

# Respiratory Viruses in Luxembourg (**ReViLux**)

Weekly report - 02 May 2023

## Executive summary

The sentinel network detected a low epidemic activity over the last week (2023/17), based on 4.0% of consultations being associated with influenza- like illness.

Among the specimen collected by the sentinel network over the last two weeks, the percentage of positive tests for SARS- CoV-2 was 14.4% and 10.6 % for Influenza type B.

Overall, during this season, Influenza A (H3) with 88.3% is the most frequent detected strain in submitted specimens. However, since week 2023/05 Influenza type B has been predominant.

Concerning SARS-CoV-2 genomic surveillance, the recombinant sub-variant XBB.1.5 remains the most frequent detected variant with 37.6 % (95%CI: 29.4-45.8%), followed closely by XBB.1.9 with 36.8% (95%CI: 28.6-45.0%). The proportion of other recombinant XBB (excluding XBB.1.5 and XBB.1.9) increased slightly from 17.7 to 21.8% (95%CI: 14.8-28.8%) compared to previous week.

### IN THE SPOTLIGHT

#### **XBB.1.5 sub-lineage**

**XBB.1.5** is a subtype with additional spike RBD mutation F486P. The lineage was first detected in October 2022 in the USA and is estimated to have a large growth advantage to other previously circulating lineages. Currently, there are no signals that the infection severity of XBB.1.5 is different from that of other circulating Omicron sub-lineages. ECDC categorizes lineage that have similar Spike proteins as **VOI XBB.1.5 lineages** (XBB.1.5 like), which include XBB.1.5, XBB.1.9.1, XBB.1.9.2 and XBB.1.16.

**XBB.1.16** has also a similar genetic profile as XBB.1.5, but two additional mutations E180V and K478R in the Spike protein. The sub-variant has been classified as variant of interest and is closely monitored (WHO, 2023).

## 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 interseason.

## Clinical results

Last week, 4.0% of consultations were reported as ILI, which represents a low 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 two weeks, the most frequently detected viruses (according to positivity rates) were SARS-CoV-2 (14.4%), Human rhinovirus (10.7%) and Adenovirus (10.7%). An overview of the viral circulation during the current season is displayed in Figure 2 and Table 2.

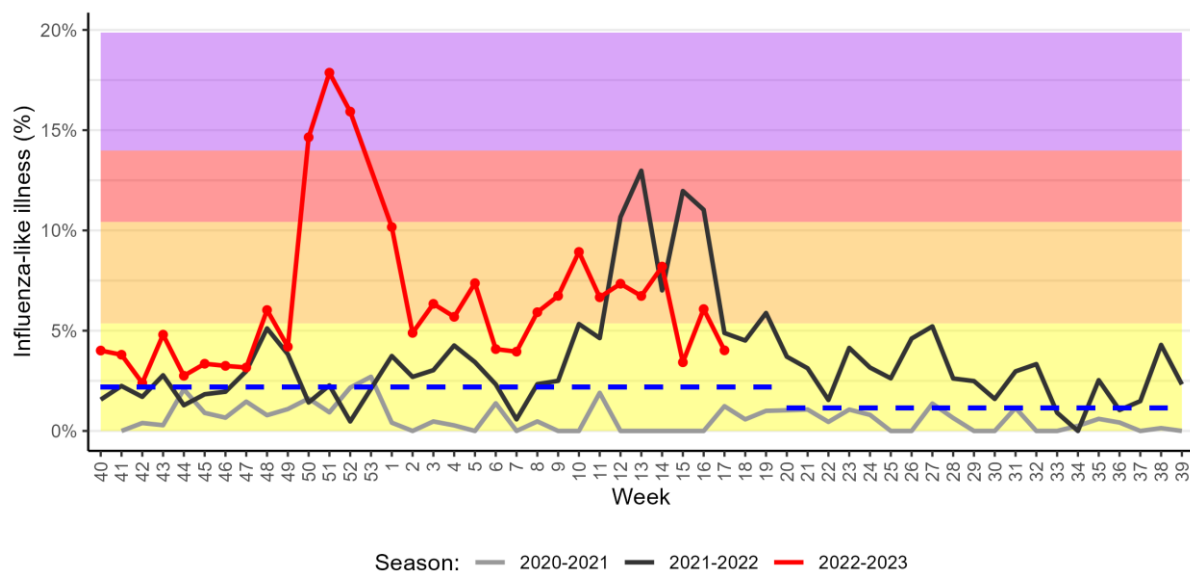


Figure 1. Percentage of patients with influenza-like illness over the last three seasons  
Background colours according to intensity of circulation: low, medium, high, very high.

