Respiratory Viruses in Luxembourg (ReViLux)

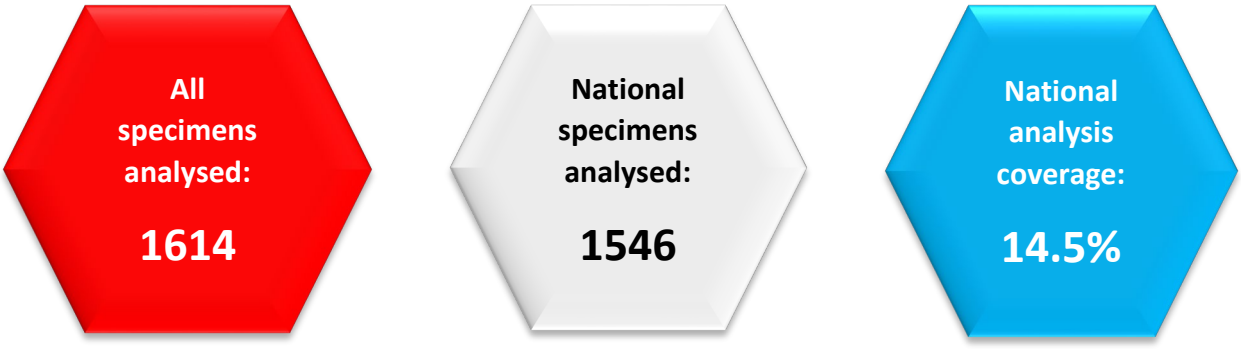
Weekly report (3 – 9 January 2022)

Executive Summary

The Sentinel Surveillance Network identified 15 cases of influenza-like illness, thus exceeding the recommended threshold for the new epidemic season, according to the European Center for Disease Prevention and Control (ECDC) guidelines.

Regarding SARS-CoV-2 genomic surveillance, the LNS analysed 665 specimens from residents in Luxembourg in week 01/2022 (from 10 680 total cases in the Grand Duchy of Luxembourg; 6.2%). This reaches the ECDC recommendations to detect emerging variants at 2.5% prevalence (minimum sample size of 568). Including PCR screening results, 1546 national specimens were analysed globally (14.5%).

The Omicron variant was assigned to 89.6% of national cases collected during week 01/2022, remaining the dominant one.



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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 on which the Revilux provides updates:

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.

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. Results of syndromic surveillance during the last four weeks are displayed in Table 1 and the history of ILI consultations since the 2019-2020 season is shown in Figure 1. The number of ILI cases identified in the week of study was 15 (out of 347 consultations); therefore, **the percentage of ILI (4.32%) exceeds the threshold for the epidemic season** (2.59%), according to the ECDC.

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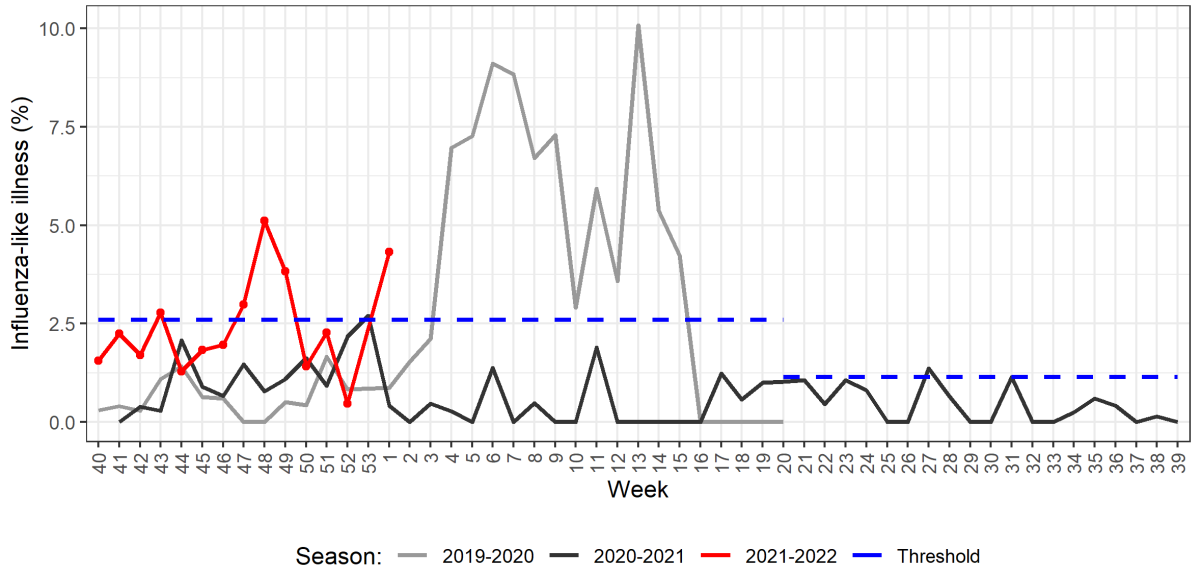
Table 1. Syndromic surveillance during week 01/2022

