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

Highlights

- Omicron sublineage BA.2 remains dominant among recent isolates

- Large BA.2 clusters were detected by grapevine-anywhere

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	1 (0.4)	1 (0.1)	2765
Beta	B.1.351	VOC	6 (2.3)	0	3250
Delta	B.1.617.2/AY.x	VOC	5 (1.9)	4 (0.3)	3334
Gamma	P.1	VOC	0	0	3
Omicron	B.1.1.529/BA.x	VOC	135 (51.1)	1403 (95.1)	1406
Eta	B.1.525	VUM	0	0	8
Theta	P.3	VUM	2 (0.8)	0	520

Table 1. Number of available sequences by variant in the Philippines as of 28 March 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 December 2021 to 28 March 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.
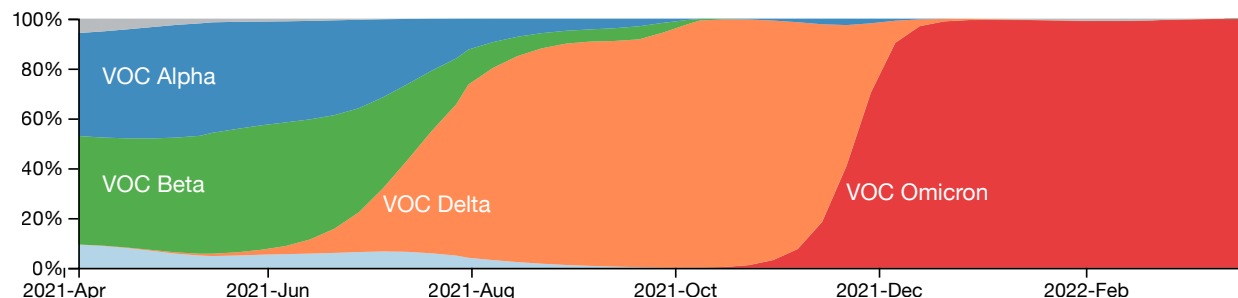

Figure 1. Temporal frequencies of SARS-CoV-2 variants in the Philippines. The figure is constructed with a subsampled genomic data set from all available sequences (methods). A more detailed illustration of SARS-CoV-2 lineages isolated in the country can be visualised by selecting PANGO Lineage as the option for coloring in the control panel (icon on top left/right). **Note** that the latest available Philippine sequences were isolated on 12 March, 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).

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	85 (32.2)	Omicron (98.4)	642 (43.5)	4783
Ilocos	17 (6.4)	Omicron (98.1)	54 (3.7)	417
CAR	13 (4.9)	Omicron (88.9)	36 (2.4)	789
Cagayan Valley	14 (5.3)	Omicron (88.9)	45 (3.1)	1031
Central Luzon	0	Omicron (100)	161 (10.9)	1125
Calabarzon	39 (14.8)	Omicron (95.8)	190 (12.9)	2381
Mimaropa	4 (1.5)	Omicron (73.7)	19 (1.3)	387
Bicol	10 (3.8)	Omicron (100)	12 (0.8)	257
Western Visayas	1 (0.4)	Omicron (94.8)	96 (6.5)	594

Region	New submission	Dominant variant in 4 months	Isolated in 4 months	Total
Central Visayas	8 (3)	Omicron (97.1)	69 (4.7)	666
Eastern Visayas	0	Omicron (100)	35 (2.4)	176
Zamboanga Peninsula	1 (0.4)	-	0	436
Northern Mindanao	2 (0.8)	Omicron (76.9)	13 (0.9)	361
Davao	2 (0.8)	Omicron (100)	24 (1.6)	788
Soccsksargen	16 (6.1)	Omicron (91.3)	23 (1.6)	223
Caraga	5 (1.9)	Omicron (100)	11 (0.7)	293
BARMM	0	Omicron (100)	1 (0.1)	103