Table 1. Syndromic surveillance over the last 4 weeks

Week	ARI		ILI		Total consultations
	N	%	N	%	
2023/14	40	21.86	15	8.20	183
2023/15	11	7.53	5	3.42	146
2023/16	41	11.33	22	6.08	362
2023/17	25	12.56	8	4.02	199

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

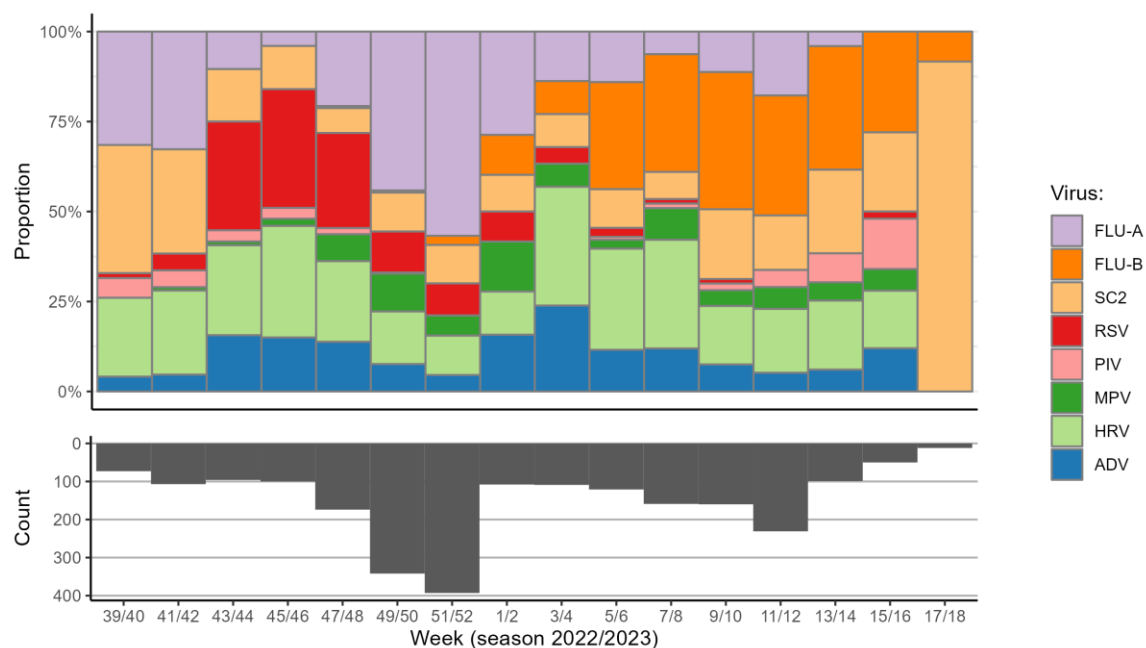


Figure 2. Distribution of respiratory viruses detected within the Sentinel Network, by two-week periods. Results from last weeks are not yet consolidated.

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.

