

GECHO Philippines SARS-CoV-2 Situation Report - 2022 April

Highlights

- Recombinant variants and Omicron BA.4/BA.5 are closely monitored but no evidence of introduction of these strains

SARS-CoV-2 variants detected in the Philippines

WHO label	Pango lineage	Classification	New submission	Isolated in 4 months	Total
Alpha	B.1.1.7/Q.x	VOC	0	0	2780
Beta	B.1.351	VOC	1 (0.5)	0	3250
Delta	B.1.617.2/AY.x	VOC	88 (45.4)	0	3431
Gamma	P.1	VOC	0	0	3
Omicron	B.1.1.529/BA.x	VOC	84 (43.3)	842 (87.7)	1516
Eta	B.1.525	VUM	0	0	8
Theta	P.3	VUM	0	0	527

Table 1. Number of available sequences by variant in the Philippines as of 25 April 2022. The variants (VOC/VUM) here only include sequences that present in the GISAID or GECHO 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 4 months*, sequences isolated from 1 January 2022 to 25 April 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.

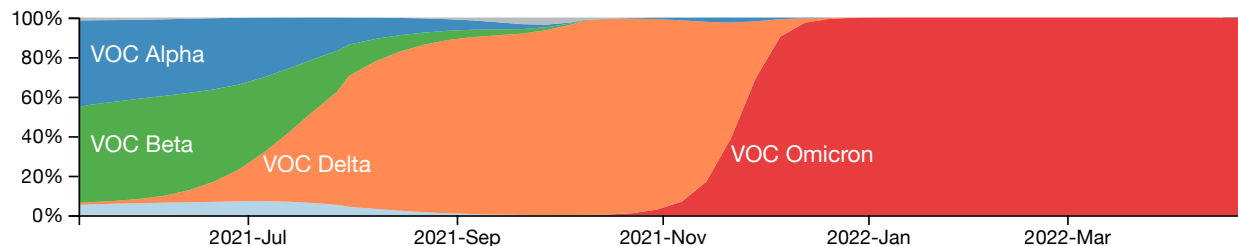


Figure 1. Temporal frequencies of SARS-CoV-2 variants in the Philippines. The figure is constructed with a subsampled genomic data set from all available sequences ([methods](#)). A more detailed illustration of SARS-CoV-2 lineages isolated in the country can be visualised by selecting PANGO Lineage as the option for coloring in the control panel (icon on top left/right). **Note** that the latest available Philippine sequences were isolated on 4 April, 2022, thus the frequencies after the time point could harbor great uncertainty.

Diversity within the Omicron variant

The two main sublineages of the Omicron variant, denoted as BA.1 and BA.2, have been identified in the Philippines since November 2021. Based on the available data, BA.2 had more sustained transmission in the country compared with BA.1. Results from the grapevine-anywhere pipeline also show large BA.2 clusters. Phylogenetic relationship of the sublineages of Omicron variant is available [here](#). Note that the BA.2 viruses do not have 69-70 deletions in the S protein, and therefore the SGTF (S-gene target failure) may not be used to detect the lineage (see *mutations of interest* section).

The BA.4 and BA.5 infections have increased since March 2022 in South Africa. These Omicron lineages showing potential growth advantages over BA.2 have not been found in our data base. On the other hand, about 10 BA.3 sequences have been isolated in the Philippines as early as December 2021.

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 4 months	Isolated in 4 months	Total
NCR	31 (16)	Omicron (96)	322 (33.5)	4809
Ilocos	4 (2.1)	Omicron (96)	50 (5.2)	421
CAR	70 (36.1)	Omicron (26.8)	97 (10.1)	859
Cagayan Valley	14 (7.2)	Omicron (75)	48 (5)	1051
Central Luzon	0	Omicron (100)	32 (3.3)	1122

