

Summary of Study

July 11, 2022 (Rev.0)

***In silico* analysis of SARS-CoV-2 variant
(BA.4, BA.5)**

This study was conducted for analyzing detectability of the GenBody COVID-19 Ag Home Test for SARS-CoV-2 Omicron subvariant BA.4 and BA.5 by in silico analysis. This study was performed with NCBI reference sequence (accession no.: NC_045512 and Global Initiative for Sharing All Influenza Data (GISAID) variant sequence.

1. Reference of variant and standard

Virus Detail	
Virus name	Severe acute respiratory syndrome coronavirus 2 isolate Wuhan-Hu-1 (NCBI reference sequence)
Accession ID	NCBI, NC_045512

Virus Detail (Omicron sub-variant, BA.4)	
Virus name	hCoV-19/USA/IN-CDC-LC0739294/2022
Accession ID	GISAID, EPI_ISL_13720917
Type	betacoronavirus
Clade	GRA
Pango Lineage	BA.4 (Pango v.4.1.1 PLEARN-v1.11), Omicron (BA.4-like) (Scorpio)

Virus Detail (Omicron sub-variant, BA.5)	
Virus name	hCoV-19/USA/IN-CDC-LC0739243/2022
Accession ID	EPI_ISL_13721095
Type	betacoronavirus
Clade	GRA
Pango Lineage	Unassigned (Pango 4.1 PLEARN-v1.11) - last assigned as BA.5 (Pango v.4.1.1 PANGO-v1.11), Omicron (BA.5-like) (Scorpio)

2. Alignment Result

2.1. Sequence alignment of BA.4 variant

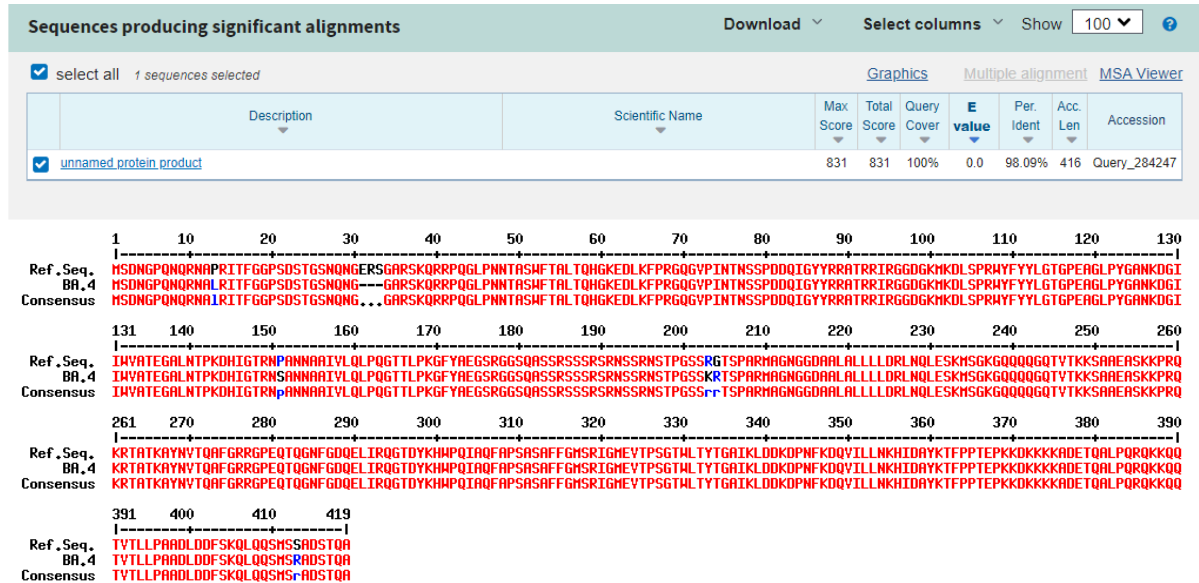
Sequence ID: Query_284247 Length: 416

Range 1: 1 to 416

Score:831 bits(2147), Expect:0.0,

Method: Compositional matrix adjust.,

Identities:411/419(98%), Positives:412/419(98%), Gaps:3/419(0%)



Upper (Ref): Nucleocapsid amino acid sequences which were identical to GenBody COVID-19 Ag's target.

Lower (BA.4): Nucleocapsid amino acid sequences of BA.4

Red: Identical, Blue: Unmatched

Amino acid substitutions is described as below;

→ N P13L, N E31del, N R32del, N S33del, N P151S, N R203K, N G204R, N S413R,

2.2. Sequence alignment of BA.5 variant

Sequence ID: Query_485489 Length: 416

Range 1: 1 to 416

Score:833 bits(2153), Expect:0.0,

Method:Compositional matrix adjust.,

Identities:412/419(98%), Positives:413/419(98%), Gaps:3/419(0%)

Sequences producing significant alignments		Download	Select columns	Show	100																																																																																																																																																																																																																																			
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Upper (Ref): Nucleocapsid amino acid sequences which were identical to GenBody COVID-19 Ag's target.

