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Abstract

Role of *APOE* Gene Polymorphisms in Coronary Artery Disease †

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Abstract: Coronary artery disease (CAD) is one of the major causes of global mortality and morbidity. It is a multifactorial disease as it involves a complex relationship between environmental, biochemical, and genetic factors. Single nucleotide polymorphisms (SNPs) are the most promising and commonly used genetic markers for disease risk association. Apolipoprotein E (APOE) is listed among the top genes that play a crucial role in coronary artery disease pathophysiology. Our current meta-analysis aims to find the association of two extensively studied variants, including rs429385 and rs7412, with coronary artery disease. Eligible articles were retrieved using different MeSH terms, keywords, and databases, including PubMed, Ovid, Cochrane Library, web of science, and Embase. Our study was conducted according to the Preferred Reporting Items for Systematic Reviews, and Meta-Analyses2009 (PRISMA 2009) guidelines. Our pooled analysis suggests the ε4 allele of APOE was significantly associated with CAD (odds ratio 2.00; 95% and CI, 1.48–2.71). In addition, meta-analysis results, including the shape of funnel plots, showed no publication bias. However, we recommend more studies with larger cohort sizes, should be conducted in different ethnic groups that may provide more conclusive findings.

Keywords: SNPs; *APOE*; CAD

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