GMR Genetics and Molecular Research
Online Journal
ISSN:1676-5680

Polymorphism of the *OLR1* 3'UTR potential microRNA binding site and risk of Alzheimer's disease: a meta-analysis

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Genet. Mol. Res. 13 (4): 10162-10172 (2014)
Received December 10, 2013
Accepted March 7, 2014
Published December 4, 2014
DOI http://dx.doi.org/10.4238/2014.December.4.10

ABSTRACT. Alzheimer's disease (AD) is a progressive neurodegenerative disorder that contributes to dementia in the elderly population. Genome-wide linkage analysis has identified chromosome 12p as the AD-susceptible region, which includes lectin-like oxidized low-density lipoprotein receptor 1 (*OLR1*). The *OLR1* +1073 C/T single-nucleotide polymorphism is located in the 3'-untranslated region of the gene and may influence the binding of regulatory microRNAs (miRNAs) and OLR1 protein homeostasis. A number of studies have reported an association between this variant and AD. However, the results are controversial. A meta-analysis of case-control studies examining the relationship between the *OLR1* +1073 C/T single-nucleotide polymorphism and AD risk was performed. Five studies were selected that included 2419 cases and 2381 controls. The results revealed a significantly decreased AD risk in the recessive model (TT *vs* TC + CC: odds ratio (OR) = 0.79, 95% confidence interval (CI) = 0.65-0.96). The control group in one of the studies was in Hardy-Weinberg disequilibrium, so we performed additional meta-analysis excluding this study. The significance was much more pronounced in

the recessive model (TT *vs* TC + CC: OR = 0.72, 95%CI = 0.62-0.85). Using miRanda and RNA hybrid methods, the polymorphic allele was shown to influence the binding of various miRNAs. Our results suggested that the +1073 C/T polymorphism decreased the risk of AD. The polymorphic allele was also predicted to affect the binding site of many miRNAs, which may explain the relationship between the +1073 C/T variant and AD.

Key words: Alzheimer's disease; Meta-analysis; MicroRNA; Oxidized low density lipoprotein receptor 1; Polymorphism

