Respiratory Viruses in Luxembourg (ReViLux)

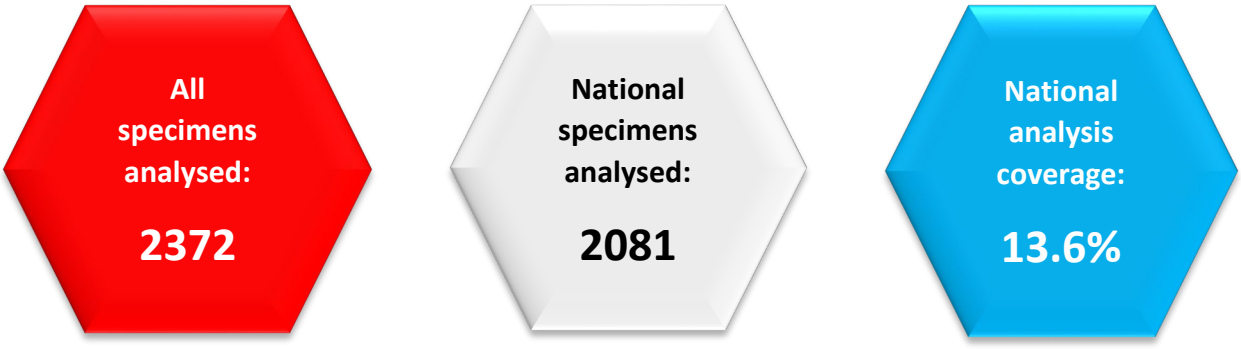
Weekly report (17 – 23 January 2022)

Executive Summary

The Sentinel Surveillance Network identified 13 cases of influenza-like illness, thus remaining over the recommended threshold for the epidemic season, according to the European Center for Disease Prevention and Control (ECDC) guidelines.

Regarding SARS-CoV-2 genomic surveillance, the LNS analysed 1013 specimens from residents in Luxembourg in week 3 (from 15 293 total cases in the Grand Duchy of Luxembourg; 6.6%). This exceeds the ECDC recommendations to detect emerging variants at 2.5% prevalence (minimum sample size of 577). Including PCR screening results, 2081 national specimens were analysed globally (13.6%).

The Omicron variant was assigned to 99.1% of national cases collected during week 3, remaining the dominant one. The most frequent lineage was BA.1.



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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:

- **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. 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 13 (out of 429 consultations); therefore, **the percentage of ILI (3.03%) remains over the threshold for the epidemic season** (2.59%) according to the ECDC.

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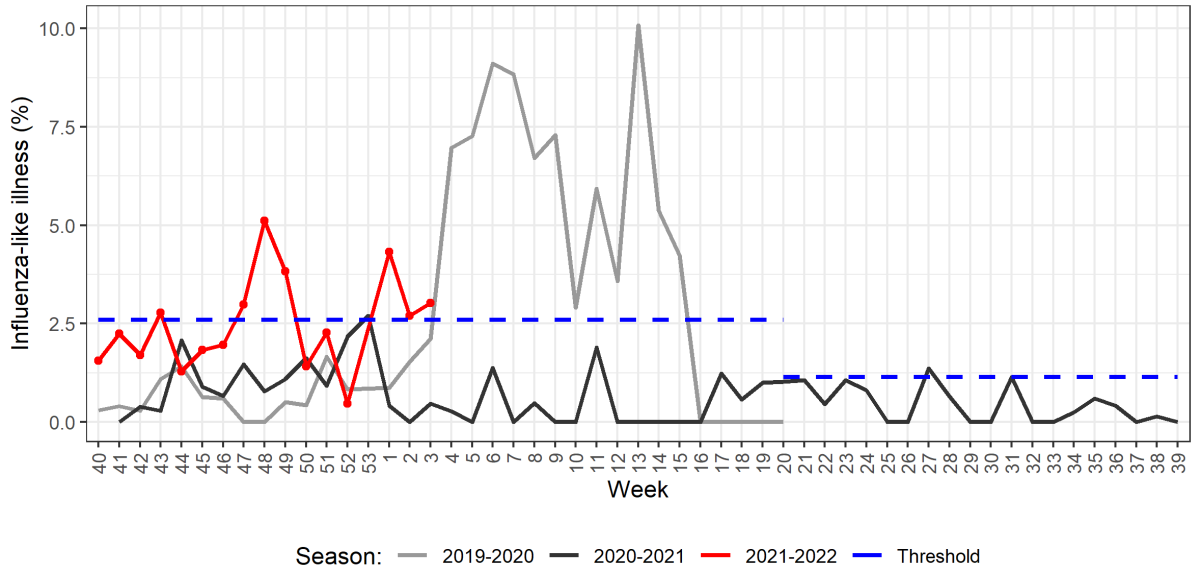
Table 1. Syndromic surveillance over the last 4 weeks.

