Modifying effects of TNF-α, IL-6 and VDR genes on the development risk and the course of COVID-19. Pilot study

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Abstract

Objectives: COVID-19 continues to range around the world and set morbidity and mortality antirecords. Determining the role of genetic factors in the development of COVID-19 may contribute to the understanding of the pathogenetic mechanisms that lead to the development of complications and fatalities in this disease. The aim of our study was to analyze the effect of TNF-α (rs1800629), IL-6 (rs1800795) and VDR (rs731236 and rs1544410) genes variants on the development risk and the course of COVID-19 in intensive care patients.

Methods: The study group included 31 patients with diagnosis "viral COVID-19 pneumonia". All patients underwent standard daily repeated clinical, instrumental and laboratory examinations. Determination of IL-6, TNF-α, and VDR genes variants was performed using the PCR-RFLP method.

Results: It was found a significant increase in the rate of the CC genotype and C allele (38.7 vs. 12.0% and 0.6 vs. 0.4%, respectively) of the IL-6 gene in all patients of the study in comparison with population frequencies. There was a significantly higher rate of heterozygous genotypes TC and GA of the VDR gene in group of died patients. The rs1800629 variant of the TNF-α gene is associated with the need for respiratory support and its longer duration in patients with COVID-19.

Conclusions: The obtained results support a hypothesis about the influence of variants of IL-6, TNF-α and VDR genes on severity of COVID-19. However, in order to draw definite conclusions, further multifaceted research in this area are need.

Keywords: IL-6; TNF-α; VDR; COVID-19; gene.

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