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

Highlights

- A probable BA.4 sequence was isolated on 8 May 2022

- Sequences of BA.2.12.1 (an emerging lineage in the US) were identified in late April
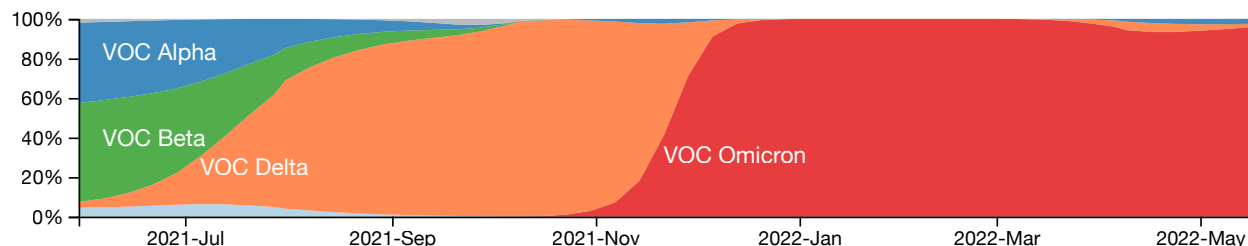
SARS-CoV-2 variants detected in the Philippines

WHO label	Pango lineage	Classification	New submission	Isolated in 3 months	Total
Alpha	B.1.1.7/Q.x	VOC	21 (10.9)	1 (0.7)	2794
Beta	B.1.351	VOC	30 (15.6)	0	3284
Delta	B.1.617.2/AY.x	VOC	11 (5.7)	2 (1.3)	3443
Gamma	P.1	VOC	0	0	3
Omicron	B.1.1.529/BA.x	VOC	118 (61.5)	135 (88.2)	1615
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 21 May 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 March 2022 to 21 May 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 9 May, 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).

As of 21 May 2022, **254** BA.1.x and **1359** BA.2.x sequences have been isolated in the Philippines. Only one BA.1 virus was isolated in the country after 5 January, and thus BA.2 and its sublineages have accounted for nearly all isolates of Omicron since January. Among BA.2 sublineages, BA.2.3 is the dominant (n=1246) strain followed by BA.2.12.x lineages (BA.2.12.1, n=13). The BA.2.12.1 lineage currently rising in the North Americas possess a L452Q antigenic mutation in the S gene.

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. A probable BA.4 sequence (PH-RITM-1379) was isolated on 8 May 2022 in the Philippines. While it's classified as unassigned or BA.2 depending on the Pangolin used, the sequence carries important mutations, including 452R and 486V in the S gene, signifying lineage BA.4. Global lineage dynamics warrants close monitoring of emerging Omicron lineages including BA.4, BA.5, BA.2.12.1.

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	46 (24)	Omicron (94.1)	34 (22.2)	4855
Ilocos	1 (0.5)	Omicron (80)	5 (3.3)	422
CAR	1 (0.5)	Omicron (66.7)	3 (2)	860
Cagayan Valley	10 (5.2)	Omicron (71.4)	28 (18.3)	1061
Central Luzon	5 (2.6)	Omicron (100)	1 (0.7)	1127
Calabarzon	45 (23.4)	Omicron (81.8)	11 (7.2)	2457
Mimaropa	13 (6.8)	Omicron (100)	21 (13.7)	408
Bicol	0	-	0	257
Western Visayas	1 (0.5)	-	0	595
Central Visayas	4 (2.1)	Omicron (100)	4 (2.6)	670
Eastern Visayas	0	-	0	176
Zamboanga Peninsula	4 (2.1)	-	0	436
Northern Mindanao	4 (2.1)	-	1 (0.7)	362
Davao	47 (24.5)	Omicron (94.4)	36 (23.5)	926
Soccsksargen	7 (3.6)	Omicron (85.7)	7 (4.6)	230
Caraga	1 (0.5)	Omicron (100)	1 (0.7)	294
BARMM	2 (1)	-	0	103

