

Respiratory Viruses in Luxembourg (ReViLux)

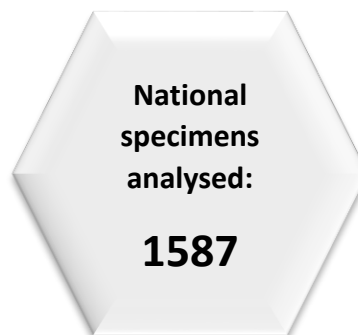
Weekly report (21 – 27 February 2022)

Executive Summary

The Sentinel Surveillance Network reported 2.59% of influenza-like illness, thus staying at baseline circulation according to the European Center for Disease Prevention and Control (ECDC). SARS-CoV-2 remains the most frequently detected virus over the last four weeks (50.0%), followed by influenza virus type A (23.4%) and human rhinovirus (12.5%).

Regarding SARS-CoV-2 genomic surveillance, the LNS sequenced 745 specimens from residents in Luxembourg in week 8 (from 4670 total cases in the Grand Duchy of Luxembourg; 16.0%). This exceeds the ECDC recommendations to detect emerging variants at 2.5%. Including PCR screening results, 1587 national specimens were analysed globally (34.0%).

The Omicron variant was assigned to all cases in the representative sample. The BA.2 lineage kept its increasing trend and is now close to BA.1 (47.9% and 52.1%, respectively). However, the analysis of target groups showed no statistically significant difference in the distribution of BA.1 and BA.2 according to collection setting and vaccination status.



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, 2.53% of consultations were reported as ILI, thus staying at baseline circulation, according to the ECDC threshold (2.59%).

Table 1. Syndromic surveillance over the last 4 weeks.

Week	ARI		ILI		Total consultations
	N	%	N	%	
2022/5	36	17.65	7	3.43	204
2022/6	65	16.80	9	2.33	387
2022/7	26	15.03	1	0.58	173
2022/8	49	20.68	6	2.53	237

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

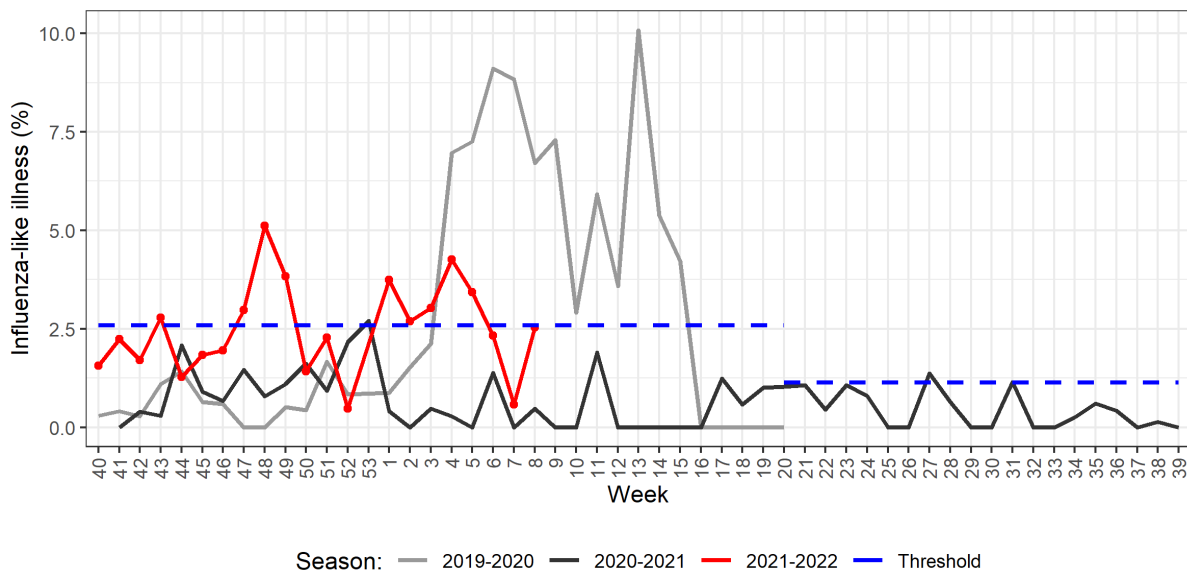


Figure 1. Percentage of patients with influenza-like illness over the last three seasons

Additionally, a selection of cases is further studied in order to monitor the circulation of respiratory viruses in the country, as shown in Figure 2. Over the last 4 weeks, influenzavirus-A was detected in 23.4% of positive specimens from the Sentinel Network, and influenzavirus-B in 4.7% of positive specimens, including 1 co-infection of the latter with metapneumovirus. These results are displayed more in detail in Table 2.

