. Results more recent than the week of study are not yet consolidated.

Circulating lineages detection

The distribution of successfully assigned lineages within the national selection is shown in Figure 6, and it is further detailed in Table 4 (last two weeks). A summary of the VOCs assigned among all specimens sequenced (including non-residents) during the last two weeks and since the beginning of the sequencing activity is shown in Table 5.

The Omicron variant remains the dominant one within the representative sample, the most frequent lineage being Omicron BA.2 (92.7%), followed by Omicron BA.5 (5.5%). Additionally, three recombinant specimens (BA.1+BA.2) were also detected, but could not be assigned to any lineage.

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Table 4. Distribution of SARS-CoV-2 lineages detected within the representative sample during the last two weeks. Previously reported cases might be updated by retrospective analysis.

Lineage	Previous week			Current week		
	N	%	CI %	N	%	CI %
Omicron BA.2	498	98.2	97.1 - 99.4	455	92.7	90.4 - 95.0
Omicron BA.4	5	1.0	0.1 - 1.8	9	1.8	0.6 - 3.0
Omicron BA.5	4	0.8	0.0 - 1.6	27	5.5	3.5 - 7.5
Total	**507**	**100.0**	**-**	**491**	**100.0**	**-**

CI: Confidence Interval at 95%.

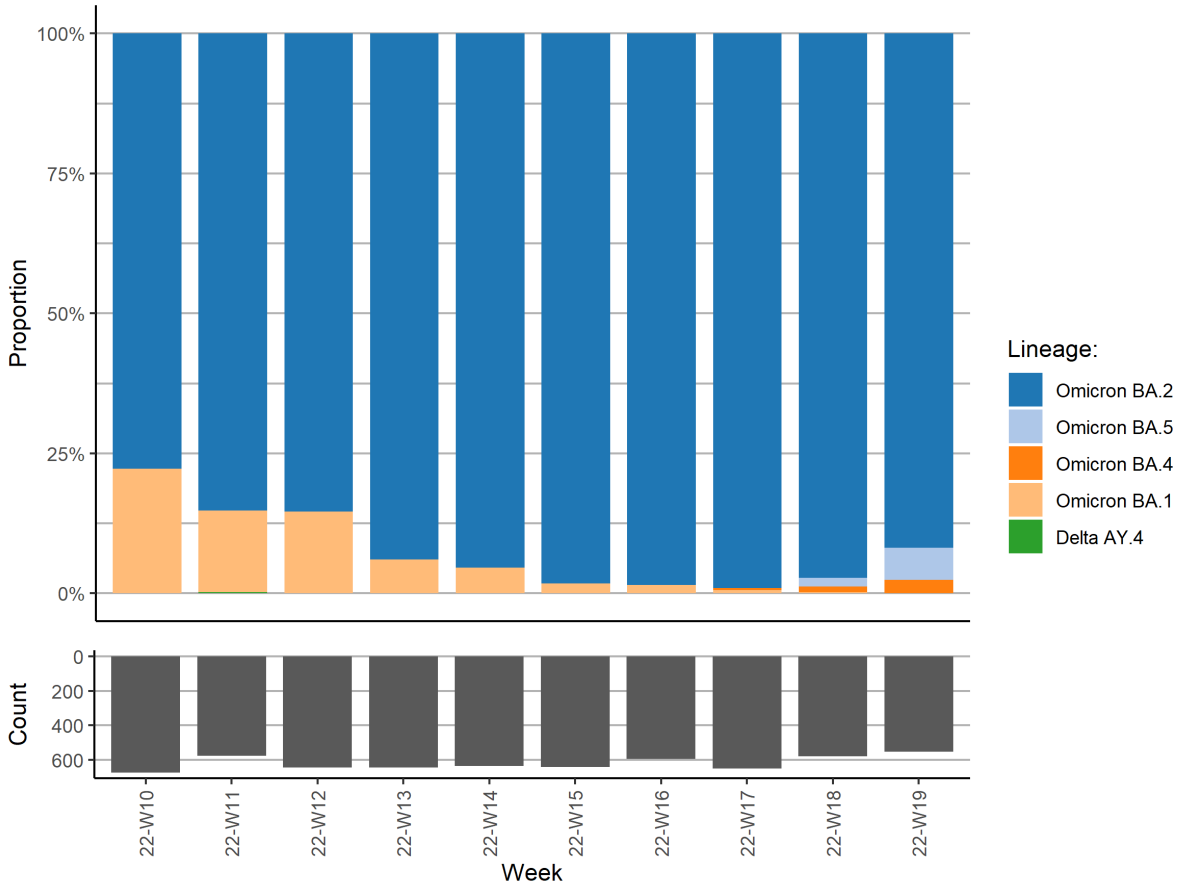

Figure 6. Distribution of lineages within the representative sample during the last 10 weeks.

Table 5. Distribution SARS-CoV-2 lineages detected within all samples sequenced since the beginning of the pandemic.

