

GECO Philippines SARS-CoV-2 Situation Report - 2022 December

Highlights

- 300+ XBB sequences, isolated from September-early November, were identified by the latest PANGOLIN. Almost all the XBB samples were collected in Western Visayas.
- BA.2.3.20, previously believed dominant strain during September-October, and XBC continue to circulate in early November.
- More recent genomic data are required to understand lineage dynamics and the geographical distribution of these lineages before the end of 2022.

SARS-CoV-2 variants detected in the Philippines

WHO label	Pango lineage	Classification	New submission	Isolated in 3 months	Total
Alpha	B.1.1.7/Q.x	VOC	0	0	2808
Beta	B.1.351	VOC	0	0	3282
Delta	B.1.617.2/AY.x	VOC	1 (0.1)	0	3496
Gamma	P.1	VOC	0	0	5
Omicron	B.1.1.529/BA.x	VOC	930 (85.2)	916 (85.5)	12310
Eta	B.1.525	VUM	0	0	8
Theta	P.3	VUM	0	0	528

Table 1. Number of available sequences by variant in the Philippines as of 31 December 2022.

The variants (VOC/VUM) here only include sequences that present in the GISAID or GECO data base and fulfill the definitions of WHO at the time the report is prepared. *New submission*, new sequences submitted from the last report. *Isolated in 3 months*, sequences isolated from 1 October 2022 to 31 December 2022. Numbers in the parentheses are percentage of the category (%). Note that recombinant strains involving Omicron sublineages (e.g. XBB, XBC) are provisionally classified as “Omicron”.

- **VOC (Variant of Concern):** A SARS-CoV-2 variant that meets the definition of a VOI (see below) and, through a comparative assessment, has been demonstrated to be associated with (a) increase in transmissibility, (b) increase in clinical disease presentation or (c) decrease in effectiveness of public health measures including diagnostics, vaccines, therapeutics.
- **VOI (Variant of Interest):** A SARS-CoV-2 variant: (a) with genetic changes that are predicted or known to affect virus characteristics such as transmissibility, disease severity, immune escape, diagnostic or therapeutic escape; AND (b) identified to cause significant community transmission or multiple COVID-19 clusters, in multiple countries with increasing relative prevalence alongside increasing number of cases over time.

- **VUM (Variant Under monitoring):** A SARS-CoV-2 variant with genetic changes that are suspected to affect virus characteristics with some indication that it may pose a future risk, but evidence of phenotypic or epidemiological impact is currently unclear, requiring enhanced monitoring and repeat assessment pending new evidence.
- **Pango lineage:** A dynamic SARS-CoV-2 naming system that uses a phylogenetic framework (methods that involve a tree-like structure inferred based on genetic information of viruses) to identify actively spreading lineages. The Pango system is designed to track the transmission and spread of SARS-CoV-2, but does not attempt to identify or define VOCs or VOIs.

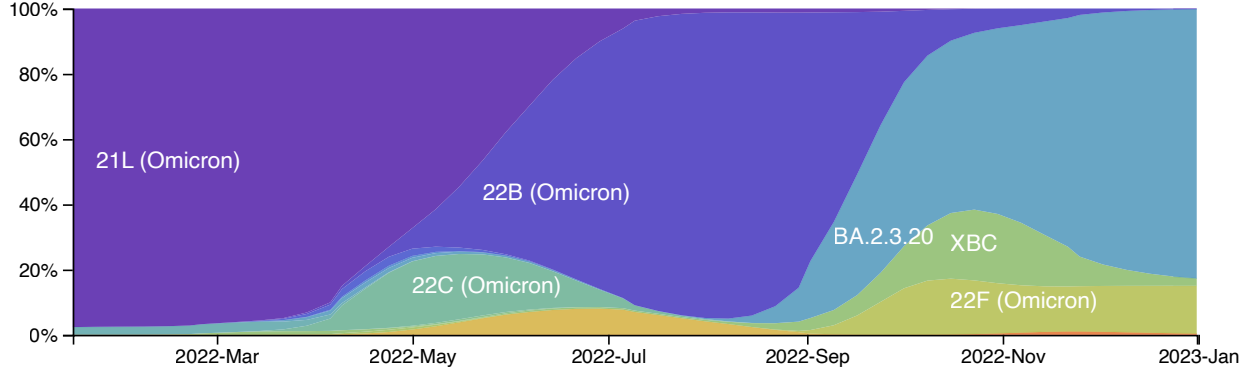


Figure 1. Temporal frequencies of SARS-CoV-2 variants in the Philippines. The figure is constructed with a subsampled genomic data set from all available sequences (methods). Different ways of classification of SARS-CoV-2 lineages isolated in the country can be visualised by selecting options for coloring in the control panel (icon on top left/right). **Note** that the latest available Philippine sequences were isolated on 29 November 2022, thus the frequencies after the time point could harbor great uncertainty.