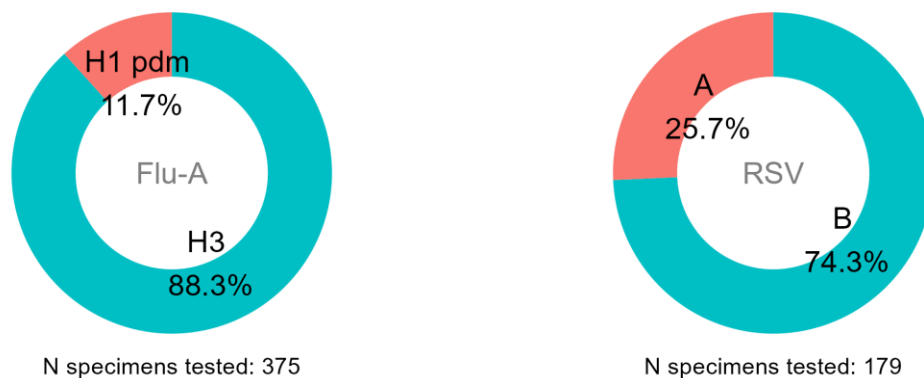
Table 2. Distribution of respiratory viruses detected within the Sentinel Network over the last 2 weeks compared to the whole current season.

Virus	Last 2 weeks		Season 2022/2023	
	N*	Positivity rate (%)	N*	Positivity rate (%)
SARS-CoV-2	15	14.4	323	22.7
Human rhinovirus	3	10.7	445	19.0
Adenovirus	3	10.7	217	9.3
Influenzavirus B	11	10.6	310	12.1
Metapneumovirus	2	7.1	143	6.1
Parainfluenzavirus	2	7.1	50	2.1
Respiratory syncytial virus	1	3.6	209	8.9
Influenzavirus A	0	0.0	407	15.8
<b>Total</b>	<b>37</b>		<b>2104</b>	

\*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 current season, the most frequently detected strain for Influenzavirus A was H3 (88.3%), and for RSV it was type B (74.3%).



*Figure 3. Detection of influenzavirus-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, and it is still a challenge for health systems. For this reason, the National Reference Laboratory for Acute Respiratory Infections at LNS continues to monitor the genomic characteristics of the SARS-CoV-2 virus detected in Luxembourg.

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 respectively. 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 (4.2, pango-data 1.19, mode UShER). In order to allow easier visualisation, WHO and Nextstrain categorisations are also used.

### Sequencing activity

In week 2023/16, 244 new cases were registered in Luxembourg; hence, the minimum sample size required to detect emerging variants at a 5% incidence is estimated to be 133 specimens (54.5%). The microbial genomics unit at LNS sequenced 176 specimens from the week of study, including 163 national ones (sequencing coverage: 66.8%; see Figure 4). This reaches the recommended sample size.

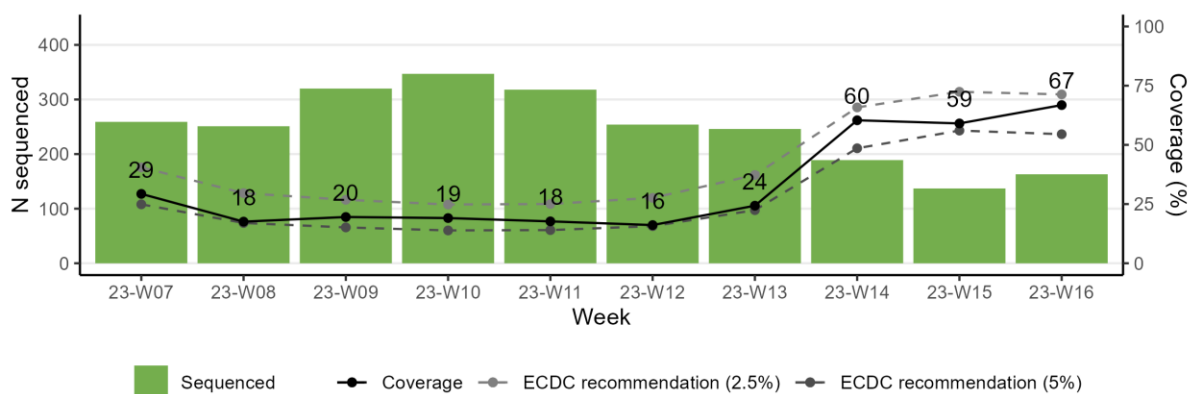


Figure 4. Number of specimens sequenced and national coverage based on weekly number of positive cases in Luxembourg. The coverage from the last two weeks is not consolidated yet.