Variant	Previous week		Current week		Cumulative count
	N	%	N	%	
Omicron	603	100	589	100	15 101
BA.1	1	0.2	0	0	7 541
BA.2	587	97.3	544	92.4	7 498
BA.4	6	1.0	13	2.2	21
BA.5	9	1.5	32	5.4	41
Delta	0	0	0	0	13 678
Gamma	0	0	0	0	1 416
Beta	0	0	0	0	1 330
Others	0	0	0	0	12 259
Total	**603**	**100**	**589**	**100**	**43 784**

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 7), sampling setting (community vs. hospital, Table 6) and vaccination status (not vaccinated vs. fully vaccinated, Table 7).

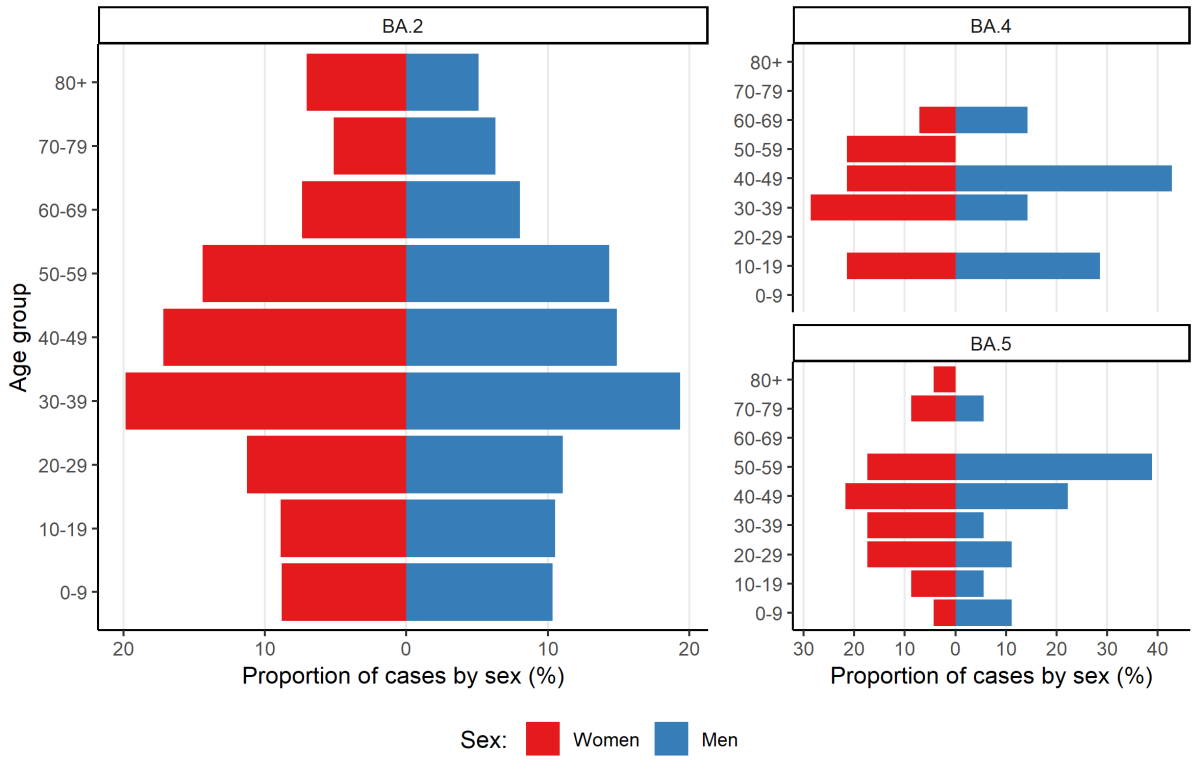

Figure 7. Age group and sex distribution of specimens sequenced over the last 4 weeks, by lineage.

Table 6. Comparison of lineage distribution by sampling setting.

Lineage	Community			Hospital		
	Women	Men	Total	Women	Men	Total
Omicron BA.2	97.1%	97.2%	97.1%	94.9%	97.8%	96.3%
Omicron BA.5	1.6%	2.1%	1.8%	4.1%	1.1%	2.6%
Omicron BA.4	1.3%	0.7%	1.0%	1.0%	1.1%	1.0%
Total	**100.0%**	**100.0%**	**100.0%**	**100.0%**	**100.0%**	**100.0%**

Table 7. Comparison of lineage distribution by vaccination status.

Lineage	Not vaccinated			Fully vaccinated		
	Women	Men	Total	Women	Men	Total
Omicron BA.2	97.3%	98.7%	98.0%	96.6%	97.0%	96.8%
Omicron BA.5	1.6%	1.3%	1.5%	2.4%	1.9%	2.2%
Omicron BA.4	1.1%	0.0%	0.6%	1.0%	1.1%	1.0%
Total	**100.0%**	**100.0%**	**100.0%**	**100.0%**	**100.0%**	**100.0%**

Mutation surveillance

In addition to the surveillance of SARS-CoV-2 variants, the LNS monitors the occurrence of SARS-CoV-2 mutations reported to have a clinical and epidemiological relevance. Newly acquired mutations may occur and their early detection might be key to expect changes in the epidemic evolution. Following ECDC guidance, the LNS is currently monitoring a selection of mutations to the spike protein frequently associated to VOCs. As each VOC is characterised by a set of defining mutations, which are expected to be highly present, it is interesting to analyse the non-defining ones.

Among the specimens collected over the last four weeks, we did not detect any non-defining mutation (present in at least 1% of any VOC).

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