

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

Highlights

- The latest genomic data available in the Philippines were isolated in August, 2022
- BA.5.2 remains the dominant among the most recent isolates
- No BQ.1.* or XBB.* has been identified
- Four recombinant sublineage XBC sequences were collected in August

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	2805
Beta	B.1.351	VOC	0	0	3276
Delta	B.1.617.2/AY.x	VOC	0	0	3490
Gamma	P.1	VOC	0	0	4
Omicron	B.1.1.529/BA.x	VOC	406 (98.1)	409 (90.3)	9065
Eta	B.1.525	VUM	0	0	8
Theta	P.3	VUM	0	0	525

Table 1. Number of available sequences by variant in the Philippines as of 28 October 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 August 2022 to 28 October 2022. Numbers in the parentheses are percentage of the category (%).

- **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.

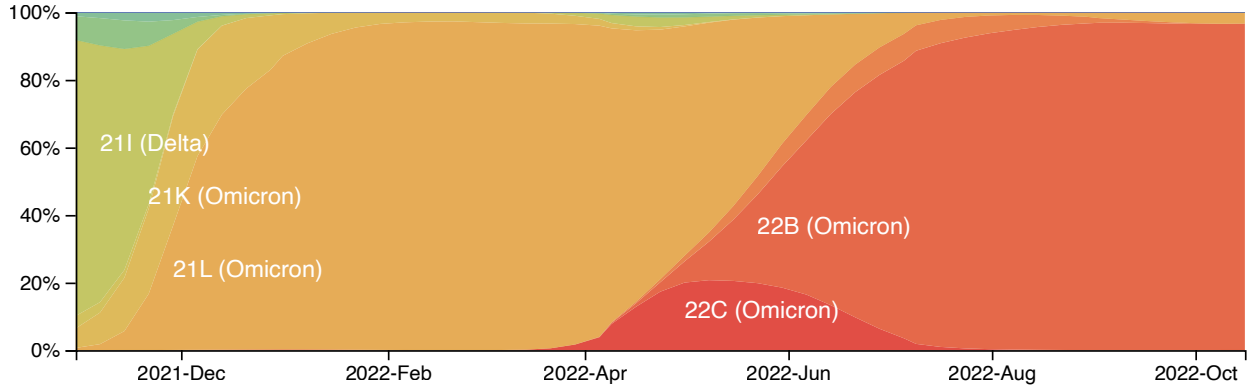


Figure 1. Temporal frequencies of SARS-CoV-2 variants in the Philippines. The figure is constructed with a subsampled genomic data set from all available sequences ([methods](#)). A more detailed illustration of SARS-CoV-2 lineages isolated in the country can be visualised by selecting Pango Lineage as the option for coloring in the control panel (icon on top left/right). **Note** that the latest available Philippine sequences were isolated on 31 August 2022, thus the frequencies after the time point could harbor great uncertainty.

- **Nextstrain clade** and the corresponding Pango lineage name: **22B** = BA.5, **22C** = BA.2.12.1, **22A** = BA.4, **21L** = BA.2, **21K** = BA.1.

Diversity within the Omicron variant

Pango lineage	New submission	Isolated in 3 months	Total
BA.1.*	0	0	598
BA.2	1 (0.2)	3 (0.2)	475
BA.2.3	2 (0.5)	9 (0.7)	5948
BA.2.12.1	0	4 (0.3)	118
BA.2.75.*	1 (0.2)	1 (0.1)	1
Other BA.2.*	1 (0.2)	7 (0.5)	211
BA.4.*	13 (3.1)	64 (4.7)	105
BA.5	6 (1.4)	15 (1.1)	15
BA.5.2.*	341 (82.4)	996 (73.7)	1318
Other BA.5.*	29 (7)	156 (11.5)	208
BE.1.*	1 (0.2)	11 (0.8)	14
BQ.1.*	0	0	0

Table 1b. Number of available Omicron sequences in the Philippines as of 28 October 2022. *New submission*, new sequences submitted from the last report. *Isolated in 3 months*, sequences isolated from 1 August 2022 to 28 October 2022. Numbers in the parentheses are percentage of the category (%). Phylogenetic relationship of the sublineages of Omicron variant is available [here](#).