- **Nextstrain clade** and the corresponding Pango lineage name: **21L** = BA.2, **22B** = BA.5, **22C** = BA.2.12.1, **22A** = BA.4, **22F** = XBB.

Diversity within the Omicron variant

Pango lineage	New submission	Isolated in 3 months	Total
BA.1.*	0	0	598
BA.2	34 (3.1)	33 (3.1)	505
BA.2.3	92 (8.4)	90 (8.4)	6045
BA.2.3.20.*	304 (27.9)	298 (27.8)	491
BA.2.12.1	0	0	118
BA.2.75.*	2 (0.2)	2 (0.2)	7
Other BA.2.*	3 (0.3)	3 (0.3)	243
BA.4.*	0	0	120
BA.5	1 (0.1)	1 (0.1)	14
BA.5.2.*	51 (4.7)	43 (4)	3112
Other BA.5.*	5 (0.5)	6 (0.6)	405
BE.1.*	2 (0.2)	3 (0.3)	17
BQ.1.*	1 (0.1)	1 (0.1)	1
XBB.*	335 (30.7)	331 (30.9)	356
XBC.*	70 (6.4)	72 (6.7)	100

Table 1b. Number of available Omicron sequences in the Philippines as of 31 December 2022. *New submission*, new sequences submitted from the last report. *Isolated in 3 months*, sequences isolated from 1 October 2022 to 31 December 2022. Numbers in the parentheses are percentage of the category (%). Phylogenetic relationship of the sublineages of Omicron variant is available [here](#).

- **BA.2.3.20** includes its descending sublineages CM. **BE.1** = BA.5.3.1.1, a sublineage of BA.5.3; **BQ.1** = BE.1.1.1.1, a sublineage of BE.1 (and also a sublineage of BA.5.3). **XBB** sublineages are recombinant viruses between BJ.1 (BA.2.10.1.1) and BA.2.75, whereas **XBC** are recombinant viruses between BA.2 and Delta.

Diversity within the Delta variants

More than 70 Pango lineages have been found among Delta variants isolated in the Philippines, with >40 sublineages that have more than 2 isolated sequences as of March 2022. Phylogenetic relationship of the sublineages of Delta variant is available [here](#).

SARS-CoV-2 variants detected by administrative region

Region	New submission	Dominant variant in 3 months	Isolated in 3 months	Total
NCR	14 (1.3)	BA.2.3.20 (28.6)	14 (1.3)	5792
Ilocos	28 (2.6)	BA.2.3 (31)	29 (2.7)	743
CAR	3 (0.3)	BA.2.3 (6.2)	16 (1.5)	1334
Cagayan Valley	2 (0.2)	-	2 (0.2)	1561
Central Luzon	20 (1.8)	BA.2.3 (36.4)	22 (2.1)	1674
Calabarzon	133 (12.2)	BA.2.3.20 (18.2)	132 (12.3)	3479
Mimaropa	11 (1)	BA.2.3.20 (40)	10 (0.9)	619
Bicol	27 (2.5)	BA.2.3 (44.4)	27 (2.5)	701
Western Visayas	577 (52.9)	XBB (55.2)	567 (52.9)	3646
Central Visayas	5 (0.5)	BA.2 (20)	5 (0.5)	1192
Eastern Visayas	3 (0.3)	BA.2.3 (50)	2 (0.2)	237
Zamboanga Peninsula	0	-	0	778
Northern Mindanao	4 (0.4)	BA.2.3 (25)	4 (0.4)	526
Davao	89 (8.2)	XBC.1 (41.8)	98 (9.2)	2534
Soccsksargen	161 (14.8)	BA.2.3 (21.8)	133 (12.4)	779
Caraga	11 (1)	BA.2.3 (20)	5 (0.5)	564
BARMM	5 (0.5)	BA.2.3 (40)	5 (0.5)	136

Table 2. Number of available sequences by administrative region in the Philippines as of 31 December 2022. *New submission*, new sequences submitted from the last report. *Dominant variant in 3 months*, the major variant isolated from 1 October 2022 to 31 December 2022. A dash indicates no sequence isolated. *Isolated in 3 months*, sequences isolated from 1 October 2022 to 31 December 2022. Numbers next to the dominant variant indicate percentage of the variant in the region, whereas other numbers in the parentheses are percentage of the category.

