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Genomic Characterization of a Novel SARS-CoV-2
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Abstract:	A new severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) associated with human to human transmission and extreme human sickness has been announced from the city of Wuhan in China. Our objectives were to perform mutation analysis between recent reported genomes in various times and locations and to characterize the genomic structure of SARS-CoV-2 using bioinformatics programs. Information on the variation of viruses is of considerable medical and biological importance for the prevention, diagnosis, and therapy of infectious diseases. In order to understand the genomic structure and variations of the SARS-CoV-2, the study analyzed 94 SARS-CoV-2 complete genome sequences available in GenBank, National Microbiology Data Center (NMDC) and NGDC Genome Warehouse from December-2019 until 22 of March-2020. The genomic signature analysis demonstrates that a strong association between the time of sample collection, location of sample and accumulation of genetic diversity. We found 114 mutations, three most common mutations were 8782C>T in ORF1ab gene, 28144T>C in ORF8 gene and 29095C>T in N gene. The mutations might affect the severity and spread of the SARS-CoV-2. The finding heavily supports an intense requirement for additional prompt, inclusive investigations that combine genomic detail, epidemiological information and graph records of the clinical features of patients with COVID-19.
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