## Variant circulation

The 'XBB.1.5 like' variants remain the main variants of interest within the selected sample, the most frequent sub-variants being XBB.1.5 as well as XBB.1.9. The proportion of XBB.1.5 dropped slightly from 40.8% in week 2023/15 to 37.6% in week 2023/16, whereas proportions of XBB.1.9 increased from 32.2 to 36.8%, respectively. The proportion of XBB (excluding XBB.1.5 and XBB.1.9) continues to increase from 17.7 to 21.8%, compared to previous week. An overview of the variants and lineages circulating over the last 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 6.

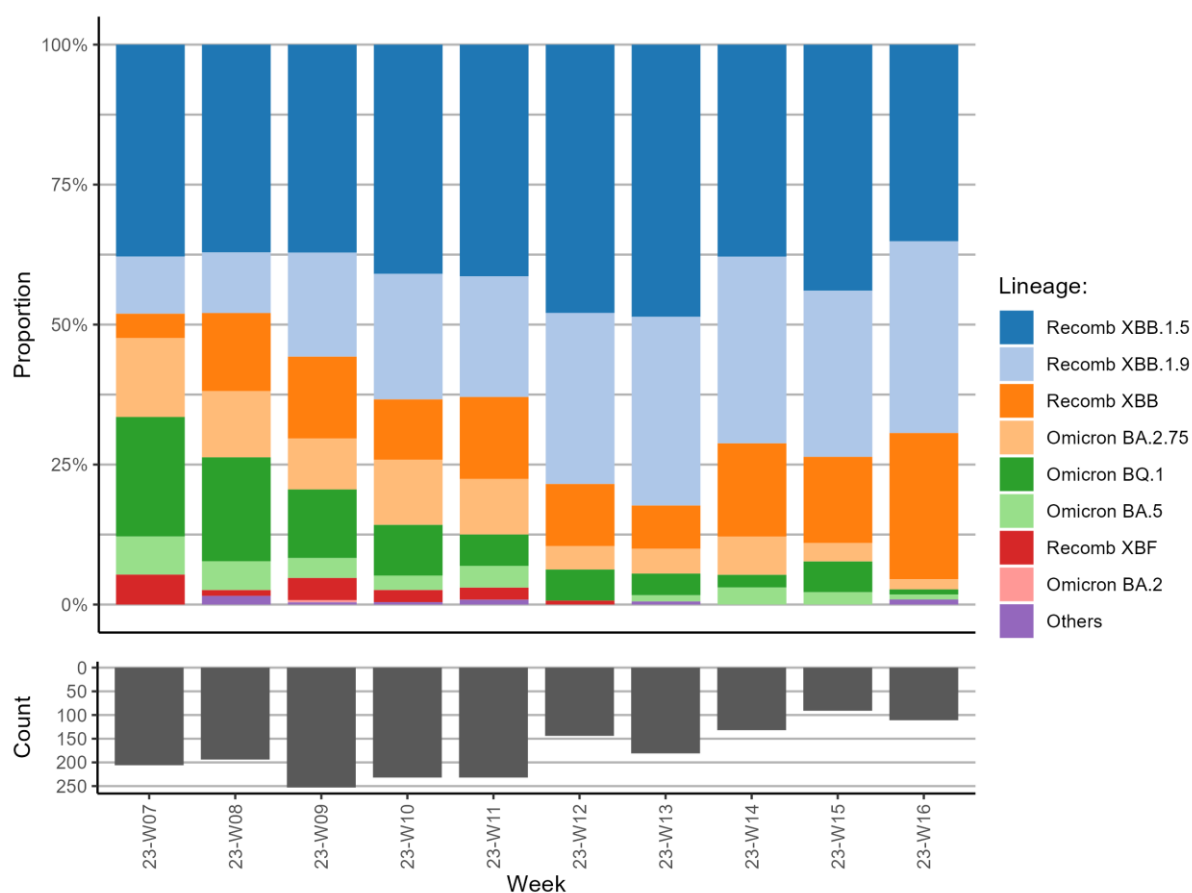


Figure 5. Distribution of lineages within the representative sample during the last 10 weeks.

