

**Genom and Gene Mutation of SARS-CoV-2 Edy Parwanto\***

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**Abstract**

The SARS-CoV-2 genome consists of the: 5' UTR, ORF 1ab gene, S gene, ORF 3a gene, E gene, M gene, ORF 6 gene, ORF 7a gene, ORF 7b gene, ORF 8 gene, N gene, ORF 10 gene and 3' UTR. Gene mutations in SARS-CoV-2 can occur in all genes that make up the genome of SARS-CoV-2. Due to mutations in the SARS-CoV-2 gene, various variants of SARS-CoV-2 appear. Several variants of SARS-CoV-2 recorded since December 2020 include of B.1.1.7, B.1.351, B. 1.429, B.1.1.28, B.1.617 and B.1.618 variants. Due to the emergence of various variants of SARS-CoV-2, we must be more careful to avoid COVID-19. People who have co-morbidities of COVID-19 should be more careful to avoid COVID-19. We must continue to apply health protocols at the community level to prevent the transmission of SARS-CoV-2

**Keywords:** SARS-CoV-2; Genom of SARS-CoV-2; Gene mutation; COVID-19

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**Letter**

It has been stated that the COVID-19 pandemic is caused by the corona virus (2019-nCoV) or severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) [1]. We first need to understand the structure of the SARS-CoV-2 genome that is causing the COVID-19 pandemic. In the review, the SARS-CoV-2 genome contained 29.903 nucleotides (nt). The SARS-CoV-2 genome consists of the: 5' UTR, ORF 1ab gene, S gene, ORF 3a gene, E gene, M gene, ORF 6 gene, ORF 7a gene, ORF 7b gene, ORF 8 gene, N gene, ORF 10 gene and 3' UTR [2]. The 5' UTR consists of 265 nt, is a non-coding sequence. The ORF 1ab gene consists of 21.290 nt which encodes the ORF1a polyprotein and the ORF1ab polyprotein. The ORF 1ab gene ID is 43740578 (updated on 3<sup>rd</sup> January 2021 at <https://www.ncbi.nlm.nih.gov/gene/43740578>). The S gene consists of 3.822 nt which encodes the surface glycoprotein. The S gene ID is 43740568 (updated on 3<sup>rd</sup> January 2021 at <https://www.ncbi.nlm.nih.gov/gene/43740568>). The ORF 3a gene consists of 828 nt which encodes of ORF 3a protein. The gene ID of ORF 3a gene is 43740569 (updated on 3<sup>rd</sup> January 2021 at <https://www.ncbi.nlm.nih.gov/gene/43740569>). The E gene consists of 228 nt which encodes of envelope protein. The gene ID of E gene is 43740570 (updated on 3<sup>rd</sup> January 2021 at <https://www.ncbi.nlm.nih.gov/gene/43740570>). The M gene consists of 669 nt which encodes of membrane glycoprotein. The gene ID of M gene is 43740571 (updated on 3<sup>rd</sup> January 2021 at <https://www.ncbi.nlm.nih.gov/gene/43740571>). The ORF 6 gene consists of 186 nt which encodes of ORF 6 protein (viral accessory protein). The gene ID of ORF 6 gene is 43740572 (updated on 3<sup>rd</sup> January 2021 at <https://www.ncbi.nlm.nih.gov/gene/43740572>). The ORF 7a gene consists of 366 nt which encodes of ORF7a protein (viral accessory protein). The gene ID of ORF 7a gene is 43740573 (updated on 3<sup>rd</sup>

