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GENOME SEQUENCES

Coding-Complete Genome Sequences of 11 SARS-CoV-2 B.1.1.7 and B.1.351 Variants from Metro Manila, Philippines

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ABSTRACT Here, we report the complete genome sequences of 11 severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) variants from the Philippines. Lineage analysis showed 3 B.1.1.7 and 8 B.1.351 sequences. One B.1.1.7 sequence contained two additional mutations, F318N and V320F, with V320F located in the receptor binding domain of the S1 subunit.

Severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2), belonging to the family *Coronaviridae* and the genus *Betacoronavirus*, is the causative agent of coronavirus disease 2019 (COVID-19) in humans (1). The first case of the SARS-CoV-2 B.1.1.7 variant was detected in a Filipino returning from the United Arab Emirates who arrived in the Philippines on 7 January 2021 (2, 3). The B.1.351 and the P.1. variants were detected by early March (4, 5) from returning overseas Filipino workers (3–5). Here, we announce the genome sequences of 11 SARS-CoV-2 strains collected from 12 March to 8 April 2021 from COVID-19 reverse transcription-PCR (RT-PCR)-positive Filipino patients (4). Viral RNA was extracted from nasopharyngeal/oropharyngeal swabs using a QIAamp viral RNA minikit (Qiagen) and used as the template for amplicon sequencing using ARTIC SARS-CoV-2 v3 primers (6). DNA libraries were constructed and multiplexed using the Illumina DNA preparation kit and then pooled before sequencing. Sequencing was performed on the iSeq100 platform using the iSeq reagent kit v2 (Illumina, USA) at the AFP-AFRIMS Molecular Laboratory, V. Luna Medical Center, Quezon City, Philippines. Primer region trimming and variant calling (Phred quality [Q] score, ≥25) were performed using iVAR v1.2.2 (7) and SAMtools (8), respectively. Consensus sequences were generated using iVAR v1.2.2 (7) (Q, ≥25; depth of coverage, ≥10×). Gaps, deletions, and ambiguous bases were identified and confirmed by genome-guided assembly using the reference sequence (GenBank accession no. NC_045512.2) with Trinity v2.11.0 (9). The lineage and clade were determined using Pangolin v2.1.10 (10) and GISAID clade nomenclature (11). MAFFT v7.475 (12) was used to examine the nucleotide and amino acid substitutions. All tools were run with default parameters. The raw reads yielded a total of 1.03 gigabases (84.3% of the clusters with Q ≥ 30). The lengths of the reads obtained were 35 to 151 nucleotides, and the range of the number of reads obtained per library was 2.4 million to 11.1 million reads. The consensus sequence lengths were similar to those of strain Wuhan-Hu-1 (NC_045512.2), with the mean coverage ranging from 563× to 2,469×. Table 1 shows the strain details and mutations. In total, 3/11 genomes were classified under clade GRY/lineage B.1.1.7, and 8/11 genomes were classified under clade GH/lineage B.1.351. All of the 11 sequenced samples collected from 12 March to 8 April 2021 were either B.1.1.7 or B.1.351 variants and were collected from patients with no history of travel, which

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TABLE 1 Genome features of 11 SARS-CoV-2 samples from the National Capital Region, Philippines

