史凯蕾1*, 朱 毅1, 缪应新2, 郭新贵1.脂联素基因SNPs＋45T＞G和SNPs＋276G＞T与老年非糖尿病冠心病的相关性[J].中华老年多器官疾病杂志,2012,11(3):187~191

# 脂联素基因SNPs＋45T＞G和SNPs＋276G＞T与老年非糖尿病冠心病的相关性

# Two single nucleotide polymorphisms (＋45T＞G and＋276G＞T) of adiponectin gene and coronary artery diseases in the elderly without diabetes

**DOI：**

**中文关键词:** 脂联素; 单核苷酸基因多态性; 冠心病; 老年人

**英文关键词:**adiponectin; single nucleoside polymorphism; coronary artery disease; elderly

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**中文摘要:**

目的 探讨老年人脂联素基因SNPs＋45T＞G和SNPs＋276G＞T与老年非糖尿病冠心病的相关性。方法 选择2005年11月至2009年12月入住我院心血管内科病房, 行冠状动脉造影、年龄≥65岁的非糖尿病患者688例, 根据冠状动脉造影结果分为冠心病组396例和对照组292例。采用聚合酶链式反应/连接酶检测反应方法检测多态性位点。结果 SNPs＋45T＞G基因表型为突变型GG者发生冠心病的危险性较TT型者显著增加（OR = 2.65, P＜0.01）; SNPs＋276G＞T基因表型为GG型者发生冠心病的危险性较TT型者显著增加（OR = 2.36, P＜0.01）; 杂合子GT型者发生冠心病的危险性也较TT型者显著增加（OR = 1.66, P＜0.05）。logistic回归分析显示, SNPs＋45T＞G基因表型为GG型, SNPs＋276G＞T基因表型为GG和GT型是冠心病发病独立的危险因素。SNPs＋45T＞G和SNPs＋276G＞T位点存在连锁不平衡, 脂联素基因SNPs＋45T＞G基因表型为突变型GG型者SNPs＋276G＞T基因表型均为GG型, 而SNPs＋276G＞T基因表型为突变型TT型者SNPs＋45T＞G基因表型均为TT型, 即GGGG基因表型和TTTT基因表型, 且SNPs＋45T＞G和SNPs＋276G＞T位点基因表型为GGGG型者发生冠心病的危险性显著高于TTTT型者（OR = 4.77, P＜0.01）。结论 在老年非糖尿病者中, 脂联素基因SNPs＋45T＞G基因表型为GG型者和SNPs＋276G＞T基因表型为GG或GT型者可能是冠心病的易感人群。

**英文摘要:**

Objective To investigate the association between two single nucleotide polymorphisms (SNPs＋45T＞G and SNPs＋276G＞T) of adiponectin gene and coronary artery diseases(CAD) in elderly patients without diabetes. Methods Coronary angiography were performed in 688 subjects ≥65 years without diabetes who were admitted to department of cardiology during November 2005 to December 2009. The subjects were divided into CAD group and control group according to coronary angiography. Genotype of two SNPs was measured by polymerase chain reaction/ligase detection reaction (PCR/LDR) assay. Results At＋45position, the risk rate of CAD in GG genotype was significantly increased compared with that in TT genotype(OR = 2.65, P＜0.01). At＋276position, the risk rate of CAD in GG or GT genotype was significantly higher than that in TT genotype(GG: OR = 2.36, P＜0.01; GT: OR =1.66, P＜0.05). Logistic regression analysis showed that GG genotype at SNPs＋45T＞G, GG genotype and GT genotype at SNPs＋276G＞T were independent risk factors of CAD. Furthermore, adiponectin gene SNPs＋45T＞G and SNPs＋276G＞T displayed strong linkage disequilibrium. GG genotype was shown at SNPs＋276G＞T when SNPs＋45T＞G genotype was GG and TT genotype was shown at SNPs＋45T＞G when SNPs＋276G＞T genotype was TT, that is GGGG and TTTT genotypes. Homozygous GGGG subjects showed a significantly higher risk of CAD(OR = 4.77, P＜0.01) than homozygous TTTT subjects. Conclusion In non-diabetic elderly subjects, those with GG genotype at SNPs＋45T＞G, GG genotype and GT genotype at SNPs＋276G＞T are the susceptible population of CAD.

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