1st INTERNATIONAL SYMPOSIUM of DOHaD and Pandemic: LESSONS FROM COVID-19
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Maringá - PR / Brazil
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1º SIMPÓSIO INTERNACIONAL de DOHaD e Pandemia: LIÇÕES DO COVID-19
10, 11 e 12 de Maio 2023
Maringá - PR / Brasil
Universidade Estadual de Maringá

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ASSOCIATION OF POLYMORPHISM IN *TICAM1* GENE WITH PROTECTION TO MODERATE/SEVERE COVID-19

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Clinical outcomes of Covid-19 have shown variability between individuals and populations**.** *TICAM1* gene encodes the TRIFF protein, essential in the antiviral response, then the purpose of the study was to assess the effect of the polymorphism (rs2292151) G>A of *TICAM1* gene on the severity of COVID-19 in individuals from the northern region of Paraná. A case-control study was performed, including patients, 100 mild and 50 moderate/severe Covid-19 cases, classified according to the WHO, by Hospital Paraná, Maringá, Brazil. The exclusion criteria used were: patients with heart disease, liver disease, other respiratory diseases, HIV, and cancer. The (rs2292151) G>A polymorphism was genotyped by qPCR and statistical analysis was performed using logistic regression in the SNPStats software. The genotype distribution was according to the expected in the Hardy-Weinberg equilibrium. There was an association between the A/A genotype in a codominant model with protection against the severity of the disease (OR=0.14, 95% CI 0.03.-0.75, *P* = 0.01). The frequency of genotype A/A was 12% in mild cases and 4% in serious cases; the G/A was 44% in mild cases and 30% in serious cases, and the G/G was 44% in mild cases and 66% in serious cases. We can conclude that the A/A genotype (in a codominant genetic model) of the polymorphism (rs2292151) G>A was associated with a protection factor for moderate/severe Covid-19 in this population, however, the genotype determination should be done in a high number of patients.

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