- **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).

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	2 (0.5)	Omicron (100)	2 (0.4)	5755
Ilocos	2 (0.5)	Omicron (100)	18 (4)	690
CAR	0	Omicron (100)	1 (0.2)	1317
Cagayan Valley	0	-	0	1559
Central Luzon	1 (0.2)	Omicron (50)	6 (1.3)	1630
Calabarzon	0	Omicron (43.5)	23 (5.1)	3229
Mimaropa	14 (3.4)	Omicron (83.3)	36 (7.9)	550
Bicol	24 (5.8)	Omicron (56.8)	37 (8.2)	650
Western Visayas	1 (0.2)	Omicron (100)	1 (0.2)	1247
Central Visayas	3 (0.7)	Omicron (100)	1 (0.2)	1184
Eastern Visayas	0	-	0	234
Zamboanga Peninsula	0	-	0	778
Northern Mindanao	2 (0.5)	Omicron (100)	2 (0.4)	522
Davao	322 (77.8)	Omicron (99.3)	293 (64.7)	2256
Soccsksargen	36 (8.7)	Omicron (84)	25 (5.5)	577
Caraga	3 (0.7)	Omicron (100)	4 (0.9)	539
BARMM	4 (1)	Omicron (100)	4 (0.9)	131

Table 2. Number of available sequences by administrative region in the Philippines as of 28 October 2022. The variant definition is identical to Table 1 based on the WHO website. *New submission*, new sequences submitted from the last report. *Dominant variant in 3 months*, the major variant isolated from 1 August 2022 to 28 October 2022. A dash indicates no sequence isolated. *Isolated in 3 months*, sequences isolated from 1 August 2022 to 28 October 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.