NCR, National Capital Region; CAR, Cordillera Administrative Region; BARMM, Bangsamoro Autonomous Region in Muslim Mindanao.

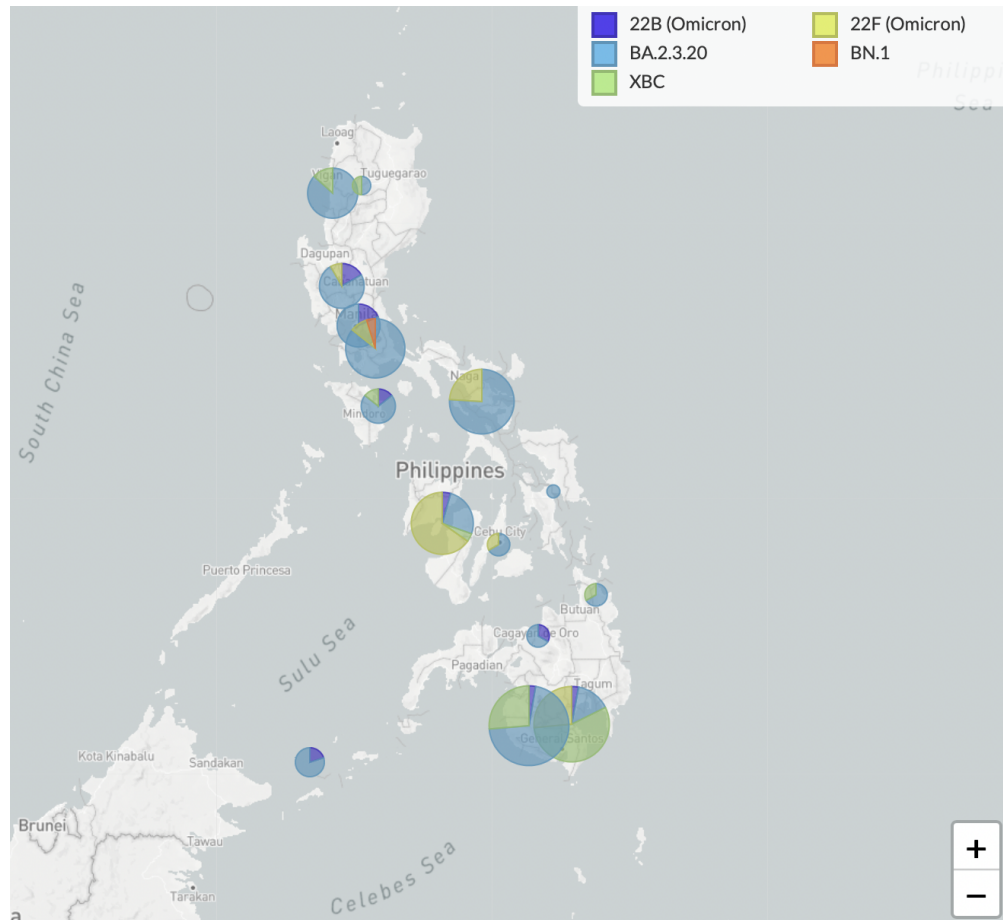


Figure 2. Frequencies of SARS-CoV-2 variants by administrative region in the Philippines since 1 October 2022. The figure is constructed with a subsampled genomic data set from all available sequences as Figure 1. Frequencies of isolates in a particular time frame and frequencies classified with the Pango lineage can be adjusted with the control panel (icon on top left/right).

- Nextstrain clade and the corresponding Pango lineage name: **22B** = BA.5, **22F** = XBB.