Week	ARI		ILI		Total consultations
	N	%	N	%	
2021/52	50	23.70	1	0.47	211
2022/1	64	18.44	15	4.32	347
2022/2	62	13.93	12	2.70	445
2022/3	72	16.78	13	3.03	429

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:

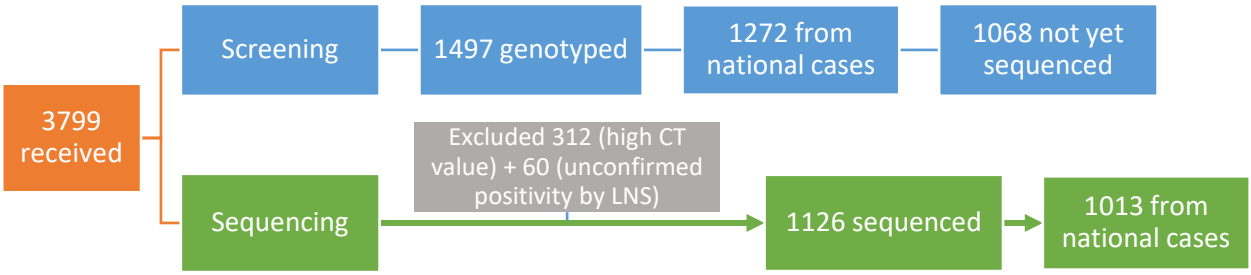
1) Sequencing all specimens from hospital cases.
2) Sequencing all specimens from post-vaccination cases.
3) Sequencing specimens from clusters with high transmission.
4) Sequencing a representative sample of community cases.

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 2022-01-20). 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 3/2022, 15 293 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 577 specimens (3.8%).

As shown in Figure 2, 3799 specimens were received from the week of study. Of them, 1497 were screened by targeted PCR for the Omicron variant (including 1272 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 1126 specimens, including 1008 national ones. The weekly sequencing coverage remains at 6.6% (1008 out of 15 293 cases registered in Luxembourg; see coverage trend in Figure 2). Overall, 2081 national specimens were analysed by either sequencing or screening (13.6%).