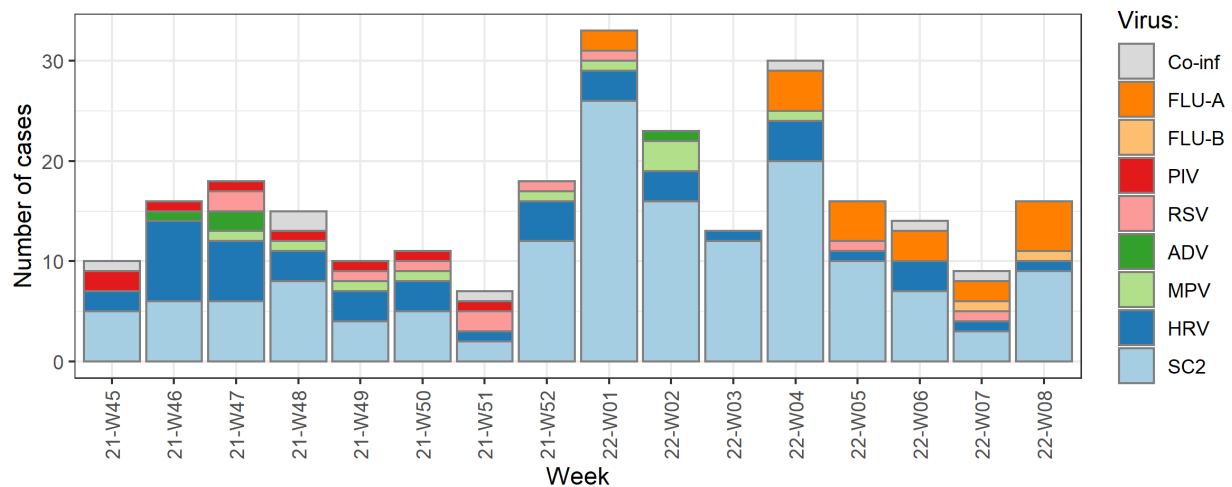


Figure 2. Distribution of respiratory viruses detected within the Sentinel Network, by week. Results from last two weeks are not yet consolidated.

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

Virus	Last 4 weeks		Current season	
	N*	%	N*	%
SARS-CoV-2	32	50.0	243	58.7
Human rhinovirus	8	12.5	98	23.7
Influenzavirus A	15	23.4	22	5.3
Respiratory Syncytial virus	3	4.7	15	3.6
Parainfluenzavirus	0	0.0	14	3.4
Metapneumovirus	2	3.1	14	3.4
Adenovirus	1	1.6	5	1.2
Influenzavirus B	3	4.7	3	0.7
Total	64	100.0	414	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 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 (v3.1.20, pangoLEARN 2022-02-02). 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

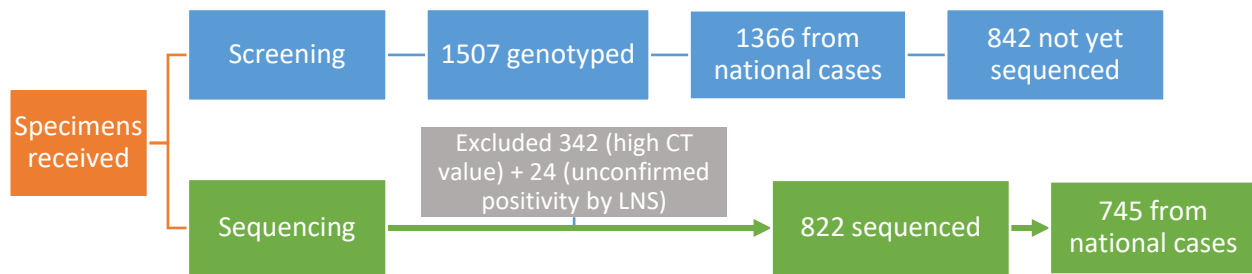


Figure 3. Flowchart of specimens collected during week 8/2022

In week 8, 4670 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 532 specimens (11.4%).

