# SARS-CoV-2 variants – molecular properties, virulence, and epidemiology

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## Abstract

SARS-CoV-2 are enveloped RNA viruses that belong to the family Coronaviridae of genus Beta coronavirus, responsible for the COVID-19 pandemic. The mutation rate is high among RNA viruses and in particular, coronavirus replication is error prone with an estimated mutation rate of $4x10^{-4}$ nucleotide substitutions per site per year. Different variants of SARS-CoV-2 have been reported from various countries including United Kingdom, South Africa, Denmark and Brazil. These variants were evolved due to mutations on spike gene responsible for the synthesis of spike (S) protein of SARS-CoV-2. These variants / lineages from different countries were designated as cluster 5 or SARS-CoV-2 variant of Denmark, B.1.351 lineages or 501.V2 variant or SARS-CoV-2 variant of South Africa, lineage B.1.1.248 or lineage P.1 of Brazil and lineage B.1.1.7 or Variant of Concern (VOC) 202012/01 from United Kingdom. Due to mutations in S gene, the variants acquired changes in S protein resulting in increased transmissibility of the mutated virus. As on date, alterations in virulence or pathogenicity have been reported from these lineages, from many parts of the globe. In our opinion, since the S protein is significantly altered, the suitability of existing vaccine targeting the S protein of SARS-CoV-2 variants is a major concern. We also presume that the mutations in SARS-CoV-2 is a continuous and evolving process that may result in the transformation of naïve SARS-CoV-2 into totally new subsets of antigenically different SARS-CoV-2 viruses over a period of time.

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