Region	New submission	Dominant variant in 4 months	Isolated in 4 months	Total
Calabarzon	34 (17.5)	Omicron (92.4)	158 (16.5)	2412
Mimaropa	6 (3.1)	Omicron (82.6)	23 (2.4)	395
Bicol	0	Omicron (100)	8 (0.8)	257
Western Visayas	0	Omicron (100)	92 (9.6)	594
Central Visayas	0	Omicron (100)	38 (4)	666
Eastern Visayas	0	Omicron (100)	32 (3.3)	176
Zamboanga Peninsula	0	-	0	432
Northern Mindanao	0	Omicron (75)	12 (1.2)	358
Davao	93 (47.9)	Omicron (100)	17 (1.8)	879
Soccsksargen	0	Omicron (95)	20 (2.1)	223
Caraga	0	Omicron (100)	11 (1.1)	293
BARMM	0	-	0	101

Table 2. Number of available sequences by administrative region in the Philippines as of 25 April 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 4 months*, the major variant isolated from 1 January 2022 to 25 April 2022. A dash indicates no sequence isolated. *Isolated in 4 months*, sequences isolated from 1 January 2022 to 25 April 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.

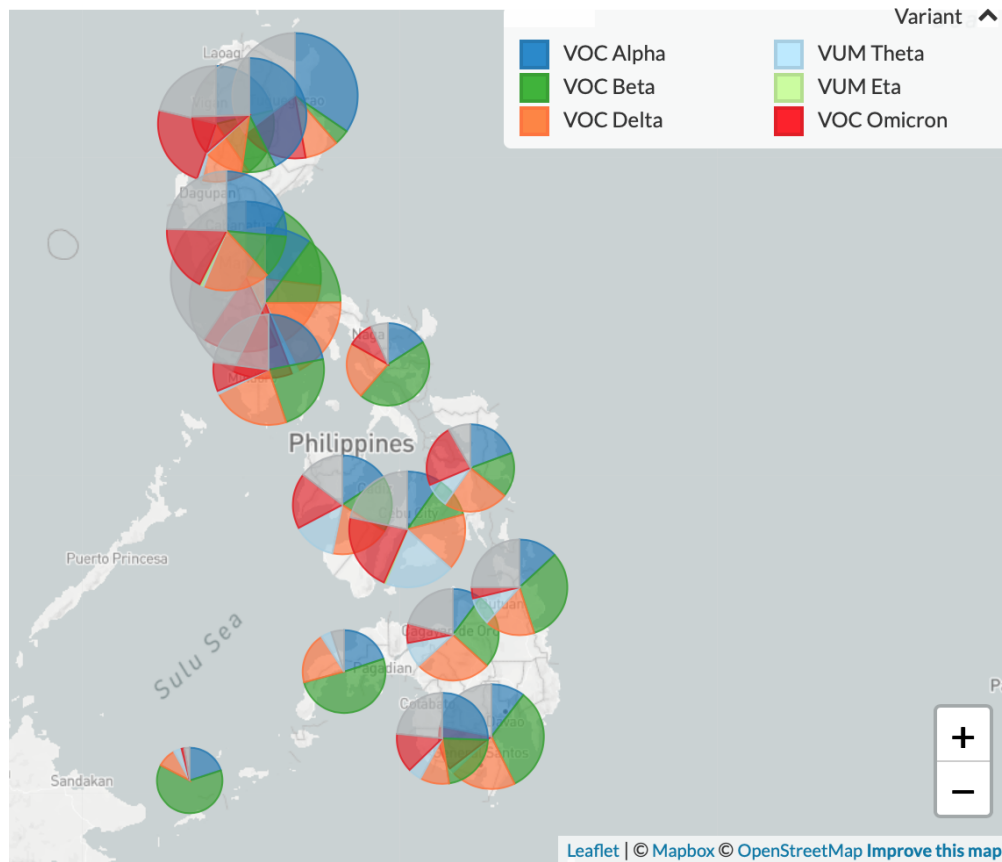


Figure 2. Frequencies of SARS-CoV-2 variants by administrative region in the Philippines. The figure is constructed with a subsampled genomic data set from all available sequences as Figure 1. Frequencies of isolates in a particular time frame can be adjusted with the control panel (icon on top left/right).

