

The Association between IFNAR2 and Dpp9 Genes Single Nucleotide Polymorphisms Frequency with COVID-19 Severity in Iranian Patients

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Abstract : Background: SARS-CoV-2, a single-stranded RNA betacoronavirus causes the global outbreak of coronavirus disease 2019 (COVID-19). Several clinical and scientific concerns are raised by this pandemic. Genetic factors can contribute to pathogenesis and disease susceptibility. There are single nucleotide polymorphisms (SNPs) in many of the genes in the immune system that affect the expression of specific genes or functions of some proteins related to immune responses against viral infections. In this study, we analyzed the impact of polymorphism in the interferon alpha and beta receptor subunit 2 (IFNAR2) and dipeptidyl peptidase 9 (Dpp9) genes and clinical parameters on the susceptibility and resistance to Coronavirus disease (COVID-19). Methods: A total of 330- SARS-CoV-2 positive patients (188 survivors and 142 nonsurvivors) were included in this study. All single-nucleotide polymorphisms (SNPs) on IFNAR2 (rs2236757) and Dpp9 (rs2109069) were genotyped by the polymerase chain reaction-restriction fragment length polymorphism (PCR-RFLP) method. Results: In survivor patients, the frequency of the favourable genotypes of IFNAR2 SNP (rs2236757 GC) was significantly higher than in nonsurvivor patients, and also Dpp9 (rs2109069 AT) genotypes were associated with the severity of COVID-19 infection. Conclusions: This study demonstrated that the severity of COVID-19 patients was strongly associated with clinical parameters and unfavourable IFNAR2, Dpp9 SNP genotypes. In order to establish the relationship between host genetic factors and the severity of COVID-19 infection, further studies are needed in multiple parts of the world.

Keywords : SARS-CoV-2, COVID-19, interferon alpha and beta receptor subunit 2, dipeptidyl peptidase 9, single-nucleotide polymorphisms

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