Sequence name	GenBank accession no.	SRA accession no.	Collection date (day-mo-yr)	Patient data					Ct value[b]	Genome size (bp)	GC content (%)	Mean depth of coverage (×)	Coverage[c] (%)	Clade	Lineage	Gene region	Nucleotide substitution[d]	Amino acid substitution[d]
				Sex[a]	Age (yr)	Location	Symptoms	Clinical outcome										
SARS-CoV-2/Philippines/AFRIMS-COVID51005	MZ068151	SRR14460628	12-Mar-21	M	55	Quezon City, National Capital Region	None	No data	21.72	29,885	39	1,648	99.5	GH	B.1.351	ORF1a	1059: C > T	T265I
																ORF1a	3037: C > T	F924F
																ORF1a	4213: T > C	A1316A
																ORF1a	5230: G > T	K1655N
																ORF1a	10323: A > G	K3353R
																ORF1a	11812: C > A	G3849G
																ORF1b	Deletion 11288–11296	SGF position 3675–3677
																ORF1b	14408: C > T	P314L
																ORF1b	15925: C > T	L820F
																ORF1b	17970: T > C	D1501D
																S	21641: G > T	A27S
																S	21801: A > C	D80A
																S	22206: A > G	D215G
																S	Deletion 22281–22289	LLA position 241–243
																S	22813: G > T	K417N
																S	23012: G > A	E484K
																S	23063: A > T	N501Y
																S	23403: A > G	D614G
																S	23664: C > T	A701V
																S	23764: A > T	T734T
																ORF3a	25563: G > T	Q57H
																ORF3a	25904: C > T	S171L
																E	26456: C > T	P71L
																ORF8	28253: C > T	F120F
																N	28642: T > C	Y123Y
																N	28887: C > T	T205I
																ORF14	28887: C > T	L52F
SARS-CoV-2/Philippines/AFRIMS-COVID52511	MZ068152	SRR14460627	18-Mar-21	M	46	Pasay City, National Capital Region	Fever, cough, sore throat, diarrhea, body malaise, anosmia	Quarantine, discharged stable	19.25	29,885	38	1,618	99.7	GH	B.1.351	ORF1a	1059: C > T	T265I
																ORF1a	3037: C > T	F924F
																ORF1a	4213: T > C	A1316A
																ORF1a	5230: G > T	K1655N
																ORF1a	10323: A > G	K3353R
																ORF1a	11812: C > A	G3849G
																ORF1b	Deletion 11288–11296	SGF position 3675–3677
																ORF1b	14408: C > T	P314L
																ORF1b	15925: C > T	L820F
																ORF1b	17970: T > C	D1501D
																S	21641: G > T	A27S
																S	21801: A > C	D80A
																S	22206: A > G	D215G
																S	Deletion 22281–22289	LLA position 241–243
																S	22813: G > T	K417N
																S	23012: G > A	E484K
																S	23063: A > T	N501Y
																S	23403: A > G	D614G
																S	23664: C > T	A701V
																S	23764: A > T	T734T
																ORF3a	25563: G > T	Q57H
																ORF3a	25904: C > T	S171L
																E	26456: C > T	P71L
																ORF8	28253: C > T	F120F
																N	28642: T > C	Y123Y

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TABLE 1 (Continued)

Sequence name	GenBank accession no.	SRA accession no.	Collection date (day-mo-yr)	Patient data					Ct value[b]	Genome size (bp)	GC content (%)	Mean depth of coverage (×)	Coverage[c] (%)	Clade	Lineage	Gene region	Nucleotide substitution[d]	Amino acid substitution[d]
				Sex[a]	Age (yr)	Location	Symptoms	Clinical outcome										
																N	28887: C > T	T205I
																ORF14	28887: C > T	L52F
																N	28928: C > A	L219I
																ORF14	28928: C > A	L65L
SARS-CoV-2/Philippines/AFRIMS-COVID53359	MZ068153	SRR14460625	20-Mar-21	F	51	Taguig City, National Capital Region	Fever, chills, runny nose, cough	Admitted to hospital, discharged stable	23.29	29,885	39	563	95.3	GH	B.1.351	ORF1a	1 059: C > T	T265I
																ORF1a	3037: C > T	F924F
																ORF1a	4213: T > C	A1316A
																ORF1a	5144: C > T	L1627L
																ORF1a	5230: G > T	K1655N
																ORF1a	10323: A > G	K3353R
																ORF1a	11812: C > A	G3849G
																ORF1b	Deletion 11288–11296	SGF position 3675–3677
																ORF1b	14408: C > T	P314L
																ORF1b	15925: C > T	L820F
																ORF1b	17970: T > C	D1501D
																S	21641: G > T	A27S
																S	21801: A > C	D80A
																S	22206: A > G	D215G
																S	Deletion 22281–22289	LLA position 241–243
																S	22813: G > T	K417N
																S	23012: G > A	E484K
																S	23063: A > T	N501Y
																S	23403: A > G	D614G
																S	23664: C > T	A701V
																S	23764: A > T	T734T
																ORF3a	25563: G > T	Q57H
																ORF3a	25904: C > T	S171L
																E	26456: C > T	P71L
																ORF8	28253: C > T	F120F
																N	28642: T > C	Y123Y
SARS-CoV-2/Philippines/AFRIMS-COVID53656	MZ068154	SRR14460624	22-Mar-21	M	56	Taguig City, National Capital Region	Difficulty breathing	Diagnosed with pulmonary tuberculosis and pneumonia; admitted to hospital and discharged stable	22.01	29,885	39	2,468	98.9	GH	B.1.3 51	ORF1a	1059: C > T	T265I
																ORF1a	3037: C > T	F924F
																ORF1a	4213: T > C	A1316A
																ORF1a	5230: G > T	K1655N
																ORF1a	10323: A > G	K3353R
																ORF1a	11812: C > A	G3849G
																ORF1b	Deletion 1 1288–11296	SGF position 3675–3677
																ORF1b	14408: C > T	P314L
																ORF1b	15925: C > T	L820F
																ORF1b	17577: A > G	E1370E
																ORF1b	17970: T > C	D1501D
																S	21641: G > T	A27S
																S	21801: A > C	D80A
																S	22206: A > G	D215G
																S	Deletion 22281–22289	LLA position 241–243
																S	22813: G > T	K417N
																S	23012: G > A	E484K
																S	23063: A > T	N501Y
																S	23277: C > T	T572I
																S	23403: A > G	D614G
																S	23664: C > T	A701V
																S	23764: A > T	T734T
																ORF3a	25563: G > T	Q57H
																ORF3a	25904: C > T	S171L
																E	26456: C > T	P71L
																ORF8	28093: C > T	S67F
																ORF8	28253: C > T	F120F
																N	28887: C > T	T205I