Philippines specific SARS-CoV-2 lineages

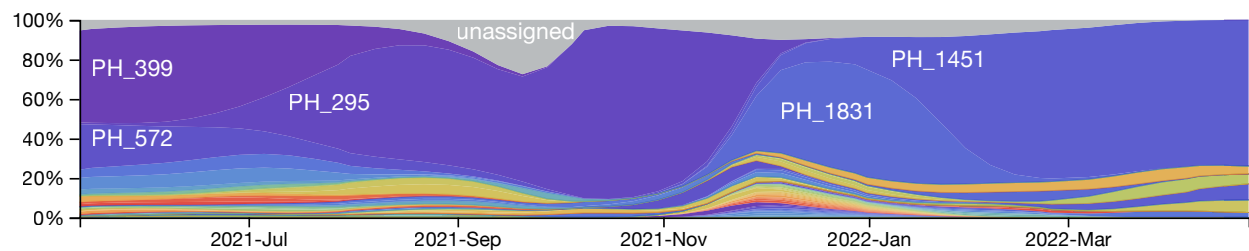


Figure 3. Temporal frequencies of Philippine lineages (clusters) identified by [Grapevine-anywhere](#). Each sequence submitted to GECO database would undergo *Grapevine-anywhere* pipeline to detect sustain local transmission. A cluster is defined based on multiple sequences isolated in the Philippines 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 sub-mission	Isolated in 4 months	Total
PH_1831	2021-12-02	BA.2.3	>3 regions	0	331	591
PH_1451	2021-12-19	BA.2.3	>3 regions	47	286	346
PH_1595	2021-12-26	BA.2.3	>3 regions	3	37	53
PH_1458	2021-12-22	BA.2.3	>3 regions	1	20	26
PH_1778	2021-12-23	BA.2.3	NCR; Calabarzon; CAR	2	4	11
PH_1437	2021-12-29	BA.2	Central Luzon; Ilocos; NCR	2	3	11
PH_1440	2021-12-28	BA.2	Central Luzon; Ilocos	0	2	10
PH_2098	2021-12-24	BA.1.1	Central Luzon; Central Visayas; Davao	0	1	8
PH_2165	2021-12-06	BA.1.14	>3 regions	0	1	8
PH_2090	2021-12-22	BA.1.1	Central Luzon; Central Visayas; NCR	0	0	6
PH_2102	2021-12-18	BA.1.1	NCR; Central Luzon; Central Visayas	0	0	18
PH_2211	2021-12-13	BA.1.15	Central Luzon; Central Visayas	0	0	8
PH_2161	2021-11-24	BA.1	Central Luzon; CAR	0	0	5
PH_213	2021-07-24	AY.98.1	NCR	0	0	6
PH_257	2021-07-23	AY.1	>3 regions	0	0	9
PH_182	2021-07-16	AY.107	>3 regions	0	0	28
PH_239	2021-07-14	AY.1	NCR; Ilocos; Central Luzon	0	0	14
PH_194	2021-07-13	AY.107	Central Luzon; NCR	0	0	6
PH_267	2021-07-12	AY.125	NCR; Calabarzon	0	0	12
PH_75	2021-07-10	AY.23	Calabarzon	0	0	5
PH_218	2021-07-08	AY.112	Northern Mindanao; Cagayan Valley; BARMM	0	0	8
PH_178	2021-07-07	AY.122	>3 regions	0	0	7
PH_208	2021-07-05	B.1.617.2	>3 regions	0	0	6
PH_73	2021-07-05	AY.23	>3 regions	0	0	23
PH_271	2021-07-02	AY.116	NCR; Calabarzon	0	0	6
PH_220	2021-06-30	AY.122	>3 regions	0	0	29
PH_245	2021-06-29	AY.1	>3 regions	0	0	19
PH_113	2021-06-28	AY.122	>3 regions	0	0	65
PH_269	2021-06-27	AY.112	>3 regions	0	0	28
PH_280	2021-06-27	AY.106	>3 regions	0	0	92
PH_224	2021-06-25	AY.1	>3 regions	0	0	107
PH_223	2021-06-23	AY.1	>3 regions	0	0	83
PH_263	2021-06-23	AY.1	>3 regions	0	0	34
PH_92	2021-06-21	AY.122	>3 regions	0	0	141
PH_857	2021-05-06	B.1.1.7	>3 regions	0	0	7
PH_905	2021-04-30	B.1.1.7	Davao; Caraga; NCR	0	0	19
PH_295	2021-04-24	B.1.617.2	>3 regions	1	0	2299
PH_830	2021-04-19	B.1.1.7	Davao; Soccsksargen	0	0	18
PH_973	2021-04-19	B.1.1.7	>3 regions	0	0	16
PH_729	2021-04-14	B.1.1.7	>3 regions	0	0	21
PH_900	2021-04-13	B.1.1.7	Davao; Caraga; Central Luzon	0	0	13
PH_298	2021-04-12	B.1.1.7	>3 regions	0	0	5
PH_1423	2021-04-02	B.1.1.519	NCR	0	0	5
PH_378	2021-03-28	B.1.351.3	NCR; Central Visayas	0	0	14
PH_885	2021-03-25	B.1.1.7	>3 regions	0	0	28