As shown in Figure 3, of all specimens received from the week of study, 1507 were screened by targeted PCR for the Omicron variant (including 1366 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 822 specimens, including 745 national ones. The weekly sequencing coverage remains at 16.0% (745 out of 4670 cases registered in Luxembourg; see coverage trend in Figure 4), which exceeds the recommended sample size. Overall, 1587 national specimens were analysed either by sequencing or screening (34.0%).

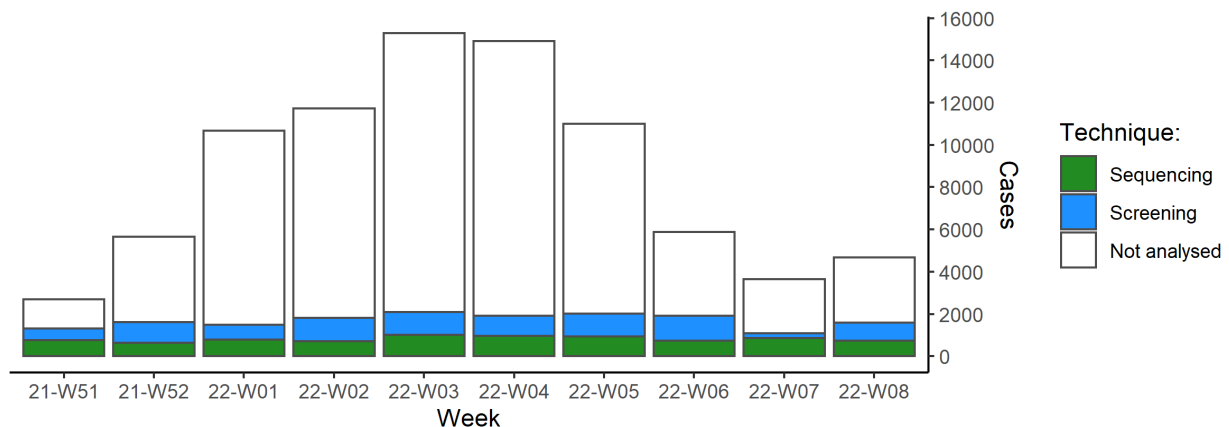


Figure 4. National coverage based on weekly number of positive cases in Luxembourg. The coverage from the latest weeks might not be consolidated yet.

Omicron screening results

As shown in Figure 5, of the 1507 specimens from week 8 which were screened by targeted PCR, all were identified as potential Omicron cases (100%).