Philippines specific SARS-CoV-2 lineages

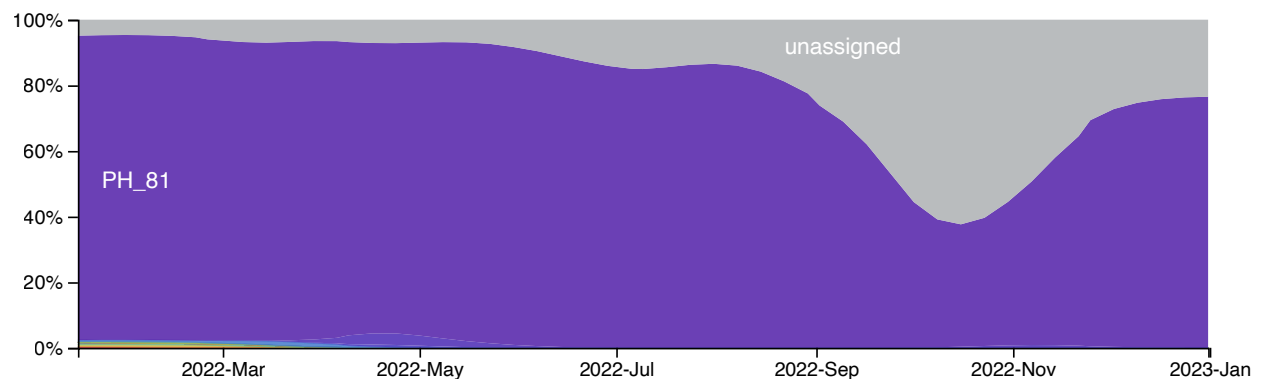


Figure 3. Temporal frequencies of Philippine lineages (clusters) identified by *Grapevine-anywhere*. Each sequence submitted to GECO database would undergo *Grapevine-anywhere* pipeline to detect sustain local transmission. A cluster is defined based on multiple sequences isolated in the Philippines that appeared to descend from the same introductory event on a phylogenetic tree. Phylogenetic relationships of these lineages can be found [here](#). **We are currently looking into the issue in which imbalanced amount of PH/non-PH genomic data caused the base of most lineages to be inferred as Philippines-originated.**

Cluster name	Date first identified	Pango lineage	Distribution	New sub-mission	Isolated in 3 months	Total
PH_81	2021-02-16	BA.2.3	>3 regions	363	353	9630
PH_190	2020-12-01	B.1.351	>3 regions	4	3	6283
PH_309	2022-01-07	BA.1.17.2	Central Visayas	0	0	6
PH_393	2022-01-05	BA.1.1	Central Visayas; NCR	0	0	8
PH_386	2021-12-31	BA.1.1	NCR; Central Visayas	0	0	6
PH_315	2021-12-30	BA.1.17.2	Central Visayas; NCR; Calabarzon	0	0	15
PH_327	2021-12-30	BA.1.17.2	>3 regions	0	0	6
PH_331	2021-12-28	BA.1	>3 regions	0	0	15
PH_335	2021-12-28	BA.1	Central Visayas; NCR	0	0	7
PH_374	2021-12-25	BA.1.1	Central Visayas; NCR; Davao	0	0	6
PH_373	2021-12-24	BA.1.1	Central Visayas; NCR; Davao	0	0	8
PH_376	2021-12-22	BA.1.1	NCR; Central Luzon; Central Visayas	0	0	6
PH_380	2021-12-22	BA.1.1	>3 regions	0	0	74
PH_346	2021-12-21	BA.1.1	>3 regions	0	0	54
PH_349	2021-12-21	BA.1.1	NCR; Central Luzon; Central Visayas	0	0	23
PH_284	2021-12-19	BA.1.15	Central Luzon; NCR	0	0	11
PH_328	2021-12-16	BA.1	Central Luzon; Central Visayas	0	0	5
PH_307	2021-12-14	BA.1.17.2	Central Visayas; NCR; Davao	0	0	16
PH_316	2021-12-06	BA.1	>3 regions	0	0	22
PH_294	2021-11-20	BA.1	Central Luzon; Central Visayas; NCR	0	0	11
PH_121	2021-05-06	B.1.1.7	>3 regions	0	0	7
PH_126	2021-04-30	B.1.1.7	Davao; Caraga; NCR	0	0	19
PH_123	2021-04-19	B.1.1.7	Davao; Soccsksargen	0	0	18
PH_144	2021-04-19	B.1.1.7	>3 regions	0	0	16
PH_134	2021-04-14	B.1.1.7	>3 regions	0	0	21
PH_125	2021-04-13	B.1.1.7	Davao; Caraga; Central Luzon	0	0	13
PH_259	2021-04-02	B.1.1.519	NCR	0	0	5
PH_127	2021-03-25	B.1.1.7	>3 regions	0	0	29
PH_124	2021-03-22	B.1.1.7	>3 regions	0	0	31
PH_140	2021-03-19	B.1.1.7	>3 regions	0	0	12
PH_143	2021-03-15	B.1.1.7	Bicol; NCR; Calabarzon	0	0	13
PH_142	2021-03-08	B.1.1.7	>3 regions	0	0	25
PH_117	2021-03-06	B.1.1.7	>3 regions	0	0	31
PH_118	2021-03-05	B.1.1.7	>3 regions	0	0	24