Cluster name	Date first identified	Pango lineage	Distribution	New sub-mission	Isolated in 4 months	Total
PH_957	2021-03-22	B.1.1.7	>3 regions	0	0	31
PH_929	2021-03-19	B.1.1.7	>3 regions	0	0	12
PH_386	2021-03-18	B.1.351	Central Luzon; NCR	0	0	5
PH_827	2021-03-11	B.1.1.7	>3 regions	0	0	43
PH_487	2021-03-05	B.1.1.7	>3 regions	0	0	32
PH_863	2021-03-05	B.1.1.7	>3 regions	0	0	32
PH_978	2021-03-05	B.1.1.7	>3 regions	0	0	24
PH_623	2021-03-04	B.1.1.7	>3 regions	0	0	47
PH_611	2021-02-22	B.1.1.7	>3 regions	0	0	14
PH_412	2021-02-15	B.1.1.7	>3 regions	0	0	55
PH_518	2021-02-12	B.1.1.7	>3 regions	0	0	72
PH_476	2021-02-11	B.1.1.7	>3 regions	0	0	14
PH_572	2021-02-06	B.1.1.7	>3 regions	0	0	1391
PH_1304	2021-02-05	B.1.1.63	NCR; Calabarzon	0	0	6
PH_399	2021-01-31	B.1.351	>3 regions	0	0	2939
PH_1193	2021-01-27	B.1.1.63	NCR; Calabarzon	0	0	7
PH_509	2021-01-26	B.1.1.7	>3 regions	0	0	48
PH_1291	2021-01-25	B.1.1.63	Calabarzon	0	0	5
PH_348	2021-01-21	B.1.466.1	Calabarzon; NCR	0	0	21
PH_1061	2021-01-19	B.1.1	>3 regions	0	0	29
PH_1129	2021-01-15	B.1.1.28	Davao; NCR; Soccsksargen	0	0	9
PH_565	2021-01-14	B.1.1.7	NCR; Central Visayas; CAR	0	0	5
PH_331	2021-01-12	B.1.441	NCR; Central Visayas	0	0	5
PH_1116	2021-01-11	B.1.1.28	Davao	0	0	14
PH_1124	2021-01-09	B.1.1.28	Davao; Soccsksargen; Calabarzon	0	0	13
PH_1041	2021-01-08	B.1.1	Calabarzon; Central Visayas; NCR	0	0	6
PH_1422	2021-01-08	P.3	>3 regions	0	0	460
PH_1015	2021-01-07	B.1.1.7	NCR	0	0	6
PH_993	2021-01-07	B.1.1.7	>3 regions	0	0	342
PH_998	2021-01-07	B.1.1.7	NCR; Central Luzon; Central Visayas	0	0	6
PH_1142	2021-01-06	B.1.1.28	>3 regions	0	0	44
PH_424	2021-01-05	B.1.1.7	>3 regions	0	0	133
PH_1145	2021-01-03	B.1.1.28	Davao; Soccsksargen	0	0	17
PH_994	2020-12-29	B.1.1.7	>3 regions	0	0	8
PH_318	2020-12-28	B.1.524	>3 regions	0	0	10
PH_1227	2020-12-18	B.1.1.63	Cagayan Valley; NCR	0	0	7
PH_1390	2020-12-17	B.1.1.263	CAR; Cagayan Valley; Central Luzon	0	0	65
PH_1258	2020-12-15	B.1.1.63	NCR; Calabarzon; CAR	0	0	11
PH_1266	2020-12-10	B.1.1.63	Calabarzon; NCR	0	0	5
PH_468	2020-12-10	B.1.1.7	NCR; Calabarzon; Central Visayas	0	0	5
PH_1175	2020-12-09	B.1.1	>3 regions	0	0	93
PH_1345	2020-12-04	B.1.1	NCR; Central Luzon	0	0	10
PH_1154	2020-12-02	B.1.1.28	>3 regions	0	0	36
PH_1157	2020-12-02	B.1.1.28	NCR; Calabarzon; Caraga	0	0	20
PH_1072	2020-11-25	B.1.1.370	Calabarzon; NCR	0	0	11

