Classifications of Variants in COVID-19

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About the Study

The novel coronavirus disease (COVID-19), caused by severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2), still remains a global challenge. Genetic variations of SARS-CoV-2 have been developing and spreading across the world throughout the COVID-19 pandemic. SARS-CoV-2 is highly contagious, so application of preventive methods, sensitive diagnostic approaches, and using current available drugs was initially practiced till the development of novel treatment. Only real-world experience can offer answers on the effectiveness of COVID-19 vaccinations against disease and mortality from SARS-CoV-2 variations without immunological correlates of protection.

The sequence-based monitoring as well as laboratory research and epidemiological studies routinely monitors viral mutations and variations. The three classes of SARS-CoV-2 variants developed by a US government interagency group effectively classify the variants as:

Variant of interest

Variation of particular genetic markers linked with alterations in receptor binding, reduced neutralization by antibodies generated against previous infection or vaccination, reduced therapeutic effects, potentially diagnostic impacts, or anticipated increased transmissibility or severity of disease. Possible attributes of a variant of interest include specific genetic markers expected to impact