Influence of Apo E Polymorphism on Coronary Artery Disease

S. Fallah, M. Seifi, M. Firoozrai, T. Godarzi, M. Jafarzadeh, and L. H. Ghohari

Abstract—The ε4 allele of the ε2, ε3 and ε4 protein isoform polymorphism in the gene encoding apolipoprotein E (Apo E) has previously been associated with increased cardiac artery disease (CAD); therefore to investigate the significance of this polymorphism in pathogenesis of CAD in Iranian patients with stenosis and control subjects. To investigate the association between Apo E polymorphism and coronary artery disease we performed a comparative case control study of the frequency of Apo E polymorphism in One hundred CAD patients with stenosis who underwent coronary angiography (>50% stenosis) and 100 control subjects (<10% stenosis). The Apo E alleles and genotypes were determined by polymerase chain reaction (PCR) and restriction fragment length polymorphism (RFLP). We observed an association between the Apo E polymorphism and CAD in this study. These data suggest that the Apo ε4 and ε3 alleles increase the risk for CAD in Iranian population (χ² =4.26, p= 0.05, OR=2 and χ² =0.38, p=0.53, OR=1.2). These results suggest that ε4 and ε3 alleles are risk factors for stenosis.

Keywords—Arterial blood vessels, atherosclerosis, cholesterol.

I. INTRODUCTION

Apolipoprotein E is a plasma protein that serves as a ligand for low density lipoprotein receptors and through its interaction with these receptors participates in the transport of cholesterol and other lipids among various cells of the body [1]. Apo E is an exchangeable protein which acts as ligand for low density lipoprotein (LDL) receptors. It also has a repair function in response to tissue injury. It plays an essential role in lipid metabolism, especially in removal atherogenic remnants of triglyceride rich lipoproteins [1-2] and by reversing cholesterol transport in plasma and intercellular lipid transport within tissues. The human Apo E gene is 3.7 Kb including 4 exons and 3 introns (3-4) and is mapped on the short arm of chromosome 19[3-4]. The mature protein is composed of 299 amino acids i.e. 34 KD with several function domains [4-7]. The three common isoforms of Apo E2, E3 and E4 are encoded by the Apo ε2, ε3 and ε4 genes, respectively [6] that give rise to different genotypes (ε2/2, ε3/3, ε4/4, ε2/ε3, ε2/ε4, ε3/ε4 and ε4/ε4). The primary sequence of these proteins is identical except at amino acids 112 and 158, where there can be cysteines (E2), arginines (E4) and arginine at position 158 (E3) [6]. Apo E2 has a lower binding affinity to LDL receptor (1% of the Apo ε3 binding affinity), whereas the binding affinity of E4 to the LDL receptor is higher [7]. The genetic variations at Apo E have been shown to affect on lipid and lipoprotein levels in the general population [8-9]. The ε4 isoform is associated with increased levels of total cholesterol (TC) and beta lipoprotein [1] and increased susceptibility [11].

A number of studies have investigated association between genetic susceptibility factor for cardiac heart disease (CHD) or atherosclerosis in divers ethnic populations [12]. The knowledge of lipid profile may predict the potential victims of cardiovascular disease before its initiation and progression and offer the opportunity for primary prevention. Therefore it is very important to identify factors that may influence blood lipids concentrations. The correlation of the most common Apo E polymorphism with CHD has been extensively investigated in the last three decades [2]. A Meta analysis of 48 diseases [13] showed that the Apo ε allele is a significant risk factor for CHD. On the other hand a trend for the ε4 allele to be associated with a higher prevalence of target organ damage in patients with mild to moderate hypertension has been proposed [14]. Therefore the current study specially aimed to find whether genetic polymorphism in Apo E gene is a risk factor for CHD in a population from Tehran Iran.

II. MATERIALS AND METHODS

A. Study Subjects

The study group consisted of 100 patients (74 males, 25 females, mean age 58.61± 9.35) who were admitted to the cardiology unit of Shahid Rajaee Hospital who had been diagnosed to have atherosclerosis. The diagnosis was based on the complete physical and clinical examination of patients by the cardiologist followed by investion. For the present study, only patients with atherosclerosis were included while patients with Alzheimer's disease, pulmonary, renal, hepatic disease, cardiomyopathy congestive heart failure and acute myocardial infarction were excluded.