Table 2. Number of available sequences by administrative region in the Philippines as of 28 March 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 December 2021 to 28 March 2022. A dash indicates no sequence isolated. *Isolated in 4 months*, sequences isolated from 1 December 2021 to 28 March 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.
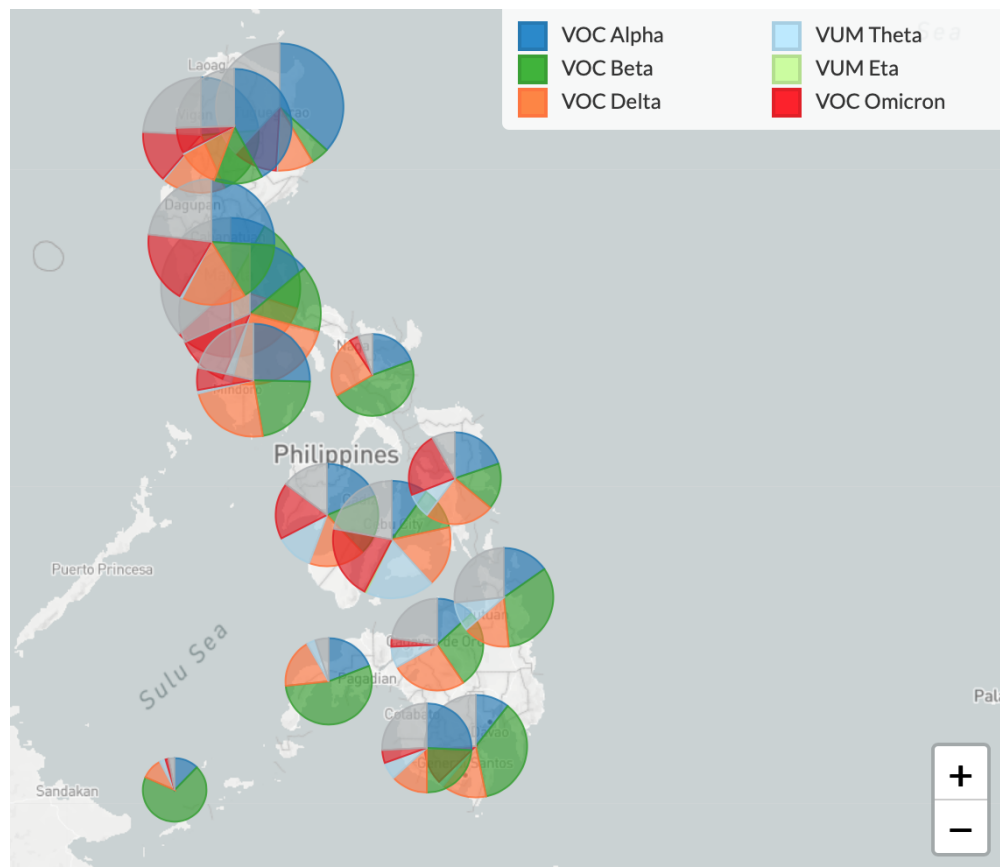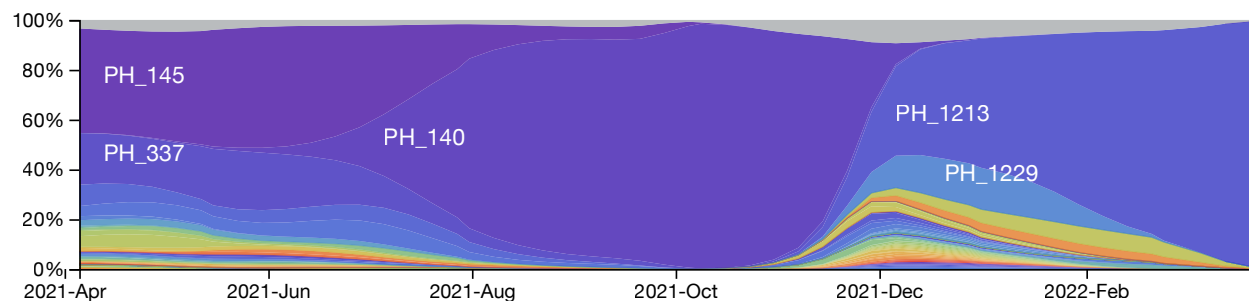
Philippines specific SARS-CoV-2 lineages