Week	ARI		ILI		Total consultations
	N	%	N	%	
2021/50	88	17.85	7	1.42	493
2021/51	42	13.64	7	2.27	308
2021/52	50	23.70	1	0.47	211
2022/01	64	18.44	15	4.32	347

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



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

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:

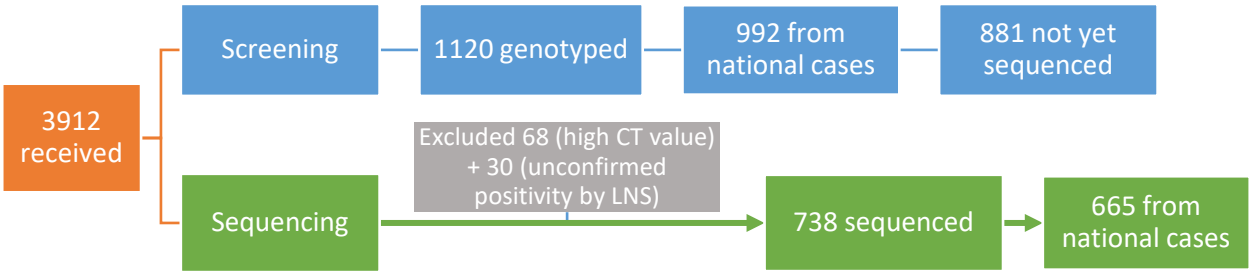
1) Sequencing all specimens from hospital cases.
2) Sequencing all specimens from post-vaccination cases.
3) Sequencing specimens from clusters with high transmission.
4) Sequencing a representative sample of community cases.

The representative sample of community cases 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.

Due to the emergence of the new Omicron variant of concern, as well as the high incidence rates in the European context, targeted PCR tests are carried systematically in order to detect potential Omicron cases within 24h from reception of the specimen. The PCR kits used target the following spike mutations: 69/70del, K417N, N501Y. The potential cases identified this way are then prioritised for confirmation by sequencing.

The LNS shares its sequencing results with GISAID EpiCov database periodically. SARS-CoV-2 lineages have been assigned based on Rambaut et al. using the Phylogenetic Assignment of Named Global Outbreak LINeages (pangolin) software (v3.1.17, pangoLEARN 2021-12-06). The Pango nomenclature is used in addition to the WHO nomenclature to enable easier visualization of links between any evolving variants and their ancestor (See nomenclature equivalences in Appendix 1).

Screening and sequenced specimens



In week 01/2022, 10 680 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 568 specimens (5.3%).

Last week, 3912 specimens were received. Of these, 1120 specimens (including 992 national specimens) were screened by targeted PCR for the Omicron variant, 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 738 specimens, including 665 specimens having been collected from residents. The weekly sequencing coverage remains at 6.2% (665 out of 10 680 cases registered in Luxembourg; see coverage trend in Figure 2). Overall, 1546 national specimens were analysed either by sequencing or screening (14.5%).