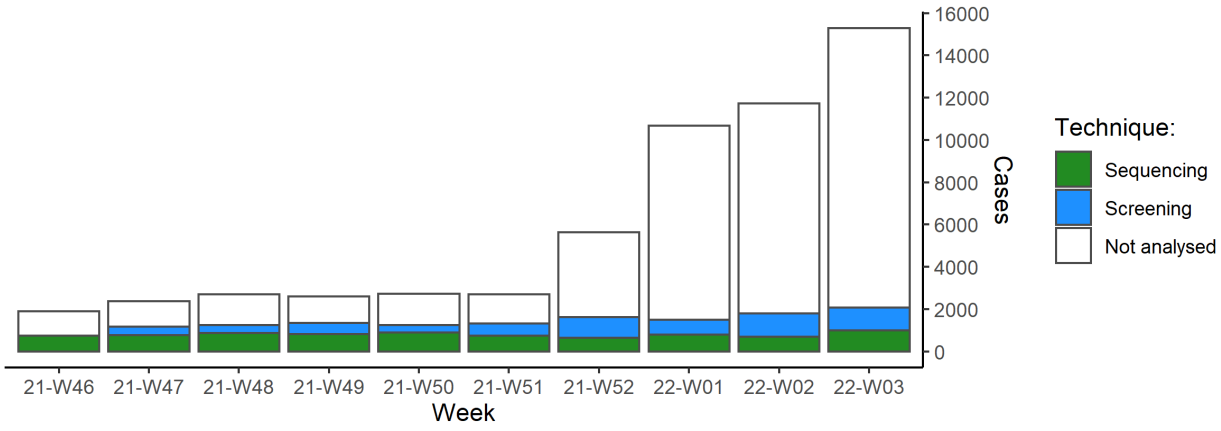
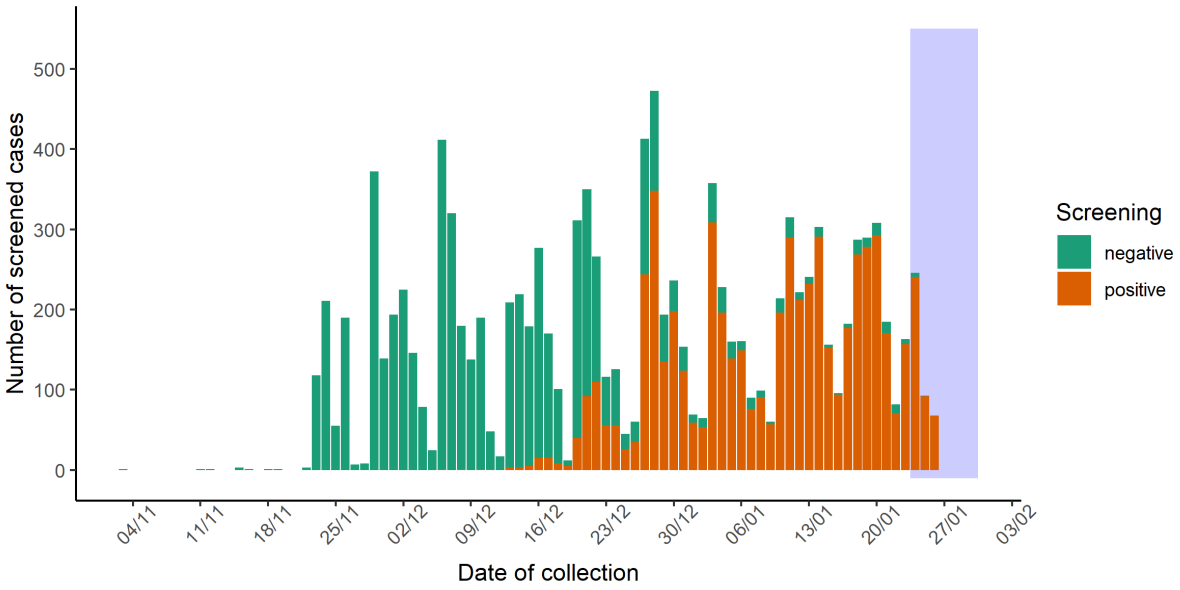


Figure 2. National coverage based on weekly number of positive cases in Luxembourg. The coverage from the latest weeks might not be consolidated yet.

Omicron screening results

As shown in Figure 3, of the 1497 specimens from week 3 screened by targeted PCR, 1416 were identified as potential Omicron cases (94.6%).