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 4 months	Total
PH_1213	2021-12-02	BA.2	>3 regions	94	615	615
PH_1229	2021-12-23	BA.2	>3 regions	0	221	221
PH_1353	2021-12-22	BA.2	>3 regions	8	77	77
PH_1598	2021-12-26	BA.2	>3 regions	6	50	50
PH_1724	2021-12-18	BA.1.1	Central Luzon; NCR; Central Visayas	0	12	12
PH_1587	2021-12-23	BA.2	NCR; Calabarzon; CAR	1	10	10
PH_1716	2021-12-21	BA.1.1	Central Luzon; Central Visayas; Davao	0	10	10
PH_1628	2021-12-29	BA.2	Central Luzon; Calabarzon; NCR	1	9	9
PH_1710	2021-12-22	BA.1.1	Central Luzon; NCR; Central Visayas	0	9	9
PH_1619	2021-12-28	BA.2	Central Luzon; Ilocos	0	7	7
PH_1635	2021-12-16	BA.1	>3 regions	0	7	7
PH_1682	2021-12-16	BA.1	>3 regions	0	7	7
PH_1645	2021-11-24	BA.1	Central Luzon; CAR	0	6	7
PH_1661	2021-12-28	BA.1	Central Luzon	0	5	5
PH_1692	2021-12-14	BA.1	Central Luzon; CAR; NCR	0	4	4
PH_1657	2021-12-13	BA.1	Central Visayas; NCR	0	4	4
PH_1208	2021-12-29	BA.2	Central Luzon; Central Visayas	0	3	3
PH_1624	2021-12-29	BA.2	Central Luzon	0	3	3

Cluster name	Date first identified	Pango lineage	Distribution	New submission	Isolated in 4 months	Total
PH_1292	2021-12-24	BA.2	NCR	0	3	3
PH_1717	2021-12-24	BA.1.1	NCR; Central Luzon	0	3	3
PH_1672	2021-12-21	BA.1	Bicol; Davao; NCR	0	3	3
PH_1701	2021-12-19	BA.1	Central Luzon; NCR	0	3	3
PH_140	2021-04-15	AY.61	>3 regions	5	3	3128
PH_1674	2021-11-22	BA.1	Central Luzon; Central Visayas; CAR	0	2	3
PH_337	2021-02-06	B.1.1.7	>3 regions	1	1	1411
PH_1105	2021-06-11	B.1.1	Zamboanga Peninsula	0	0	3
PH_435	2021-05-23	B.1.1.7	Central Luzon; NCR	0	0	3
PH_614	2021-05-06	B.1.1.7	>3 regions	0	0	7
PH_710	2021-04-30	B.1.1.7	Davao; Caraga; NCR	0	0	19
PH_647	2021-04-19	B.1.1.7	Davao; Soccsksargen	0	0	18
PH_618	2021-04-15	B.1.1.7	Bicol; Ilocos; NCR	0	0	3
PH_411	2021-04-14	B.1.1.7	>3 regions	0	0	21
PH_709	2021-04-13	B.1.1.7	Davao; Caraga; Central Luzon	0	0	13
PH_1202	2021-04-02	B.1.1.519	NCR	0	0	5
PH_587	2021-03-31	B.1.1.7	Northern Mindanao; Calabarzon	0	0	3
PH_693	2021-03-25	B.1.1.7	>3 regions	0	0	28
PH_659	2021-03-22	B.1.1.7	>3 regions	0	0	31
PH_742	2021-03-19	B.1.1.7	>3 regions	0	0	12
PH_723	2021-03-15	B.1.1.7	Bicol; NCR; Calabarzon	0	0	13
PH_155	2021-03-09	B.1.1.7	Calabarzon; Mimaropa	0	0	5
PH_1134	2021-03-08	B.1.1.28	Soccsksargen; Davao	0	0	3
PH_340	2021-03-06	B.1.1.7	>3 regions	0	0	31
PH_292	2021-03-05	B.1.1.7	>3 regions	0	0	32
PH_351	2021-03-05	B.1.1.7	>3 regions	0	0	24
PH_633	2021-03-05	B.1.1.7	>3 regions	0	0	32
PH_951	2021-03-05	B.1.1.63	NCR; Calabarzon	0	0	5
PH_989	2021-03-05	C.38	NCR; Caraga	0	0	3
PH_499	2021-03-04	B.1.1.7	>3 regions	0	0	8
PH_536	2021-03-04	B.1.1.7	>3 regions	0	0	46
PH_736	2021-02-22	B.1.1.7	NCR; Calabarzon; Central Luzon	0	0	13
PH_325	2021-02-20	B.1.1.7	NCR	0	0	3
PH_769	2021-02-20	B.1.1.7	Central Luzon; NCR	0	0	3
PH_208	2021-02-15	B.1.1.7	>3 regions	0	0	55
PH_172	2021-02-12	B.1.1.7	>3 regions	0	0	71
PH_281	2021-02-11	B.1.1.7	>3 regions	0	0	14
PH_1180	2021-01-31	B.1.1.28	Central Visayas	0	0	3
PH_145	2021-01-31	B.1.351	>3 regions	6	0	2993
PH_327	2021-01-31	B.1.1.7	NCR; Central Luzon	0	0	3
PH_168	2021-01-27	B.1.1.7	Central Luzon; NCR	0	0	4
PH_861	2021-01-27	B.1.1.63	NCR; Calabarzon	0	0	7
PH_163	2021-01-26	B.1.1.7	>3 regions	0	0	48
PH_312	2021-01-26	B.1.1.7	NCR; Calabarzon; Central Visayas	0	0	5
PH_931	2021-01-25	B.1.1.63	Calabarzon	0	0	5
PH_918	2021-01-24	B.1.1.63	NCR	0	0	3

