## **Abstract**

## **COVID-19 Variant Surveillance Study in the Republic of Korea**

Kim II-Hwan, Park Ae Kyung, Kim Jeong-Min, Kim Heui Man, Lee Nam-Joo, Woo SangHee, Lee Chae young, Lee Jaehee, Rhee JeeEun, Kim Eun-Jin Division of Emerging Infectious Diseases, Bureau of Infectious Diseases Diagnosis Control, Korea Disease Control and Prevention Agency (KDCA)

Recently, the coronavirus disease (COVID-19) virus variants originating in the United Kingdom (UK), South Africa, and Brazil are spreading all over the world, and the variants are known to be different from non-variants in their transmissibility and immune effect. Accordingly, the World Health Organization (WHO) recommended public health measures for variants and proposed working definitions of a variant of concern (VOC) and a variant of interest (VOI).

The Korea Disease Control and Prevention Agency (KDCA) has been continuously monitoring the genotype and the variations of COVID-19 virus through whole genome sequencing analysis from the outbreak of COVID-19 in January 20, 2020, to the present. As a result, 162 VOCs originating from the UK (138), South Africa (18), and Brazil (6) and 61 VOIs originating from California, USA (55), New York, USA (3) and the UK/Nigeria (3). were identified early, and the genome information of the variants confirmed through surveillance were shared in the GISAID DB for international cooperation. To cope with the continuing spread of COVID-19 variants, the KDCA is continuing to strengthen its surveillance system by expanding its analysis capacity. This report was intended to help establish countermeasures to prevent the spread of variants by providing information on the characteristics of variants occurring at domestic and overseas, and the results of domestic surveillance.

**Keywords:** Coronavirus disease (COVID-19), Virus variant, Whole genome sequencing analysis

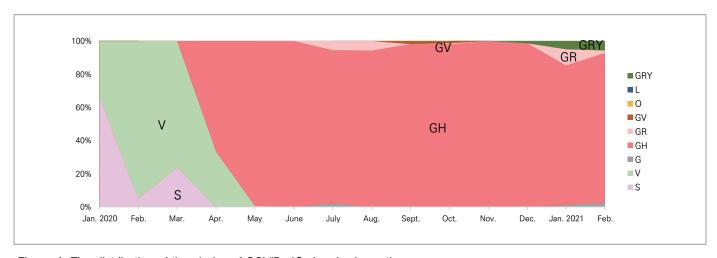


Figure 1. The distribution of the clades of COVID-19 virus in domestic cases

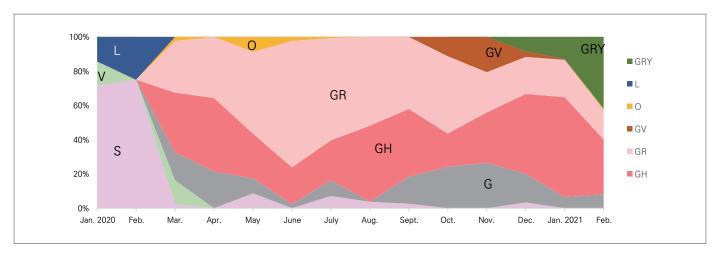


Figure 2. The distribution of the clades of COVID-19 virus in imported cases

Table 1. The occurrence status of COVID-19 variants in the Republic of Korea (As of March 1st, 2021)

	No. of _	Variant of Concern (VOC)				Variant of Interest (VOI)			
		Total	501Y.V1	501Y.V2	501Y.V3	Total	452R.V1	B.1.526	484K.V3
Total	1,516	162 (10.7%) <sup>-</sup>	138 (9.1%)	18 (1.2%)	6 (0.4%)	61 (4.0%)	55 (3.6%)	3 (0.2%)	3 (0.2%)
Dec. 2020	495	16 (3.2%)	15 (3.0%)	1 (0.2%)	0 (0.0%)	14 (2.8%)	14 (2.8%)	0 (0.0%)	0 (0.0%)
Jan. 2021	551	67 (12.2%)	51 (9.3%)	10 (1.8%)	6 (1.1%)	20 (3.6%)	20 (3.6%)	0 (0.0%)	0 (0.0%)
Feb. 2021	470	79 (16.8%)	72 (15.3%)	7 (1.5%)	0 (0.0%)	27 (5.7%)	21 (4.5%)	3 (0.6%)	3 (0.6%)

<sup>\*</sup> Confirmation rate of variants = (No. of variants / No. of Samples)  $\times 100$ 

Table 2. The routes in which the COVID-19 variants were identified in the Republic of Korea (As of March 1st, 2021)

		Route	No. of Variants	Countries
Variant of Concern (VOC)	501Y.V1 (138)	Imported	104	Total 21 countries: Hungry (28), United Kingdom (18), Ghana (10), UAE (9), Poland (9), Jordan (7), USA (5), Serbia (3), Pakistan (2), Iraq (2), Maldives (1), Nigeria (1), Norway (1), France (1), China(1), Slovakia (1), Libya (1), Ethiopia (1), Germany(1), Russia (1), Philippines (1)
		Domestic	34	-
	501Y.V2	Imported	17	Total 7 countries: Tanzania (7), UAE(4), South Africa (2), Zimbabwe (1), Malawi (1), Zambia (1), USA (1)
	(18)	Domestic	1	-
	501Y.V3	Imported	6	Total 3 countries: Brazil (4), Canada (1), Saudi Arabia (1)
	(6)	Domestic	0	-
	452R.V1	Imported	23	Total 2 countries: USA (21), Mexico (2)
	(55)	Domestic	32	-
Variant of Interest	B.1.526	Imported	3	Total 1 country: USA (3)
(VOI)	(3)	Domestic	0	_
	484K.V3	Imported	3	Total 1 country: Nigeria (2), Sudan (1)
	(3)	Domestic	0	-