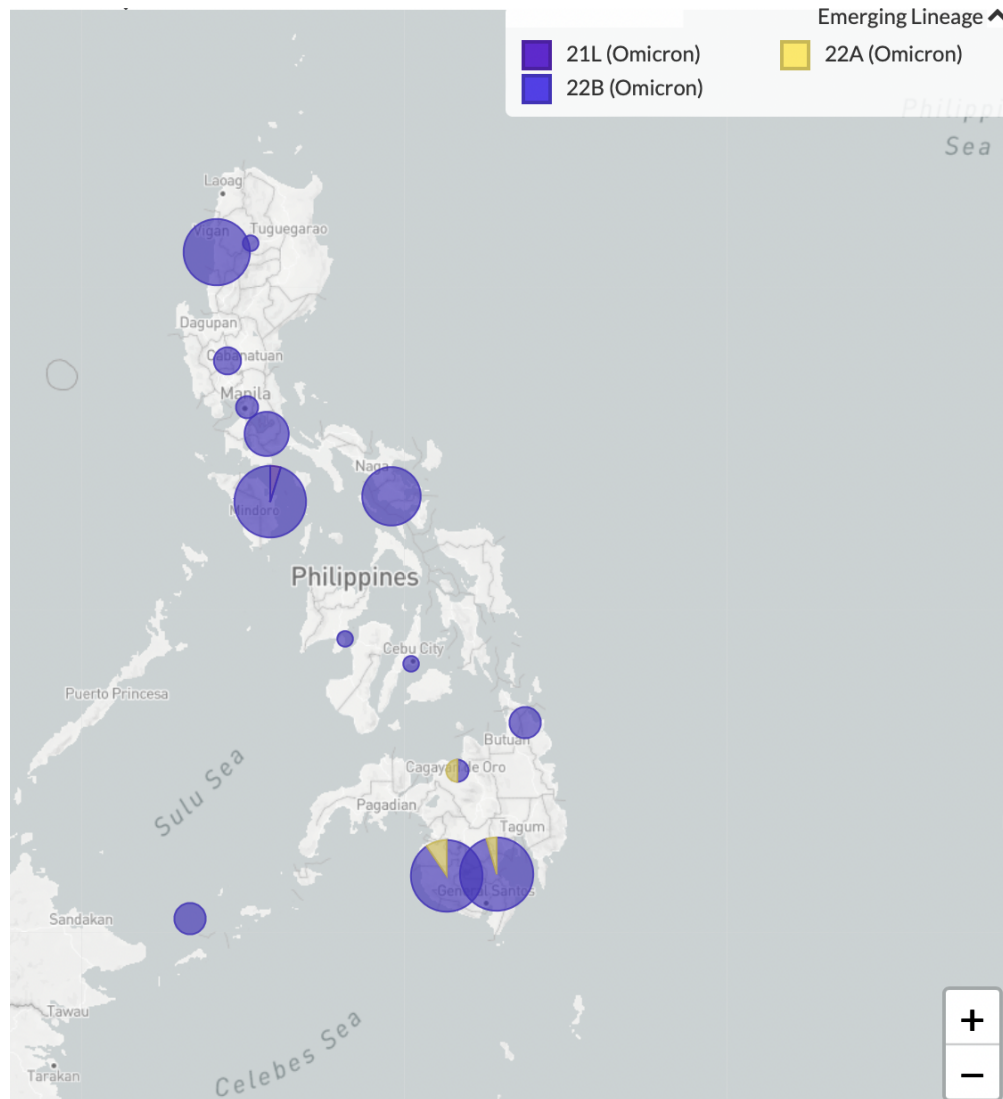


Figure 2. Frequencies of SARS-CoV-2 variants by administrative region in the Philippines since 1 August 2022. The figure is constructed with a subsampled genomic data set from all available sequences as Figure 1. Frequencies of isolates in a particular time frame and frequencies classified with the Pango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

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

Philippines specific SARS-CoV-2 lineages

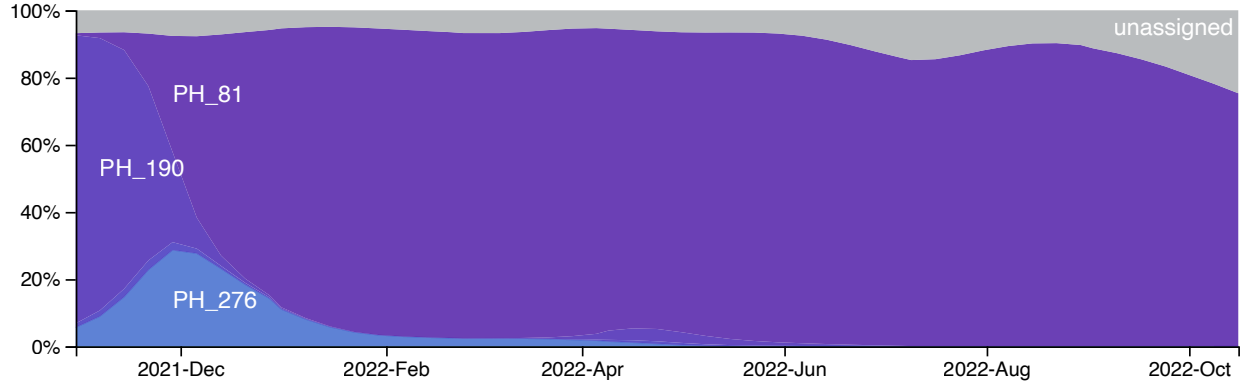


Figure 3. Temporal frequencies of Philippine lineages (clusters) identified by *Grapevine-anywhere*. Each sequence submitted to GECO database would undergo *Grapevine-anywhere* pipeline to detect sustain local transmission. A cluster is defined based on multiple sequences isolated in the Philippines that appeared to descend from the same introductory event on a phylogenetic tree. Phylogenetic relationships of these lineages can be found [here](#).

