

Research Article

APOE Gene Polymorphism and Risk of Coronary Stenosis in Pakistani Population

Asma Naseer Cheema,¹ Attya Bhatti,¹ Xingbin Wang,² Jabar Ali,³ Mikhil N. Bamne,² F. Yesim Demirci,² and M. Ilyas Kamboh²

¹Atta-Ur-Rahman School of Applied Biosciences, National University of Sciences & Technology, H/12, Islamabad 44000, Pakistan ²Department of Human Genetics, University of Pittsburgh, Pittsburgh, PA 15261, USA ³Department of Cardiology, Lady Reading Hospital, Peshawar 25000, Pakistan

Correspondence should be addressed to Asma Naseer Cheema; asma.cheema4@gmail.com

Received 26 January 2015; Accepted 15 March 2015

Academic Editor: Sarah H. Elsea

Copyright © 2015 Asma Naseer Cheema et al. This is an open access article distributed under the Creative Commons Attribution License, which permits unrestricted use, distribution, and reproduction in any medium, provided the original work is properly cited.

Genetic variation in lipid regulatory genes, particularly *APOE*, significantly influences the risk of coronary artery disease (CAD). This study aimed to assess the association between *APOE* polymorphism and angiographically assessed coronary stenosis in Pakistani population. A total of 695 subjects (22.3% female, mean age = 54 ± 11 years) presenting with chest pain were enrolled after obtaining written informed consent. CAD stenosis/extent was assessed by angiography. Patients were classified as having severe stenosis ($\geq 70\%$), moderate stenosis (30-69%), and mild stenosis (<30%). CAD patients with $\geq 70\%$ stenosis (n = 491) were further categorized based on possessing one, two, or three vessel diseases to assess the disease extent. Genomic DNA from leukocytes was isolated with DNA purification kit (Qiagen) and *APOE* polymorphisms (E2/E3/E4) were determined using TaqMan assays. Six hundred and seventy-two of 695 subjects were successfully genotyped. The frequency of *APOE* *4 carriers (3/4 and 4/4 genotypes) was significantly higher in severe stenosis group ($\geq 70\%$) as compared to mild group (<30%) (22.8% versus 13.01%; P = 0.01). In multiple regression, the odds ratio for *APOE* *4 carriers to develop $\geq 70\%$ stenosis was 2.16 (95% CI: 1.29–3.79; P < 0.005). In conclusion, the presence of *APOE* *4 allele is a significant risk factor to develop severe coronary stenosis (>70%) among Pakistanis.

1. Introduction

Coronary artery disease (CAD) is a complex and multifactorial disorder involving the interplay of both genetic and environmental factors. Despite significant improvement in clinical management of the CAD, it is still reported as the most common cause of adult deaths worldwide [1]. Geographically, there is asymmetrical pattern of CAD distribution such that the disease burden is projected to be double by 2020 in developing countries as compared to the only 50% rise in developed countries [2]. The integrative approach of analyzing the disease both clinically and genetically provides the opportunity to disentangle the complex interactions underlying disease pathways. While lifestyle modification has reduced the mortality rate, the candidate gene approach has provided new insights for exploring diagnostic and therapeutic approaches. The important role of lipid regulatory genes in

CAD pathogenesis has been an essential aspect of research for the past many years [3, 4]. Apolipoprotein E (ApoE protein; APOE gene), one of the key regulators of lipid metabolism, plays an important role in the uptake of ApoE-containing lipoprotein particles by the cells. There is a common ApoE protein polymorphism with three alleles, APOE*2, APOE*3, and APOE*4, which are differentiated by amino acid substitution at codons 112 and 158 in exon 4. ApoE2 has cysteine at both positions; E3 has cysteine at 112 and arginine at 158 while E4 has arginine at both positions [5]. The three alleles show marked variation in distribution among different racial groups and are associated with variation in plasma cholesterol levels in the general population [6]. APOE polymorphism is also associated with atherosclerosis where the APOE*4 allele is linked with elevated risk of CAD [7, 8]. However, epidemiological studies have shown inconsistent association of APOE polymorphism with clinical CAD [9-12].