Cluster name	Date first identified	Pango lineage	Distribution	New sub-mission	Isolated in 3 months	Total
PH_122	2021-03-05	B.1.1.7	>3 regions	0	0	32
PH_155	2021-03-05	B.1.1.7	>3 regions	0	0	33
PH_247	2021-03-05	B.1.1.63	NCR; Calabarzon	0	0	5
PH_145	2021-03-04	B.1.1.7	>3 regions	0	0	28
PH_73	2021-03-04	B.1.1.7	>3 regions	0	0	9
PH_128	2021-02-22	B.1.1.7	NCR; Calabarzon; Central Luzon	0	0	13
PH_27	2021-02-18	B.1.1.7	Calabarzon; Mimaropa; NCR	0	0	6
PH_79	2021-02-15	B.1.1.7	>3 regions	0	0	55
PH_84	2021-02-12	B.1.1.7	>3 regions	0	0	72
PH_156	2021-02-11	B.1.1.7	>3 regions	0	0	14
PH_130	2021-02-10	B.1.1.7	>3 regions	0	0	328
PH_217	2021-01-27	B.1.1.63	NCR; Calabarzon	0	0	7
PH_80	2021-01-26	B.1.1.7	>3 regions	0	0	48
PH_234	2021-01-25	B.1.1.63	Calabarzon	0	0	5
PH_43	2021-01-21	B.1.466.1	Calabarzon; NCR	0	0	21
PH_253	2021-01-19	B.1.1	>3 regions	0	0	29
PH_264	2021-01-15	B.1.1.28	Davao; NCR; Soccsksargen	0	0	9
PH_104	2021-01-14	B.1.1.7	NCR; Central Visayas; CAR	0	0	5
PH_30	2021-01-12	B.1.441	NCR; Central Visayas	0	0	5
PH_266	2021-01-11	B.1.1.28	Soccsksargen; Davao; Calabarzon	0	0	14
PH_271	2021-01-11	B.1.1.28	Davao	0	0	14
PH_197	2021-01-08	B.1.1	Calabarzon; Central Visayas; NCR	0	0	6
PH_111	2021-01-07	B.1.1.7	NCR; Central Luzon; Central Visayas	0	0	6
PH_152	2021-01-07	B.1.1.7	>3 regions	0	0	342
PH_78	2021-01-05	B.1.1.7	>3 regions	0	0	133
PH_116	2020-12-29	B.1.1.7	>3 regions	0	0	8
PH_59	2020-12-28	B.1.524	>3 regions	0	0	10
PH_47	2020-12-26	B.1.2	NCR; Calabarzon	0	0	5
PH_222	2020-12-18	B.1.1.63	Cagayan Valley; NCR	0	0	7
PH_187	2020-12-17	B.1.1.263	CAR; Cagayan Valley; Central Luzon	0	0	65
PH_229	2020-12-15	B.1.1.63	NCR; Calabarzon; CAR	0	0	11
PH_157	2020-12-10	B.1.1.7	NCR; Calabarzon; Central Visayas	0	0	5
PH_225	2020-12-10	B.1.1.63	Calabarzon; NCR	0	0	5
PH_240	2020-12-04	B.1.1.63	NCR; Central Luzon	0	0	10
PH_272	2020-12-02	B.1.1.28	>3 regions	0	0	36
PH_273	2020-12-02	B.1.1.28	NCR; Calabarzon; Caraga	0	0	20
PH_176	2020-11-25	B.1.1	Calabarzon; NCR	0	0	11
PH_214	2020-11-22	B.1.1.63	Calabarzon; NCR	0	0	9
PH_180	2020-11-15	B.1.1.263	CAR; Cagayan Valley; Calabarzon	0	0	9
PH_14	2020-11-10	B.6	NCR; Calabarzon	0	0	5