Cluster name	Date first identified	Pango lineage	Distribution	New submission	Isolated in 4 months	Total
PH_68	2021-01-21	B.1.466.1	Calabarzon; NCR	0	0	21
PH_996	2021-01-19	B.1.1	>3 regions	0	0	29
PH_1130	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_304	2021-01-14	B.1.1.7	NCR; Central Visayas; CAR	0	0	5
PH_82	2021-01-12	B.1.441	NCR; Central Visayas	0	0	5
PH_1159	2021-01-11	B.1.1.28	Davao	0	0	14
PH_1125	2021-01-09	B.1.1.28	Davao; Soccsksargen; Calabarzon	0	0	13
PH_7	2021-01-09	A.23.1	NCR; Ilocos	0	0	3
PH_87	2021-01-09	B.1.36.29	NCR	0	0	4
PH_97	2021-01-09	B.1.2	NCR	0	0	3
PH_1106	2021-01-08	B.1.1	Calabarzon; Central Visayas; NCR	0	0	6
PH_1122	2021-01-08	P.3	>3 regions	2	0	454
PH_1080	2021-01-07	R.1	NCR	0	0	3
PH_311	2021-01-07	B.1.1.7	NCR; Central Luzon; Central Visayas	0	0	6
PH_317	2021-01-07	B.1.1.7	NCR	0	0	7
PH_775	2021-01-07	B.1.1.7	>3 regions	0	0	342
PH_1138	2021-01-06	B.1.1.28	>3 regions	0	0	44
PH_220	2021-01-05	B.1.1.7	>3 regions	0	0	134
PH_1141	2021-01-03	B.1.1.28	Davao; Soccsksargen	0	0	17
PH_259	2021-01-03	B.1.1.7	NCR; CAR	0	0	4
PH_995	2020-12-30	B.1.1.174	NCR	0	0	3
PH_333	2020-12-29	B.1.1.7	>3 regions	0	0	8
PH_106	2020-12-28	B.1.524	>3 regions	0	0	10
PH_92	2020-12-26	B.1.2	NCR; Calabarzon	0	0	3
PH_66	2020-12-22	B.1.466.1	NCR	0	0	4
PH_58	2020-12-19	B.1	NCR; Calabarzon	0	0	3
PH_788	2020-12-18	B.1.1.63	Cagayan Valley; NCR	0	0	7
PH_1010	2020-12-17	B.1.1.263	CAR; Cagayan Valley; Central Luzon	0	0	65
PH_829	2020-12-15	B.1.1.63	NCR; Calabarzon; CAR	2	0	11
PH_277	2020-12-10	B.1.1.7	NCR; Calabarzon; Central Visayas	0	0	5
PH_847	2020-12-10	B.1.1.63	Calabarzon; NCR	0	0	5
PH_1103	2020-12-09	B.1.1	Central Luzon; NCR; Calabarzon	0	0	22
PH_957	2020-12-06	B.1.1.63	NCR; Central Luzon	0	0	4
PH_986	2020-12-04	B.1.1.63	NCR; Central Luzon	0	0	10
PH_1181	2020-12-02	B.1.1.28	>3 regions	0	0	36
PH_1184	2020-12-02	B.1.1.28	NCR; Calabarzon; Caraga	0	0	20
PH_1098	2020-12-01	B.1.1	Calabarzon; NCR	0	0	4
PH_1087	2020-11-25	B.1.1	Calabarzon; NCR	1	0	11
PH_885	2020-11-24	B.1.1.63	NCR	0	0	4
PH_1045	2020-11-23	B.1.1.263	NCR	0	0	3
PH_910	2020-11-22	B.1.1.63	Calabarzon; NCR	0	0	9
PH_98	2020-11-20	B.1.2	NCR	0	0	3