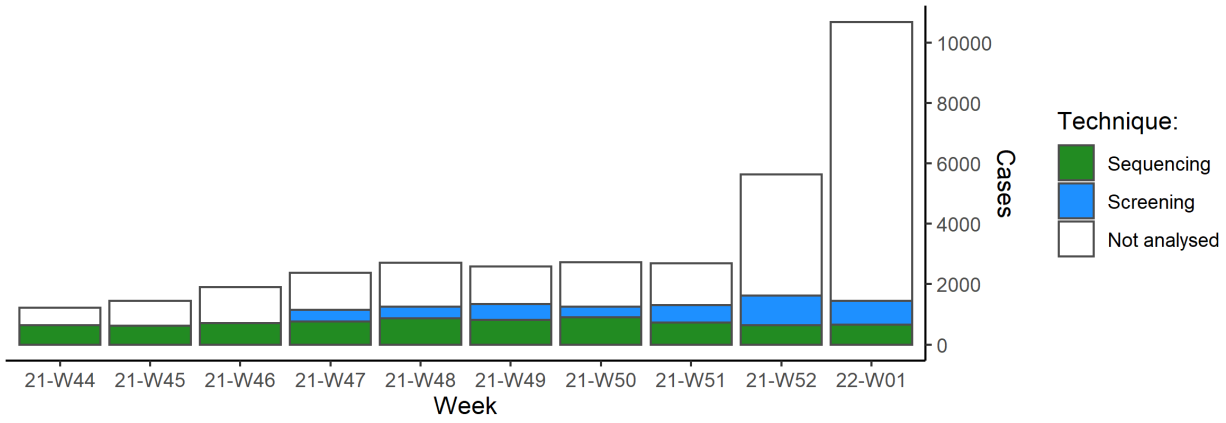


Figure 2. National coverage based on weekly number of positive cases in Luxembourg. The coverage from the latest weeks might not be consolidated yet.

Omicron screening results

As shown in Figure 3, of the 1120 specimens from week 01/2022 which were screened by targeted PCR, 984 were identified as potential Omicron cases (87.9%).

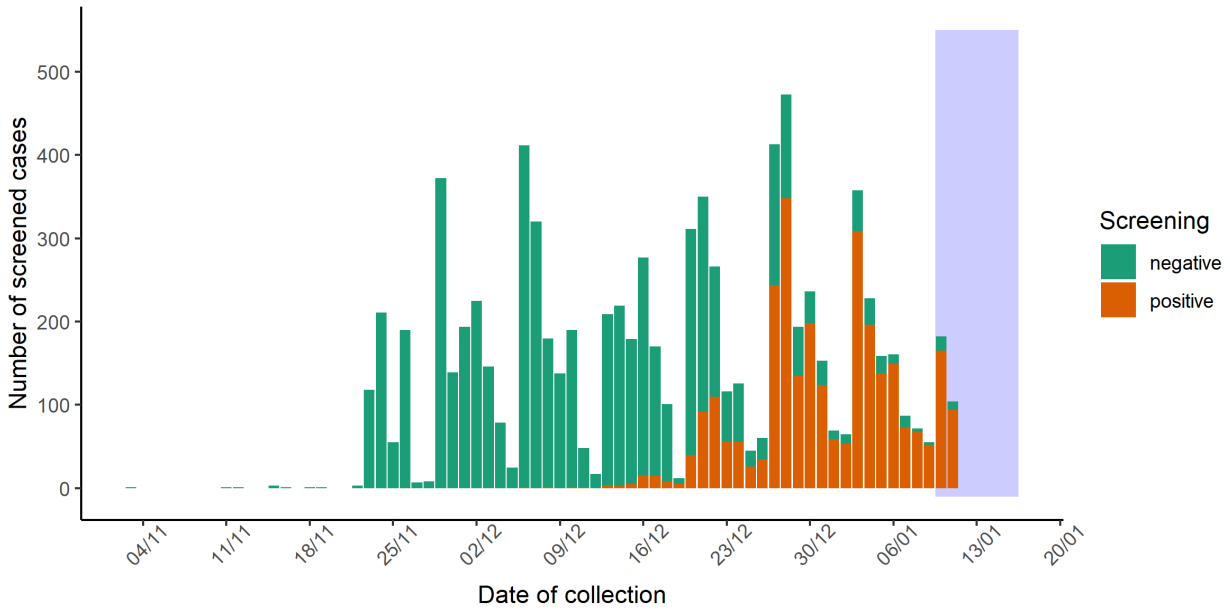


Figure 3. Number of specimens included in the screening for the Omicron variant by date of collection. Results more recent than the week of study are not yet consolidated (purple shade).

Circulating lineage detection

The distribution of successfully assigned lineages within the national selection is shown in Figure 4. Regarding Delta AY sublineages, only a selection is displayed, based on their prevalence during the last 10 weeks (min. 1%). This distribution is further detailed for the last 2 weeks in Table 2.

