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

Highlights

- Over 80% of a batch of >1000 sequences by PGC isolated during Nov. 2021-Jan. 2022 are BA.2.
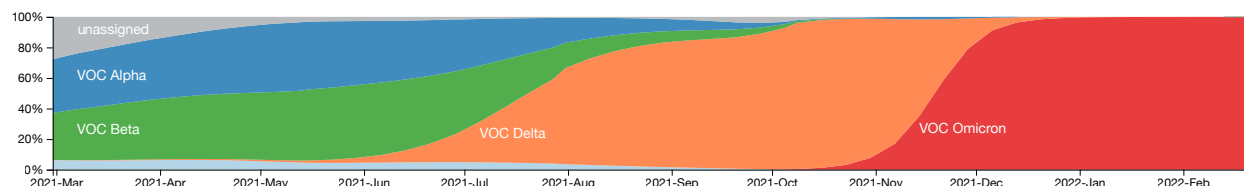
SARS-CoV-2 variants detected in the Philippines

WHO label	Pango lineage	Classification	New submission	Isolated in 4 months	Total
Alpha	B.1.1.7/Q.x	VOC	5 (0.4)	2 (0.1)	2767
Beta	B.1.351	VOC	5 (0.4)	0	3244
Delta	B.1.617.2/AY.x	VOC	34 (2.4)	37 (2.8)	3329
Gamma	P.1	VOC	0	0	3
Omicron	B.1.1.529/BA.x	VOC	1207 (85.2)	1269 (94.7)	1269
Eta	B.1.525	VUM	0	0	8
Theta	P.3	VUM	0	0	518

Table 1. Number of available sequences by variant in the Philippines as of 22 February 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 4 months*, sequences isolated from 1 November 2021 to 22 February 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 in the online version. **Note** that the latest available Philippine sequences were isolated on 22 February, 2022, thus the frequencies after the time point could harbor great uncertainty.

Diversity within the Omicron variant

The two 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, most BA.2 sequences isolated in the Philippines were likely originated from the same introduction. These sequences were also identified by the grapevine-anywhere pipeline as 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).

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 February 2022. Among the sublineages of Delta variant, AY.26 is the most frequently isolated lineage in the Philippines, followed by AY.61. Phylogenetic relationship of the sublineages of Delta variant is available here.
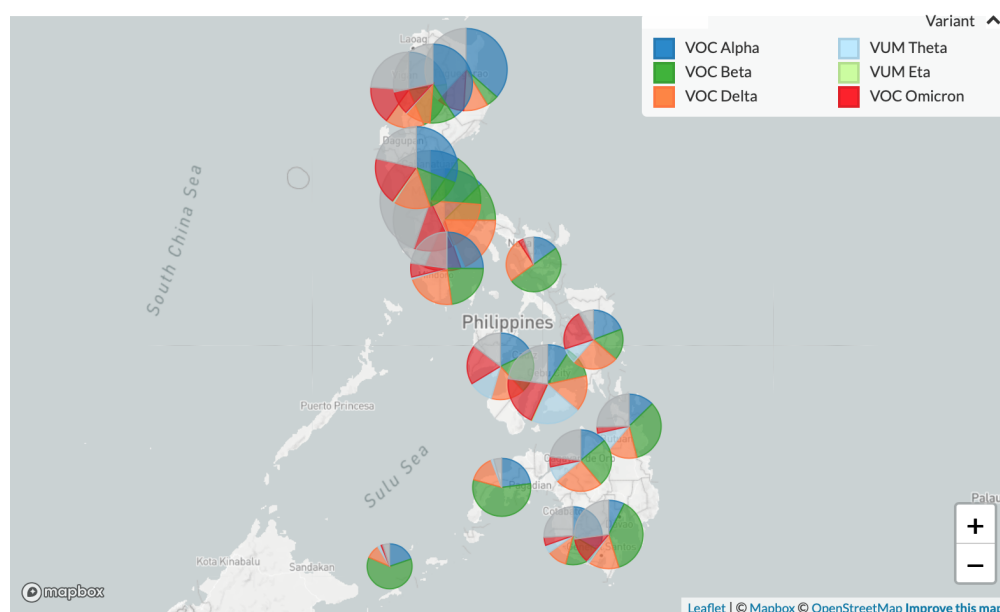
SARS-CoV-2 variants detected by administrative region