Cluster name	Date first identified	Pango lineage	Distribution	New submission	Isolated in 4 months	Total
PH_104	2020-11-18	B.1	Calabarzon; NCR	0	0	3
PH_1095	2020-11-16	B.1.1	>3 regions	0	0	70
PH_1051	2020-11-15	B.1.1.263	CAR; Cagayan Valley; Calabarzon	0	0	9
PH_146	2020-11-14	B.1.177	Calabarzon; NCR	0	0	4
PH_34	2020-11-10	B.6	NCR; Calabarzon	1	0	5
PH_932	2020-11-09	B.1.1.63	Mimaropa; Calabarzon; NCR	0	0	4
PH_1150	2020-11-07	B.1.1.28	Calabarzon; NCR; Central Luzon	0	0	6
PH_83	2020-11-06	B.1.36	Calabarzon; NCR	0	0	9
PH_906	2020-11-03	B.1.1.63	Calabarzon	0	0	6
PH_859	2020-11-02	B.1.1.63	>3 regions	0	0	35
PH_949	2020-11-01	B.1.1.63	>3 regions	0	0	14
PH_1064	2020-10-11	B.1.1.263	>3 regions	0	0	67
PH_1152	2020-08-24	B.1.1.28	>3 regions	0	0	15
PH_110	2020-08-22	B.1	NCR; Calabarzon; Davao	0	0	12
PH_879	2020-08-13	B.1.1.63	>3 regions	4	0	189
PH_1083	2020-08-07	B.1.1	NCR	0	0	5
PH_982	2020-08-07	B.1.1.63	>3 regions	1	0	21
PH_36	2020-08-06	B.6	>3 regions	0	0	37
PH_1090	2020-08-05	B.1.1	Calabarzon; NCR	0	0	5
PH_1137	2020-08-05	B.1.1.28	>3 regions	1	0	228
PH_865	2020-07-22	B.1.1.63	>3 regions	1	0	126
PH_874	2020-07-19	B.1.1.63	Calabarzon; NCR; Western Visayas	1	0	24
PH_54	2020-07-15	B.1	>3 regions	0	0	30
PH_998	2020-07-12	B.1.1	NCR; Calabarzon; Mimaropa	1	0	12
PH_780	2020-07-09	B.1.1.63	>3 regions	3	0	121
PH_113	2020-07-08	B.1	Mimaropa; NCR; Central Visayas	1	0	9
PH_936	2020-07-08	B.1.1.63	>3 regions	1	0	79
PH_994	2020-07-08	B.1.1	>3 regions	2	0	163
PH_779	2020-07-07	B.1.1.63	>3 regions	1	0	29
PH_943	2020-07-07	B.1.1.63	NCR; Calabarzon; Cagayan Valley	0	0	12
PH_1165	2020-07-05	B.1.1.28	>3 regions	0	0	6
PH_776	2020-07-01	B.1.1.63	Calabarzon; NCR; CAR	1	0	9
PH_923	2020-07-01	B.1.1.63	>3 regions	2	0	234
PH_818	2020-06-29	B.1.1.63	>3 regions	2	0	133
PH_975	2020-06-23	B.1.1.63	NCR	0	0	5
PH_40	2020-06-17	B.6	NCR; Calabarzon	0	0	3
PH_1007	2020-06-16	B.1.1.263	>3 regions	0	0	145
PH_121	2020-06-11	B.1	NCR; Western Visayas	2	0	8
PH_29	2020-03-11	B.6	NCR; Cagayan Valley	0	0	6
PH_12	2020-03-10	B.6	>3 regions	3	0	19