The Omicron variant remains the dominant one (89.6%) within national specimens. All Omicron cases were assigned to the lineage BA.1 (the most common worldwide). Within the Delta variant, the lineage AY.43 remained the most frequent one.

Table 2. Distribution of SARS-CoV-2 lineages detected within the national sample in weeks 52/2021 and 01/2022 (previously reported cases might be updated by retrospective analysis).

Variant	**Week 52**			**Week 01**		
	N	***%***	***CI %***	***N***	***%***	***CI %***
Omicron	422	77.9	74.4 – 81.4	509	89.6	87.1 – 92.1
Delta	120	22.1	18.6 – 25.6	59	10.4	7.9 – 12.9
Beta	0	-	-	0	-	-
Gamma	0	-	-	0	-	-
Others	0	-	-	0	-	-
Total	**542**	**100.0**	**-**	**568**	**100.0**	**-**

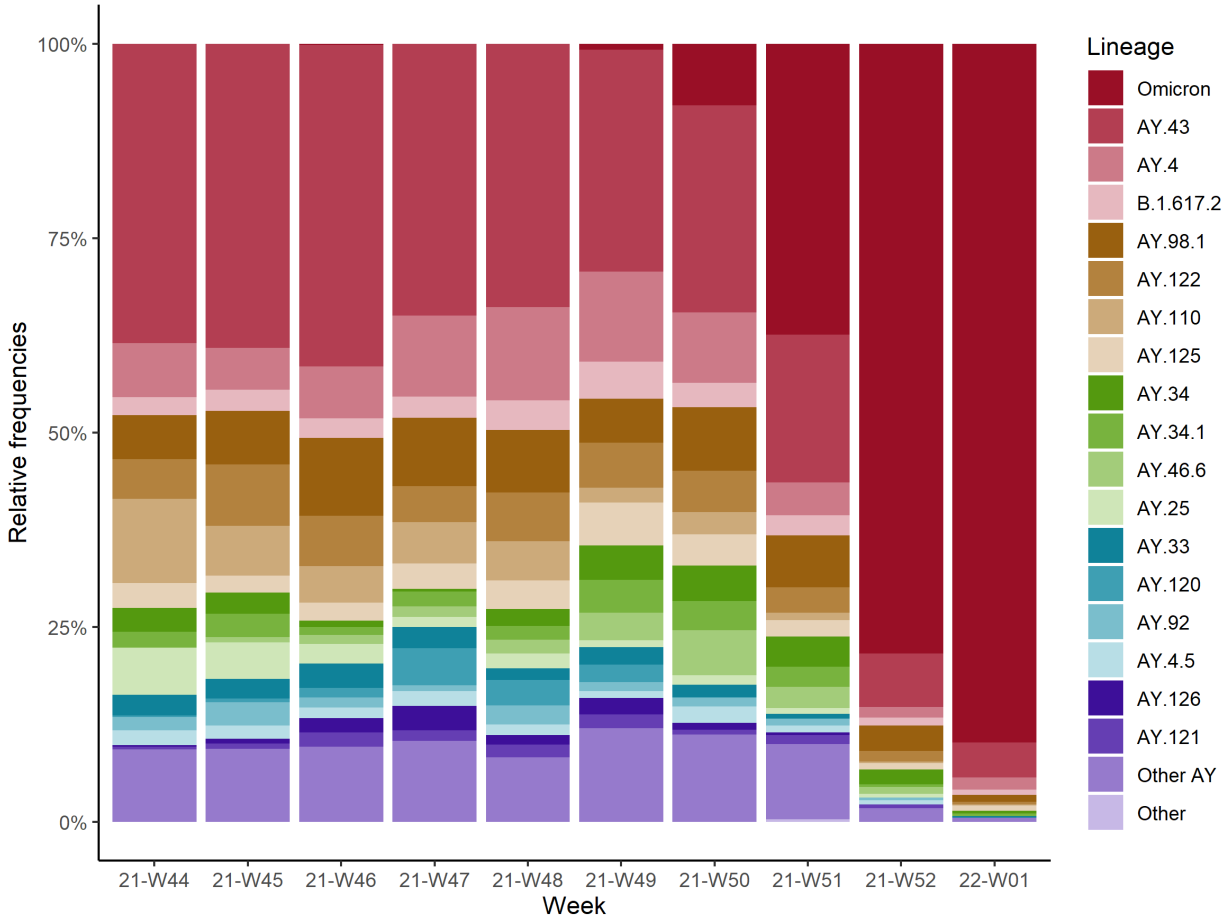


Figure 4. Distribution of lineages within the national selection during the last 10 weeks.

