

## Mutations of SARS-CoV-2

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### Editorial Note

Mutation is a transformation in the nucleotide sequence of the genome of a virus when they are exposed to environmental selection pressures. This influences the enhancement of virulence variants that mutate and evolve. The mutation rate of ssRNA viruses is found to be much greater than the organisms that possess ssDNA and several times higher than those with dsDNA. Research says that in most cases, mutations are actually detrimental or inconsequential and only few necessarily increase virulence. As a result, organisms must find a balance between high mutation rates in order to adapt to changing environmental conditions, and a low one that reduces the incidence of catastrophic mutations. Small DNA viruses can encode to repair their own DNA. Although DNA viruses typically rely on transcription machines for the host cell. Some RNA viruses also share the ability to verify and correct replication errors and also encode their own transcription unit, which ensures their reproduction. As their degree of mutation is more specifically related to their own genome and is subject to the same forces of evolution.

Generally the RNA virus with genomes usually falling within a range of 7-12 kb in length and it appears to have one or two distinct mutations per nucleotide site. But Extreme acute respiratory syndrome coronavirus-2 (SARS-CoV-2) genome is believed to be between 27-31 kb in length and even increase the total number of mutations gained, without actually increasing the occurrence rate. As it has the ability to easily develop new genetic traits makes it possible for new viruses to evolve in the host system and escape immunity caused by vaccination, and becoming more virulent. SARS-CoV-2 uses the spike protein to interact with ACE2 receptors in the organism. This consists of two subunits, the first of which forms the domain that binds the receptor.

Especially with the replacement of asparagine amino acid with tyrosine at position 5011. Therefore, the mutation is called N501Yit occur in B.1.1.7 lineage. In comparison, the strain also indicates that amino acids 69 and 70 are deleted. Often seen in other strains to emerge spontaneously and inducing a conformational modification of the protein spike and the improved transmissibility is correlated with this version. Compared to other variants, it was associated with an increased risk of mortality. P681H: a region of increased heterogeneity in coronaviruses near the S1/S2 furin cleavage site. This mutation has spontaneously arisen many times as well.

SARS has had a very significant influence on culture. Tension has risen in the city throughout the early phase of the SARS epidemic. Due to a lack of accurate official statistics, there are folk stories about the disease condition spread by word of mouth, short texts from cell phones, transmission of social media, among other means. Not only did the SARS outbreak do considerable damage to the physical and mental health of individuals, but also to the economy. SARS had a huge influence on tourism and its associated sectors and further they can lead to serious infection, marked by high fever, severe respiratory symptoms and death, and there are no clear antiviral medications and vaccines available for them. A significant public health problem is infections caused by these viruses. They are a big cause of death and have negative socio-economic ramifications that are constantly compounded. They are a big cause of death and have negative socio-economic ramifications that are constantly compounded. Therefore, there is a need to improve potential recovery initiatives and alternatives.