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TABLE 1 (Continued)

Sequence name	GenBank accession no.	SRA accession no.	Collection date (day-mo-yr)	Patient data					Ct value[b]	Genome size (bp)	GC content (%)	Mean depth of coverage (×)	Coverage[c] (%)	Clade	Lineage	Gene region	Nucleotide substitution[d]	Amino acid substitution[d]
				Sex[a]	Age (yr)	Location	Symptoms	Clinical outcome								ORF14	28887: C > T	L52F
SARS-CoV-2/Philippines/AFRIMS-COVID53909	MZ068155	SRR14460623	22-Mar-21	M	24	Taguig City, National Capital Region	Fever, cough, general weakness, sore throat, vomiting	Home quarantine, stable, recovered	25.95	29,884	39	1,768	96.7	GRY	B.1.1.7	ORF1a	913: C > T	S216S
																ORF1a	3037: C > T	F924F
																ORF1a	3267: C > T	T1001I
																ORF1a	5388: C > A	A1708D
																ORF1a	5986: C > T	F1907F
																ORF1a	6954: T > C	I2230T
																ORF1a	7097: A > G	I2278V
																ORF1a	11114: G > A	G3617S
																ORF1b	Deletion 11288–11296	SGF position 3675–3677
																ORF1b	14408: C > T	P314L
																ORF1b	14676: C > T	P403P
																ORF1b	15279: C > T	H604H
																ORF1b	16176: T > C	T903T
																ORF1b	17615: A > G	K1383R
																ORF1b	19079: A > G	E1871G
																ORF1b	19854: C > T	D2129D
																S	Deletion 21765–21770	HV position 69–70
																S	Deletion 21991–21993	Y position 144
																S	23063: A > T	N501Y
																S	23271: C > A	A570D
																S	23403: A > G	D614G
																S	23604: C > A	P681H
																S	23709: C > T	T716I
																S	24506: T > G	S982A
																S	24914: G > C	D1118H
																ORF8	27972: C > T	Q27*
																ORF8	28048: G > T	R52I
																ORF8	28111: A > G	Y73C
																Nontranslation region	Deletion 28271	NA[e]
																N	28280: G > C	NA
																N	28281: A > T	D3L
																N	28282: T > A	NA
																N	28881: G > A	R203K
																N	28882: G > A	NA
																N	28883: G > C	G204R
																ORF14	28881: G > A	NA
																ORF14	28882: G > A	G50N
																ORF14	28883: G > C	NA
																N	28977: C > T	S235F
SARS-CoV-2/Philippines/AFRIMS-COVID55604	MZ068156	SRR14460622	26-Mar-21	M	28	Tanay, Rizal, Calabarzon (Region 4-A)	None	Home quarantine, stable, recovered	19.66	29,885	39	1,254	96.6	GH	B.1.351	ORF1a	1059: C > T	T265I
																ORF1a	1441: C > T	G392G
																ORF1a	3037: C > T	F924F
																ORF1a	4213: T > C	A1316A
																ORF1a	5230: G > T	K1655N
																ORF1a	10323: A > G	K3353R
																ORF1a	11812: C > A	G3849G
																ORF1b	Deletion 11288–11296	SGF position 3675–3677
																ORF1b	14408: C > T	P314L
																ORF1b	15925: C > T	L820F
																ORF1b	17970: T > C	D1501D
																S	21641: G > T	A27S
																S	21801: A > C	D80A