Lower (BA.5): Nucleocapsid amino acid sequences of BA.5

Red: Identical, Blue: Unmatched

Amino acid substitutions is described as below;

→ N P13L, N E31del, N R32del, N S33del, N R203K, N G204R, N S413R

3. Discussion

SARS-CoV-2 is a (+)ssRNA virus that is highly mutated, and many variants have been generated. The WHO designated SARS-CoV-2 as Variants of Interest (VOIs), Variants of Concern (VOCs) and Variants under monitoring (VUM) depending on the transmissibility, virulence and risk posed to global public health. BA.4 and BA.5 are Omicron subvariants and omicron is VOC currently. These public health threats were mainly caused by mutations in the spike protein related to immune evasion or increased infectivity. Amino acid mutations also appear in the case of the nucleocapsid protein (Fig. 1), which binds to the genomic RNA of the virus, but with a lower frequency of mutations than in the spike protein.

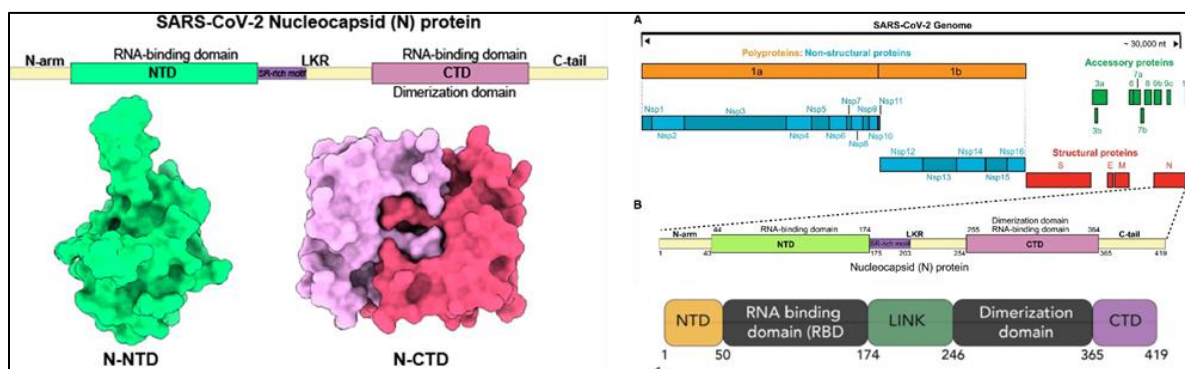


Fig 1. Genome organization of coronavirus and the domain composition of the SARS-CoV-2 nucleocapsid (N) protein.¹

It is known that the BA.4 variant differs in one amino acid sequence from the NP compared to the BA.2 variant, and the BA.5 variant is known as the NP sequence that is not different from the BA.2 variant (Fig. 2).

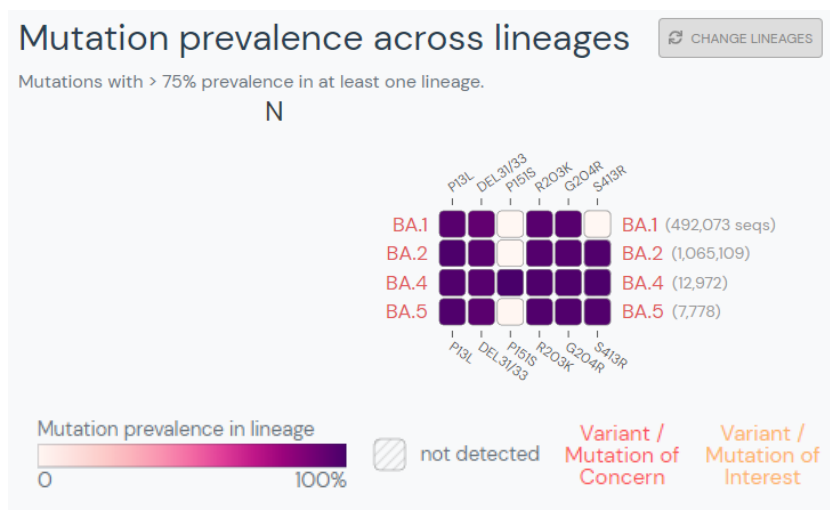


Fig 2. Amino acids variation of SARS-CoV-2 Omicron sub-variant at nucleocapsid protein.²

¹ Ref: Peng, Ya, et al. "Structures of the SARS-CoV-2 nucleocapsid and their perspectives for drug design." *The EMBO Journal* 39.20 (2020): e105938.

² Ref: <https://outbreak.info/>

4. Conclusion

GenBody COVID-19 Ag, GenBody COVID-19 Ag Home Test, GenBody Influenza/COVID19 Ag Triple, and GenBody FIA COVID-19 Ag were developed using with the same mouse monoclonal antibody pair. GenBody has completed the evaluation of the detection ability for Omicron sub-variant BA.2 using the COVID-19 Ag kit. There was no significant differences between standard strain isolated at Korea for the first time and BA.2 variant when tested with GenBody COVID-19 Ag Kit. Accordingly, it is presumed that the GenBody COVID-19 Ag, GenBody COVID-19 Ag Home Test, GenBody Influenza/COVID-19 Ag Triple, and GenBody FIA COVID-19 Ag have no significant problem when detecting Omicron sub-variant (BA.4, BA.5).