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

Highlights

- Delta variant accounts for the majority of sequence output isolated since August.
- High genetic diversity of the Delta variant viruses suggests frequent introductory events.

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	7 (5.5)	80 (3.8)	2736
Beta	B.1.351	VOC	20 (15.6)	87 (4.1)	3217
Delta	B.1.617.2/AY.x	VOC	10 (7.8)	1908 (89.5)	3230
Gamma	P.1	VOC	0	0	3
Eta	B.1.525	VUM	0	0	8
Theta	P.3	VUM	3 (2.3)	37 (1.7)	522

Table 1. Number of available sequences by variant in the Philippines as of 22 November 2021. The variants (VOC/VOI/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. Since there has been a major change in the format of the GECO report, the column here indicates the sequences isolated from 1 November to 22 November, 2021. *Isolated in 4 months*, sequences isolated from 1 August 2021 to 22 November 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.
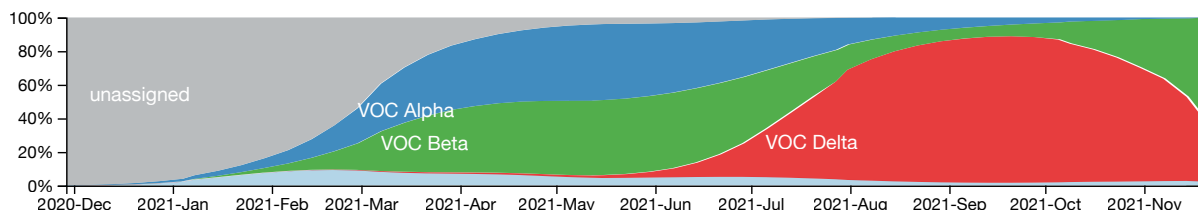

Figure 1. Temporal frequencies of SARS-CoV-2 variants in the Philippines. The figure is constructed with a subsampled genomic data set from all available sequences. A more detailed illustration of SARS-CoV-2 lineages isolated in the country can be visualised by selecting PANGO Lineage as the option for color in the control panel (left hand side). **Note** that the latest available Philippine sequences were isolated on 9 September, 2021, thus the frequencies after the time point could harbor great uncertainty.

Diversity within Delta

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 22 November 2021. Among the sublineages of Delta variant, AY.61 is the most isolated lineages in the Philippines (31%), followed by AY.71 (11.5%) and AY.75.x (11.1%). Transmission and the spread of the Delta sublineages should be closely monitored. Phylogenetic relationship of the sublineages in 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	26 (20.3)	Delta (97.5)	483 (22.7)	3957
Ilocos	0	Delta (90.1)	111 (5.2)	363
CAR	0	Delta (92.1)	89 (4.2)	747
Cagayan Valley	0	Delta (86.8)	167 (7.8)	984
Central Luzon	0	Delta (96)	225 (10.6)	965
Calabarzon	44 (34.4)	Delta (92.7)	260 (12.2)	2016
Mimaropa	0	Delta (62.2)	82 (3.8)	332
Bicol	0	Delta (81)	84 (3.9)	242
Western Visayas	0	Delta (77.3)	132 (6.2)	498
Central Visayas	0	Delta (98.5)	68 (3.2)	595
Eastern Visayas	0	Delta (88.2)	51 (2.4)	140
Zamboanga Peninsula	0	Delta (81.7)	82 (3.8)	417
Northern Mindanao	11 (8.6)	Delta (96.4)	112 (5.3)	336
Davao	34 (26.6)	Delta (72.5)	91 (4.3)	764
Soccsksargen	12 (9.4)	Delta (90.9)	11 (0.5)	200
Caraga	0	Delta (83.8)	74 (3.5)	282
BARMM	1 (0.8)	Delta (77.8)	9 (0.4)	81

Table 2. Number of available sequences by administrative region in the Philippines as of 22 November 2021 The varaitns definition is identical to Table 1 based on the WHO website. *New submission*, new sequences submitted from the last report. Since there has been a major change in the format of the GECO report, the column here indicates the sequences isolated from 1 November to 22 November, 2021. *Isolated in 4 months*, sequences isolated from 1 August 2021 to 22 November 2021. *Dominant variant in 4 months*, the major variant isolated from 1 August 2021 to 22 November 2021.