Table 2. Number of available sequences by administrative region in the Philippines as of 21 May 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 March 2022 to 21 May 2022. A dash indicates no sequence isolated. *Isolated in 3 months*, sequences isolated from 1 March 2022 to 21 May 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 submission	Isolated in 3 months	Total
PH_81	2021-03-20	BA.2.3	>3 regions	19	43	373
PH_358	2022-04-29	BA.2.12.1	Mimaropa	8	8	8
PH_392	2021-12-29	BA.2	>3 regions	5	5	7
PH_182	2020-08-13	B.1.617.2	>3 regions	10	2	3410
PH_368	2021-12-26	BA.2.3	>3 regions	0	1	50
PH_334	2021-12-21	BA.1.1	Central Luzon; Davao; Cagayan Valley	0	1	9
PH_382	2021-12-02	BA.2.3	>3 regions	0	1	529
PH_36	2021-01-25	B.1.1.7	>3 regions	19	1	1441
PH_394	2021-12-29	BA.2	Central Luzon; NCR	0	0	7
PH_388	2021-12-28	BA.2	Central Luzon	0	0	8
PH_384	2021-12-27	BA.2.3	>3 regions	0	0	54
PH_385	2021-12-27	BA.2.3	>3 regions	0	0	10
PH_386	2021-12-27	BA.2.3	NCR; Calabarzon; Davao	0	0	6
PH_340	2021-12-24	BA.1.1	Central Luzon; Central Visayas	0	0	5
PH_379	2021-12-23	BA.2.3	NCR; Calabarzon; CAR	1	0	12
PH_335	2021-12-22	BA.1.1	Central Luzon; NCR	0	0	6
PH_366	2021-12-22	BA.2.3	>3 regions	0	0	24
PH_296	2021-12-18	BA.1.15	Central Luzon; Central Visayas	0	0	7
PH_341	2021-12-18	BA.1.1	NCR; Central Luzon; Central Visayas	0	0	17
PH_318	2021-12-06	BA.1	>3 regions	0	0	10
PH_321	2021-11-24	BA.1	Central Luzon; CAR	0	0	5
PH_141	2021-05-06	B.1.1.7	>3 regions	0	0	7
PH_137	2021-04-30	B.1.1.7	Davao; Caraga; NCR	0	0	19
PH_148	2021-04-19	B.1.1.7	Davao; Soccsksargen	0	0	18
PH_132	2021-04-14	B.1.1.7	>3 regions	0	0	21
PH_136	2021-04-13	B.1.1.7	>3 regions	1	0	14
PH_266	2021-04-02	B.1.1.519	NCR	0	0	5
PH_138	2021-03-25	B.1.1.7	>3 regions	0	0	29
PH_144	2021-03-22	B.1.1.7	>3 regions	0	0	31
PH_152	2021-03-19	B.1.1.7	>3 regions	0	0	12
PH_145	2021-03-08	B.1.1.7	>3 regions	1	0	27
PH_139	2021-03-06	B.1.1.7	>3 regions	0	0	32
PH_113	2021-03-05	B.1.1.7	>3 regions	0	0	32
PH_140	2021-03-05	B.1.1.7	>3 regions	0	0	24
PH_147	2021-03-05	B.1.1.7	>3 regions	0	0	32
PH_135	2021-03-04	B.1.1.7	>3 regions	0	0	18
PH_150	2021-02-22	B.1.1.7	NCR; Calabarzon; Central Luzon	0	0	13
PH_94	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_112	2021-02-11	B.1.1.7	>3 regions	0	0	14
PH_217	2021-02-05	B.1.1.63	NCR; Calabarzon	0	0	6
PH_189	2021-01-27	B.1.1.63	NCR; Calabarzon	0	0	7

