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基础医学

FADS1/FADS2基因多态性与冠心病发病的关联性分析

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摘要：

目的：探讨多不饱和脂肪酸代谢限速酶基因FADS1和FADS2单核苷酸多态性与冠心病的关系，阐明FADS1/FADS2在冠心病发生中的作用机制。方法：在我国北方汉族人群中选择237例冠心病患者和224例健康体检者作为研究对象，采用问卷调查表收集基本信息，应用聚合酶链式反应-限制性片段长度多态性（PCR-RFLP）方法检测FADS1基因的rs174556位点和FADS2基因的rs174617位点，采用遗传学软件UNPHASED 3.012和统计学软件SPSS 13.0分析2位点的联合作用及等位基因和基因型频数分布。结果：病例组和对照组的各位点基因型频数分布均符合Hardy-Weinberg平衡定律（*P*>0.05）。病例组和对照组rs174556位点的等位基因和基因型频数分布差异有统计学意义，病例组次等位基因T及基因型TT的携带者频数显著高于对照组（*P*=0.009,*P*=0.038）。rs174556-rs174617基因型系统与冠心病的发生无关联（*P*>0.05）.结论：在中国北方汉族人群中FADS1基因的rs174556位点基因多态性可能与冠心病发病有关联。

关键词： 冠心病；FADS1基因；FADS2基因；基因多态性

Association analysis between |polymorphisms of FADS1/FADS2 gene and coronary heart disease

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Abstract:

Objective To investigate the association between the single nucleotide polymorphisms of FADS1 and FADS2 (SNP) of polyunsaturated fatty acids metabolic rate-limiting enzymes and coronary heart disease(CHD) and to clarify the action mechanism of FADS1/FADS2 in the occurrence of CHD.Methods 237 patients diagnosed with CHD and 224 healthy controls from the Han population in Northern China were selected.Questionnaires were used to collect the basic information about individual objects.PCR-RFLP analysis was applied to detect the rs174556 SNP of FADS1 and the rs174617 SNP of FADS2.UNPHASED 3.012 and statistical software SPSS 13.0 were used to analyze the combined effect of two loci and frequency distribution of alleles and genotypes. Results The genotypic frequencies of various sites didn’[KG-*5]t deviate from Hardy-Weinberg equilibrium in both case and control groups (P>0.05).The allelic and genotypic frequency distributions of rs174556 in FADS1 gene showed significant difference between case and control groups.The frequency distributions of allele T and homozygote TT were significantly different between case and control groups (P=0.009,P=0.038).Conclusion Thegene polymorphisms of rs174556 in FADS1 gene is very likely to be associated with CHD in Chinese Han population.

Keywords: coronary heart disease FADS1 gene FADS2 gene gene polymorphism

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