Cluster name	Date first identified	Pango lineage	Distribution	New submission	Isolated in 3 months	Total
PH_81	2021-02-18	BA.2.3	>3 regions	371	368	7405
PH_276	2021-11-20	BA.1.1	>3 regions	0	0	473
PH_126	2021-05-06	B.1.1.7	>3 regions	0	0	7
PH_135	2021-04-30	B.1.1.7	Davao; Caraga; NCR	0	0	19
PH_130	2021-04-19	B.1.1.7	Davao; Soccsksargen	0	0	18
PH_141	2021-04-19	B.1.1.7	>3 regions	0	0	16
PH_120	2021-04-14	B.1.1.7	>3 regions	0	0	21
PH_134	2021-04-13	B.1.1.7	Davao; Caraga; Central Luzon	0	0	13
PH_171	2021-04-02	B.1.1.519	NCR	0	0	5
PH_136	2021-03-25	B.1.1.7	>3 regions	0	0	30
PH_128	2021-03-22	B.1.1.7	>3 regions	0	0	32
PH_139	2021-03-19	B.1.1.7	>3 regions	0	0	12
PH_137	2021-03-08	B.1.1.7	>3 regions	0	0	27
PH_122	2021-03-06	B.1.1.7	>3 regions	0	0	31
PH_123	2021-03-05	B.1.1.7	>3 regions	0	0	24
PH_129	2021-03-05	B.1.1.7	>3 regions	0	0	32
PH_154	2021-03-05	B.1.1.7	>3 regions	0	0	32
PH_225	2021-03-05	B.1.1.63	NCR; Calabarzon	0	0	5
PH_140	2021-03-04	B.1.1.7	>3 regions	0	0	18
PH_142	2021-03-04	B.1.1.7	>3 regions	0	0	28
PH_132	2021-02-22	B.1.1.7	>3 regions	0	0	14
PH_27	2021-02-18	B.1.1.7	Calabarzon; Mimaropa; NCR	0	0	6
PH_78	2021-02-15	B.1.1.7	>3 regions	0	0	55
PH_95	2021-02-12	B.1.1.7	>3 regions	0	0	72
PH_153	2021-02-11	B.1.1.7	>3 regions	0	0	15
PH_217	2021-01-27	B.1.1.63	NCR; Calabarzon	0	0	7
PH_108	2021-01-26	B.1.1.7	NCR; Calabarzon; Central Visayas	0	0	5

