GECO Philippines SARS-CoV-2 Situation Report - 2021 December

Highlights

- First sequences of Omicron variant were isolated from incoming travelers (by Airport Diagnostic Laboratory and PGC)

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	2746
Beta	B.1.351	VOC	0	2 (4.7)	3230
Delta	B.1.617.2/AY.x	VOC	39 (95.1)	39 (90.7)	3269
Gamma	P.1	VOC	0	0	3
Omicron	B.1.1.529/BA.x	VOC	2 (4.9)	2 (4.7)	2
Eta	B.1.525	VUM	0	0	8
Theta	P.3	VUM	0	0	521

Table 1. Number of available sequences by variant in the Philippines as of 17 December 2021. The variants (VOC/VUM) here only include sequences that present in the GIDAID 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 September 2021 to 17 December 2021. 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.
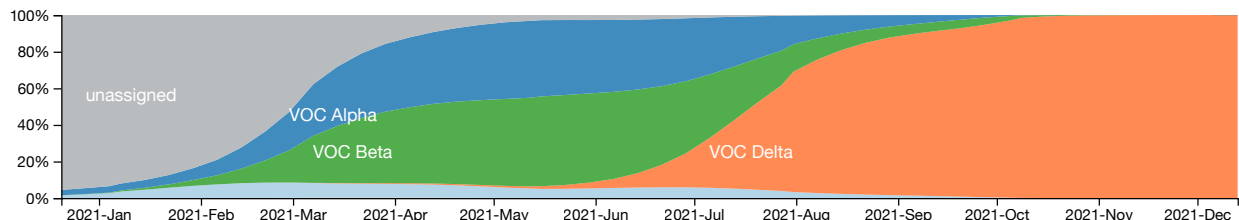

Figure 1. Temporal frequencies of SARS-CoV-2 variants in the Philippines. The figure is constructed with a subsampled genomic data set from all available sequences (methods). A more detailed illustration of SARS-CoV-2 lineages isolated in the country can be visualised by selecting PANGO Lineage as the option for coloring in the control panel (icon on top left/right). **Note** that the latest available Philippine sequences were isolated on 6 December, 2021, thus the frequencies after the time point could harbor great uncertainty.

Diversity within 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 17 December 2021. Among the sublineages of Delta variant, AY.61 is the most isolated lineages in the Philippines (27%), followed by AY.76 (16%). With the potential introduction and circulation of Omicron variant in the Philippines, it is expected to observe a major shift in local lineage dynamics depending on border control measures, vaccination campaign and viral intrinsic transmissibility. 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	8 (19.5)	Delta (75)	8 (18.6)	3965
Ilocos	0	-	0	363
CAR	0	-	0	747
Cagayan Valley	0	-	0	984
Central Luzon	0	-	0	965
Calabarzon	29 (70.7)	Delta (100)	29 (67.4)	2045
Mimaropa	3 (7.3)	Delta (100)	3 (7)	335
Bicol	0	-	0	242
Western Visayas	0	-	0	498
Central Visayas	0	-	0	595
Eastern Visayas	1 (2.4)	Delta (100)	1 (2.3)	141
Zamboanga Peninsula	0	-	0	417
Northern Mindanao	0	-	0	336
Davao	0	Beta (100)	2 (4.7)	764
Soccsksargen	0	-	0	200

Region	New submission	Dominant variant in 4 months	Isolated in 4 months	Total
Caraga	0	-	0	282
BARMM	0	-	0	81

Table 2. Number of available sequences by administrative region in the Philippines as of 17 December 2021. The variant definition is identical to Table 1 based on the WHO website. *New submission*, new sequences submitted from the last report. *Isolated in 4 months*, sequences isolated from 1 September 2021 to 17 December 2021. *Dominant variant in 4 months*, the major variant isolated from 1 September 2021 to 17 December 2021. A dash indicates no sequence isolated.

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).
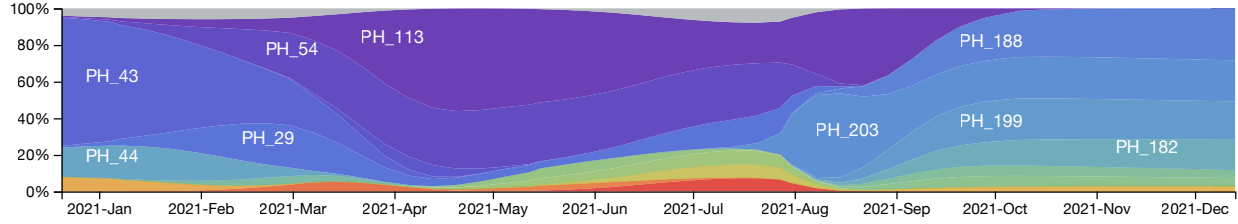
Philippines specific SARS-CoV-2 lineages