Cluster name	Date first identified	Pango lineage	Distribution	New submission	Isolated in 3 months	Total
PH_88	2021-01-26	B.1.1.7	>3 regions	0	0	48
PH_222	2021-01-25	B.1.1.63	Calabarzon	0	0	5
PH_39	2021-01-21	B.1.466.1	Calabarzon; NCR	0	0	21
PH_174	2021-01-19	B.1.1	>3 regions	0	0	29
PH_261	2021-01-15	B.1.1.28	Davao; NCR; Soccsksargen	0	0	9
PH_161	2021-01-14	B.1.1.7	NCR; Central Visayas; CAR	0	0	5
PH_40	2021-01-12	B.1.441	NCR; Central Visayas	0	0	5
PH_253	2021-01-11	B.1.1.28	Davao	0	0	14
PH_260	2021-01-09	B.1.1.28	Davao; Soccsksargen; Calabarzon	0	0	13
PH_231	2021-01-08	B.1.1	Calabarzon; Central Visayas; NCR	0	0	5
PH_402	2021-01-08	P.3	>3 regions	0	0	458
PH_120	2021-01-07	B.1.1.7	NCR; Central Luzon; Central Visayas	0	0	6
PH_125	2021-01-07	B.1.1.7	NCR	0	0	7
PH_158	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	44
PH_93	2021-01-05	B.1.1.7	>3 regions	0	0	133
PH_264	2021-01-03	B.1.1.28	Davao; Soccsksargen	0	0	17
PH_127	2020-12-29	B.1.1.7	>3 regions	0	0	8
PH_53	2020-12-28	B.1.524	>3 regions	0	0	10
PH_196	2020-12-18	B.1.1.63	Cagayan Valley; NCR	0	0	7
PH_241	2020-12-17	B.1.1.263	CAR; Cagayan Valley; Central Luzon	0	0	65
PH_201	2020-12-15	B.1.1.63	NCR; Calabarzon; CAR	0	0	11
PH_109	2020-12-10	B.1.1.7	NCR; Calabarzon; Central Visayas	0	0	5
PH_199	2020-12-10	B.1.1.63	Calabarzon; NCR	0	0	5
PH_212	2020-12-04	B.1.1.63	NCR; Central Luzon	0	0	10
PH_255	2020-12-02	B.1.1.28	>3 regions	0	0	36
PH_256	2020-12-02	B.1.1.28	NCR; Calabarzon; Caraga	0	0	20
PH_225	2020-11-25	B.1.1	Calabarzon; NCR	0	0	11
PH_184	2020-11-22	B.1.1.63	Calabarzon; NCR	0	0	9
PH_246	2020-11-15	B.1.1.263	CAR; Cagayan Valley; Calabarzon	0	0	9
PH_12	2020-11-10	B.6	NCR; Calabarzon	0	0	5
PH_257	2020-11-07	B.1.1.28	Calabarzon; NCR; Central Luzon	0	0	6
PH_42	2020-11-06	B.1.36	Calabarzon; NCR	0	0	10
PH_183	2020-11-03	B.1.1.63	Calabarzon	0	0	6
PH_190	2020-11-02	B.1.351	>3 regions	29	0	3045
PH_216	2020-11-01	B.1.1.63	>3 regions	0	0	14
PH_242	2020-10-11	B.1.1.263	>3 regions	0	0	68
PH_252	2020-08-24	B.1.1.28	>3 regions	0	0	15
PH_54	2020-08-22	B.1.524	NCR; Calabarzon; Davao	0	0	12
PH_211	2020-08-07	B.1.1.63	>3 regions	0	0	21
PH_223	2020-08-07	B.1.1	NCR	0	0	5
PH_13	2020-08-06	B.6	>3 regions	0	0	40

Cluster name	Date first identified	Pango lineage	Distribution	New submission	Isolated in 3 months	Total
PH_226	2020-08-05	B.1.1	Calabarzon; NCR	0	0	5
PH_251	2020-08-05	B.1.1.28	>3 regions	0	0	228
PH_227	2020-08-04	B.1.1	>3 regions	0	0	101
PH_92	2020-07-22	B.1.1.63	>3 regions	2	0	127
PH_23	2020-07-20	B.1	>3 regions	0	0	9
PH_181	2020-07-19	B.1.1.63	Calabarzon; NCR; Western Visayas	0	0	24
PH_27	2020-07-15	B.1	>3 regions	1	0	28
PH_172	2020-07-12	B.1.1	NCR; Calabarzon; Mimaropa	0	0	12
PH_195	2020-07-09	B.1.1.63	>3 regions	0	0	121
PH_165	2020-07-08	B.1.1	>3 regions	0	0	158
PH_193	2020-07-08	B.1.1.63	>3 regions	0	0	30
PH_206	2020-07-08	B.1.1.63	>3 regions	0	0	78
PH_55	2020-07-08	B.1	Mimaropa; NCR; Central Visayas	0	0	9
PH_210	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	6
PH_180	2020-07-01	B.1.1.63	Calabarzon; NCR; CAR	0	0	9
PH_205	2020-07-01	B.1.1.63	>3 regions	0	0	234
PH_198	2020-06-29	B.1.1.63	>3 regions	1	0	133
PH_214	2020-06-23	B.1.1.63	NCR	0	0	5
PH_238	2020-06-16	B.1.1.263	>3 regions	0	0	144
PH_58	2020-06-11	B.1	NCR; Western Visayas	0	0	9
PH_11	2020-03-11	B.6	NCR; Cagayan Valley	0	0	6
PH_2	2020-03-10	B.6	>3 regions	1	0	20

Table 3. Number of sequences by cluster identified with the Grapevine-anywhere as of 21 May 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 March 2022 to 21 May 2022.