Cluster name	Date first identified	Pango lineage	Distribution	New submission	Isolated in 4 months	Total
PH_1365	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_1097	2020-11-07	B.1.1.28	Calabarzon; NCR; Central Luzon	0	0	6
PH_332	2020-11-06	B.1.36	Calabarzon; NCR	0	0	9
PH_1197	2020-11-02	B.1.1.63	>3 regions	0	0	34
PH_1303	2020-11-01	B.1.1.63	>3 regions	0	0	14
PH_1099	2020-10-30	B.1.1.28	Central Visayas; NCR	0	0	46
PH_1363	2020-10-30	B.1.1.263	>3 regions	0	0	7
PH_1373	2020-10-11	B.1.1.263	>3 regions	0	0	78
PH_1107	2020-08-24	B.1.1.28	>3 regions	0	0	15
PH_322	2020-08-22	B.1	NCR; Calabarzon; Davao	0	0	12
PH_1068	2020-08-07	B.1.1	NCR	0	0	5
PH_1341	2020-08-07	B.1.1.63	>3 regions	0	0	21
PH_23	2020-08-06	B.6	>3 regions	0	0	37
PH_1075	2020-08-05	B.1.1.370	Calabarzon; NCR	0	0	5
PH_1102	2020-08-05	B.1.1.28	>3 regions	0	0	182
PH_1077	2020-08-04	B.1.1	>3 regions	0	0	103
PH_1178	2020-07-22	B.1.1.63	>3 regions	0	0	337
PH_1187	2020-07-19	B.1.1	Calabarzon; NCR; Western Visayas	0	0	24
PH_1029	2020-07-12	B.1.1	Calabarzon; NCR; Mimaropa	0	0	13
PH_55	2020-07-10	B.1	>3 regions	0	0	31
PH_1207	2020-07-09	B.1.1.63	>3 regions	0	0	121
PH_1025	2020-07-08	B.1.1	>3 regions	0	0	67
PH_1295	2020-07-08	B.1.1.63	>3 regions	0	0	78
PH_325	2020-07-08	B.1	Mimaropa; NCR; Central Visayas	0	0	9
PH_1201	2020-07-07	B.1.1.63	>3 regions	0	0	30
PH_1338	2020-07-07	B.1.1.63	NCR; Calabarzon; Cagayan Valley	0	0	12
PH_1101	2020-07-05	B.1.1.28	>3 regions	0	0	6
PH_1198	2020-07-01	B.1.1.63	Calabarzon; NCR; CAR	0	0	9
PH_1283	2020-07-01	B.1.1.63	>3 regions	0	0	233
PH_1240	2020-06-29	B.1.1.63	>3 regions	0	0	132
PH_1324	2020-06-23	B.1.1.63	NCR	0	0	5
PH_1356	2020-06-16	B.1.1.263	>3 regions	0	0	128
PH_308	2020-06-11	B.1	NCR; Western Visayas	1	0	9
PH_16	2020-03-11	B.6	NCR; Cagayan Valley	0	0	6
PH_13	2020-03-10	B.6	>3 regions	0	0	20

Table 3. Number of sequences by cluster identified with the Grapevine-anywhere as of 25 April 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 4 months*, sequences isolated from 1 January 2022 to 25 April 2022.