Cluster name	Date first identified	Pango lineage	Distribution	New sub-mission	Isolated in 3 months	Total
PH_89	2021-01-26	B.1.1.7	>3 regions	0	0	48
PH_219	2021-01-25	B.1.1.63	Calabarzon	0	0	5
PH_67	2021-01-21	B.1.466.1	Calabarzon; NCR	0	0	21
PH_247	2021-01-19	B.1.1	>3 regions	0	0	29
PH_259	2021-01-15	B.1.1.28	Davao; NCR; Soccsksargen	0	0	9
PH_103	2021-01-14	B.1.1.7	NCR; Central Visayas; CAR	0	0	5
PH_60	2021-01-12	B.1.441	NCR; Central Visayas	0	0	5
PH_262	2021-01-11	B.1.1.28	Soccsksargen; Davao; Calabarzon	0	0	12
PH_266	2021-01-11	B.1.1.28	Davao	0	0	14
PH_251	2021-01-08	B.1.1	Calabarzon; Central Visayas; NCR	0	0	6
PH_279	2021-01-08	P.3	>3 regions	0	0	456
PH_105	2021-01-07	B.1.1.7	NCR; Central Luzon; Central Visayas	0	0	6
PH_109	2021-01-07	B.1.1.7	NCR	0	0	7
PH_116	2021-01-07	B.1.1.7	>3 regions	0	0	343
PH_263	2021-01-06	B.1.1.28	>3 regions	0	0	45
PH_77	2021-01-05	B.1.1.7	>3 regions	0	0	134
PH_264	2021-01-03	B.1.1.28	Davao; Soccsksargen	0	0	17
PH_112	2020-12-29	B.1.1.7	NCR; Central Luzon; Eastern Visayas	0	0	5
PH_36	2020-12-28	B.1.1.7	>3 regions	0	0	1402
PH_51	2020-12-26	B.1.2	NCR; Calabarzon	0	0	5
PH_200	2020-12-18	B.1.1.63	Cagayan Valley; NCR	0	0	7
PH_207	2020-12-15	B.1.1.63	NCR; Calabarzon; CAR	0	0	11
PH_146	2020-12-10	B.1.1.7	NCR; Calabarzon; Central Visayas	0	0	5
PH_203	2020-12-10	B.1.1.63	Calabarzon; NCR	0	0	5
PH_236	2020-12-04	B.1.1.63	NCR; Central Luzon	0	0	10
PH_269	2020-12-02	B.1.1.28	>3 regions	0	0	36
PH_270	2020-12-02	B.1.1.28	NCR; Calabarzon; Caraga	0	0	21
PH_180	2020-11-25	B.1.1	Calabarzon; NCR	0	0	11
PH_212	2020-11-22	B.1.1.63	Calabarzon; NCR	0	0	9
PH_192	2020-11-15	B.1.1.263	CAR; Cagayan Valley; Calabarzon	0	0	9
PH_21	2020-11-10	B.6	NCR; Calabarzon	0	0	5
PH_182	2020-11-09	B.1.1.28	NCR; Calabarzon	0	0	11
PH_268	2020-11-07	B.1.1.28	Calabarzon; NCR; Central Luzon	0	0	6
PH_68	2020-11-06	B.1.36	Calabarzon; NCR	0	0	10
PH_211	2020-11-03	B.1.1.63	Calabarzon	0	0	6
PH_218	2020-11-02	B.1.1.63	>3 regions	0	0	34
PH_223	2020-11-01	B.1.1.63	>3 regions	0	0	14
PH_193	2020-10-11	B.1.1.263	>3 regions	0	0	68
PH_265	2020-08-24	B.1.1.28	>3 regions	0	0	15
PH_37	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

Cluster name	Date first identified	Pango lineage	Distribution	New submission	Isolated in 3 months	Total
PH_178	2020-08-07	B.1.1	NCR	0	0	5
PH_235	2020-08-07	B.1.1.63	>3 regions	0	0	21
PH_19	2020-08-06	B.6	>3 regions	0	0	40
PH_181	2020-08-05	B.1.1	Calabarzon; NCR	0	0	5
PH_242	2020-08-04	B.1.1	Calabarzon; NCR; Cagayan Valley	0	0	25
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_40	2020-07-15	B.1	>3 regions	0	0	24
PH_238	2020-07-12	B.1.1	NCR; Calabarzon; Mimaropa	0	0	9
PH_190	2020-07-10	B.1.351	>3 regions	0	0	6348
PH_199	2020-07-09	B.1.1.63	>3 regions	0	0	121
PH_175	2020-07-08	B.1.1	>3 regions	0	0	225
PH_227	2020-07-08	B.1.1.63	>3 regions	0	0	79
PH_38	2020-07-08	B.1	Mimaropa; NCR; Central Visayas	0	0	9
PH_198	2020-07-07	B.1.1.63	>3 regions	0	0	32
PH_228	2020-07-07	B.1.1.63	NCR; Calabarzon; Cagayan Valley	0	0	12
PH_258	2020-07-05	B.1.1.28	>3 regions	0	0	233
PH_194	2020-07-01	B.1.1.63	NCR; Calabarzon; CAR	0	0	8
PH_220	2020-07-01	B.1.1.63	>3 regions	0	0	234
PH_204	2020-06-29	B.1.1.63	>3 regions	0	0	133
PH_231	2020-06-23	B.1.1.63	NCR	0	0	5
PH_185	2020-06-16	B.1.1.263	>3 regions	0	0	143
PH_42	2020-06-11	B.1	NCR; Western Visayas	0	0	9
PH_18	2020-03-11	B.6	NCR; Cagayan Valley	0	0	6
PH_2	2020-03-10	B.6	>3 regions	0	0	18

Table 3. Number of sequences by cluster identified with the Grapevine-anywhere as of 28 October 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 August 2022 to 28 October 2022.