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TABLE 1 (Continued)

Sequence name	GenBank accession no.	SRA accession no.	Collection date (day-mo-yr)	Patient data					Ct value[b]	Genome size (bp)	GC content (%)	Mean depth of coverage (×)	Coverage[c] (%)	Clade	Lineage	Gene region	Nucleotide substitution[d]	Amino acid substitution[d]
				Sex[a]	Age (yr)	Location	Symptoms	Clinical outcome								S	22206: A > G	D215G
																S	Deletion 22281–22289	LLA position 241–243
																S	22813: G > T	K417N
																S	23012: G > A	E484K
																S	23063: A > T	N501Y
																S	23403: A > G	D614G
																S	23664: C > T	A701V
																S	23764: A > T	T734T
																ORF3a	25563: G > T	Q57H
																ORF3a	25904: C > T	S171L
																E	26456: C > T	P71L
																ORF8	28253: C > T	F120F
																N	28642: T > C	Y123Y
																N	28887: C > T	T205I
																ORF14	28887: C > T	L52F
SARS-CoV-2/Philippines/AFRIMS-COVID56628	MZ068157	SRR14460621	29-Mar-21	M	44	Tanay, Rizal, Calabarzon (Region 4-A)	Cough, fever, anosmia, diarrhea	Diagnosed with pneumonia, admitted to hospital, discharged stable	20.50	29,885	39	2,261	96.2	GH	B.1.351	ORF1a	1059: C > T	T265I
																ORF1a	2195: G > A	D644N
																ORF1a	3037: C > T	F924F
																ORF1a	4213: T > C	A1316A
																ORF1a	5230: G > T	K1655N
																ORF1a	9559: C > T	Y3098Y
																ORF1a	10323: A > G	K3353R
																ORF1a	11812: C > A	G3849G
																ORF1a	12008: C > T	L3915F
																ORF1a	12641: C > A	L4126I
																ORF1b	Deletion 11288–11296	SGF position 3675–3677
																ORF1b	14408: C > T	P314L
																ORF1b	15925: C > T	L820F
																ORF1b	17970: T > C	D1501D
																S	21641: G > T	A27S
																S	21801: A > C	D80A
																S	22206: A > G	D215G
																S	Deletion 22281–22289	LLA position 241–243
																S	22813: G > T	K417N
																S	23012: G > A	E484K
																S	23063: A > T	N501Y
																S	23403: A > G	D614G
																S	23664: C > T	A701V
																S	23764: A > T	T734T
																ORF3a	25563: G > T	Q57H
																ORF3a	25904: C > T	S171L
																E	26456: C > T	P71L
																ORF6	27213: C > T	L4L
																ORF8	28253: C > T	F120F
																ORF8	28254: A > C	I121L
																N	28642: T > C	Y123Y
																N	28887: C > T	T205I
																ORF14	28887: C > T	L52F
SARS-CoV-2/Philippines/AFRIMS-COVID58228	MZ068158	SRR14460620	7-Apr-21	M	43	Navotas City, National Capital Region	Colds, cough, anosmia, diarrhea	Home quarantine, stable, recovered	28.31	29,884	39	2,158	97.3	GRY	B.1.1.7	ORF1a	816: G > A	R184H
																ORF1a	913: C > T	S216S
																ORF1a	3037: C > T	F924F
																ORF1a	3267: C > T	T1001I
																ORF1a	5388: C > A	A1708D
																ORF1a	5986: C > T	F1907F
																ORF1a	6954: T > C	I2230T
																ORF1b	Deletion 11288–11296	SGF position 3675–3677

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TABLE 1 (Continued)