Table 3. 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*	Week 15		Week 16	
	%	CI %	%	CI %
Recomb XBB.1.5	40.8	32.3 - 49.2	37.6	29.4 - 45.8
Recomb XBB.1.9	32.3	24.3 - 40.3	36.8	28.6 - 45.0
Recomb XBB	17.7	11.1 - 24.3	21.8	14.8 - 28.8
Omicron BA.2.75	3.1	0.1 - 6.0	1.5	0.0 - 3.6
Omicron BQ.1	4.6	1.0 - 8.2	0.8	0.0 - 2.2
Omicron BA.5	1.5	0.0 - 3.7	0.8	0.0 - 2.2
Others	0.0	-	0.8	0.0 - 2.2

\*Sub-lineages are not included in the count of their parental lineages (e.g. BQ.1 not included in BA.5).  
CI: confidence interval at 95%.

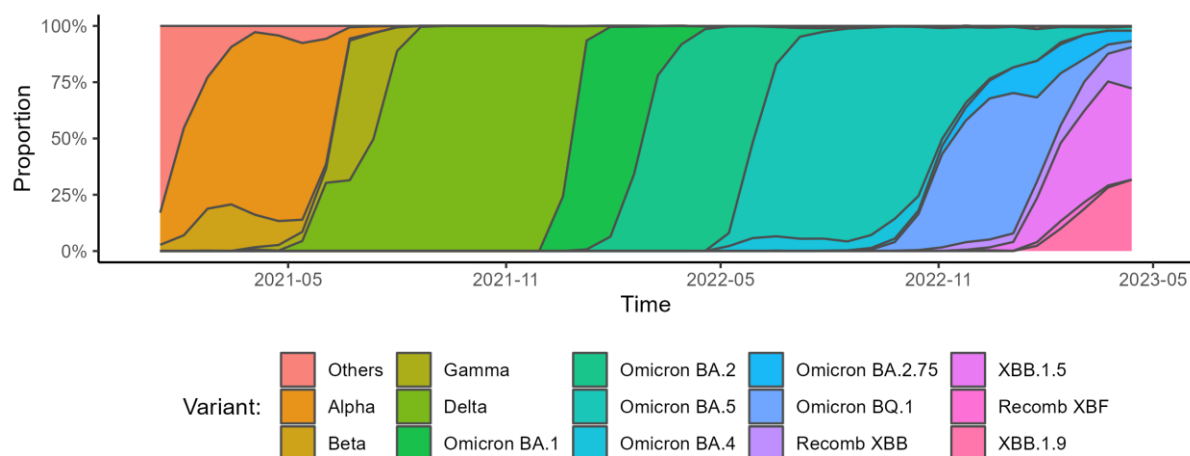


Figure 6. Proportion of each variant circulating in Luxembourg since January 2021.



