

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

Highlights

- Omicron variant accounts for most of the sequences isolated in December, 2021.
- Locally circulating Omicron viruses most likely belong to BA.2 lineage.

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	15 (6.9)	1 (1)	2761
Beta	B.1.351	VOC	9 (4.1)	0	3239
Delta	B.1.617.2/AY.x	VOC	12 (5.5)	42 (40)	3281
Gamma	P.1	VOC	0	0	12
Omicron	B.1.1.529/BA.x	VOC	60 (27.5)	62 (59)	62
B.1.640	B.1.640	VUM	0	0	2
Eta	B.1.525	VUM	0	0	8
Theta	P.3	VUM	0	0	519

Table 1. Number of available sequences by variant in the Philippines as of 20 January 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 October 2021 to 20 January 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.

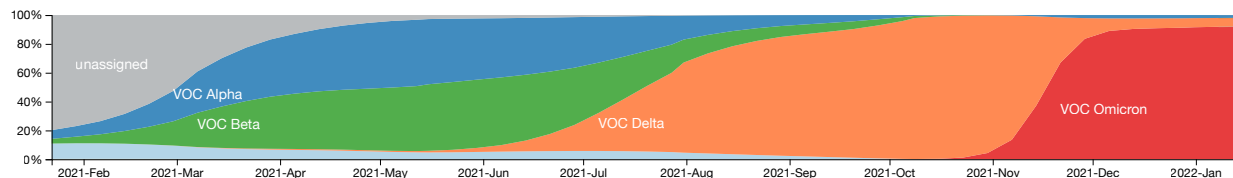


Figure 1. Temporal frequencies of SARS-CoV-2 variants in the Philippines. The figure is constructed with a subsampled genomic data set from all available sequences ([methods](#)). A more detailed illustration of SARS-CoV-2 lineages isolated in the country can be visualised by selecting PANGO Lineage as the option for coloring in the control panel (icon on top left/right). **Note** that the latest available Philippine sequences were isolated on 28 December, 2021, 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 December 2021. Based on the available data, all BA.2 sequences isolated in the Philippines (n=39) were likely originated from the same introduction. These sequences were also identified by the grapevine-anywhere pipeline as a single cluster (PH_137, see *PH specific lineages* section). 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 January 2022. Among the sublineages of Delta variant, AY.28 is the most frequently isolated lineage in the Philippines, followed by AY.9.2. 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 (39)	Omicron (88.2)	51 (48.6)	4050
Ilocos	0	-	0	363
CAR	0	-	0	747
Cagayan Valley	0	-	0	984
Central Luzon	3 (1.4)	Omicron (100)	3 (2.9)	968
Calabarzon	90 (41.3)	Delta (78)	41 (39)	2135
Mimaropa	10 (4.6)	Delta (100)	3 (2.9)	345
Bicol	2 (0.9)	Omicron (100)	2 (1.9)	244
Western Visayas	1 (0.5)	Omicron (100)	1 (1)	499
Central Visayas	3 (1.4)	Omicron (100)	3 (2.9)	598
Eastern Visayas	0	Delta (100)	1 (1)	141

Region	New submission	Dominant variant in 4 months	Isolated in 4 months	Total
Zamboanga Peninsula	0	-	0	417
Northern Mindanao	12 (5.5)	-	0	348
Davao	0	-	0	764
Soccsksargen	0	-	0	200
Caraga	0	-	0	282
BARMM	12 (5.5)	-	0	93

Table 2. Number of available sequences by administrative region in the Philippines as of 20 January 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 October 2021 to 20 January 2022. A dash indicates no sequence isolated. *Isolated in 4 months*, sequences isolated from 1 October 2021 to 20 January 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.