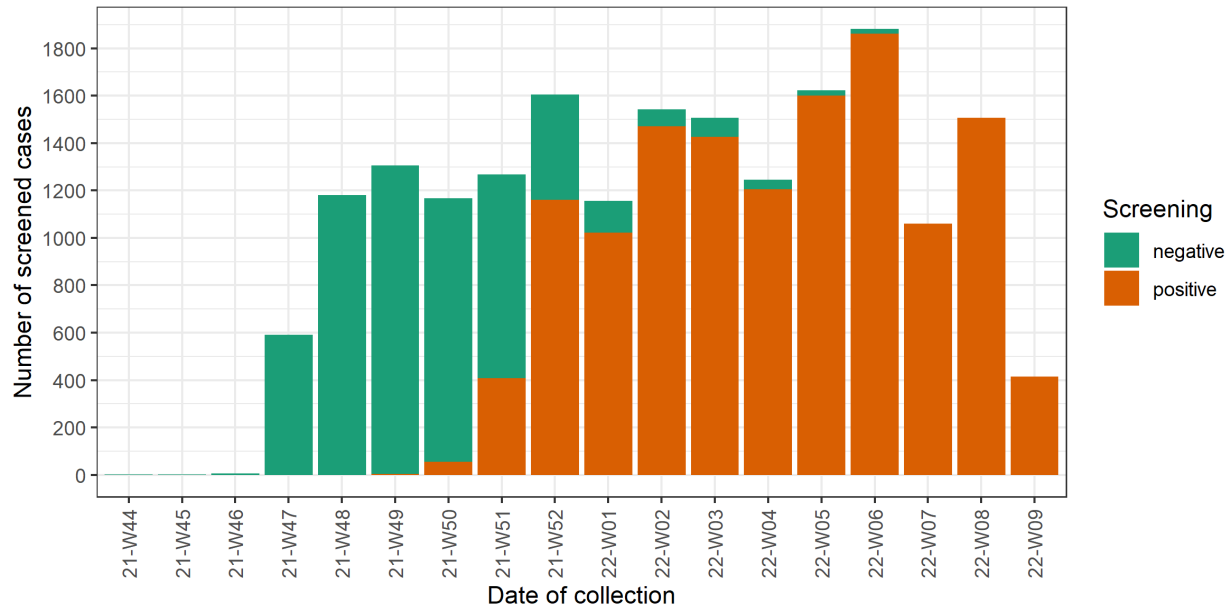


Figure 5. Number of specimens included in the screening for the Omicron variant by date of collection. Results more recent than the week of study are not yet consolidated.

Circulating lineage detection

The distribution of successfully assigned lineages within the national selection is shown in Figure 6. 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 4.

The Omicron variant remains the only one detected within the representative sample. The most frequent lineage is BA.1 (52.1%), followed closely by BA.2 (47.9%), which continues to increase.

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.

Table 4. Distribution of SARS-CoV-2 lineages detected within the representative sample in weeks 7-8 (previously reported cases might be updated by retrospective analysis).

Variant	Week 7			Week 8		
	N	%	CI %	N	%	CI %
Omicron	515	100.0	-	532	100.0	-
BA.1	355	68.9	64.9 – 72.9	277	52.1	47.8 – 56.3
BA.2	159	30.9	26.9 – 34.9	255	47.9	43.7 – 52.2
BA.1.1	1	0.2	0.0 – 0.6	0	-	-
Delta	0	-	-	0	-	-
Beta	0	-	-	0	-	-
Gamma	0	-	-	0	-	-
Others	0	-	-	0	-	-
Total	515	100.0	-	532	100.0	-