SARS-CoV-2 sequencing in the Philippines

Total available SARS-CoV-2 sequences in the Philippines: 22866

SARS-CoV-2 sequences from GECO project: 2637

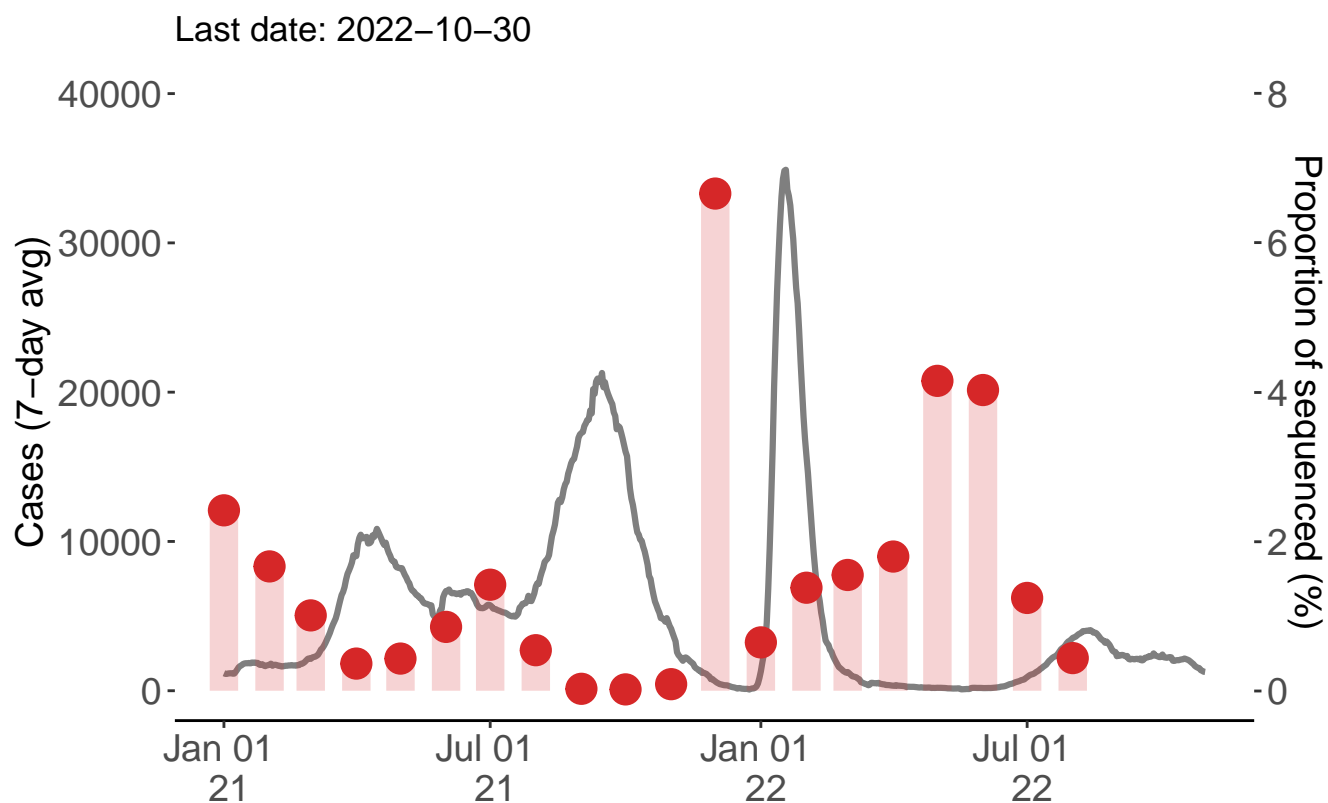


Figure 4. Number of COVID-19 cases and the proportion of sequenced samples in the Philippines from January 2021. The gray line indicates the mean cases in a 7 days window based on the JHU data base, whereas the red bars indicate the estimated percentage of sequenced samples among cases in a month.