Region	New submission	Dominant variant in 4 months	Isolated in 4 months	Total
NCR	650 (45.9)	Omicron (97.4)	626 (46.7)	4700
Ilocos	37 (2.6)	Omicron (100)	37 (2.8)	400
CAR	27 (1.9)	Omicron (88.9)	27 (2)	774
Cagayan Valley	33 (2.3)	Omicron (93.9)	33 (2.5)	1017
Central Luzon	158 (11.2)	Omicron (100)	161 (12)	1126
Calabarzon	208 (14.7)	Omicron (92)	175 (13.1)	2343
Mimaropa	38 (2.7)	Delta (52.8)	36 (2.7)	383
Bicol	3 (0.2)	Omicron (80)	5 (0.4)	247
Western Visayas	90 (6.4)	Omicron (94.5)	91 (6.8)	589
Central Visayas	60 (4.2)	Omicron (96.8)	63 (4.7)	658
Eastern Visayas	35 (2.5)	Omicron (100)	35 (2.6)	176
Zamboanga Peninsula	18 (1.3)	-	0	435

| Region	New submission	Dominant variant in 4 months	Isolated in 4 months	Total
Northern Mindanao	11 (0.8)	Omicron (72.7)	11 (0.8)	359
Davao	22 (1.6)	Omicron (100)	22 (1.6)	786
Soccsksargen	7 (0.5)	Omicron (85.7)	7 (0.5)	207
Caraga	6 (0.4)	Omicron (83.3)	6 (0.4)	288
BARMM	10 (0.7)	Omicron (100)	1 (0.1)	103

Table 2. Number of available sequences by administrative region in the Philippines as of 22 February 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 November 2021 to 22 February 2022. A dash indicates no sequence isolated. *Isolated in 4 months*, sequences isolated from 1 November 2021 to 22 February 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 in the online version.

Philippines specific SARS-CoV-2 lineages
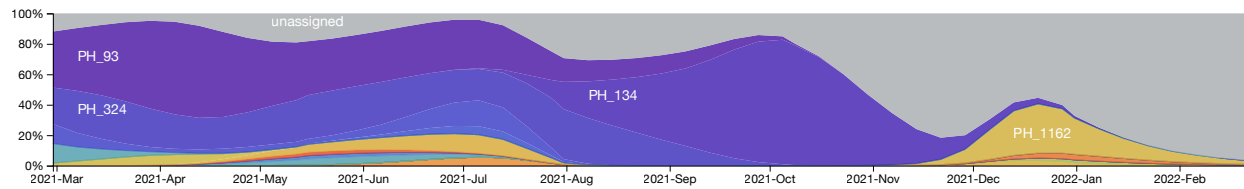
Figure 3. **Temporal frequencies of Philippine lineages (clusters) identified by Grapevine-anywhere.** Each sequence submitted to GECO database would undergo *Grapevine-anywhere* pipeline to detect sustain local transmission. A cluster is defined based on multiple sequences isolated in the Philippines 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_1162	2021-12-19	BA.2	>3 regions	36	52	52
PH_1205	2021-12-22	BA.2	NCR; Cagayan Valley; Western Visayas	4	11	11
PH_1173	2021-12-23	BA.2	NCR	5	8	8
PH_1239	2021-12-26	BA.2	NCR	0	4	4
PH_134	2021-04-09	AY.26	>3 regions	0	3	3107
PH_324	2021-02-06	B.1.1.7	>3 regions	0	1	1457
PH_789	2021-06-11	B.1.1	Zamboanga Peninsula	0	0	3
PH_441	2021-05-23	B.1.1.7	Central Luzon; NCR	0	0	3
PH_329	2021-05-06	B.1.1.7	>3 regions	0	0	7
PH_674	2021-04-30	B.1.1.7	Davao; Caraga; NCR	0	0	19
PH_132	2021-04-19	B.1	Northern Mindanao; Davao; Western Visayas	0	0	4
PH_575	2021-04-19	B.1.1.7	Davao; Soccsksargen	0	0	18
PH_327	2021-04-15	B.1.1.7	Bicol; Ilocos; NCR	0	0	3
PH_479	2021-04-14	B.1.1.7	>3 regions	0	0	21
PH_669	2021-04-13	B.1.1.7	Davao; Caraga; Central Luzon	0	0	13
PH_1156	2021-04-02	B.1.1.519	NCR	0	0	5
PH_526	2021-03-31	B.1.1.7	Northern Mindanao; Calabarzon	0	0	3
PH_632	2021-03-25	B.1.1.7	>3 regions	0	0	28
PH_603	2021-03-22	B.1.1.7	>3 regions	0	0	32
PH_690	2021-03-19	B.1.1.7	>3 regions	0	0	12
PH_648	2021-03-15	B.1.1.7	Bicol; NCR; Calabarzon	0	0	13
PH_748	2021-03-10	B.1.1.7	>3 regions	0	0	8
PH_145	2021-03-09	B.1.1.7	Calabarzon; Mimaropa	0	0	5
PH_695	2021-03-08	B.1.1.7	>3 regions	0	0	26
PH_841	2021-03-08	B.1.1.28	Soccsksargen; Davao	0	0	3
PH_1073	2021-03-05	B.1.1.63	NCR; Calabarzon	0	0	5
PH_160	2021-03-05	B.1.1.7	>3 regions	0	0	33
PH_561	2021-03-05	B.1.1.7	>3 regions	0	0	32
PH_811	2021-03-05	C.38	NCR; Caraga	0	0	3
PH_659	2021-03-04	B.1.1.7	>3 regions	0	0	17