## 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) and sampling setting (community vs. hospital, Table 4).

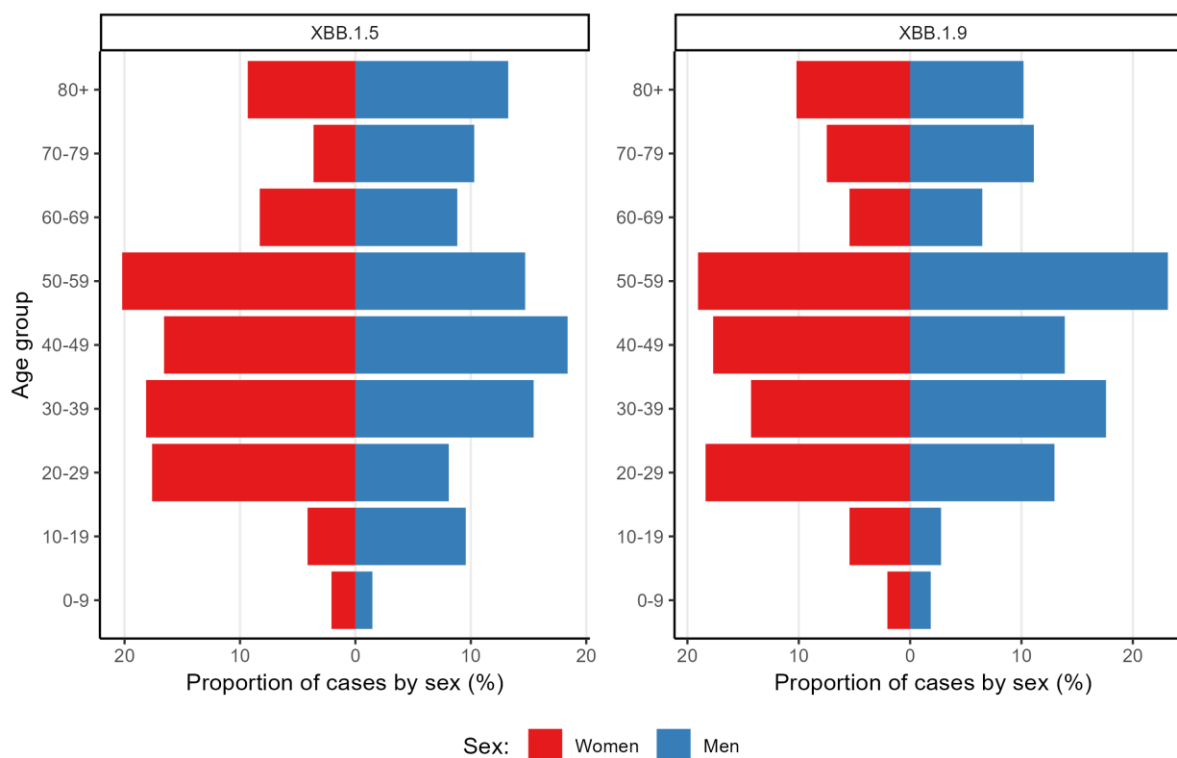


Figure 7. Age group and sex distribution of specimens sequenced over the last 4 weeks, by lineage.

Table 4. Comparison of lineage distribution by sampling setting.

Lineage	Community			Hospital		
	Women	Men	Total	Women	Men	Total
Recomb XBB.1.5	59.5%	57.2%	<b>58.6%</b>	48.9%	52.1%	<b>50.3%</b>
Recomb XBB.1.9	40.5%	42.8%	<b>41.4%</b>	51.1%	47.9%	<b>49.7%</b>
<b>Total</b>	<b>100.0%</b>	<b>100.0%</b>	<b>100.0%</b>	<b>100.0%</b>	<b>100.0%</b>	<b>100.0%</b>

## References

- Centers for Disease Control and Prevention. SARS-CoV-2 Variant Classifications and Definitions. Retrieved 02 May 2023, from <https://www.cdc.gov/coronavirus/2019-ncov/variants/variant-info.html>
- European Centre for Disease Prevention and Control. Guidance for representative and targeted genomic SARS-CoV-2 monitoring – 3 May 2021. ECDC : Stockholm ; 2021
- European Centre for Disease Prevention and Control. SARS-CoV-2 variants of concern. Retrieved 02 May 2023, 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-23-29-april-2023-week-17>
- Genomic sequencing of SARS-CoV-2: a guide to implementation for maximum impact on public health. Geneva: World Health Organization; 2021.
- GISAIID. EpiCoV – Pandemic coronavirus causing COVID-19. Retrieved 5 mai 2022, from <https://www.gisaid.org>
- GitHub - cov-lineages/pangolin: Software package for assigning SARS-CoV-2 genome sequences to global lineages. (2021). Retrieved 02 May 2023, 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
- The Luxembourgish data platform. COVID-19: Rapports hebdomadaires. Retrieved 02 May 2023, from <https://data.public.lu/en/datasets/covid-19-rapports-hebdomadaires/>
- WHO- XBB.1.16 initial risk assessment, 17 April 2023 - who. Available at: [https://www.who.int/docs/default-source/coronaviruse/21042023xbb.1.16ra-v2.pdf?sfvrsn=84577350\\_1](https://www.who.int/docs/default-source/coronaviruse/21042023xbb.1.16ra-v2.pdf?sfvrsn=84577350_1) (Accessed: April 25, 2023).