Cluster name	Date first identified	Pango lineage	Distribution	New submission	Isolated in 3 months	Total
PH_36	2020-11-09	B.1.1.7	>3 regions	0	0	1068
PH_269	2020-11-07	B.1.1.28	Calabarzon; NCR; Central Luzon	0	0	6
PH_33	2020-11-06	B.1.36	Calabarzon; NCR	0	0	10
PH_213	2020-11-03	B.1.1.63	Calabarzon	0	0	6
PH_208	2020-11-02	B.1.1.63	>3 regions	0	0	35
PH_245	2020-11-01	B.1.1.63	>3 regions	0	0	14
PH_179	2020-10-11	B.1.1.263	>3 regions	0	0	78
PH_270	2020-08-24	B.1.1.28	>3 regions	0	0	15
PH_60	2020-08-22	B.1	NCR; Calabarzon; Davao	0	0	12
PH_210	2020-08-13	B.1.1.63	>3 regions	0	0	189
PH_175	2020-08-07	B.1.1	NCR	0	0	5
PH_239	2020-08-07	B.1.1.63	>3 regions	0	0	21
PH_16	2020-08-06	B.6	>3 regions	0	0	40
PH_177	2020-08-05	B.1.1	Calabarzon; NCR	0	0	5
PH_92	2020-07-22	B.1.1.63	>3 regions	0	0	127
PH_209	2020-07-19	B.1.1.63	Calabarzon; NCR; Western Visayas	0	0	24
PH_173	2020-07-12	B.1.1	NCR; Calabarzon; Mimaropa	0	0	13
PH_237	2020-07-12	B.1.1.63	>3 regions	0	0	79
PH_205	2020-07-10	B.1.1	>3 regions	0	0	105
PH_54	2020-07-10	B.1	>3 regions	0	0	32
PH_221	2020-07-09	B.1.1.63	>3 regions	0	0	121
PH_171	2020-07-08	P.3	>3 regions	0	0	618
PH_61	2020-07-08	B.1	Mimaropa; NCR; Central Visayas	0	0	9
PH_219	2020-07-07	B.1.1.63	>3 regions	0	0	30
PH_244	2020-07-07	B.1.1.63	NCR; Calabarzon; Cagayan Valley	0	0	13
PH_267	2020-07-05	B.1.1.28	>3 regions	0	0	295
PH_206	2020-07-01	B.1.1.63	Calabarzon; NCR; CAR	0	0	9
PH_231	2020-07-01	B.1.1.63	>3 regions	0	0	235
PH_224	2020-06-29	B.1.1.63	>3 regions	0	0	133
PH_236	2020-06-23	B.1.1.63	NCR	0	0	5
PH_178	2020-06-16	B.1.1.263	>3 regions	0	0	136
PH_62	2020-06-11	B.1	NCR; Western Visayas	0	0	9
PH_13	2020-03-11	B.6	NCR; Cagayan Valley	0	0	6
PH_2	2020-03-10	B.6	>3 regions	0	0	19

Table 3. Number of sequences by cluster identified with the Grapevine-anywhere as of 31 December 2022. A cluster is defined based on multiple sequences isolated in the Philippines that appeared to descend from the same introductory event on a phylogenetic tree. *Date first identified*, the isolation date of the first identified sequence. *Pango lineage*, the major Pango lineage of the sequences that belong to the same cluster. *New submission*, new sequences submitted from the last report. *Isolated in 3 months*, sequences isolated from 1 October 2022 to 31 December 2022. **We are currently looking into the issue in which imbalanced amount of PH/non-PH genomic data caused the base of most lineages to be inferred as Philippines-originated.**

