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研究报告

低密度脂蛋白受体相关蛋白基因C766T多态性与阿尔茨海默氏病发病风险的Meta-分析

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摘要

运用Meta分析的方法综合评价低密度脂蛋白受体相关蛋白基因(low density lipoprotein receptor-related protein 1 gene, LPR-1)第三外显子C766T多态性与阿尔茨海默氏病(Alzheimer’s disease, AD)发病风险的关系。通过检索Medline、Cochrane图书馆和中国生物医学文献数据库(CBM)，纳入内容涉及LPR-1基因C766T多态性的基因型频率和(或)等位基因频率的独立病例对照研究。各文献满足研究方法相似，有综合的统计指标。研究年限为1997~2004年，语种不限。应用RevMan4.2软件进行统计分析。在AD组3764例和对照组3647例研究对象中，分别对基因型和等位基因频率做合并统计。各研究之间有显著的异质性，P<0.01，故采用随机效应模型分析合并结果。总体效应检验未发现CC基因型频率在病例对照之间统计学上的差异(Z=1.74, P=0.08, OR=1.17, 95%CI: 0.98~1.39)，C等位基因频率在病例对照之间也未发现差异(Z=1.31, P=0.19, OR=1.11, 95 % CI: 0.95~1.31)。Meta分析结果提示，LPR-1基因C766T多态性不是AD的主要风险因子，但尚不能完全排除其可能在AD发病中具有微弱的作用。

关键词

阿尔茨海默氏病；低密度脂蛋白受体相关蛋白基因；多态性；Meta分析

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Meta-Analysis of the Association of the LRP C766T Polymorphism with the Risk of Alzheimer’s Disease.

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Abstract

<P> A C-to-T polymorphism in exon 3 of the low density lipoprotein receptor-related protein 1 (LPR-1) gene has been implicated as a risk factor for Alzheimer's disease (AD). The authors performed a meta-analysis to investigate the association between the C766T polymorphism in the LPR-1 gene and the risk for AD. Nineteen references were retrieved through Medline, Cochran Library and CBM search from 1997 to 2004. Similar search strategies were applied to each of these databases. Studies which were eligible for the meta-analysis should meet the following inclusion criteria: presentation of original data and a cross-sectional design, AD as the outcome of interest, an odds ratio (or enough information to calculate it) reported to quantify the association between the frequencies of genotypes and/or alleles of LPR-1 gene C766T polymorphism and the risk for AD. All analyses were performed with Review Manager 4.2. A total of 3,560 AD patients and 3,476 control subjects were analyzed according to the random effect model because some between-study heterogeneity was found (P<0.01). The combined data statistics revealed that there was no statistical difference (test for overall effect: Z=1.74, P=0.08, OR=1.17, 95% CI: 0.98~1.39; Z=1.31, P=0.19, OR=1.11, 95%CI: 0.95~1.31) in the frequencies of allele and genotype between the AD patients and the controls. The meta-analysis showed that the LPR-1 polymorphism was not a major risk factor for AD, although a small effect of the polymorphism for AD risk could not be excluded. </P>

Key words

Alzheimer’s disease；LPR-1；polymorphism；Meta-analysis

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