SARS-CoV-2 sequencing in the Philippines

Total available SARS-CoV-2 sequences in the Philippines: 15066

SARS-CoV-2 sequences from GECO project: 1414

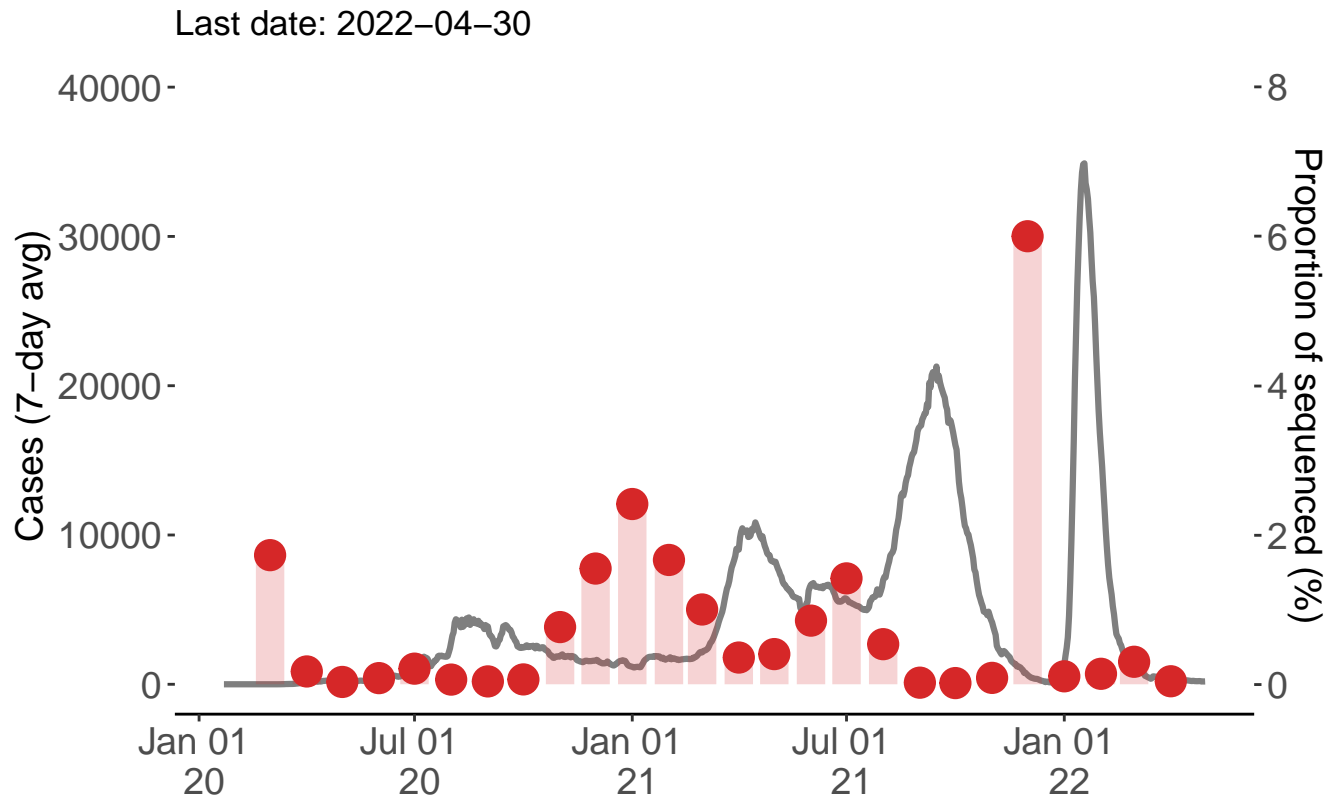


Figure 4. Number of COVID-19 cases and the proportion of sequenced samples in the Philippines. The gray line indicates the mean cases in a 7 days window based on the JHU data base, whereas the red bars indicate the estimated percentage of sequenced samples among cases in a month. The proportions in January and March, 2020 were discarded as they are outliers.