Random were included study as control (64 males, 36 females mean age 53.45± 9.35). Control subjects were also similarly evaluated the confounding risk factors included smoking and alcohol consumption, dislipidemia and family history of atherosclerosis. In the present study, evaluation of the contribution of confounding risk factors of the
development of artherosclerosis was based on the individual’s personal history findings.

B. Genetic Analysis

Leucocytes extracted following standard protocols [15] DNA was amplified by PCR in a DNA cycler (0005.416model T-cy grady) using oligonucleotide primer forward (5-ACAGAATTGCGCCGGCCTGGTACACG) and reverse (5-TAAAGCTTGCCAGGCTTCGCCAGC 3) (company) as described by Hixson et al [16]. The PCR condition included on initial step of 95°C for 30 min, followed by 33 cycles (95°C 30 S, 55°C 30 S and 70°C 1 min) and by a final extension (70°C, 7 min) with 94°C hold according to a protocol described by Hixson et al [16]. Electrophoresis of amplified products (244 bp) was performed on 10% polyacrylamide gel. After PCR implication 5 units of Hha1 enzyme (New England Biolabs) was added directly to each reaction mixture for digestion of Apo E sequence of PCR product (over night, 37°C)[16]. Each reaction mixture was loaded onto a 10% polyacrylamide gel and electrophoresed. After electrophoresis, digested fragments were visualized by UV illumination. The size of Hha I fragments were estimated by comparison with known DNA (Fermenta, Gene Ruler 50bp DNA Ladder).

Statistically analysis: Allele frequencies were deduced from genotype frequencies, and the Hardy–Weinberg equilibrium was analyzed through the chi-square test. p<0.05 was considered significant. Quantitative information was expressed as mean standard deviation. All calculations were performed by using the SPSS 11.5 program. To evaluate the association of Apo E polymorphism with artherosclerosis: Multiple logistic regressions were used with maximum likelihood estimation of the regression coefficients and their standard error. Multivariate adjusted odds ratios calculated for Apo ε4 allele (ε3ε4 and ε3ε6), ε2 allele (ε3ε2, ε3ε6 and ε6ε6) and taking allele ε3 (ε3ε3) as reference. For each odds ratios we calculated two tailed p values and 95% confidence interval 1.2to 3.8, p<0.05 in all.

III. RESULTS

In this study we identified three Apo alleles ε2, ε3 and ε4 and six genotypes ε3ε3, ε3ε4, ε3ε6, ε4ε6, ε6ε6, ε6ε4 and ε6ε3. In study population for both men and women, allele frequencies did not deviate from Hardy-Weinberg equilibrium. The distribution of Apo E genotypes in patient subjects differed significantly fro control group. As it shown in Table I, the prevalence of six genotypes ε3ε3, ε3ε4, ε3ε6, ε4ε6, ε6ε6, ε6ε4 and ε6ε3 in patient and control 30%, 4%, 8%, 18%, 6%, 34% and 15%, 6%, 12%, 8%, 8%, 51% respectively. It observed that the prevalence of ε6ε6 was 1.5 fold high in patient subjects (4% Vs 6%) when compared with controls (χ² =0.42, p=0.156, OR=0.58). While prevalence ε3ε6 and ε6ε6 genotypes were higher in patients (18% Vs 8% and 30% Vs 15%) than in controls (χ² =4.3, p=0.036, OR=2.52) and (χ² =6.4, p=0.01, OR=1.86) respectively. The frequency of ε3ε6 (χ²=0.3, P=0.57, OR=0.49) and ε6ε3 (χ² = 0.89, p=0.346, OR=0.57) in control was 1.3 and 1.5 fold high when compared with patient subjects (6% Vs 8%) and (8% Vs 12%) respectively. Statistically significant difference was not found between patients and controls (32% Vs 28%) with respect to ε4 and allele frequency (χ² =0.38, p=0.53, OR=1.2) while ε3 allele frequency was found to be much more prevalent in patients (34% Vs 51%) than in control (χ² =5.9, P=0.015, OR=0.44).

As it shown in Table II the prevalence of ε4 allele in patient subjects (34% Vs 21%) is higher than controls (χ² =4.23, p=0.04, OR=2).