SARS-CoV-2 sequencing in the Philippines

Total available SARS-CoV-2 sequences in the Philippines: 26322

SARS-CoV-2 sequences from GECO project: 3399

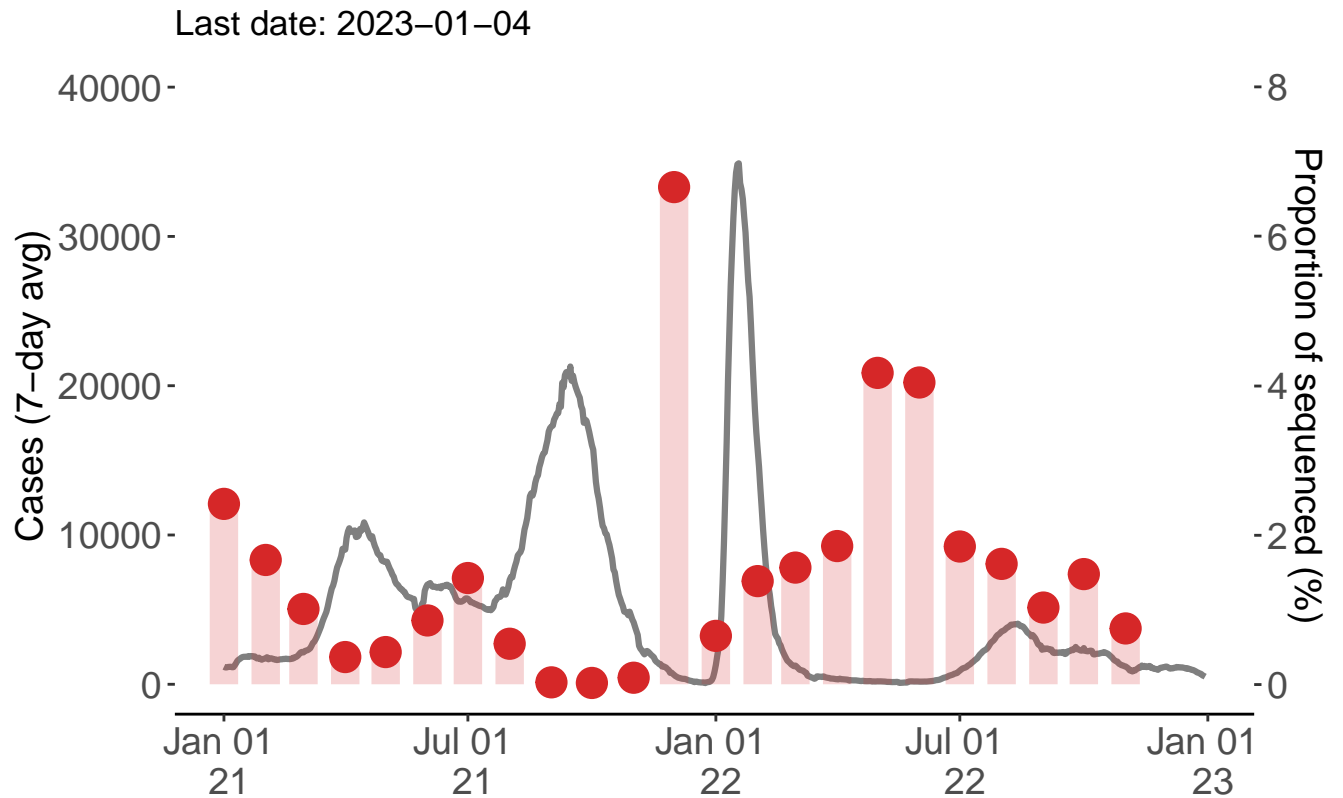


Figure 4. Number of COVID-19 cases and the proportion of sequenced samples in the Philippines from January 2021. The gray line indicates the mean cases in a 7 days window based on the JHU data base, whereas the red bars indicate the estimated percentage of sequenced samples among cases in a month.