Parameters	<30%	30-69%	≥70%	P value
	(n = 157)	(n = 30)	(n = 508)	
Age (years)	52.47 (12.56)	55.63 (13.40)	54.42 (11.32)	0.14
BMI (kg/m ²)	28.89 (4.82)	28.71 (3.09)	28.98 (4.65)	0.94
Gender (M/F)	120/37	26/6	394/112	0.82
Smoking (no/yes)	91/66	118/14	395/11	$5.7E^{-07}$
Family history (no/yes)	87/70	12/20	346/160	$7.5E^{-05}$
*TC (mg/dL)	188.58 (46.53)	198.19 (44.02)	200.01 (53.90)	0.43
*HDL-c (mg/dL)	40.53 (10.26)	34.21 (6.06)	39.18 (9.29)	0.1
*TG (mg/dL)	171.22 (61.54)	147.26 (38.95)	186.52 (62.12)	0.03

TABLE 1: Patient characteristics according to the percent of vessel's stenosis (n = 695).

*TC, HDL-c, and TG were measured on subset of 216 subjects.

TC: total cholesterol; HDL-c: high-density lipoprotein; TG: triglyceride.

The aim of our study was to seek the association between *APOE* polymorphism and angiographically assessed coronary stenosis among Pakistanis, which to the best of our knowledge has not been reported previously.

2. Materials and Methods

2.1. Subjects. A total of 695 subjects were enrolled at the Lady Reading Hospital, Peshawar, after obtaining written and oral consent. The institutional review board and ethical committee of National University of Sciences & Technology approved the study. The study was designed to enroll patients presenting with chest pain or suspected to have clinical myocardial ischemia. The study participants were classified as having severe stenosis (\geq 70%), moderate stenosis (30–69%), and mild stenosis (<30%). CAD patients with \geq 70% stenosis were further categorized based on possessing one, two, or three vessel diseases to assess the disease extent. The participants with cardiomyopathy, NYHA class IV CCF, valvular or congenital heart disease, and recent coronary angioplasty or coronary bypass surgeries were excluded from the study.

2.2. APOE Genotyping. Genomic DNA was isolated from leukocytes using DNA purification kit (Qiagen, Valencia, CA). Genotypes for two APOE single-nucleotide polymorphisms (SNPs), rs429358 (E4) and rs7412 (E2), were determined by TaqMan SNP genotyping assays on ABI Prism 7900HT Sequence Detection System (Life Technologies, Grand Island, NY). To estimate the assay error rate, 10% of samples were randomly selected and included as duplicates in genotyping run. There was only one discrepant sample, which was removed from the final analysis. The genotype outputs from the two SNPs were converted into the conventional six APOE genotypes (22, 23, 33, 34, 24, and 44) based on three alleles (APOE*2, APOE*3, and APOE*4).

2.3. Statistical Analysis. Differences in mean values for age, body mass index (BMI), and lipid levels were analyzed using one-way ANOVA. Chi-square (χ^2) test was performed to assess the distribution of sex, smoking, and family history

TABLE 2: Distribution of the *APOE* polymorphism in the genotyped sample of 672 subjects.

Genotype/allele	Count	(%)
22	2	0.3
23	36	5.36
24	6	0.89
33	491	73.07
34	129	19.2
44	8	1.19
APOE*2	46	3.42
APOE*3	1147	85.34
APOE*4	151	11.24

of CAD among the three-stenosis groups. *APOE* allele frequencies were calculated by allele counting. The Hardy-Weinberg equilibrium was tested by a χ^2 goodness-of-fit test. For association analysis between *APOE* and CAD severity, *APOE* genotypes were collapsed into three groups: E2 (2/2 and 2/3 genotypes), E3 (3/3 genotype), and E4 (3/4 and 4/4 genotypes). Because of the known opposite effects of the *APOE**2 and *APOE**4 alleles on the risk of CAD, we omitted individuals with the 2/4 genotype from the analysis. The Cochran-Armitage (C-A) trend test was applied in the analysis of the association between *APOE* and CAD severity [13]. Multiple logistic regressions were performed to determine the odds ratios (ORs) after including significant CAD risk factors: gender, age, smoking, and family history (FH) of CAD.

3. Results

A total of 695 subjects (22.3% females, mean age = 54 ± 11 years) with angiographically assessed stenosis were analyzed. The demographic and descriptive data of three stenosis groups are given in Table 1. Distributions of *APOE* genotypes and allele frequencies are presented in Table 2. Out of 695 analyzed subjects, we obtained final genotype calls for 672 samples. The distribution of *APOE* genotypes in 672 subjects was in the Hardy-Weinberg equilibrium (P = 0.721). Six

TABLE 3: Distribution of the *APOE* polymorphism by stenosis groups.