NCR, National Capital Region; CAR, Cordillera Administrative Region; BARMM, Bangsamoro Autonomous Region in Muslim Mindanao.
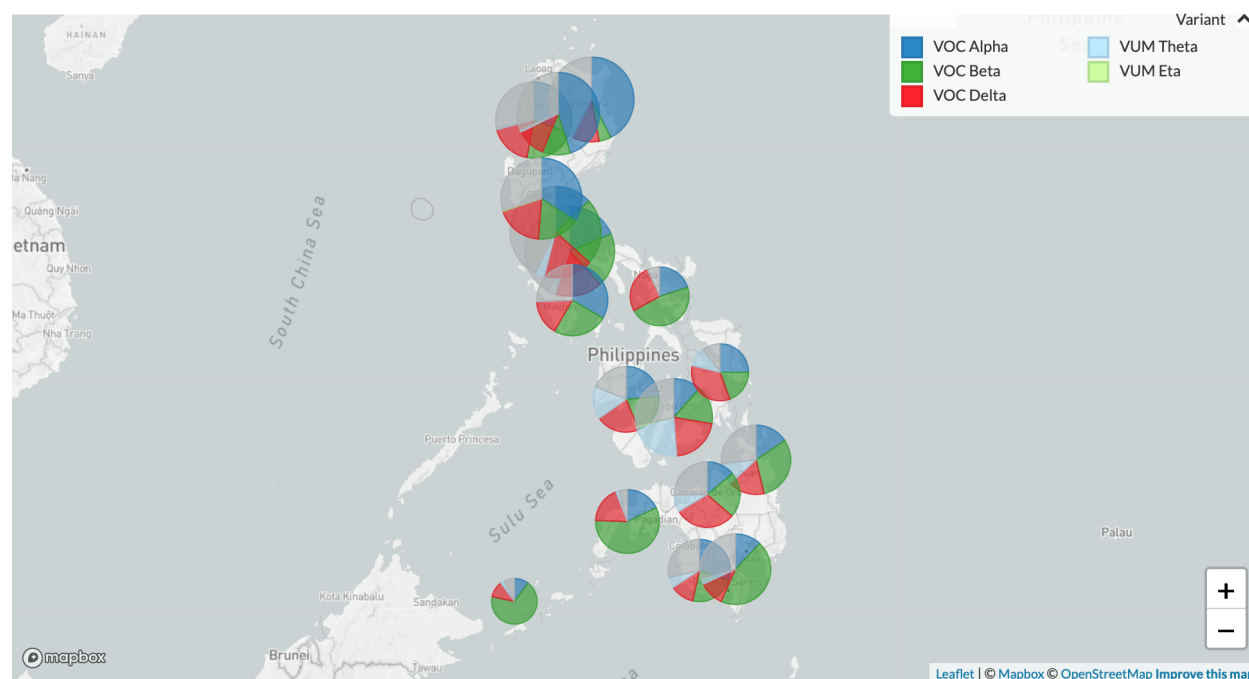