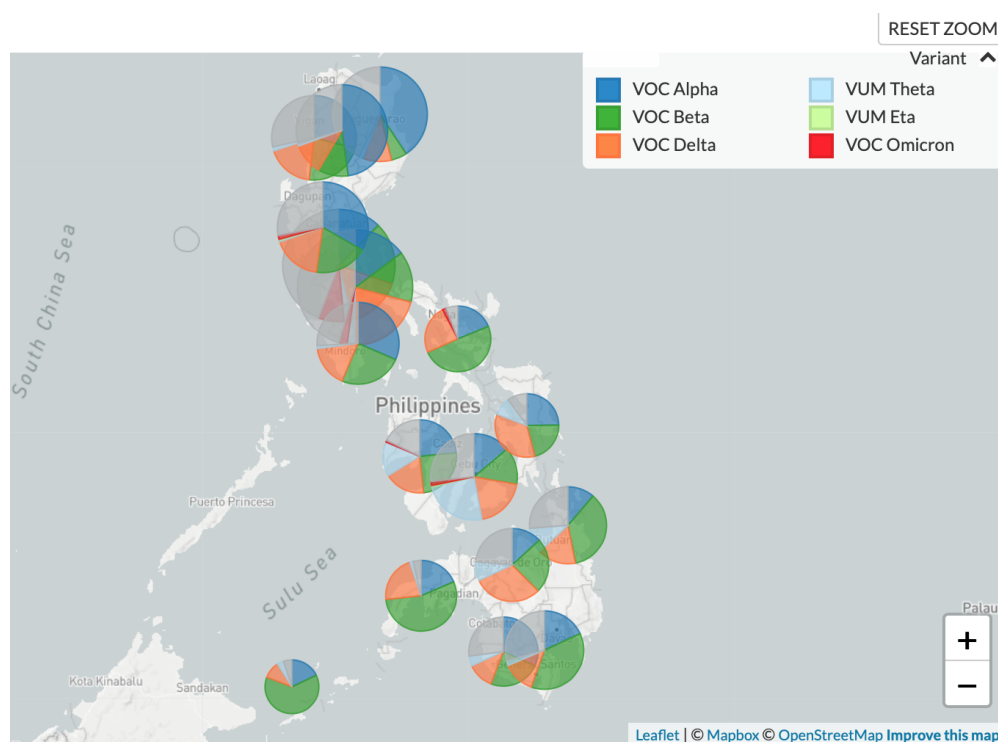


Figure 2. Frequencies of SARS-CoV-2 variants by administrative region in the Philippines. The figure is constructed with a subsampled genomic data set from all available sequences as Figure 1. Frequencies of isolates in a particular time frame can be adjusted with the control panel (icon on top left/right).

Philippines specific SARS-CoV-2 lineages

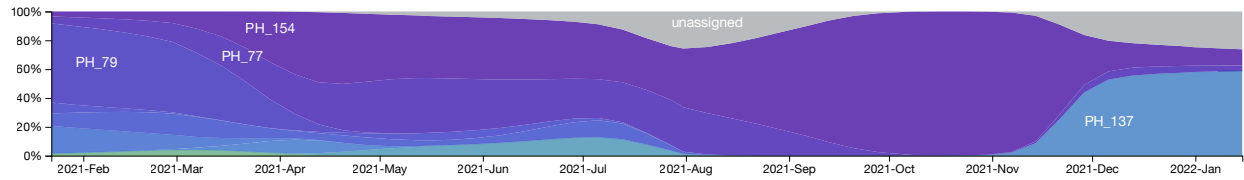


Figure 3. Temporal frequencies of Philippine lineages (clusters) identified by *Grapevine-anywhere*. Each sequence submitted to GECO database would undergo *Grapevine-anywhere* pipeline to detect sustain local transmission. A cluster is defined based on multiple sequences isolated in the Philippines 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 4 months	Total
PH_154	2020-08-18	B.1.351	>3 regions	28	42	6135
PH_137	2021-12-19	BA.2	NCR; Calabarzon	33	33	33
PH_150	2021-12-04	BA.1	NCR; Central Visayas	1	3	3
PH_77	2020-12-29	B.1.1.7	>3 regions	11	1	2131
PH_101	2021-04-02	B.1.1.519	NCR	0	0	5
PH_105	2021-03-05	C.38	NCR; Caraga	0	0	3
PH_41	2021-02-20	B.1.1.7	Central Visayas; NCR	0	0	3
PH_37	2021-02-18	B.1.1.7	Calabarzon; Central Luzon; Mimaropa	0	0	7
PH_47	2021-02-17	B.1.1.7	Central Luzon; Central Visayas; NCR	0	0	3
PH_34	2021-02-16	B.1.1.7	Central Luzon; NCR	0	0	3
PH_57	2021-02-11	B.1.1.7	>3 regions	0	0	47
PH_68	2021-01-27	B.1.1.7	Central Luzon; NCR	0	0	4
PH_62	2021-01-26	B.1.1.7	>3 regions	0	0	48
PH_78	2021-01-19	B.1.1	>3 regions	0	0	29
PH_55	2021-01-17	B.1.1.7	Central Visayas; NCR; Central Luzon	0	0	5
PH_6	2021-01-15	A.21	NCR; Calabarzon	0	0	3
PH_156	2021-01-09	B.1.525	NCR; Central Luzon; Central Visayas	0	0	6
PH_169	2021-01-09	B.1.36.29	NCR	0	0	3
PH_136	2021-01-08	P.3	>3 regions	0	0	459
PH_5	2021-01-08	A.23.1	NCR; Ilocos	0	0	4
PH_98	2021-01-07	R.1	NCR	0	0	3
PH_97	2021-01-05	B.1.1	NCR	0	0	4
PH_66	2021-01-03	B.1.1.7	>3 regions	0	0	268
PH_114	2020-12-30	B.1.1.174	NCR	0	0	3
PH_4	2020-12-30	A	NCR; Calabarzon	0	0	3
PH_163	2020-12-28	B.1	NCR	0	0	3
PH_186	2020-12-28	B.1	>3 regions	0	0	5
PH_177	2020-12-22	B.1.466.1	Calabarzon; NCR	2	0	27
PH_49	2020-12-10	B.1.1.7	NCR; Calabarzon; Central Visayas	0	0	5
PH_84	2020-12-01	B.1.1	Calabarzon; NCR	0	0	4