Epidemiology of COVID-19 in the Philippines

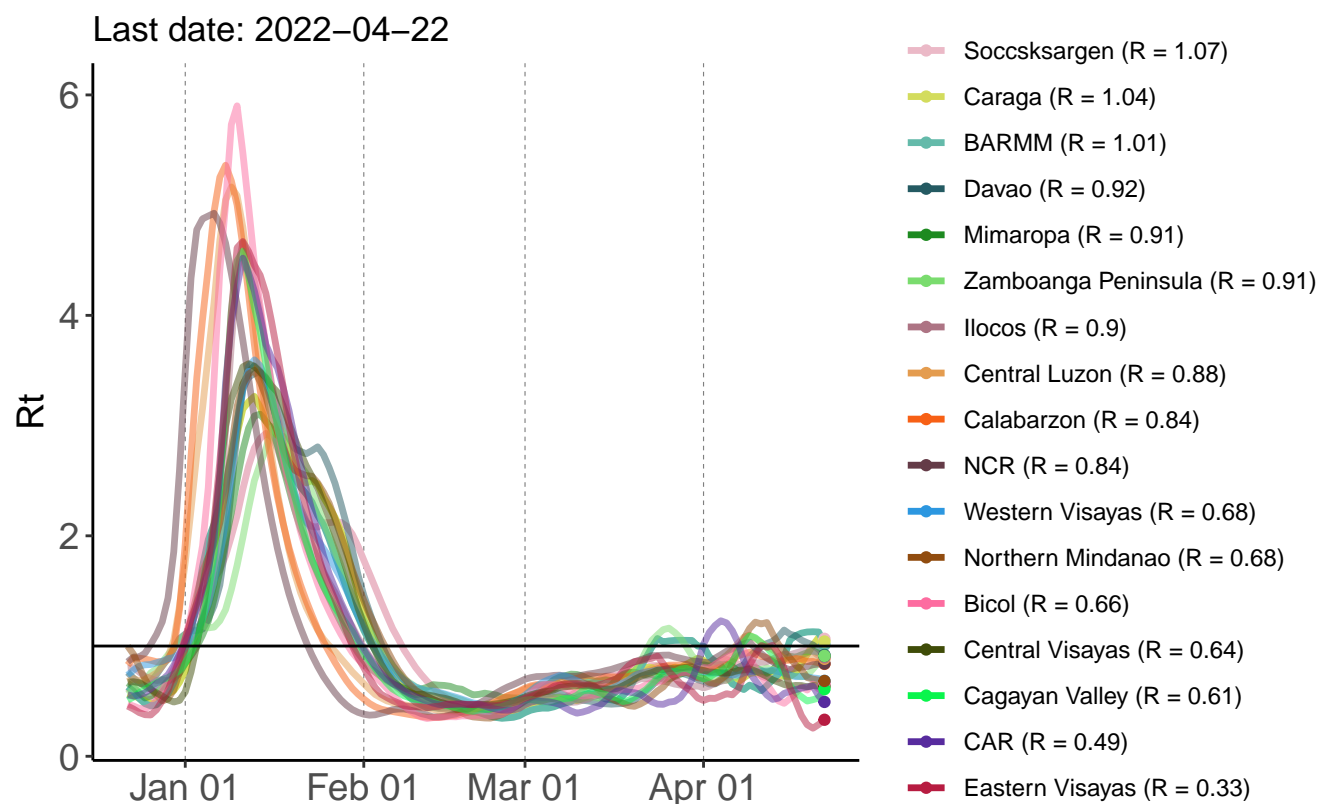


Figure 5. Mean effective reproductive number (R_t) of COVID-19 in the Philippines by region from December 2021 to April 2022. The reproductive number (R) is defined as the number of new infections that one infected patient can cause in a susceptible population. Here, *the mean effective reproductive 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

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](#)
- **L452R*** (Delta, BA.4/BA.5): [Distribution on the Philippine isolates](#)

- **T478K** (Delta, Omicron): [Distribution on the Philippine isolates](#)
- **E484K** (Beta, Gamma, Eta, Mu): [Distribution on the Philippine isolates](#)
- **F486V*** (BA.4/BA.5): [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 417, S 484) and receptor binding (S 417, S 484, S 501). 69-70Del, deletions at positions 69-70. *: mutations relevant to emerging lineages (S 452, S 486).

Data sources and references

Data

- [GECO website](#)
- [DOH Data drop](#)
- [GISAID](#) (EPI-SET: EPI_SET_20220430ca)
- [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](#)

2022-03 [pdf](#)



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