ApoE ε2 and butyrylcholinesterase K variant are associated with coronary heart disease in type 2 diabetes

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Background and Aims: Type 2 diabetic patients are at an increased risk for developing coronary heart disease (CHD) over the normal population. Hyperlipidamia is known to be associated with both Type 2 diabetes and CHD. Genetic variants at the ApoE locus, ε4 and ε2, affect lipid levels differentially from the wildtype ε3 allele. The aim of this study was to investigate whether there is an association between ApoE and CHD in Type 2 diabetic patients. Genotyping for the three major alleles ε2, 3, 4, two promoter polymorphisms, -219G/T and -491A/T and two gene variants known to interact with ApoE, butyrylcholinesterase (BCHE) K (G1615A) and α-2 macroglobulin exon 18 insertion/deletion was carried out.
Materials and Methods: A case/control study of Type 2 diabetic patients from the UKPDS was undertaken. 295 patients with fatal MI (n = 45), nonfatal MI (n = 139), or angina (n = 111) were matched with 295 patients without evidence of heart disease for gender, age, duration of disease, fasting plasma glucose, blood pressure, smoking, LDL and HDL
Results: (table)

ApoE	**Fatal and nonfatal MI**		**BCHE: All heart disease**		
Allele	**Cases**	**Controls**	**Genotype**		**n**
			Cases	**Controls**	
ε 2	43	25	AA	AA	0
ε 3	273	297	nonAA	AA	4
ε 4	52	46	AA	nonAA	13
X^2, p	11.6, 0.04		nonAA	nonAA	274
RR, (95%CI)	1.81, (1.08-3.04)		McNemar statistic 4.765, p = 0.049		

Conclusion: ApoEε2 and BCHE K are significantly associated with MI in diabetic patients.