	<30%		30	30-69%		≥70%	
	N	%	N	%	N	%	
E2	9	6.16	2	6.90	27	5.50	
E3	118	80.82	21	72.41	352	71.69	
E4	19	13.01	6	20.69	112	22.81	
Total	146		29		491		
Trend test (E2 versus E3)	$\chi^2 = 4E - 04; \ P = 0.98$						
Trend test (E3 versus E4)	$\chi^2 = 6.378; P = 0.01$						

samples with the 2/4 genotype were excluded (672 - 6 = 666) from the association analysis due to known opposite effects of the E2 and E4 on CAD. First, we assessed the association of APOE polymorphism among 666 subjects with percentage of CAD stenosis by evaluating the pattern of distribution of E2 (2/2 and 2/3), E4 (3/4 and 4/4), and E3 (3/3) genotype groups among three stenosis categories (<30%, 30-69%, and $\geq 70\%$) (Table 3). Specifically, the C-A trend test was used to detect whether the proportion of E4 or E2 increases linearly with the level of CAD severity when comparing with E3 group. The proportions of E4 (E3 versus E4) are 0.14, 0.22, and 0.24 for three stenosis categories (<30%, 30–69%, and \geq 70%), which significantly increases linearly with the level of CAD severity (P = 0.01), while the proportion of E2 (E2 versus E3) does not increase linearly with the level of CAD extent. We further examined the effect of APOE4 on the severity of CAD by performing logistic regression analysis. After adjusting for gender, age, smoking, and FH, the APOE*4 associated ORs were 1.61 (95% CI: 0.52–4.5; P = 0.377) and 2.16 (95% CI: 1.29–3.79; P = 0.005) in the 30–69% and \geq 70% stenosis groups, respectively.

Plasma lipid levels (TC, HDL-c, and TG) data were available only in subset of subjects (n = 216) and so they were not considered as covariates in the main analysis. However, we performed a post hoc analysis on this subset of individuals with available lipid levels data. Only TG showed nominally significant difference between the three stenosis groups (P = 0.03), followed by a nonsignificant trend of difference observed for TC (P = 0.43) (Table 1). In the extended post hoc analysis model, we included TG and TC as covariates in addition to gender, age, smoking, and FH. The adjusted OR associated with the E4 genotype group to develop \geq 70% stenosis was 1.61 (95% CI: 0.59–5.23; P = 0.38) in this subset of sample. For comparison, we also did post hoc analysis in this subset using only gender, age, smoking, and FH as covariates, as we did in the main analysis and found a similar outcome (OR = 1.64; 95% CI: 0.62-5.27; P = 0.35), suggesting that using lipids as covariates in the main analysis would have also given similar results in the total sample. We also examined the impact of three APOE genotype groups, E2 (2/2 and 2/3), E3 (3/3), and E4 (3/4 and 4/4), on plasma lipid levels in this subgroup of individuals using gender, age, smoking, and FH as covariates but found

	One vessel		Two vessels		Three vessels	
	N	%	N	%	N	%
E2	16	8.16	3	2.4	8	4.71
E3	133	67.86	94	75.2	125	73.53
E4	47	23.98	28	22.4	37	21.76
Total	196		125		150	
Trend test (E2 versus E3)	$\chi^2 = 2.52; P = 0.11$					
Trend test (E3 versus E4)	$\chi^2 = 0.10; P = 0.74$					

no significant association with TC (P = 0.16), HDL-c (P = 0.23), and TG (P = 0.18).

Next, we evaluated the association of the *APOE* polymorphism with the number of diseased vessels in the \geq 70% stenosis group but found no significant association (Table 4).

4. Discussion

Coronary artery disease is a major public health problem in Pakistan and is considered as the most prevalent cause of death. One out of four middle-aged men and women equally has CAD [14]. Compared with developed countries, heart disease among South Asians is studied only at limited scale [15, 16]. The genetic basis of coronary heart disease (CHD) among Pakistanis is largely an unexplored area of research. In order to fill this research gap, we examined the association of APOE polymorphism with angiographically assessed coronary stenosis in Pakistan population. APOE is an established genetic risk factor for CAD in Europeans and other populations [17, 18]. We hypothesized that the common APOE polymorphism will also affect the CAD risk among Pakistanis. To the best of our knowledge, this is the first study that has examined the association of APOE polymorphism with angiographically assessed stenosis and the number of diseased vessels among Pakistanis. The frequency of the APOE*4 allele in our sample was 11%, which is very similar to its reported frequency of 9% in a relatively older Pakistani control sample of 108 individuals [19] but slightly lower than the average frequency of 14% among Europeans [20].