Cluster name	Date first identified	Pango lineage	Distribution	New submission	Isolated in 4 months	Total
PH_713	2021-02-22	B.1.1.7	NCR; Calabarzon; Central Luzon	0	0	13
PH_322	2021-02-20	B.1.1.7	NCR	0	0	3
PH_757	2021-02-20	B.1.1.7	Central Luzon; NCR	0	0	3
PH_240	2021-02-15	B.1.1.7	>3 regions	0	0	55
PH_203	2021-02-12	B.1.1.7	>3 regions	0	0	71
PH_161	2021-02-11	B.1.1.7	>3 regions	0	0	14
PH_122	2021-02-10	B.1.525	NCR; Central Luzon	0	0	3
PH_312	2021-01-31	B.1.1.7	NCR; Central Luzon	0	0	3
PH_93	2021-01-31	B.1.351	>3 regions	0	0	2980
PH_197	2021-01-27	B.1.1.7	Central Luzon; NCR	0	0	4
PH_962	2021-01-27	B.1.1.63	NCR; Calabarzon	0	0	7
PH_192	2021-01-26	B.1.1.7	>3 regions	0	0	48
PH_302	2021-01-26	B.1.1.7	NCR; Calabarzon; Central Visayas	0	0	5
PH_1034	2021-01-25	B.1.1.63	Calabarzon	0	0	5
PH_1011	2021-01-24	B.1.1.63	NCR	0	0	3
PH_68	2021-01-21	B.1.466.1	Calabarzon; NCR	0	0	21
PH_768	2021-01-19	B.1.1	>3 regions	0	0	29
PH_837	2021-01-15	B.1.1.28	Davao; NCR; Soccsksargen	0	0	9
PH_9	2021-01-15	A.21	NCR; Calabarzon	0	0	3
PH_295	2021-01-14	B.1.1.7	NCR; Central Visayas; CAR	0	0	4
PH_85	2021-01-12	B.1.441	NCR; Central Visayas	0	0	5
PH_861	2021-01-11	B.1.1.28	Davao	0	0	14
PH_52	2021-01-09	B.1.2	NCR	0	0	3
PH_7	2021-01-09	A.23.1	NCR; Ilocos	0	0	3
PH_844	2021-01-09	B.1.1.28	Davao; Soccsksargen; Calabarzon	0	0	16
PH_90	2021-01-09	B.1.36.29	NCR	0	0	4
PH_120	2021-01-08	B.1.179	CAR	0	0	3
PH_1263	2021-01-08	P.3	>3 regions	0	0	455
PH_790	2021-01-08	B.1.1	Calabarzon; Central Visayas; NCR	0	0	6
PH_1151	2021-01-07	R.1	NCR	0	0	3
PH_307	2021-01-07	B.1.1.7	NCR	0	0	7
PH_313	2021-01-07	B.1.1.7	NCR; Central Luzon; Central Visayas	0	0	6
PH_761	2021-01-07	B.1.1.7	>3 regions	0	0	343
PH_821	2021-01-06	B.1.1.28	>3 regions	0	0	44
PH_239	2021-01-05	B.1.1.7	>3 regions	0	0	134
PH_817	2021-01-04	B.1.1.28	Davao; Soccsksargen; NCR	0	0	29
PH_201	2021-01-03	B.1.1.7	NCR; CAR	0	0	4
PH_824	2021-01-03	B.1.1.28	Davao; Soccsksargen	0	0	17
PH_764	2020-12-29	B.1.1.7	>3 regions	0	0	8
PH_108	2020-12-28	B.1.524	>3 regions	0	0	10
PH_55	2020-12-26	B.1.2	NCR; Calabarzon	0	0	4
PH_66	2020-12-22	B.1.466.1	NCR	0	0	4
PH_955	2020-12-18	B.1.1.63	Cagayan Valley; NCR	0	0	7
PH_1127	2020-12-17	B.1.1.263	CAR; Cagayan Valley; Central Luzon	0	0	65
PH_921	2020-12-15	B.1.1.63	Calabarzon; NCR; CAR	0	0	9