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<th>Genotype</th>
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<th>χ²</th>
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IV. DISCUSSION

Studies conducted in different parts of the globe reveal that gene frequencies at Apo E locus are highly heterogeneous between the populations. The ε3 is the most common form of the gene in most of the population [17-18]. In a population-based study Venkutaramana et al [19] reported that the allele frequencies in Indian population 85%-92% for ε3 allele, 3.9% for ε4 allele and 3.5% for ε2 allele. In the present study Apo ε4 allele frequencies in the control group of Tehran population are 34%, 34% and 32% for ε3, ε4 and ε2 respectively which are not comparable with the study of Venkutaramana et al and others [19]. The prevalence of ε2/ε2, ε2/ε3,ε2/ε4, ε3/ε3, ε3/ε4 and ε4/ε4 in Korean adults were 0.3%, 10.3%, 0.6%, 75.3%, 12.5% and 0.4% for men and 0.6%, 9.1%, 1.0%, 72.9%, 15.3% and 0.9% for women respectively. The reasons for these discrepancies could be genetic heterogeneity and gene environment interactions in different ethnic population. It is well known that the ε4 allele of Apo E is associated with increased prevalence of artherosclerosis and cardiac heart disease (CHD)[20-21]. However there are controversial results concerning the association between Apo E genotypes and some cardiovascular risk factors. Some studies have suggested that high blood pressure may be associated with the presence of the ε4 allele [22-24], while others have found its association with ε2 allele [25]. However no association was found in few studies [25]. In this study we evaluated the distribution of Apo E genotype and alleles in angiographically defined CAD patients and control subjects,
and found these polymorphisms as risk factors for atherosclerosis. As it shown, the distribution of \( \varepsilon_2/\varepsilon_3, \varepsilon_2/\varepsilon_4, \varepsilon_3/\varepsilon_4 \) genotypes and \( \varepsilon_3 \) and \( \varepsilon_4 \) alleles in patients group were significantly different from control group. It is suggested that the \( \varepsilon_4 \) allele and \( \varepsilon_2/\varepsilon_4 \) genotype of Apo E may be less efficient at retarding the oxidation of LDL than others. As it shown in Tables 1 the prevalence of \( \varepsilon_2/\varepsilon_4 \) genotype was 1.5 fold high in control group when compared with patients (51% Vs 34%, \( p=0.015 \)) whereas prevalence of \( \varepsilon_2/\varepsilon_3 \) and \( \varepsilon_2/\varepsilon_4 \) genotypes was 2 and 2.25 fold high in patient group than control subjects (30% Vs 15%, \( p=0.01 \)and 18% Vs 8%, \( p=0.036 \)). This finding suggests that the prevalence of \( \varepsilon_2/\varepsilon_4 \) and \( \varepsilon_3/\varepsilon_4 \) genotypes may be risk factors in this complex disease. The frequency of \( \varepsilon_2 \) allele was 1.5 fold high in control group when compared to patient (51% Vs 34%, \( p=0.015, \chi^2=5.9, \) OR=0.44), while statistically difference was found between patients and controls with respect to \( \varepsilon_2 \) allele frequency (32% Vs 28%, \( p=0.53, \chi^2=0.38, \) OR=1.2). It is suggested that \( \varepsilon_2 \) allele may be a risk factor for CAD disease in Iranian population. A significant difference was found between the prevalence of \( \varepsilon_4 \) allele in patient group as comparison with control subjects (34% Vs 21%, \( p=0.04, \chi^2=4.23, \) OR=2). These results showed an evidence of an association between the \( \varepsilon_2 \) and \( \varepsilon_4 \) alleles and CAD. This finding is accordance or different to some studies that performed in different population with coronary artery disease. These findings are accordance to the results of two meta-analysis [26a]. The results of these study showed that the odd ratios (ORs) for coronary heart disease (CHD) in \( \varepsilon_2 \) and \( \varepsilon_4 \) alleles versus persons who had with \( \varepsilon_3 \) allele. Compared with those who had the \( \varepsilon_3 \) allele, the pooled ORs for CHD among carriers of \( \varepsilon_2 \) allele were 1.3 in the classic random effects model and 1.42 in a bayesian hierarchical random effect mode. These two model showed that no evidence of association between the \( \varepsilon_4 \) allele and CHD risk (ORs= 0.93 and 0.98) respectively [26]. They showed a similar estimates for each of \( \varepsilon_2/\varepsilon_2, \varepsilon_2/\varepsilon_3, \varepsilon_2/\varepsilon_4, \varepsilon_3/\varepsilon_4, \) and \( \varepsilon_4/\varepsilon_4 \) genotypes compared with \( \varepsilon_3/\varepsilon_3 \) genotype in both classic random- effects model and a bayesian hierarchical random effect model. They showed that persons with \( \varepsilon_3/\varepsilon_3 \) and \( \varepsilon_4/\varepsilon_4 \) genotypes had higher risk for CHD ( ORs =1.41 and 1.36) respectively than those with the \( \varepsilon_3/\varepsilon_3 \) genotype, whereas there was no evidence of any association between CHD risk and \( \varepsilon_2/\varepsilon_2, \varepsilon_2/\varepsilon_3, \varepsilon_2/\varepsilon_4 \) genotypes ( ORs = 0.43, 1.04 and 1.11 ) respectively. The results of our study with respect to \( \varepsilon_2 \) allele carriers are accordance to two meta analysis studies results.