Circulating lineage detection

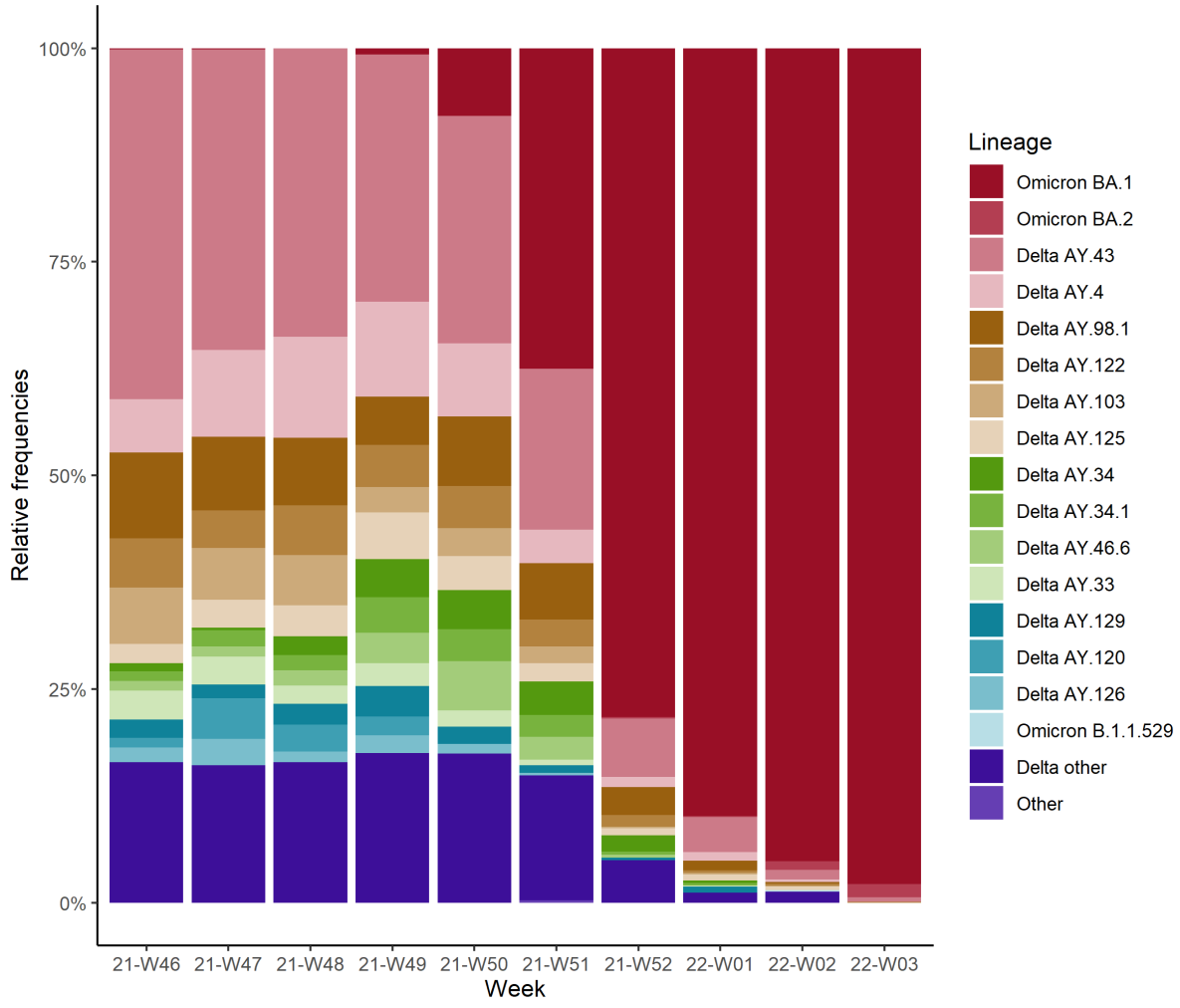
The distribution of successfully assigned lineages within the national selection is shown in Figure 4. Regarding Delta AY sublineages, only a selection is displayed, based on their prevalence during the last 10 weeks (min. 1%). This distribution is further detailed for the last 2 weeks in Table 2.

The Omicron variant remains the dominant one (99.1%) within the representative sample. Most Omicron cases (97.9%) were assigned to the lineage BA.1 (the most common worldwide). Concerning the Delta variant, the lineage AY.43 remained the most frequent one.

Considering all specimens sequenced (including non-residents), there was a new increase of BA.2 cases: 16 in week 3/2022, compared to 6 last week and 1 the previous one.

Table 2. Distribution of SARS-CoV-2 lineages detected within the representative sample in weeks 2-3 (previously reported cases might be updated by retrospective analysis).

Variant	**Week 2**			**Week 3**		
	N	***%***	***CI %***	***N***	***%***	***CI %***
Omicron	551	96.5	95.0 – 98.0	572	99.1	98.4 – 99.9
Delta	20	3.5	2.0 – 5.0	5	0.9	0.1 – 1.6
Beta	0	-	-	0	-	-
Gamma	0	-	-	0	-	-
Others	0	-	-	0	-	-
Total	**571**	**100.0**	**-**	**577**	**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. This complementary surveillance enables us to detect unexpected mutations among the specimens sequenced. 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.

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 all Omicron BA.1 sequences, the LNS found the following:

- A701V, frequently associated to the Beta variant. It is present in at least 12.26% of Omicron specimens (lower than the European region: 25.7% according to GISAID).
- P681R, frequently associated to the Delta variant. It is present in at least 0.6% of Omicron specimens (higher than the European region: 0.04% according to GISAID).
- L452R, frequently associated to the Delta variant. It is present in at least 0.2% of Omicron specimens (similar to the European region: 0.3% according to GISAID).

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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)	Reduced (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] "The observed increased growth rate may be due to increased inherent biological transmissibility, contextual factors such as transmitting in population groups with increased contact rates, or escape from immunity which increases the size of the susceptible population"

[b] "Preliminary studies show reduced risk of hospitalisation, but more data from EU/EEA countries is required to determine if this effect is observed across population groups (e.g. by age, vaccination and prior infection status). Conclusive evidence on mortality risk is not yet available"

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/)