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. This complementary surveillance enables us to detect unexpected mutations among the specimens sequenced. It is expected that VOC defining mutations share the same distribution as their corresponding VOCs. However, 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 42 mutations to the spike protein frequently associated to VOCs. Additionally to the 509 national specimens successfully assigned to the Omicron variant in the week of study, 15 sequences with insufficient quality to be assigned to any lineage were found to carry characteristic mutations of this variant.

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Appendices

Appendix 1: SARS-CoV-2 variants of concern

According to the ECDC

Table A1-a. Nomenclature for variants of concern by the European Centre for Disease Prevention and Control (ECDC)

WHO label	Pango lineage*	Spike mutations of interest	First detection	Evidence for impact on: transmission	immunity	severity
Beta	B.1.351	K417N, E484K, N501Y, D614G, A701V	South Africa, Sept 2020	Increased (v)	Increased (v)	Increased (v)
Gamma	P.1	K417T, E484K, N501Y, D614G, H655Y	Brazil, Dec 2020	Increased (v)	Increased (v)	Increased (v)
Delta	B.1.617.2	L452R, T478K, D614G, P681R	India, Dec 2020	Increased (v)	Increased (v)	Increased (v)
Omicron	B.1.1.529	**	South Africa, Botswana, Nov 2021	Unclear (v) [a]	Increased (v)	Unclear (v) [b]

WHO: World Health Organization. (v): evidence derived from the variant itself; (m): evidence derived from mutations associated with the variant.

**All sub-lineages included.*

***A67V, Δ69-70, T95I, G142D, Δ143-145, N211I, Δ212, ins215EPE, G339D, S371L, S373P, S375F, K417N, N440K, G446S, S477N, T478K, E484A, Q493R, G496S, Q498R, N501Y, Y505H, T547K, D614G, H655Y, N679K, P681H, N764K, D796Y, N856K, Q954H, N969K, L981F.*

[a] "It is not clear whether the increased growth rate is attributed only to immune evasion or also to increased inherent transmissibility."

[b] "Preliminary studies show reduced risk of hospitalisation, but further evidence from the EU/EEA countries is needed to fully determine the size of the effect and if it applies to all population groups to acknowledge differences internationally in vaccination coverages and the patient populations that are currently being hospitalised. Conclusive evidence on any change of the impact on fatalities is not available (yet)."

Adapted from ECDC – SARS-CoV-2 variants of concern (https://www.ecdc.europa.eu/en/covid-19/variants-concern).

According to the WHO

Table A1-b. Nomenclature for variants of concern by the World Health Organization (WHO)

WHO label	Pango lineage*	GISAID clade/lineage	Nextstrain clade	Additional amino acid changes monitored	Earliest documented samples	Date of designation
Alpha	B.1.1.7[#]	GRY (formerly GR/501Y.V1)	20I (V1)	+S:484K +S:452R	United Kingdom, Sep-2020	18-Dec-2020
Beta	B.1.351	GH/501Y.V2	20H (V2)	+S:L18F	South Africa, May-2020	18-Dec-2020
Gamma	P.1	GR/501Y.V3	20J (V3)	+S:681H	Brazil, Nov-2020	11-Jan-2021
Delta	B.1.617.2[§]	G/478K.V1	21A, 21I, 21J	+S:417N +S:484K	India, Oct-2020	VOI: 4-Apr-2021 VOC: 11-May-2021
Omicron	B.1.1.529	GRA	21K, 21L, 21M	+S:R346K	Multiple countries, Nov-2021	VUM: 24-Nov-2021 VOC: 26-Nov-2021

**All sublineages included. [#] includes all Q sublineages. [§] includes all AY sublineages.*

Adapted from WHO - Tracking SARS-CoV-2 variants (https://www.who.int/en/activities/tracking-SARS-CoV-2-variants/)