Epidemiology of COVID-19 in the Philippines

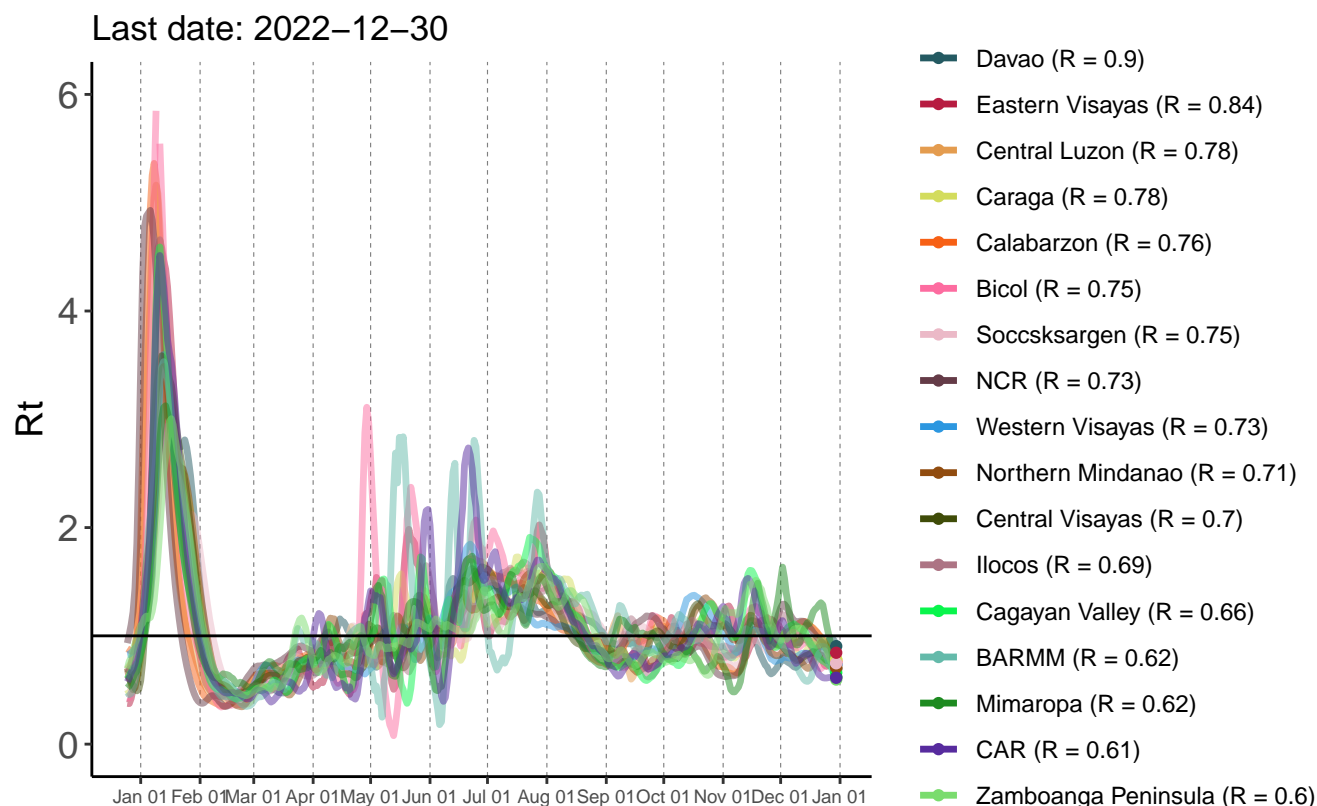


Figure 5. Mean effective reproductive number (R_t) of COVID-19 in the Philippines by region from December 2021. The reproductive number (R) is defined as the number of new infections that one infected patient can cause in a susceptible population. Here, the *mean effective reproductive number* (R_t) was inferred by daily number of cases reported in MOH, Philippines in a window of seven days. The horizontal line indicates one. If R_t is greater than 1, the case number in the region will likely continue to grow. If the R_t is below 1, the new cases may continue to appear at a slower rate. The R values denoted with the region name represent the most recent estimates. More regional epidemiological statistics can be found [here](#).

SARS-CoV-2 mutations of interest

Omicron sublineage convergent sites

- **R346X** (K: BA.1.1; T: BA.5.2, BA.2.75.2): [Distribution on the Philippine isolates](#)
- **K444X** (R: BA.2.3.20; M: BR.1 [a BA.2.75.4.*]; T: BQ.1): [Distribution on the Philippine isolates](#)
- **L452X** (R: BA.4/BA.5, BA.2.35; M: BA.2.3.20): [Distribution on the Philippine isolates](#)
- **N460X** (K: BA.2.75, BQ.1 [a BA.5.3.*], BA.2.3.20): [Distribution on the Philippine isolates](#)
- **F486X** (V: BA.4/BA.5, S: BA.2.75.2, XBB.1.5): [Distribution on the Philippine isolates](#)

- **R493X** (Q: BA.4/BA.5, BA.2.75, BA.2.3.20): [Distribution on the Philippine isolates](#)

Other Spike protein

- **69-70Del** (Alpha, Omicron): [Distribution on the Philippine isolates](#)
- **T95I** (Mu, Omicron): [Distribution on the Philippine isolates](#)
- **144-** (Alpha, Eta, Omicron): [Distribution on the Philippine isolates](#)
- **K417N** (Beta, Omicron): [Distribution on the Philippine isolates](#)
- **T478K** (Delta, Omicron): [Distribution on the Philippine isolates](#)
- **E484K** (Beta, Gamma, Eta, Mu): [Distribution on the Philippine isolates](#)
- **N501Y** (Alpha, Beta, Gamma, Mu, Omicron): [Distribution on the Philippine isolates](#)
- **H655Y** (Gamma, Omicron): [Distribution on the Philippine isolates](#)

Relevant functions including antibody escape (S 69-70Del, S 144, S 346, S 417, S 484) and receptor binding (S 417, S 484, S 501). 69-70Del, deletions at positions 69-70.

Data sources and references

Data

- [GECO website](#)
- [DOH Data drop](#)
- [GISAID](#) (EPI-SET: EPI_SET_230102wd)
- [JHU COVID data](#)

Methods

- [Analyses in this report](#)
- [Nextstrain](#) (build for GECO project)
- [Grapevine-anywhere](#)

References

- [WHO](#)
- [Pango lineage list](#)

Online version and previous reports

[GECO Monthly Report](#)

2022-11 [pdf](#)



**Genomic Epidemiology of
COVID in the Philippines
(GECO PH)**