Figure 2. Frequencies of SARS-CoV-2 variants by administrative region in the Philippines. The figure is constructed with a subsampled genomic data set from all available sequences. Frequencies of isolates in a particular timeframe can be adjusted with the control panel.
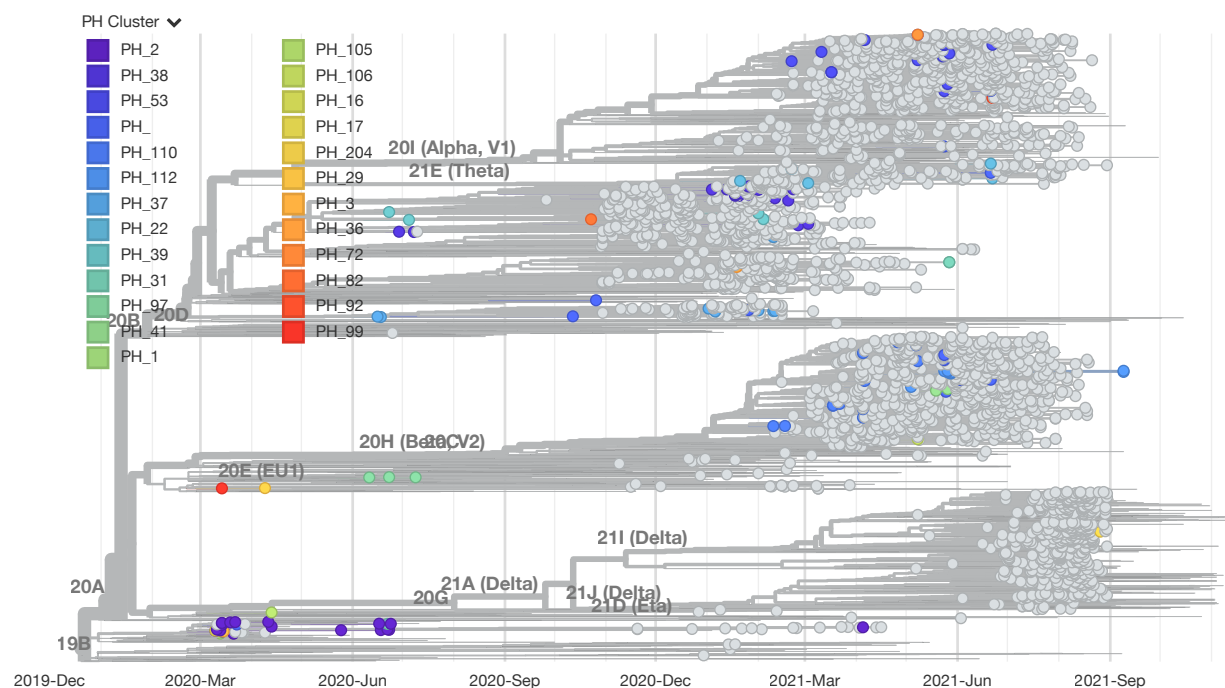
Philippines specific SARS-CoV-2 lineages

Figure 3. Phylogenetic relationships 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. A "PH_" here indicates sequences isolated by GECO without a assigned cluster name.

Cluster name	Date first identified	Pango lineage	Distribution	New submission	Isolated in 4 months	Total
PH_10	2020-03-06	B.6	NCR	0	0	6
PH_106	2021-02-21	B.1.351	Northern Mindanao; Calabarzon; NCR	1	0	4
PH_110	2021-01-31	B.1.351	>3 regions	15	0	71
PH_112	2021-02-10	B.1.351	>3 regions	4	2	26
PH_2	2020-03-10	B.6	>3 regions	0	0	21
PH_20	2021-02-02	B.1.1	NCR	2	0	4
PH_204	2021-08-22	B.1.617.2	Calabarzon	7	7	7
PH_22	2021-01-21	P.3	>3 regions	3	1	15
PH_3	2020-03-04	B.6	NCR; Calabarzon	0	0	3
PH_31	2020-06-22	B.6	NCR; Calabarzon; Davao	1	0	7
PH_33	2021-01-04	B.1	Calabarzon	0	0	4
PH_36	2021-01-19	B.1.1.28	Calabarzon; Mimaropa; NCR	0	0	3
PH_37	2020-06-16	B.1.1.370	NCR; Calabarzon	6	0	18
PH_38	2020-06-29	B.1.1.63	>3 regions	14	0	64
PH_39	2020-06-23	B.1.1.63	Calabarzon; NCR; CAR	1	0	19
PH_41	2021-03-07	B.1.351	>3 regions	0	0	10
PH_48	2021-01-10	B.1.1	Calabarzon; NCR	1	0	3
PH_53	2021-02-21	B.1.1.7	>3 regions	7	0	49

