Genetic Variants of Toll Like Receptor-4 in Patients with Premature Coronary Artery Disease, South of Iran

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Abstract

Introduction: Ischemic cardiovascular diseases are the leading causes of morbidity and mortality in most developed and developing countries including Iran. Premature myocardial infarction has a polygenic base with a complex relation with environmental factors. Since expression of different inflammatory genes especially toll like receptor-4(TLR4) has increased considerably in human atherosclerotic plaques, we have decided to study variants of TLR4 inpremature coronary artery disease in patients in Jahrom city, Iran.
Methods: In this case-control study, 100 patients with a history of premature coronary artery diseases and 100 healthy control subjects referred to health centers in Jahrom city were studied. Target sequences of TLR4 gene were amplified by PCR amplification and digestion was done by StyI restriction enzyme (PCR-RFLP method).
Results: There was no significant difference regarding age (P>0.05). The distribution of TC heterozygote genotype inthe premature myocardial infarction group is significantly higher than in the healthy group (P<0.05) but the homozygote mutated genotype showed no significant difference (P>0.05). In addition, the genotype carrying the mutated allele (TC+CC) showed a significant difference when compared to TC variant (P<0.05). The genotype distribution in rs1927911 in both genders shows no concomitance between males and females (P>0.05).
Conclusion: According to the results derived from this study, it seems like the existence of the genotype carrying the mutated allele (TC+CC) in rs1927911's mononucleotide polymorphism of TLR gene is associated with an increased risk of premature myocardial infarction.

Keywords

Premature coronary artery disease; TLR4 gene; rs1927911 polymorphism