

عنوان مقاله:

Highly Conserve Sequences in Envelope, Nucleoprotein and RNA-Dependent RNA Polymerase of SARS-CoV-2 in Nasopharyngeal Samples of the COVID-19 Patients; a Diagnostic Target for Further Studies

محل انتشار:

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خلاصه مقاله:

Background: The etiological agent of coronavirus diseases 2019 (COVID-19) is severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2). Conventional molecular methods are used to detect viruses in COVID-19 infected patients. This study aimed to investigate escape mutations from molecular detection on SARS-CoV-2 targeted genes, which indicates the importance of mutations in false-negative PCR test results in the detection of virus in clinical specimens of patients with COVID-19. Materials and Methods: The 20 nasopharyngeal swabs samples collected from COVID-19 confirmed patients. The SARS-CoV-2 E, nsp12, and N genetic regions are amplified by RT-PCR assay. PCR products were sequenced using the Sanger sequencing method and Multiple sequence alignment (MSA) to assess the polymorphism and mutations performed using MEGA X software and the Maximum likelihood method for the phylogenetic evaluation. Results: Among all COVID-19 cases, 60% and 40% were male and female, respectively. The MSA showed high conservation between all evaluated samples and VOCs in all N, E, and nsp12 genes. Also, the phylogenetic evaluation by the Maximum likelihood method reported high similarity between all SARS-CoV-2 sequenced samples, VOCs, and Wuhan reference sequences in the evaluated region. Conclusion: Our study results approved the relatively conserved suitability of the E, N, and RdRp-gene regions with no diversity, therefore, making them perfect candidates for first-line screening.

کلمات کلیدی:

SARS-CoV-2, COVID-19, Mutation, Phylogenetic

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