Cluster name	Date first identified	Pango lineage	Distribution	New submission	Isolated in 4 months	Total
PH_72	2021-03-11	B.1.1.7	Calabarzon; Northern Mindanao; Soccsksargen	0	0	3
PH_82	2020-09-18	B.1.1	Calabarzon; Mimaropa	0	0	3
PH_97	2020-06-11	B.1	NCR; Western Visayas	0	0	3

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

SARS-CoV-2 sequencing in the Philippines

Total available SARS-CoV-2 sequences in the Philippines: 12932

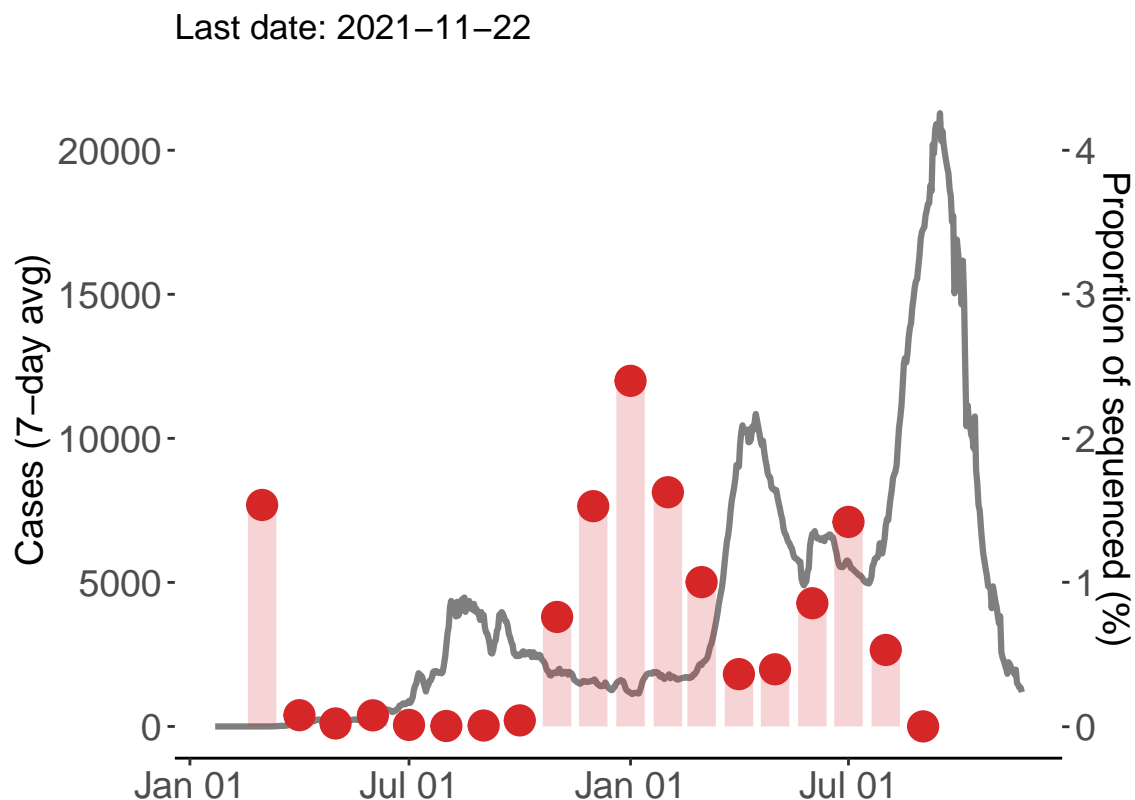**SARS-CoV-2 sequences from GECO project: 474**