Cluster name	Date first identified	Pango lineage	Distribution	New sub-mission	Isolated in 4 months	Total
PH_961	2020-12-12	B.1.1.63	Calabarzon; NCR; CAR	0	0	7
PH_153	2020-12-10	B.1.1.7	NCR; Calabarzon; Central Visayas	0	0	5
PH_903	2020-12-10	B.1.1.63	Calabarzon; NCR	0	0	5
PH_1076	2020-12-06	B.1.1.63	NCR; Central Luzon	0	0	4
PH_1039	2020-12-04	B.1.1.63	NCR; Central Luzon	0	0	10
PH_871	2020-12-02	B.1.1.28	>3 regions	0	0	36
PH_874	2020-12-02	B.1.1.28	NCR; Calabarzon; Caraga	0	0	19
PH_784	2020-12-01	B.1.1	Calabarzon; NCR	0	0	4
PH_1086	2020-11-25	B.1.1.370	Calabarzon; NCR	0	0	10
PH_1002	2020-11-24	B.1.1.63	NCR	0	0	4
PH_1112	2020-11-23	B.1.1.263	NCR	0	0	3
PH_982	2020-11-22	B.1.1.63	Calabarzon; NCR	0	0	9
PH_100	2020-11-18	B.1	Calabarzon; NCR	0	0	3
PH_1106	2020-11-15	B.1.1.263	CAR; Cagayan Valley; Calabarzon	0	0	9
PH_1121	2020-11-14	B.1.1.263	>3 regions	0	0	63
PH_139	2020-11-14	B.1.177	Calabarzon; NCR	0	0	4
PH_1049	2020-11-13	B.1.1.63	Calabarzon; NCR	0	0	3
PH_33	2020-11-10	B.6	NCR; Calabarzon	0	0	4
PH_1030	2020-11-09	B.1.1.63	Mimaropa; Calabarzon; NCR	0	0	4
PH_891	2020-11-07	B.1.1.28	Calabarzon; NCR; Central Luzon	0	0	6
PH_86	2020-11-06	B.1.36	Calabarzon; NCR	0	0	10
PH_976	2020-11-05	B.1.1.63	Calabarzon; NCR; Western Visayas	0	0	22
PH_978	2020-11-03	B.1.1.63	Calabarzon	0	0	6
PH_1020	2020-11-02	B.1.1.63	>3 regions	0	0	35
PH_1069	2020-11-01	B.1.1.63	>3 regions	0	0	13
PH_103	2020-09-15	B.1	Mimaropa; NCR; Central Visayas	0	0	6
PH_1084	2020-08-29	B.1.1	NCR	0	0	4
PH_852	2020-08-24	B.1.1.28	>3 regions	0	0	15
PH_102	2020-08-22	B.1	NCR; Calabarzon; Davao	0	0	12
PH_46	2020-08-18	B.1	>3 regions	0	0	27
PH_977	2020-08-13	B.1.1.63	>3 regions	0	0	183
PH_1035	2020-08-12	B.1.1.63	>3 regions	0	0	20
PH_35	2020-08-06	B.6	>3 regions	0	0	36
PH_1041	2020-08-05	B.1.1.63	>3 regions	0	0	69
PH_1089	2020-08-05	B.1.1.370	Calabarzon; NCR	0	0	5
PH_818	2020-08-05	B.1.1.28	>3 regions	0	0	203
PH_769	2020-08-04	B.1.1	>3 regions	0	0	250
PH_782	2020-08-03	B.1.1	Calabarzon; NCR; Mimaropa	0	0	8
PH_966	2020-07-22	B.1.1.63	>3 regions	0	0	117
PH_935	2020-07-09	B.1.1.63	>3 regions	0	0	113
PH_895	2020-07-08	B.1.1.63	>3 regions	0	0	26
PH_1062	2020-07-07	B.1.1.63	NCR; Cagayan Valley; Calabarzon	0	0	11
PH_1022	2020-07-05	B.1.1.63	>3 regions	0	0	226