In a study by Bhavani et al [27] the prevalence of genotypes and allele frequencies among hypertension patients and controls were identified. They showed that prevalence of \( \varepsilon_2/\varepsilon_4 \) genotypes was 1.5 fold high in patients when compared to controls (14.5% Vs 10.0 %, \( p=0.05 \)) while prevalence of \( \varepsilon_2/\varepsilon_4 \) genotype was high in controls than in patients (6.5% Vs 4.3%). They showed that statistically significant difference was not found between patients and controls with respect to \( \varepsilon_2 \) and \( \varepsilon_3 \) allele frequencies, while \( \varepsilon_4 \) allele frequency was found to be more prevalent in patients (12.16%) than in controls (5.75%), \( \chi^2=10.87, p=0.05 \). They found that this allelic association should higher relative incidence of \( \varepsilon_4 \) allele (\( \chi^2=9.13, p<0.05 \)) as compared to other alleles and also in case with family history of hypertension (\( \chi^2=6.79, p<0.05 \)). Analysis of the apolipoprotein E gene polymorphism in large Caucasian population by Hubacle et al [28], the carrier of mutant allele Arg 136 / Ser in C Zech region was identified. They estimated that the population frequency of this Apo E mutation is very low. They suggested that this mutation in subjects not necessarily connected with elevated lipid in all cases. In present study the mutant allele (Arg 136 Ser) in Iranian population was not found. The results of a study by Merho [29] showed that Apo E polymorphism had a significant effect on lipid levels in Koreans, that the association between the Apo E allele type and CAD. This finding is accordance or [30-32]. It is suggested that the association between Apo E polymorphism and different lipoproteins (Triglyceride- HDL-C and LDL-C) levels are not entirely similar among different populations. Gene – environment interaction may contribute to the discrepancies observed between studies. Previous studies have shown that HDL-C levels vary with physical activity, alcohol consumption and diet [33-34]. Reznik et al [35] showed that the association between and Apo E polymorphism postprandial triglyceride clearance was modified by age, bodyweight and triglyceride pool level. As shown by Alessandro [36] in young adults, the Apo \( \varepsilon_4 \) allele and cigarette smoking act synergistically increasing an individual's propensity to have a cerebral ischemic event. However the mechanism underlying of Apo E polymorphism to CHD risk is not completely understood and deserves further investigation. Although the impact of Apo E polymorphism on plasma levels of total and low density lipoprotein cholesterol, apolipoprotein B and apolipoprotein E is well established, the triglycerides, high density lipoprotein cholesterol, apolipoprotein A-1 and lipoprotein (a) remain equivocal [37-39]. It has been suggested that the \( \varepsilon_2 \) allele is related to HDL-C and LDL-C levels, while the potential antiatherogenic of the \( \varepsilon_2 \) involving lower levels of LDL-C may be offset by accumulation of atherogenic large very low density lipoprotein cholesterol and remnant rich lipoproteins [37-39]. Beyond the effect on lipid metabolism, Apo E genotypes may also affect CHD risk through antioxidative, inflammatory and immune activities [37-39].

In conclusion, our results support the notion that a significant association of \( \varepsilon_4 \) allele is observed with coronary heart disease (CHD) in addition to the other well known risk factors and positive family history. Carriers of \( \varepsilon_4 \) allele form a high risk group showing greater susceptibility to CHD while the \( \varepsilon_2 \) allele has no effect. Further, this observation interplay between genetic and environmental factors must be thoroughly considered in order to evaluate the etiological role.
of Apo E in CHD. There is convincing evidence that the relationship between Apo E genotype and plasma lipoprotein lipid levels is context-dependent, being significantly influenced by age [40] and sex [41-42]. Some evidence [43-44] also indicates that the responses of plasma lipoprotein – lipid levels to different lipid lowering interventions may be affected by an individual's Apo E genotype, indicating the significance of gene-environment interactions.

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