عنوان مقاله:

Association of rs۲۹۵۴۰۲۹ and rs۶۹۸۲۵۰۲ Variants with Coronary Artery Disease by HRM Technique: A GWAS Replication Study in an Iranian Population

محل انتشار:

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خلاصه مقاله:

Background: Genome-wide association studies (GWAS) have been the primary tool for an unbiased study of the genetic background of coronary artery disease (CAD). They have identified a list of single-nucleotide polymorphisms (SNPs) associated with coronary artery disease (CAD). In this study, we aimed to replicate the association of rs۲۹۵۴۰۲۹ and rs۶۹۸۲۵۰۲, a GWAS identified SNP, to CAD in an Iranian population. Methods: A sample of ۲۸۵ subjects undergoing coronary angiography, including ۱۳۴ CAD patients and ۱۵۱ healthy. The genotype determination of rs۲۹۵۴۰۲۹ and rs۶۹۸۲۵۰۲ SNPs performed using the high-resolution melting analysis (HRM) technique. Results: Our results revealed that the TT genotype of rs۲۹۵۴۰۲۹ (p= ۰.۰۰۹) and rs۶۹۸۲۵۰۲ (p< ۰.۰۰۱) were significantly higher in CAD patients compared with controls. Binary logistic regression showed that rs۶۹۸۲۵۰۲ and rs۲۹۵۴۰۲۹ increase the risk of CAD incidence (۲.۴۷۰ times, p= ۰.۰۱۱, ۹۵% CI= [۱.۲۱۹-۴.۷۵۱], and ۲.۱۷۴ times, p= ۰.۰۳۳, ۹۵% CI= [۱.۰۶۶-۴.۴۳۳] respectively). After adjusting for confounders, we found that rs۶۹۸۲۵۰۲ and rs۲۹۵۴۰۲۹ are significantly associated with CAD risk. Conclusions: These data showed that the TT genotype of rs۲۹۵۴۰۲۹ and rs۶۹۸۲۵۰۲ is associated with the risk of CAD in a hospital-based sample of the Iranian population, which has replicated the result of recent GWAS studies.

کلمات کلیدی:

Coronary Artery Disease (CAD), Genome-Wide Association Studies (GWAS), High-Resolution Melting (HRM), Single-Nucleotide Polymorphisms (SNP).