Sequence name	GenBank accession no.	SRA accession no.	Collection date (day-mo-yr)	Patient data					Ct value[b]	Genome size (bp)	GC content (%)	Mean depth of coverage (×)	Coverage[c] (%)	Clade	Lineage	Gene region	Nucleotide substitution[d]	Amino acid substitution[d]
				Sex[a]	Age (yr)	Location	Symptoms	Clinical outcome										
																ORF1b	14408: C > T	P314L
																ORF1b	14676: C > T	P403P
																ORF1b	15096: T > C	N543N
																ORF1b	15279: C > T	H604H
																ORF1b	16176: T > C	T903T
																ORF1b	16323: C > T	C952C
																S	Deletion 21765–21770	HV position 69–70
																S	Deletion 21991–21993	Y position 144
																S	**22514: T > A**	**F318N**
																S	**22515: T > A**	**F318N**
																S	**22520: G > T**	**V320F**
																S	23063: A > T	N501Y
																S	23271: C > A	A570D
																S	23403: A > G	D614G
																S	23604: C > A	P681H
																S	23709: C > T	T716I
																S	24109: C > T	L849L
																S	24506: T > G	S982A
																S	24914: G > C	D1118H
																ORF3a	25427: C > T	T12I
																ORF7a	27503: C > T	S37F
																ORF8	27972: C > T	Q27[c]
																ORF8	28048: G > T	R52I
																ORF8	28095: A > T	K68[c]
																ORF8	28111: A > G	Y73C
																Nontranslation region	Deletion 28271	NA
																N	28280: G > C	NA
																N	28281: A > T	D3L
																N	28282: T > A	NA
																N	28881: G > A	R203K
																N	28882: G > A	NA
																N	28883: G > C	G204R
																ORF14	28881: G > A	NA
																ORF14	28882: G > A	G50N
																ORF14	28883: G > C	NA
																N	28977: C > T	S235F
SARS-CoV-2/Philippines/AFRIMS-COVID58236	MZ068159	SRR14460619	7-Apr-21	M	39	Paco, Manila City, National Capital Region	Cough	Home quarantine, stable, recovered	24.47	29,884	39	1,695	97.6	GRY	B.1.1.7	ORF1a	816: G > A	R184H
																ORF1a	913: C > T	S216S
																ORF1a	3037: C > T	F924F
																ORF1a	3267: C > T	T1001I
																ORF1a	5388: C > A	A1708D
																ORF1a	5986: C > T	F1907F
																ORF1a	6954: T > C	I2230T
																ORF1b	Deletion 11288–11296	SGF position 3675–3677
																ORF1b	14408: C > T	P314L
																ORF1b	14676: C > T	P403P
																ORF1b	15096: T > C	N543N
																ORF1b	15279: C > T	H604H
																ORF1b	16176: T > C	T903T
																ORF1b	16323: C > T	C952C
																S	Deletion 21765–21770	HV position 69–70

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TABLE 1 (Continued)

Sequence name	GenBank accession no.	SRA accession no.	Collection date (day-mo-yr)	Patient data				Clinical outcome	Ct value[b]	Genome size (bp)	GC content (%)	Mean depth of coverage (×)	Coverage[c] (%)	Clade	Lineage	Gene region	Nucleotide substitution[d]	Amino acid substitution[d]
				Sex[a]	Age (yr)	Location	Symptoms									S	Deletion 21991–21993	Y position 144
																S	23063: A > T	N501Y
																S	23271: C > A	A570D
																S	23403: A > G	D614G
																S	23604: C > A	P681H
																S	23709: C > T	T716I
																S	24109: C > T	L849L
																S	24506: T > G	S982A
																S	24914: G > C	D1118H
																ORF3a	25427: C > T	T12I
																ORF7a	27503: C > T	S37F
																ORF8	27972: C > T	Q27*
																ORF8	28048: G > T	R52I
																ORF8	28095: A > T	K68*
																ORF8	28111: A > G	Y73C
																Nontranslation region	Deletion 28271	NA
																N	28280: G > C	NA
																N	28281: A > T	D3L
																N	28282: T > A	NA
																N	28881: G > A	R203K
																N	28882: G > A	NA
																N	28883: G > C	G204R
																ORF14	28881: G > A	NA
																ORF14	28882: G > A	G50N
																ORF14	28883: G > C	NA
																N	28977: C > T	S235F
SARS-CoV-2/Philippines/AFRIMS-COVID58693	MZ068160	SRR14460618	8-Apr-21	F	47	Caloocan City, National Capital Region	Fever	Home quarantine, stable, recovered	17.92	29,885	38	1,939	98.9	GH	B.1.351	ORF1a	337: C > G	R24R
																ORF1a	1059: C > T	T265I
																ORF1a	3037: C > T	F924F
																ORF1a	4213: T > C	A1316A
																ORF1a	5230: G > T	K1655N
																ORF1a	10323: A > G	K3353R
																ORF1a	11812: C > A	G3849G
																ORF1b	Deletion 11288–11296	SGF position 3675–3677
																ORF1b	14408: C > T	P314L
																ORF1b	15925: C > T	L820F
																ORF1b	17970: T > C	D1501D
																S	21641: G > T	A27S
																S	21801: A > C	D80A
																S	22206: A > G	D215G
																S	Deletion 22281–22289	LLA position 241–243
																S	22813: G > T	K417N
																S	23012: G > A	E484K
																S	23063: A > T	N501Y
																S	23403: A > G	D614G
																S	23664: C > T	A701V
																S	23764: A > T	T734T
																ORF3a	25563: G > T	Q57H
																ORF3a	25904: C > T	S171L
																E	26456: C > T	P71L
																ORF8	28253: C > T	F120F
																N	28642: T > C	Y123Y
																N	28887: C > T	T205I
																ORF14	28887: C > T	L52F