Different epidemiologic studies have shown inconsistent results between APOE polymorphism and CAD severity and extent. We found significant association between APOE*4 and CAD stenosis like most reported studies. The risk of having significant CAD measured by stenosis was two times higher among APOE*4 carriers than other genotypes. However, we did not observe an association between APOE*4 and number of diseased vessels in our sample as a determinant of disease extent. In Women's Ischemic Syndrome Evaluation (WISE) study, APOE*4 was associated with both severity of stenosis and number of diseased vessels [3]. On the other hand, APOE*4 was found to be associated with number of diseased vessels and not with stenosis in a study conducted by Wang et al. [17]. The protective role of APOE*2 against CAD was not observed in our study, most likely due to its low frequency in this population. This is consistent with previous studies where the association of APOE*2 with CAD was only detected in large-scale datasets [5, 16]. Moreover, all the meta-analyses done so far contained a variety of covariates and the specific adjustment for different covariates was not clear [4, 10].

A limitation of our study is that cholesterol and other lipid values were available only in a subset of individuals, and in this subgroup *APOE* polymorphism did not show any association with lipid levels. However, we observed an expected trend of association of cholesterol levels among the three stenosis groups in this subgroup where highest levels of TC were observed in the \geq 70% stenosis group, intermediate in the 30–69% group, and lowest in the <30% group (Table 1). In our post hoc analysis in this subgroup with lipid levels, the association of *APOE**4 with CAD severity was independent of lipid levels, suggesting that we would have likely seen this independent association in the total sample, had the lipid data been available on all subjects.

In case of multifactorial disorders, it has always been challenging to establish a mechanistic relationship between a particular allele and disease development. Coronary artery disease results from a sequence of events starting from endothelial cell injury followed by sequestration of oxidized LDL particles, smooth muscle cell proliferation, and intense inflammatory reaction. In addition to the opposite effect of the *APOE**4 and *APOE**2 alleles on cholesterol levels, different *APOE* genotypes have diverse antioxidant properties too, among which *APOE**4 is the least antioxidant [21]. Furthermore, the ancillary role of *APOE* in lymphocyte recruitment makes it an important candidate gene responsible for inflammation in CAD [22]. The *APOE* polymorphism with divergent properties at cellular level could predispose to CAD by using multiple pathways that needs further probing.

5. Conclusion

In conclusion, we report the first study with the aim of evaluating the genetic determinants of CAD in Pakistanis, which confirms that persons with *APOE**4 have significant risk of developing coronary artery disease in the Pakistani population.

Conflict of Interests

The authors declare that there is no conflict of interests.

Acknowledgment

The authors acknowledge the Higher Education Commission of Pakistan for partial support of this project.

References

 C. J. O'Donnell and E. G. Nabel, "Genomics of cardiovascular disease," *The New England Journal of Medicine*, vol. 365, no. 22, pp. 2098–2109, 2011.