Table 3. Number of sequences by cluster identified with the Grapevine-anywhere as of 28 March 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 December 2021 to 28 March 2022.

SARS-CoV-2 sequencing in the Philippines

Total available SARS-CoV-2 sequences in the Philippines: 14872

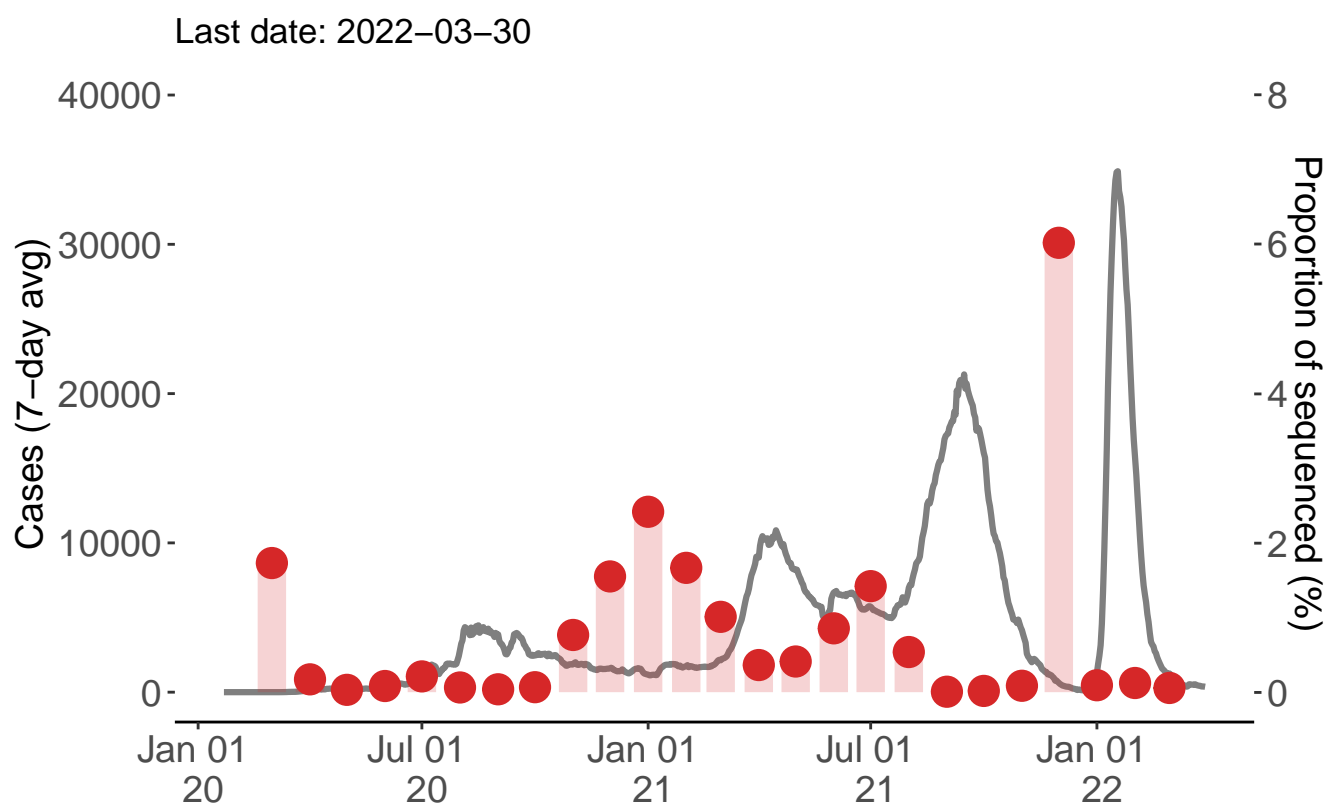**SARS-CoV-2 sequences from GECO project: 1314**