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

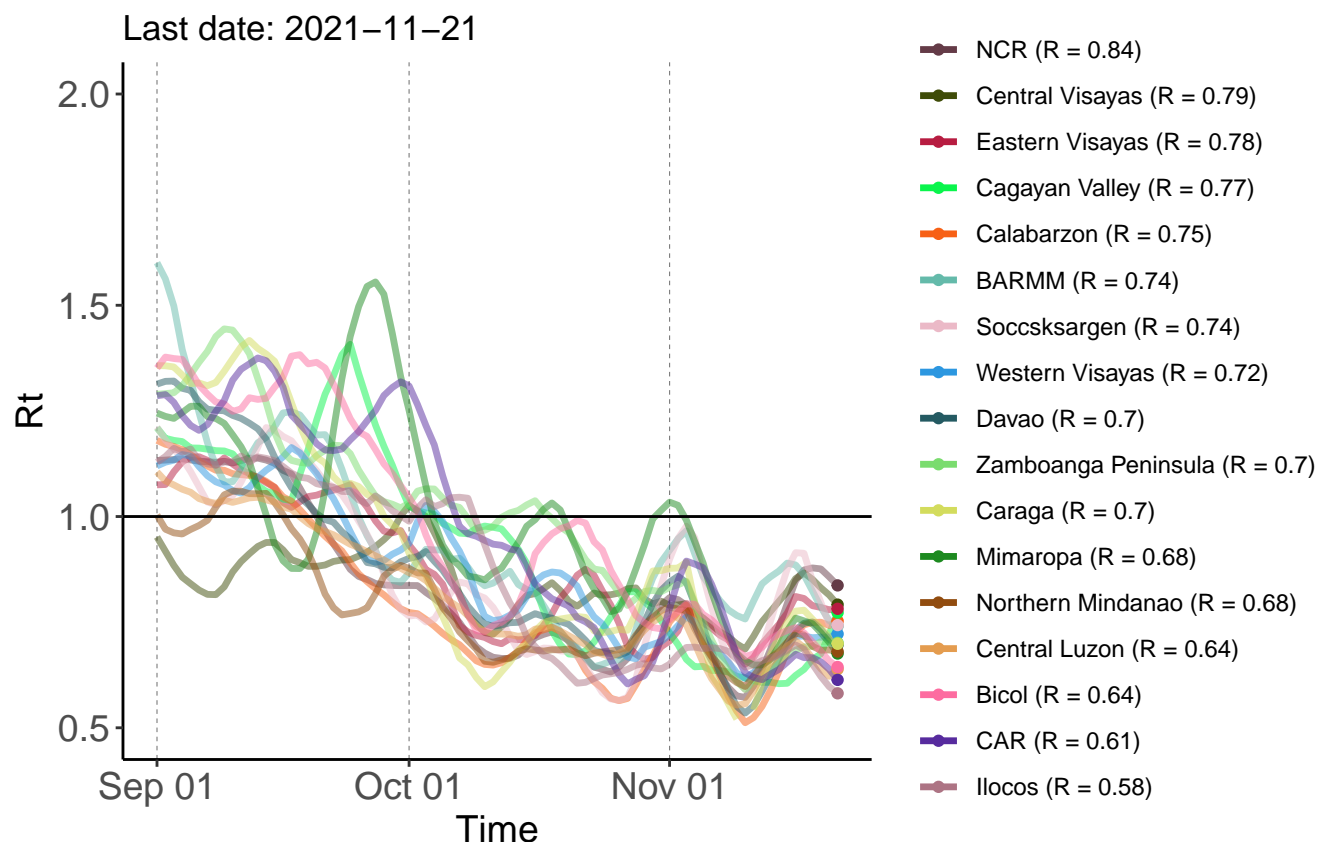## Epidemiology of COVID-19 in the Philippines

Figure 5. Mean effective reproductive number (Rt) of COVID-19 in the Philippines by region. 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.

SARS-CoV-2 mutaions of interest

Spike protein

- **E484K:** Distribution on the Philippine isolates

- **D614G:** Distribution on the Philippine isolates

Data sources and references

Data

- GECO website
- DOH Data drop
- GISAID (acknowledgement table)
- JHU COVID data

Methods

- Nextstrain
- Grapevine-anywhere

References

- WHO
- Pango lineage list

Previous reports

Genomic Epidemiology of COVID in the Philippines (GECO PH)