

**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 3rd 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 3rd 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 3rd 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 3rd 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 3rd 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 3rd 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 3rd January

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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 3rd 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 3rd January 2021 at <https://www.ncbi.nlm.nih.gov/gene/43740577>). The N gene consists of 908 nt which encodes of nucleocapsidphosphoprotein. The Gene ID of N gene is 43740575 (updated on 3rd 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 3rd 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-month12/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 hereinafter 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, Prete Jr 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 Spss*: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.