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_3	2020-03-04	B.6	NCR; Calabarzon	0	0	3
PH_10	2020-03-06	B.6	NCR	0	0	6
PH_2	2020-03-10	B.6	>3 regions	0	0	20
PH_29	2020-04-09	P.3	>3 regions	0	0	17
PH_102	2020-06-11	B.1	NCR; Western Visayas	0	0	3
PH_21	2020-06-16	B.1.1.370	NCR; Calabarzon	0	0	18
PH_44	2020-06-23	B.1.1.63	Calabarzon; NCR; CAR	0	0	19
PH_43	2020-06-29	B.1.1.63	>3 regions	0	0	64
PH_82	2020-09-18	B.1.1	Calabarzon; Mimaropa	0	0	3
PH_33	2021-01-04	B.1	Calabarzon	0	0	4
PH_40	2021-01-10	B.1.1	Calabarzon; NCR	0	0	3
PH_28	2021-01-19	B.1.1.28	Calabarzon; Mimaropa; NCR	0	0	3
PH_23	2021-01-21	B.1.1.28	Calabarzon; Davao; NCR	0	0	6
PH_113	2021-01-31	B.1.351	>3 regions	0	2	107
PH_20	2021-02-02	B.1.1	NCR	0	0	4
PH_109	2021-02-21	B.1.351	Northern Mindanao; Calabarzon; NCR	0	0	4
PH_54	2021-02-21	B.1.1.7	>3 regions	0	0	54
PH_41	2021-03-07	B.1.351	>3 regions	0	0	10
PH_72	2021-03-11	B.1.1.7	Calabarzon; Northern Mindanao; Soccsksargen	0	0	3
PH_51	2021-05-24	B.1.1.7	Northern Mindanao; Soccsksargen	0	0	4
PH_203	2021-08-22	B.1.617.2	Calabarzon; NCR	9	9	16
PH_218	2021-08-24	AY.1	Calabarzon; Eastern Visayas; NCR	2	2	3
PH_188	2021-10-09	B.1.617.2	Calabarzon; NCR; Mimaropa	9	9	9
PH_199	2021-10-09	B.1.617.2	Calabarzon; NCR; Mimaropa	10	10	10
PH_182	2021-10-11	B.1.617.2	Calabarzon; Mimaropa	5	5	5

Table 3. Number of sequences by cluster identified with the Grapevine-anywhere as of 17

December 2021. 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 September 2021 to 17 December 2021.

SARS-CoV-2 sequencing in the Philippines

Total available SARS-CoV-2 sequences in the Philippines: 12973

SARS-CoV-2 sequences from GECO project: 514
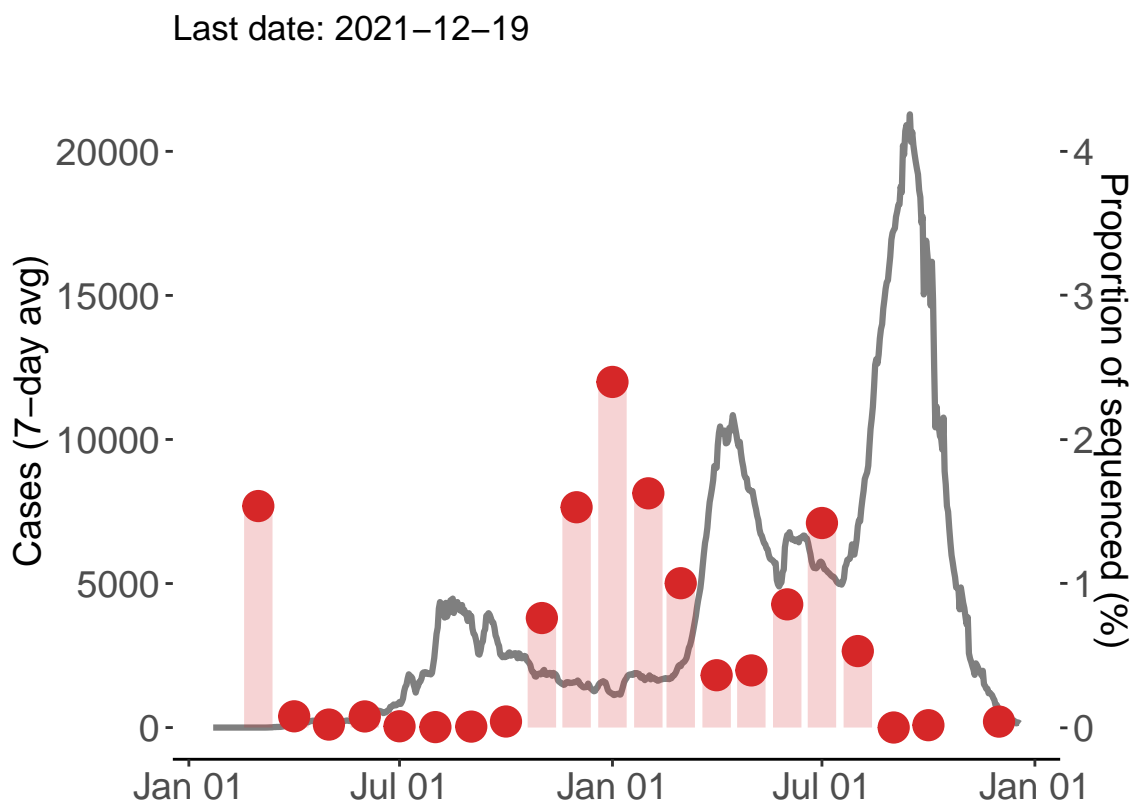
Figure 4. Number of COVID-19 cases and the proportion of sequenced samples in the Philippines. The gray line indicates the mean cases in a 7 days window based on the JHU data base, whereas the red bars indicate the estimated percentage of sequenced samples among cases in a month. The proportions in January and February, 2020 were discarded as they are outliers.