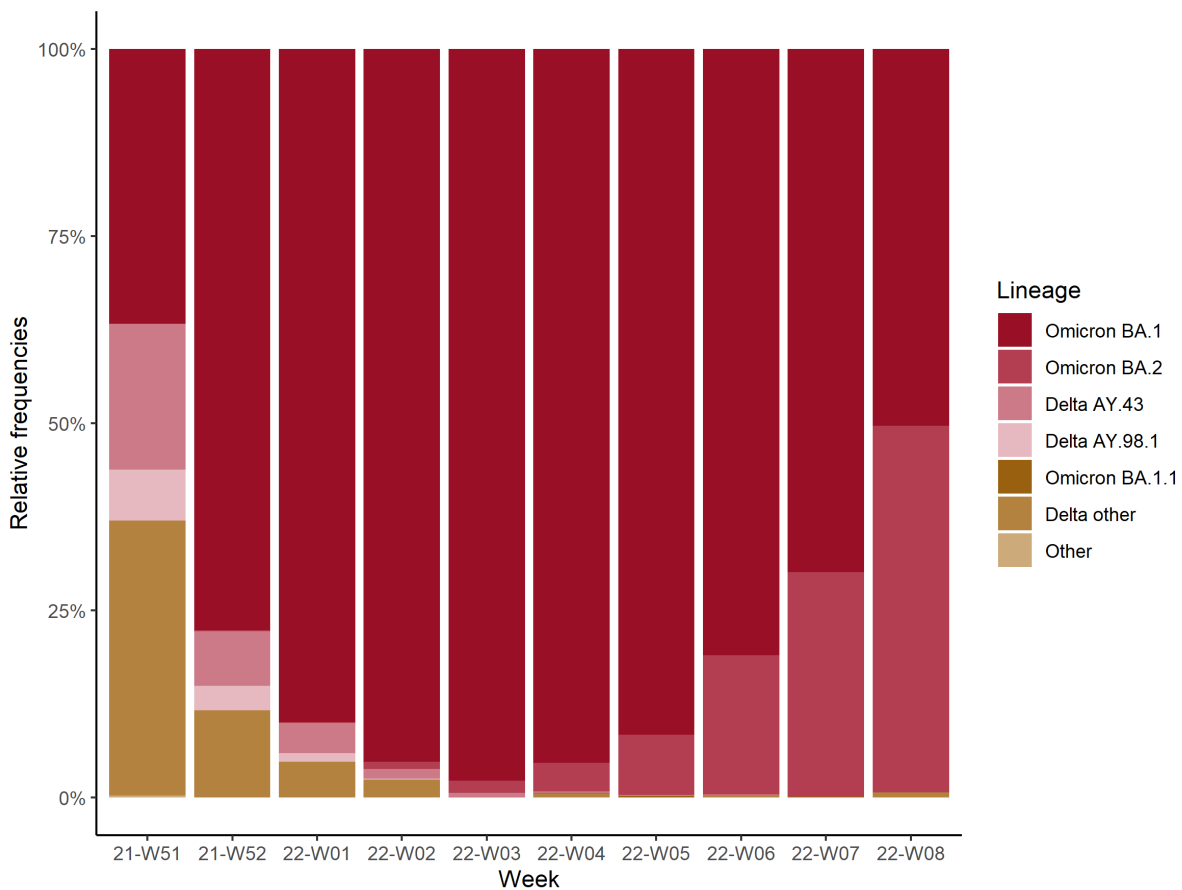


Figure 6. Distribution of lineages within the national selection during the last 10 weeks.

Table 5. Distribution of VOCs within all samples sequenced (including non-residents)

Variant	Week 7		Week 8		Cumulative count
	N	%	N	%	N
Delta	0	-	5	0.6	12 499
Omicron	686	100.0	772	99.4	7913
BA.1	477	69.5	387	49.8	6931
BA.2	208	30.3	385	49.5	978
BA.1.1	1	0.1	0	-	4
Gamma	0	-	0	-	1305
Beta	0	-	0	-	1255
Other	0	-	0	-	12 181
Total	686	100.0	777	100.0	35 153

Target groups

The LNS prioritises the sequencing of specimens collected at hospitals. These may belong to either outpatients or inpatients, and patients hospitalised for reasons other than COVID-19 might also be included. Therefore, not all hospital specimens can be attributed to severe COVID-19 cases. The distribution of Omicron lineages (BA.1 and BA.2) was studied by origin of the specimen (hospital or community) (Table 6), but no statistically significant difference was found ($p > 0.05$). Only specimens from the latest 3 weeks were included in order to avoid bias by differing epidemiological contexts.

Table 6. Comparison of Omicron lineages distribution by sampling setting.

	Community	Hospital
Omicron BA.1	66.7%	71.2%
Omicron BA.2	33.3%	28.8%
Total	100.0%	100.0%

Number of cases: General = 2004, Hospital = 524. P value > 0.05 (χ^2).

Similarly, the distribution of VOC cases was studied by vaccination status (fully vaccinated with 2 or more doses vs non-vaccinated) (Table 7), but no statistically significant difference was found ($p > 0.1$). This suggests that BA.1 and BA.2 may have a similar vaccine escape rate, which should be further studied as well.

Table 7. Comparison of VOC distribution by vaccination status.

	Not vaccinated	Fully vaccinated
Omicron BA.1	68.1%	67.6%
Omicron BA.2	31.9%	32.4%
Total	100.0%	100.0%

Number of cases: Not vaccinated = 548, Fully vaccinated = 1030. P value > 0.1 (χ^2).

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 the specimens collected over the last four weeks, the LNS found the following mutations (minimum 1% prevalence):

- BA.1 specimens:
 - o A701V (in at least 4.6%), frequently associated to the Beta variant.
- BA.2 specimens:
 - o A67V, del69-70, T95I, L981F (each in at least 1.2%), frequently associated to Omicron BA.1.
 - o T547K and N856K (each in at least 1.1%), frequently associated to Omicron BA.1.

Concerning BA.1 specimens, the A701V mutation continues to show a decreasing trend and remains below the rate in the European region. Concerning BA.2 specimens, all aforementioned mutations also showed decreasing trends, but still higher than in the European region (<1%, according to GISAID), so they will remain under monitoring.

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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	transmission	Evidence for impact on:	
					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	Increased (v)	Increased (v)	Reduced (v)

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.

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 [§]	GK	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. [°] includes all BA sublineages

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