Epidemiology of COVID-19 in the Philippines

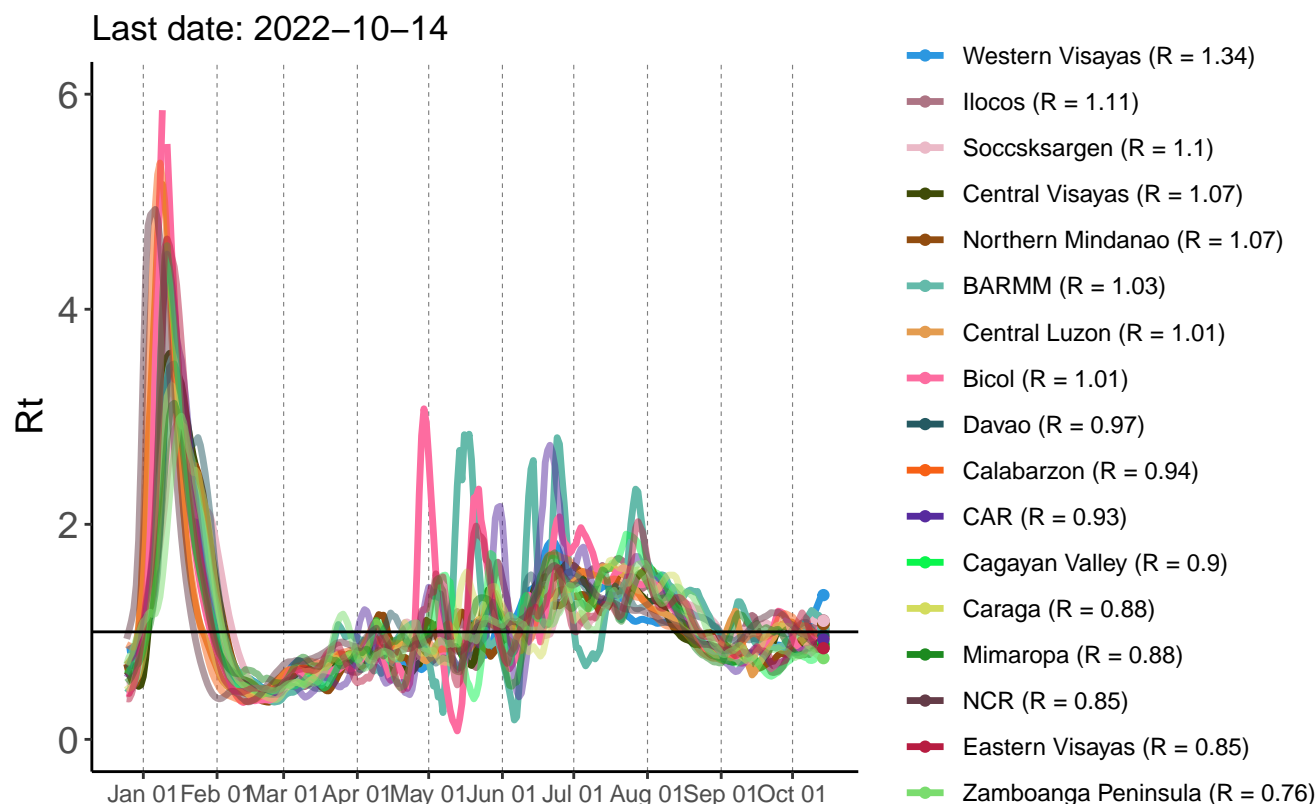


Figure 5. Mean effective reproductive number (R_t) of COVID-19 in the Philippines by region from December 2021. The reproductive number (R) is defined as the number of new infections that one infected patient can cause in a susceptible population. Here, the *mean effective reproductive number* (R_t) 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.*]): [Distribution on the Philippine isolates](#)
- **F486X** (V:BA.4/BA.5, S: BA.2.75.2): [Distribution on the Philippine isolates](#)

- **R493X** (Q:BA.4/BA.5, BA.2.75): [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_220930td)
- [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](#)

2022-09 [pdf](#)



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