- [2] G. Abraham, O. G. Bhalala, P. I. W. de Bakker, S. Ripatti, and M. Inouye, "Towards a molecular systems model of coronary artery disease," *Current Cardiology Reports*, vol. 16, no. 6, article 488, 2014.
- [3] Q. Chen, S. E. Reis, C. M. Kammerer et al., "APOE polymorphism and angiographic coronary artery disease severity in the Women's Ischemia Syndrome Evaluation (WISE) study," *Atherosclerosis*, vol. 169, no. 1, pp. 159–167, 2003.
- [4] Y.-W. Yin, Q.-Q. Sun, B.-B. Zhang et al., "Association between apolipoprotein E gene polymorphism and the risk of coronary artery disease in Chinese population: evidence from a metaanalysis of 40 Studies," *PLoS ONE*, vol. 8, no. 6, Article ID e66924, 2013.
- [5] P. D. Zende, M. P. Bankar, P. S. Kamble, and A. A. Momin, "Apolipoprotein e gene polymorphism and its effect on plasma lipids in arteriosclerosis," *Journal of Clinical and Diagnostic Research*, vol. 7, no. 10, pp. 2149–2152, 2013.
- [6] A. M. Bennet, E. Di Angelantonio, Z. Ye et al., "Association of apolipoprotein e genotypes with lipid levels and coronary risk," *Journal of the American Medical Association*, vol. 298, no. 11, pp. 1300–1311, 2007.
- [7] S. B. Damani and E. J. Topol, "Emerging genomic applications in coronary artery disease," *JACC: Cardiovascular Interventions*, vol. 4, no. 5, pp. 473–482, 2011.
- [8] L. F. Abu. Marrzoq, F. A. Sharif, and A. A. Abed, "Relationship between ApoE gene polymorphism and coronary heart disease in Gaza Strip," *Journal of Cardiovascular Disease Research*, vol. 2, no. 1, pp. 29–35, 2011.
- [9] K. Wu, R. Bowman, A. A. Welch et al., "Apolipoprotein E polymorphisms, dietary fat and fibre, and serum lipids: the EPIC Norfolk study," *European Heart Journal*, vol. 28, no. 23, pp. 2930–2936, 2007.
- [10] J. E. Eichner, S. T. Dunn, G. Perveen, D. M. Thompson, K. E. Stewart, and B. C. Stroehla, "Apolipoprotein E polymorphism and cardiovascular disease: a HuGE review," *American Journal of Epidemiology*, vol. 155, no. 6, pp. 487–495, 2002.
- [11] F. D. A. Ince, A. Atay, M. Köseoğlu, M. Yeşil, and E. Deveci, "Relationship between severity of coronary artery disease and apolipoprotein E gene polymorphism," *Anadolu Kardiyoloji Dergisi*, vol. 10, no. 3, pp. 202–208, 2010.
- [12] H. Ward, P. N. Mitrou, R. Bowman et al., "APOE genotype, lipids, and coronary heart disease risk: a prospective population study," *Archives of Internal Medicine*, vol. 169, no. 15, pp. 1424– 1429, 2009.
- [13] P. Armitage, "Tests for linear trends in proportions and frequencies," *Biometrics*, vol. 11, no. 3, pp. 375–386, 1955.
- [14] T. H. Jafar, F. H. Jafary, S. Jessani, and N. Chaturvedi, "Heart disease epidemic in Pakistan: women and men at equal risk," *American Heart Journal*, vol. 150, no. 2, pp. 221–226, 2005.
- [15] T. H. Jafar, Z. Qadri, and N. Chaturvedi, "Coronary artery disease epidemic in Pakistan: more electrocardiographic evidence of ischaemia in women than in men," *Heart*, vol. 94, no. 4, pp. 408–413, 2008.
- [16] A. Aggarwal, S. Aggarwal, and V. Sharma, "Cardiovascular risk factors in young patients of coronary artery disease: differences over a decade," *Journal of Cardiovascular and Thoracic Research*, vol. 6, no. 3, pp. 169–173, 2014.
- [17] X. L. Wang, R. M. McCredie, and D. E. L. Wilcken, "Polymorphisms of the apolipoprotein E gene and severity of coronary artery disease defined by angiography," *Arteriosclerosis, Thrombosis, and Vascular Biology*, vol. 15, no. 8, pp. 1030–1034, 1995.

- [18] P. W. F. Wilson, R. H. Myers, M. G. Larson, J. M. Ordovas, P. A. Wolf, and E. J. Schaefer, "Apolipoprotein E alleles, dyslipidemia, and coronary heart disease: the framingham offspring study," *Journal of the American Medical Association*, vol. 272, no. 21, pp. 1666–1671, 1994.
- [19] M. Chaudhry, S. Hasnain, B. E. Snitz et al., "Association of APOE polymorphisms and stressful life events with dementia in a Pakistani population," *Neuroscience Letters*, vol. 570, pp. 42– 46, 2014.
- [20] D. Burman, A. Mente, R. A. Hegele, S. Islam, S. Yusuf, and S. S. Anand, "Relationship of the ApoE polymorphism to plasma lipid traits among South Asians, Chinese, and Europeans living in Canada," *Atherosclerosis*, vol. 203, no. 1, pp. 192–200, 2009.
- [21] M. Miyata and J. D. Smith, "Apolipoprotein E allele-specific antioxidant activity and effects on cytotoxicity by oxidative insults and β -amyloid peptides," *Nature Genetics*, vol. 14, no. 1, pp. 55–61, 1996.
- [22] T. Mazzone, "Apolipoprotein E secretion by macrophages: its potential physiological functions," *Current Opinion in Lipidol*ogy, vol. 7, no. 5, pp. 303–307, 1996.



BioMed Research International









International Journal of Genomics









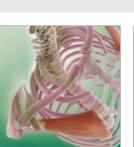


The Scientific World Journal

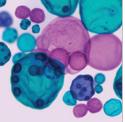


Genetics Research International

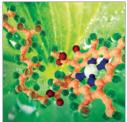
Archaea



Anatomy Research International



International Journal of Microbiology



Biochemistry Research International



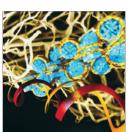


Journal of Marine Biology





International Journal of Evolutionary Biology



Molecular Biology International