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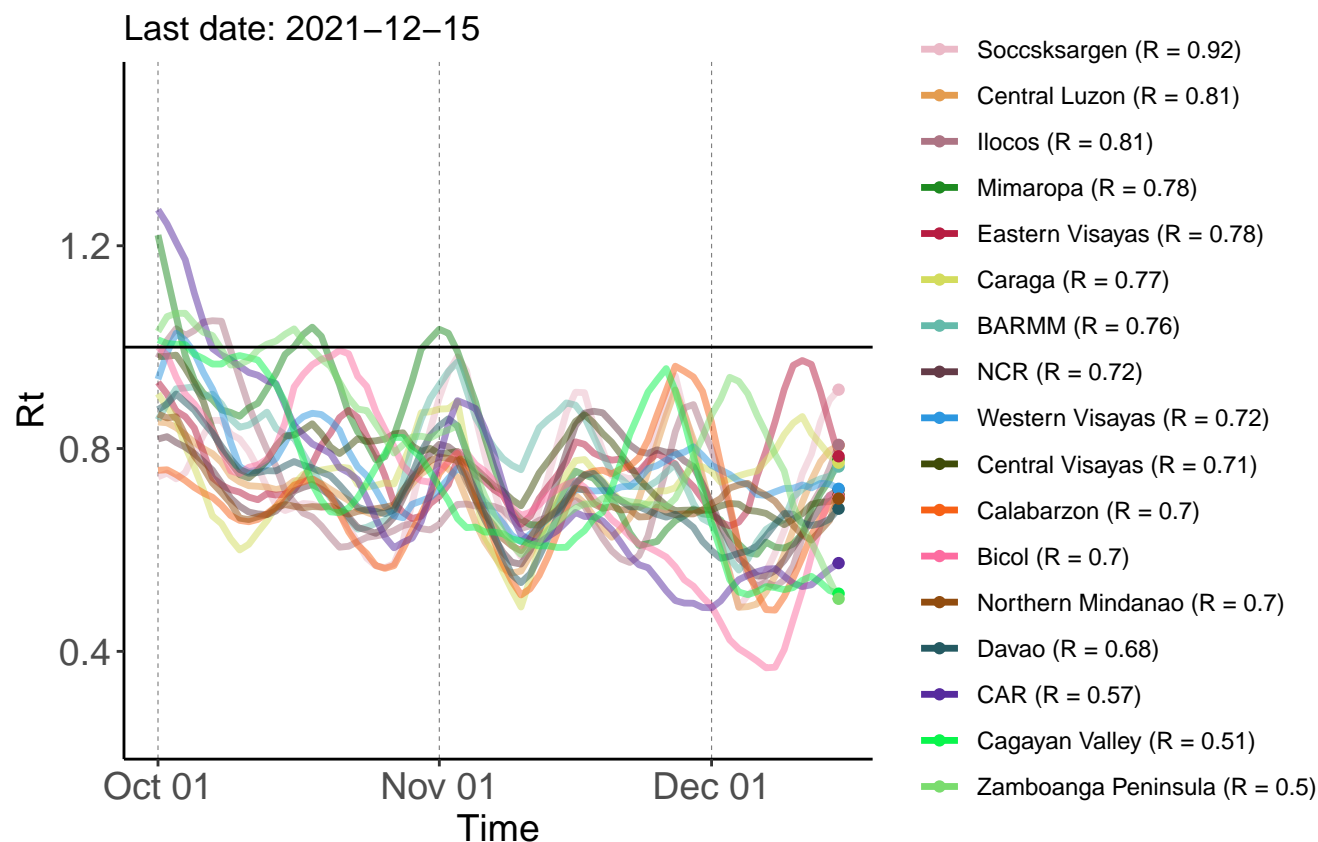# Epidemiology of COVID-19 in the Philippines

Figure 5. Mean effective reproductive number (Rt) of COVID-19 in the Philippines by region. 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 appear but in a more 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 mutaions of interest

Spike protein

- **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 144, S 417, S 484) and receptor binding (S 417, S 484, S 501).

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

2021-11 pdf

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