Cluster name	Date first identified	Pango lineage	Distribution	New submission	Isolated in 4 months	Total
PH_900	2020-06-29	B.1.1.63	>3 regions	0	0	108
PH_1043	2020-06-23	B.1.1	NCR	0	0	3
PH_1091	2020-06-16	B.1.1.263	>3 regions	0	0	140
PH_118	2020-06-11	B.1	NCR; Western Visayas	0	0	3
PH_39	2020-03-11	B.6	NCR; Cagayan Valley	0	0	5
PH_11	2020-03-10	B.6	>3 regions	0	0	18

Table 3. Number of sequences by cluster identified with the Grapevine-anywhere as of 22 February 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 November 2021 to 22 February 2022.

SARS-CoV-2 sequencing in the Philippines

**Total available SARS-CoV-2 sequences in the Philippines: 14608**

SARS-CoV-2 sequences from GECO project: 1055
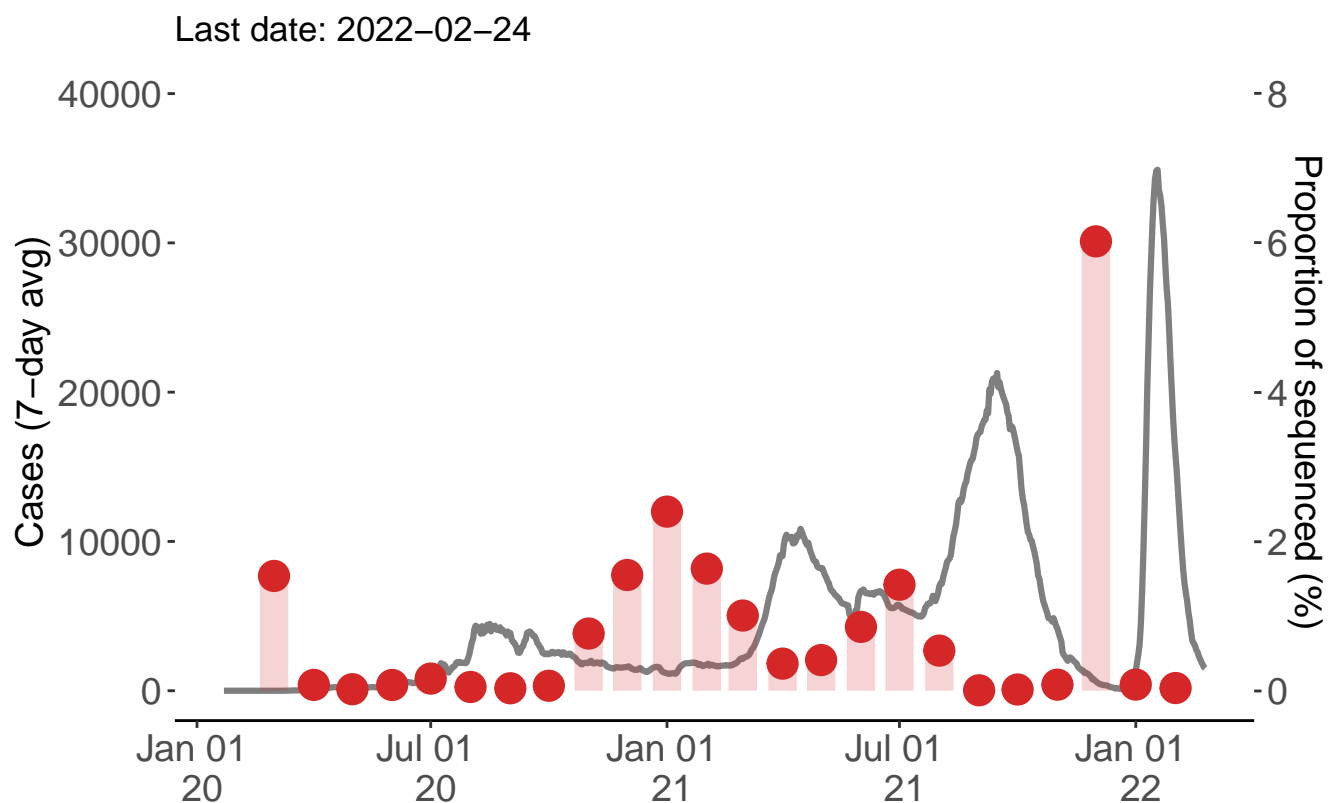
Figure 4. Number of COVID-19 cases and the proportion of sequenced samples in the Philippines. The gray line indicates the mean cases in a 7 days window based on the JHU data base, whereas the red bars indicate the estimated percentage of sequenced samples among cases in a month. The proportions in January and February, 2020 were discarded as they are outliers.