SARS-CoV-2 sequencing in the Philippines

**Total available SARS-CoV-2 sequences in the Philippines: 15258**

SARS-CoV-2 sequences from GECO project: 1559
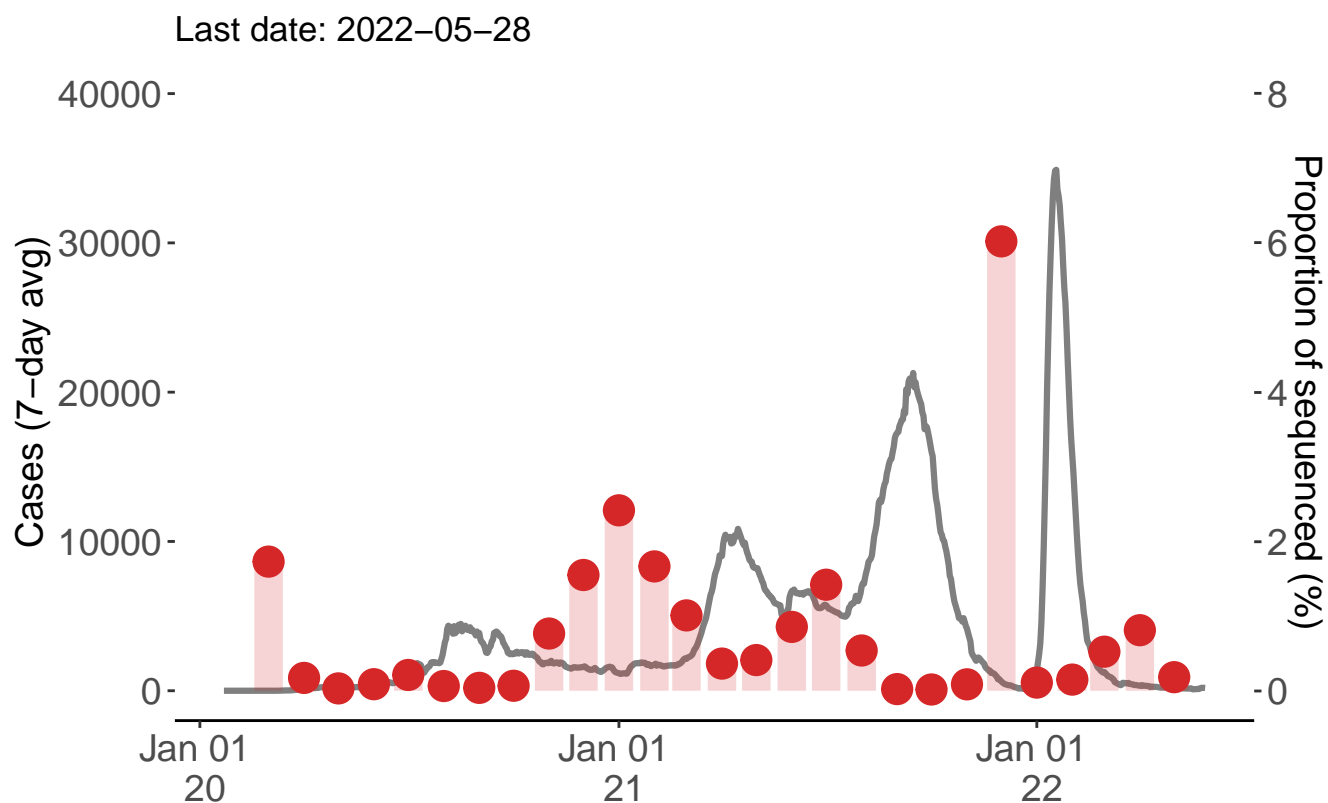
Figure 4. Number of COVID-19 cases and the proportion of sequenced samples in the Philippines. The gray line indicates the mean cases in a 7 days window based on the JHU data base, whereas the red bars indicate the estimated percentage of sequenced samples among cases in a month. The proportions in January and March, 2020 were discarded as they are outliers.