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.
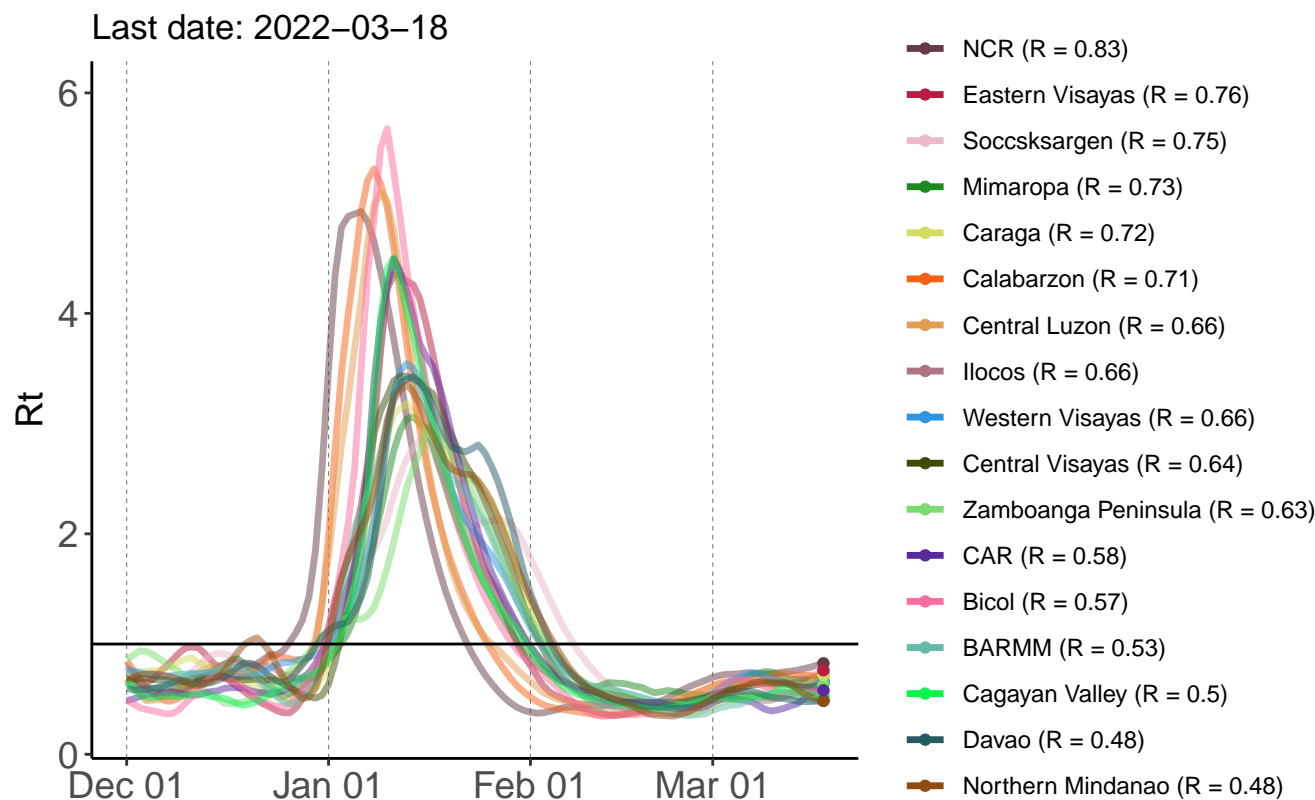
Epidemiology of COVID-19 in the Philippines

Figure 5. Mean effective reproductive number (Rt) of COVID-19 in the Philippines by region from December 2021 to March, 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

2022-03 pdf

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