

## SARS-CoV-2: Genome, New Variant and Risk of Infection in Immunized Individuals

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### ABSTRACT

The COVID-19 outbreak was caused by SARS-CoV-2. This situation is concerning because it has created uncertainty and has become a world problem. Regarding the COVID-19 outbreak, a genomic analysis of SARS-CoV-2 has been carried out. The genome of SARS-CoV-2 contains 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. It has been reported about the discovery of a new variant namely B.1.1.7 (20I/501Y.V1), B.1.351 (20H/501Y.V2), B.1.429 (452R.V1), P.1-lineage (20J/501Y.V3). Consequently, the presence of the new variant of SARS-CoV-2 described above affects the risk of infection in immunized individuals.

**Keywords:** COVID-19; SARS-CoV-2; Mutation; New variant of SARS-CoV-2

## DESCRIPTION

The COVID-19 outbreak was caused by SARS-CoV-2 [1]. This situation is concerning because it has created uncertainty and has become a world problem. It has become a reality that as a result of the COVID-19 pandemic, many people have died. Victims who died due to COVID-19 occurred both in people who had comorbidities and those who did not have comorbidities. Therefore, people who have comorbidities to COVID-19, including diabetes ketoacidosis and hypertension [2], and heart disease [3] should be more careful to avoid being infected with SARS-CoV-2. A special message for the elderly who suffer from hypertension and diabetes mellitus must also be careful to avoid COVID-19 [4]. Of course the warning "be more careful to avoid COVID-19" not only for people with comorbidities described above, but also for people with other comorbidities.

Regarding the COVID-19 outbreak, a genomic analysis of SARS-CoV-2 has been carried out. The genome of SARS-CoV-2 contains 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 [5]. During the COVID-19 pandemic, the genes of SARS-CoV-2 had mutated to produce new variants. A new variants of SARS-CoV-2 has been

detected in several countries, including, UK [6], South Africa [7] and USA [8].

It has been reported about the discovery of a new variant namely B.1.1.7 or variants below investigation, 2020, month 12, variant 01 (VUI 202012/01) in UK on 18 December 2020 [6]. One of the mutations that produced the new variant of SARS-CoV-2 had an N501Y mutation in the spike protein. The new variant may be associated with the recent rise in cases in southeast England. Even so it is stated that the new variant of SARS-CoV-2 which is more contagious does not necessarily make it more dangerous. It is further stated that a number of new variants have been detected in the UK, for example the D614G variant [9]. Then it was reported that there is an increase in the proportion of VUI-202012/01 with the number of SARS-CoV-2 isolates in the UK (as of 20 December 2020) [10]. Furthermore, the variant B.1.1.7 was known as 20I/501Y.V1. And also referred to as Variant of Concern 202012/01 (VOC-202012/01) [11,12]. It was further reported that the D614G variant was also discovered during the COVID-19 outbreak in the first and second waves in Hiroshima, Japan [13].

In addition to the variant of B.1.1.7 or 20I/501Y.V1, has also been reported the 501Y.V2 variant of SARS-CoV-2. The 501Y.V2 variant has 8 gene mutations in the spike protein. The variant of 501Y.V2 emerged in South Africa [7], and then

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known as 20H/501Y.V2 or B.1.351.[14]. Apart from the two variants of SARS-CoV-2 earlier, another variant of SARS-CoV-2 has been identified successfully, namely B.1.429. The B.1.429 variant also known as CAL.20C or 452R.V1 and has been identified in California, USA. There are 5 mutations in ORF1a as a feature of B.1.429 variant. The mutations are: I4205V, ORF1b: D1183Y, S: S13I; W152C; L452R [8].

Another variant reported as P.1-lineage (known as 20J/501Y.V3 variant) is the result of the B.1.1.28 mutation. These mutations occur in the spike protein receptor binding domains, namely: K417T, E484K, and N501Y. The 20J/501Y.V3 variant was first reported by the National Institute of Infectious Diseases (NIID) in Japan. Samples that containing the 20J/501Y.V3 variant were obtained from four Brazilians travelers [14]. The new variant has been confirmed as reinfection in Brazil [15]. We know that the B.1.617.2 variant of SARS-CoV-2 increased the number of COVID-19 cases in India. Today, this variant is detected almost all over the world [16].

Consequently, the presence of the new variant of SARS-CoV-2 described above affects the risk of infection in immunized individuals [17]. To fight the COVID-19 pandemic, currently many people have been vaccinated. Several types of vaccines have been tested for their effectiveness to neutralize SARS-CoV-2 [18-21].

## TAKE HOME MESSAGE

In the current situation of the COVID-19 pandemic, we must be aware of the emergence of a new variant of SARS-CoV2. New variants of SARS-CoV-2 have increased the number of COVID-19 cases in several countries. In addition, the emergence of a new variant of SARS-CoV-2 also has an effect on the risk of infection for individuals who have been vaccinated against COVID-19. Therefore, we must remain vigilant against SARS-CoV-2 variants; continue to carry out health protocols and a healthy lifestyle to avoid COVID-19.

## CONFLICT OF INTEREST

The author declares that there is no conflict of interest.

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