(Continued on next page)

TABLE 1 (Continued)

Sequence name	GenBank accession no.	SRA accession no.	Collection date (day-mo-yr)	Patient data					Ct value[b]	Genome size (bp)	GC content (%)	Mean depth of coverage (×)	Coverage[c] (%)	Clade	Lineage	Gene region	Nucleotide substitution[d]	Amino acid substitution[d]
				Sex[a]	Age (yr)	Location	Symptoms	Clinical outcome										
SARS-CoV-2/Philippines/AFRIMS-COVID58620	MZ068161	SRR14460626	8-Apr-21	F	26	Indang, Cavite, Calabarzon (Region 4-A)	None	No data	23.26	29,903	39	1,961	98.5	GH	B.1.351	ORF1a	1059: C > T	T265I
																ORF1a	3037: C > T	F924F
																ORF1a	4213: T > C	A1316A
																ORF1a	5230: G > T	K1655N
																ORF1a	10323: A > G	K3353R
																ORF1a	11812: C > A	G3849G
																ORF1a	12159: A > G	E3965G
																ORF1b	Deletion 11288–11296	SGF position 3675–3677
																ORF1b	14408: C > T	P314L
																ORF1b	15925: C > T	L820F
																ORF1b	17970: T > C	D1501D
																S	21641: G > T	A27S
																S	21801: A > C	D80A
																S	22206: A > G	D215G
																S	Deletion 22281–22289	LLA position 241–243
																S	22813: G > T	K417N
																S	23012: G > A	E484K
																S	23063: A > T	N501Y
																S	23403: A > G	D614G
																S	23664: C > T	A701V
																S	23764: A > T	T734T
																ORF3a	25546: C > T	L52F
																ORF3a	25563: G > T	Q57H
																ORF3a	25904: C > T	S171L
																E	26456: C > T	P71L
																ORF8	28253: C > T	F120F
																N	28642: T > C	Y123Y
																N	28887: C > T	T205I
																ORF14	28887: C > T	L52F

[a] M, male; F, female.
[b] Ct, threshold cycle.
[c] The strain Wuhan-Hu-1 (GenBank accession no. NC_045512.2) reference genome was used for estimation of the horizontal coverage.
[d] Unique mutations are in bold.
[e] NA, not applicable.

suggests sustained, increasing community transmission and high numbers of these variants in the National Capital Region (NCR) starting in early March 2021. Both the B.1.351 and B.1.1.7 variants have been associated with increased transmissibility (13, 14), reduced neutralizing titers, reduced vaccine efficacy (15–21), and significantly higher adjusted odds ratio for hospitalization and intensive care admission (22). We compared the S gene mutations in our sequences with 542,800 B.1.1.7 and 14,359 B.1.351 GISAID sequences accessed on 8 May 2021 using outbreak.info (23), and one of our B.1.1.7 sequences (MZ068158) contained two unique mutations, F318N and V320F. The F318N mutation was located in an unknown function region between the N-terminal domain and the receptor binding domain, while the V320F mutation was located in the receptor binding domain in the S1 subunit. The surge of COVID-19 cases starting in early March 2021 (24) in the NCR may be explained by the circulation of these variants in addition to the relaxation of quarantine measures, increased mobility of the population, and lower compliance with health standards. Informed consent was obtained from the patients for SARS-CoV-2 real-time RT-PCR (rRT-PCR) testing and sequencing. The sample collection was considered a public health effort and did not require an institutional review board-approved human use protocol.

Data availability. The SARS-CoV-2 genome sequences from the Philippines were deposited in the GenBank database (accession no. MZ068151 to MZ068161). The raw reads have been deposited in the NCBI Sequence Read Archive (SRA accession no. SRR14460618 to SRR14460628). The BioProject accession number is PRJNA726840. The BioSample accession numbers are SAMN18976036 to SAMN18976046.

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