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January 2021 at <https://www.ncbi.nlm.nih.gov/gene/43740573>). The ORF 7b gene consists of 132 nt which encodes of ORF 7b protein (viral accessory protein). The gene ID of ORF 7b gene is 43740574 (updated on 3<sup>rd</sup> January 2021 at <https://www.ncbi.nlm.nih.gov/gene/43740574>). The ORF 8 gene consists of 193 nt which encodes of ORF 8 protein. The gene ID of ORF 8 gene yaitu 43740577 (updated on 3<sup>rd</sup> January 2021 at <https://www.ncbi.nlm.nih.gov/gene/43740577>). The N gene consists of 908 nt which encodes of nucleocapsid phosphoprotein. The Gene ID of N gene is 43740575 (updated on 3<sup>rd</sup> January 2021 at <https://www.ncbi.nlm.nih.gov/gene/43740575>). The ORF 10 gene consists of 117 nt which encodes of ORF 10 protein. The gene ID of ORF 10 is 43740576 (updated on 3<sup>rd</sup> January 2021 at <https://www.ncbi.nlm.nih.gov/gene/43740576>). The 3' UTR consists of 229 nt which is non-coding sequence.

We know that gene mutations in SARS-CoV-2 can occur in all genes that make up the genome of SARS-CoV-2. Due to mutations in the SARS-CoV-2 gene, various variants of SARS-CoV-2 appear. Several variants of SARS-CoV-2 recorded since December 2020 include of B.1.1.7, B.1.351, B. 1.429, B.1.1.28, B.1.617 and B.1.618 variants.

The B.1.1.7 variant of SARS-CoV-2 was formerly known as VUI-202012/01 (Variant Under Investigation-2020-month 12/variant 01). The B.1.1.7 variant debuted in the UK in December 2020 [3]. Subsequently, the B.1.1.7 variant was known as 20V/501Y.V1 [4] with mutation characteristics 69-70 del, 145 del, N501Y, A570D,

D614G, P681H, T716I, S982A and D1118H [5]. The B.1.1.7 variant has a fast spreading rate [4] and increases the risk of death by 30% [6].

The B.1.351 variant was first discovered in South Africa [7]. The B.1.351 variant is here in after known as the 20H/501Y.V2 variant. Mutation characteristics of B.1.351 variant include D80A, D215G, K417N, E484K, N501Y, D614G and A701V [5]. It has also been reported that B.1.351 variant has a significantly greater affinity for the ACE2 receptor compared with the SARS-CoV-2 that caused COVID-19 outbreak in Wuhan, China [8].

The B.1.429 variant was first discovered in California, USA. Mutation characteristic of B.1.429 variant occurs in the ORF 1a, ORF 1b and S genes. Mutation of I4205V occurs in the ORF1a gene, D1183Y occurs in the ORF1b gene and S13I, W152C, L452R occurs in the S gene [5]. It was reported that the B.1.429 variant had a rapid deployment in the United States [9].

The B.1.1.28 variant also known as P.1. variant. These variant discovered in North Brazilia [10]. The B.1.1.28 variant also identification in Japan, and known as 20 J/501Y.V3. Characteristic of B.1.1.28 variant has gene mutation such as L18F, T20N, P26S, D138Y, R190S, K417T, E484K, N501Y, D614G, H655Y, T1027I and V1176F. Further also reported that a sample of someone returning from Africa to Japan in March 2021 who were positive for SARS-CoV-2 with the D614G mutation [5]. In addition, a variant with D614G mutation in the S gene of SARS-CoV-2 has also been reported in Pakistan [11].

## References

- 1 Parwanto MLE (2020) Virus Corona (2019-nCoV) Penyebab COVID-19. *J Biomed Kes* 3:1-2.
- 2 Khailany RA, Safdar M, Ozaslan M (2020) Genomic characterization of a novel SARS-CoV-2. *Gene Reports* 19:1-6.
- 3 New and Emerging Respiratory Virus Threats Advisory Group (NERVTAG) (2020) NERVTAG meeting on SARS-CoV-2 variant under investigation VUI-202012/01.
- 4 Rambaut A, Loman N, Pybus O, Barclay W, Barrett J, et al. (2021) Preliminary genomic characterisation of an emergent SARS-CoV-2 lineage in the UK defined by a novel set of spike mutations. *ARTIC Network*.
- 5 Hirotsu Y, Omata M (2021) Discovery of a SARS-CoV-2 variant from the P.1 lineage harboring K417T/E484K/N501Y mutations in Kofu, Japan. *J Infect* 82:276-316.
- 6 Horby P, Huntley C, Davies N, Edmunds J, Ferguson N, et al. (2021) Paper from the New and Emerging Respiratory Virus Threats Advisory Group (NERVTAG) on new coronavirus (COVID-19) variant B.1.1.7.
- 7 Tegally H, Wilkinson E, Giovanetti M (2020) Emergence and rapid spread of a new severe acute respiratory syndrome-related coronavirus 2 (SARS-CoV-2) lineage with multiple spike mutations in South Africa. *MedRxiv*.
- 8 Zhou D, Dejnirattisai W, Supasa P, Liu C, Mentzer AJ, et al. (2021) Evidence of escape of SARS-CoV-2 variant B.1.351 from natural and vaccine-induced sera. *Cell* 189: 2348-2361.