Cluster name	Date first identified	Pango lineage	Distribution	New submission	Isolated in 4 months	Total
PH_31	2020-11-14	B.1.177	Calabarzon; NCR	0	0	4
PH_161	2020-11-09	B.1.441	NCR; Calabarzon; Central Visayas	0	0	7
PH_194	2020-10-30	B.1	>3 regions	0	0	23
PH_165	2020-09-17	B.1.36	Calabarzon; NCR; Central Luzon	1	0	11
PH_116	2020-08-05	B.1.1.28	>3 regions	4	0	422
PH_79	2020-06-23	B.1.1.63	>3 regions	61	0	1337
PH_89	2020-06-16	B.1.1.263	>3 regions	15	0	285
PH_182	2020-06-11	B.1	NCR; Western Visayas	0	0	3
PH_160	2020-04-13	B.1.2	NCR; Calabarzon; Central Visayas	0	0	13
PH_8	2020-03-10	B.6	>3 regions	3	0	70

Table 3. Number of sequences by cluster identified with the Grapevine-anywhere as of 20 January 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 October 2021 to 20 January 2022.

SARS-CoV-2 sequencing in the Philippines

Total available SARS-CoV-2 sequences in the Philippines: 13191

SARS-CoV-2 sequences from GECO project: 698

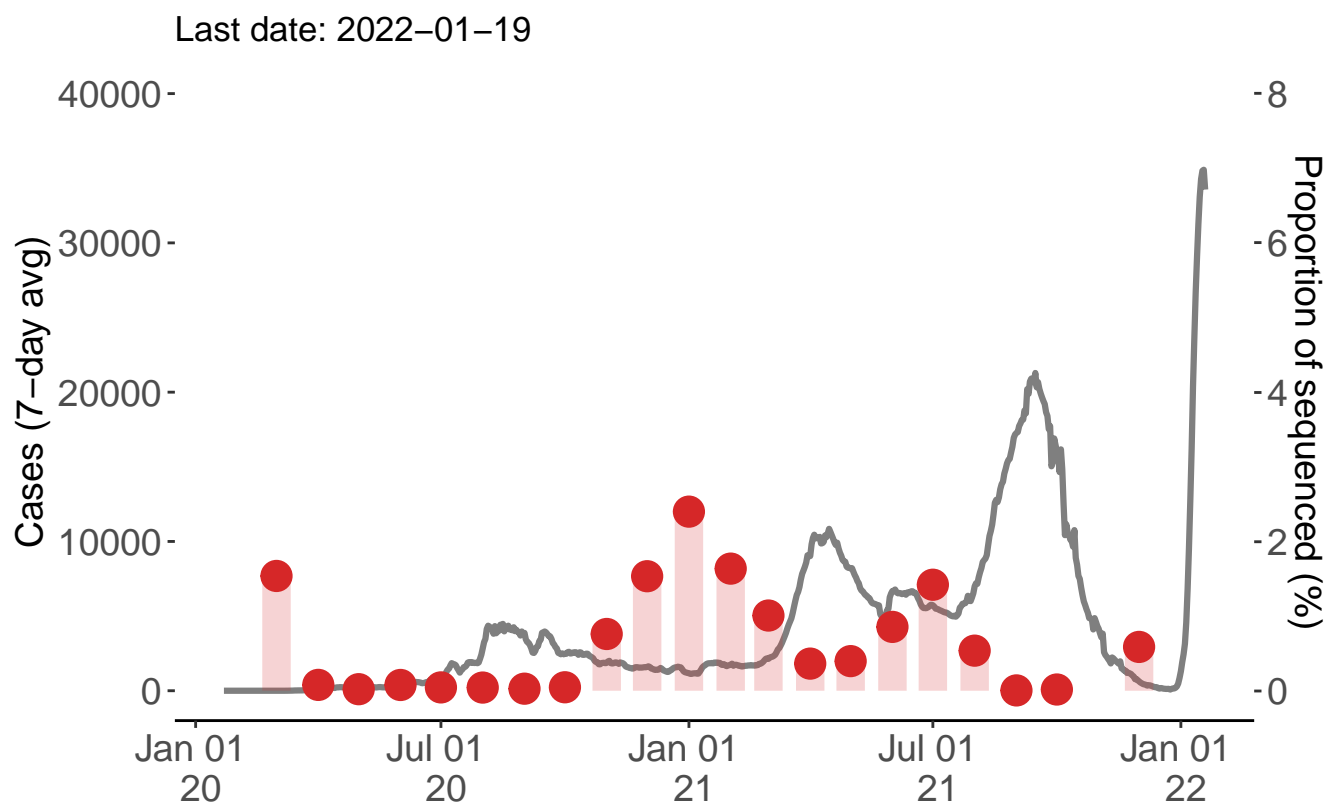


Figure 4. Number of COVID-19 cases and the proportion of sequenced samples in the Philippines. The gray line indicates the mean cases in a 7 days window based on the JHU data base, whereas the red bars indicate the estimated percentage of sequenced samples among cases in a month. The proportions in January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

Epidemiology of COVID-19 in the Philippines

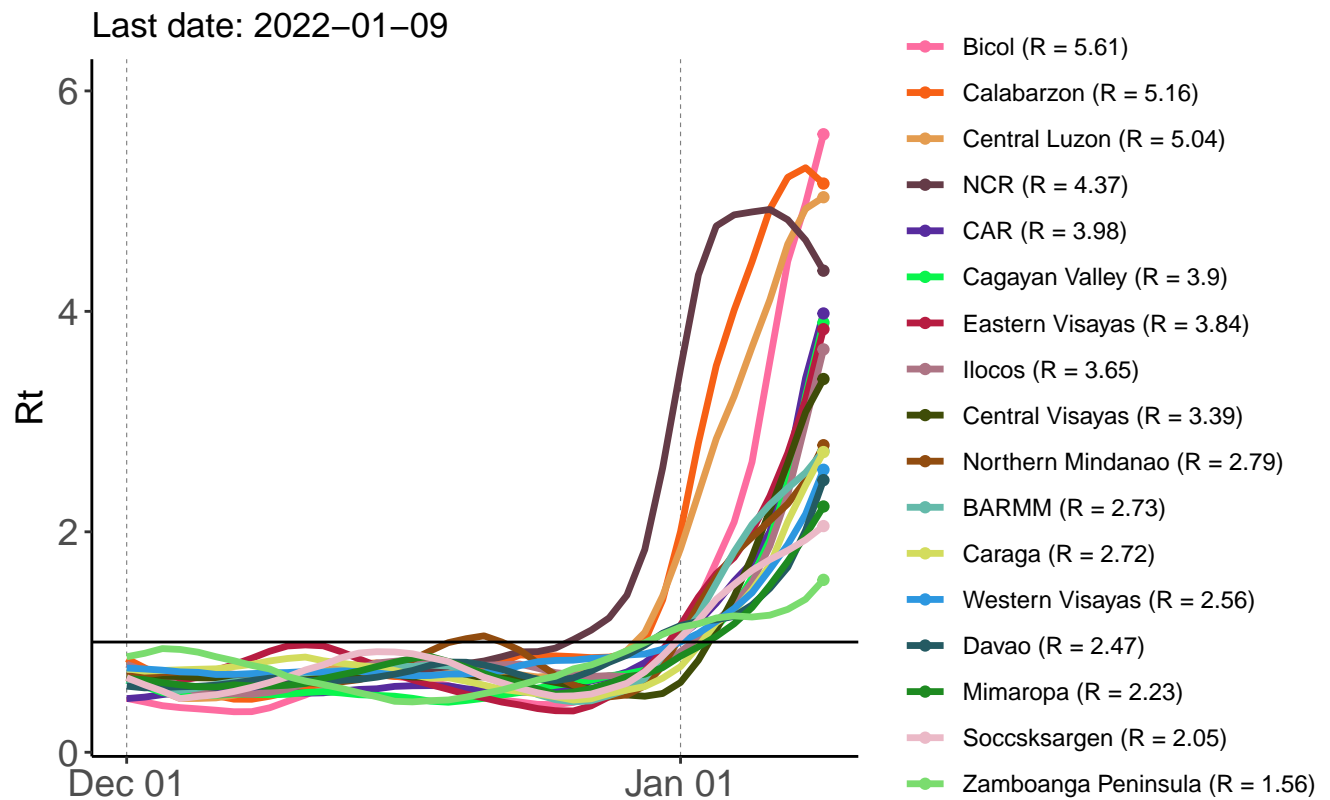


Figure 5. Mean effective reproductive number (R_t) of COVID-19 in the Philippines by region from December 2021 to January, 2022. The reproductive number (R) is defined as the number of new infections that one infected patient can cause in a susceptible population. Here, *the mean effective reproductive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

2021-12 [pdf](#)



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