Epidemiology of COVID-19 in the Philippines
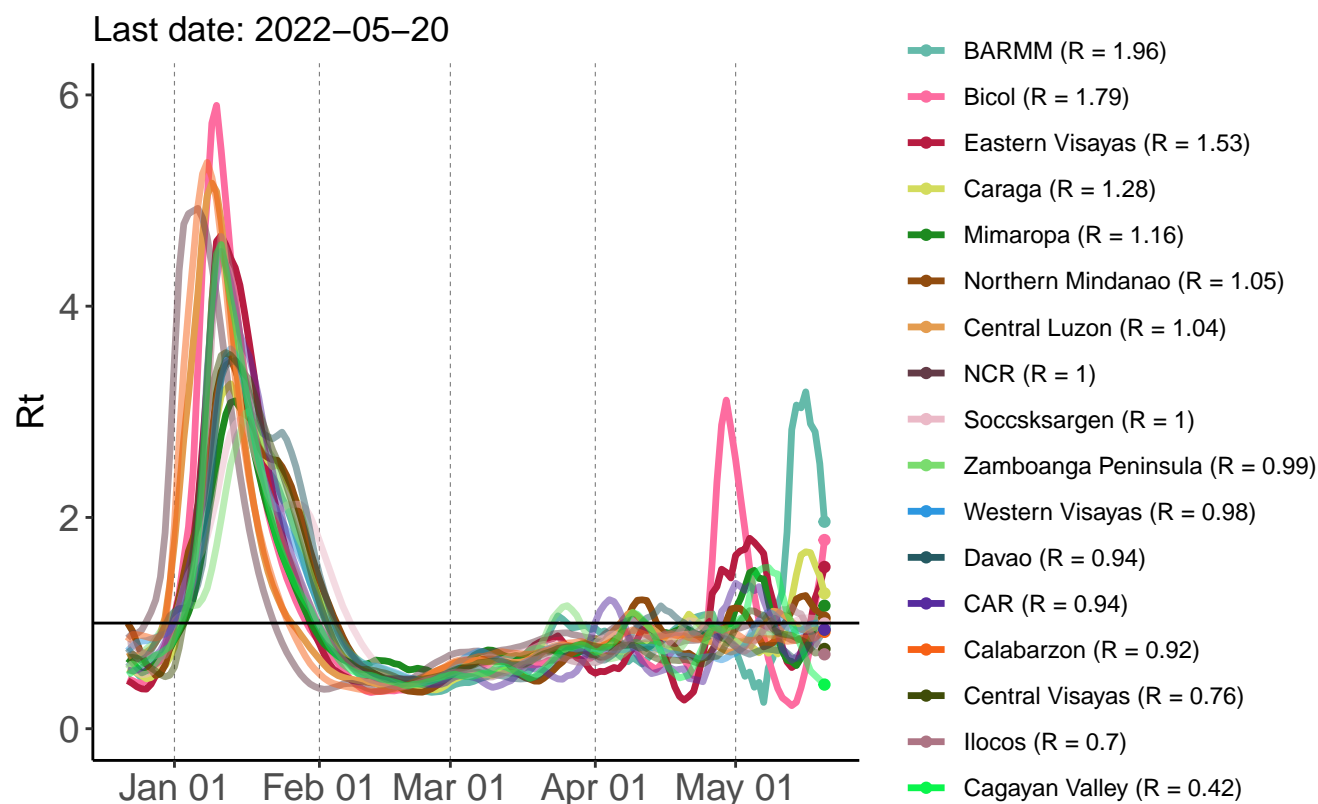
Figure 5. Mean effective reproductive number (Rt) of COVID-19 in the Philippines by region from December 2021 to May 2022. The reproductive number (R) is defined as the number of new infections that one infected patient can cause in a susceptible population. Here, *the mean effective reproductive number* (Rt) was inferred by daily number of cases reported in MOH, Philippines in a window of seven days. The horizontal line indicates one. If Rt is greater than 1, the case number in the region will likely continue to grow. If the Rt 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_20220530ca)
- 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

2022-04 pdf

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