Variants of B.1.617 and B.1.618 have been identified in India. The two variants are a concern in the development of COVID-19 cases in India [12]. The B.1.617 variant has mutation characteristics in the S gene, namely: L452R, E484Q, D614G. In addition to the B.1.617 variant, also identified the B.1.617.1 variant with characteristics of mutations in the S gene are T95I, G142D, E154K, L452R, E484Q, D614G, P681R and Q1071H. Beside that, another variant was first detected in India, namely the B.1.617.2 variant (delta variant) [13]. Mutation characteristic of B.1.618 variant such as  $\Delta$ 145-146, E484K and D614G [14].

The appearance of SARS-CoV-2 variants that mentioned above, We have to be more careful to avoid COVID-19. People who have comorbidities of COVID-19 include diabetic ketoacidosis and hypertension [15], heart disease [16], as well as diabetes mellitus and hypertension [17] to be more careful to avoid COVID-19. We have also written about the importance of implementing health protocols at the community level to prevent the transmission of SARS-CoV-2 [18].

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## Competing Interests

We declare that there is no conflict of interest in the writing of this paper. The author completed the ICMJE form, download from <http://www.icmje.org/disclosure-of-interest/>

- 9 Washington NL, Gangavarapu K, Zeller M, Bolze A, Cirulli ET, et al. (2021) Genomic epidemiology identifies emergence and rapid transmission of SARS-CoV-2 B.1.1.7 in the United States. *Med Rxiv*.
- 10 Faria NR, Claro IM, Candido D, PreteJR CA, Crispim MAE, et al. (2020) Genomic characterisation of an emergent SARS-CoV-2 lineage in Manaus: preliminary findings. *Virological* 397: P452-455.
- 11 Umair M, Ikram A, Salman M (2021) Whole-genome sequencing of SARS-CoV-2 reveals the detection of G614 variant in Pakistan. *PLoS ONE* 16: e0248371.
- 12 Singh J, Rahman SA, Ehtesham NZ, Hira S, Hasnain SE (2021) SARS-CoV-2 variants of concern are emerging in India. *Nat Med*.
- 13 CDC (2021) SARS-CoV-2 Variant Classifications and Definitions.
- 14 Tada T, Zhou H, Dcosta BM, Samanovic MI, Mulligan MJ, et al. (2021) The spike proteins of sars-cov-2 b.1.617 and b.1.618 variants identified in india provide partial resistance to vaccine-elicited and therapeutic monoclonal antibodies. *BioRxiv*.
- 15 Parwanto MLE, Digambiro RA, Nusantara DU, Rarasati T (2020) Coronavirus disease 2019 (COVID-19): A case report in a patient with diabetic ketoacidosis and hypertension. *Bali Med J* 9: 520-526.
- 16 Parwanto MLE (2020) People with Heart Disease have to be more Vigilant so as to Avoid COVID-19. *Health Sci J Spiss*:1-2.
- 17 Parwanto MLE, Guyansyah A (2020) Hello Indonesia, Be Careful with COVID-19 in the Elderly with Hypertension and Diabetes Mellitus. *Clinics Mother Child Health* 17:369.
- 18 Parwanto E (2021) Response to mutation and variants of the SARS-CoV-2 gene. *Universa Medicina* 40: 77-78.