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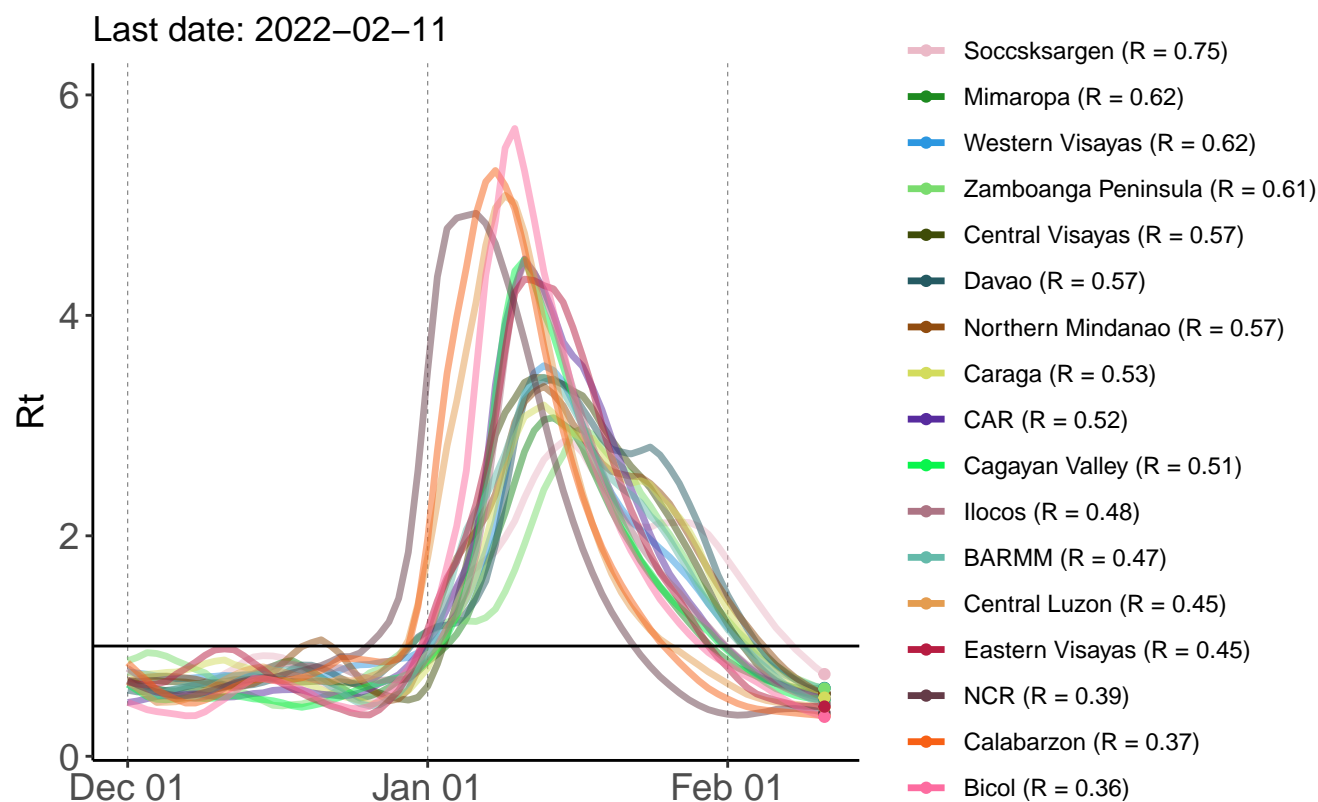
Figure 5. Mean effective reproductive number (Rt) of COVID-19 in the Philippines by region from December 2021 to February, 2022. The reproductive number (R) is defined as the number of new infections that one infected patient can cause in a susceptible population. Here, *the mean effective reproductive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

- **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 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 (acknowledgement table)
- 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

2022-01 pdf

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