



Global Analysis of Tracking the Evolution of SARS-CoV-2 Variants

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Message from the Guest Editor

SARS-CoV-2, a positive-sense β -coronavirus, is the etiological agent of COVID-19. Although it possesses an error-prone viral RNA-dependent RNA polymerase with limited 3'-5' exoribonuclease activity, it can cause progeny viruses with new mutations, affecting its infectivity, transmissibility, and virulence. Moreover, recently, a sharp decline in PCR testing due to high cost and reliance on antigen testing kits could lead to the potential underreporting of new emerging variants. Therefore, the continuous monitoring and tracking of new variants on a globe scale, as well as the characterization of mutations, is crucial because of their effect on adaptive immunity, neutralizing antibody response, and impact on vaccine efficacy.

The detailed maps of mutations highlighting their prospective role in therapeutics and vaccine development can better prepare us for future waves of continuously evolving SARS-CoV-2. With this aim, we invite original research and review articles which address the tracking and genomic surveillance of emerging variants, their virulence, transmissibility, mathematical modeling, and therapeutic aspects of COVID-19.





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Message from the Editor-in-Chief

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