Association of PS1 Gene Polymorphisms with Alzheimer’s Disease in Chinese Population: A Meta-Analysis of Case-Control Studies

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Abstract. The aim of our study was to assess the association of PS1 gene polymorphisms with Alzheimer’s disease in Chinese population using a meta-analysis. We identified 11 studies and found significant associations with Alzheimer’s disease for 1/2 genotype of PS1 gene polymorphism (odds ratio 0.69, 95% confidence interval 0.50–0.94, P=0.02), under dominant and recessive genetic models, associations were also exited. The heterogeneity existed among all studies (P<0.05). The present meta-analysis suggested a significant association of PS1 gene polymorphisms with Alzheimer’s disease in Chinese population. The 1/2 genotype of PS1 gene is associated with risk for Alzheimer’s disease in the Chinese population.

Keywords: Alzheimer’s disease (AD), Presently 1 gene, Polymorphism, Meta analysis.

1 Introduction

Alzheimer’s disease (AD) is a common cause of morbidity and mortality in the elderly. The key features of AD brains are neuronal and synapse loss, extracellular plaques composed of Amyloid-β peptides and intrapersonal neurofibrillary tangles consisting of hyperphosphorylated tau protein. Genetic factors are believed to contribute substantially to an individual’s risk for developing Alzheimer disease. The APOE4 allele is the only genetic factor that is unequivocally associated with an increased risk of late-onset AD [1, 2]. But it has been estimated to account for less than half of the genetic contribution to AD risk, Beyond this, nearly 1,000 papers have been published claiming or refuting association between Alzheimer disease and literally hundreds of putative risk alleles in other genes [3].

Wragg.et al. [4] firstly described an association with variation in balletic polymorphism of the presenilin 1 gene (PS1 gene in the intron region 3 to exon8). Subsequent studies of this polymorphism have shown inconsistent results. In some studies, PS1 allele1 was found to be associated with the risk for AD[5,6], while in other studies, PS1 allele1 was found to have no association with the risk for AD [7,8].

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In China, genetic association studies are also widely carried out to evaluate the relationship between these three polymorphisms and Alzheimer disease. Like the same situation in the worldwide populations, the obtained conclusions in Chinese populations are also inconsistent.

Therefore, we performed a meta-analysis with the aim of assessing the association of PS1 gene polymorphism with Alzheimer’s disease in Chinese case-control studies.

2 Methods

2.1 Selection of Studies

We conducted a systematic computerized literature search for studies published before 12 August 2010. We searched the Chinese Biomedicine Database, the China National Knowledge Infrastructure platform, Pubmed and Medline, using the search terms ‘Alzheimer’s disease’, ‘PS-1’, ‘polymorphism’, ‘China’ and ‘Chinese’, without limiting to specific language. The full texts of the retrieved studies were carefully read to assess if they should be included in the meta-analysis. All of the references cited in the studies were also searched to identify potentially relevant articles.

2.2 Selection Criteria

The data were included in the following meta-analysis if the research papers fulfilled the subsequent two conditions: the association of Alzheimer’s disease and PS-11/2 polymorphism was examined in Chinese individuals; the genotype frequencies were reported in both patients and controls. After that, we re-evaluated the Hardy-Weinberg equilibrium (HWE) for every included study result, and the studies that did not follow HWE were excluded.

2.3 Data Extraction

Two workers examined the retrieved studies to extract…” Instead, try “R.B.G. thanks …” Put sponsor acknowledgments in the unnumbered footnote on the first page. the standard information from independent studies. From each study, the following information was collected: first author, year of publication, distribution of genotypes and alleles in both control and AD groups, average case and control characteristics (age, sex, and sample size).

2.4 Statistical Analysis

The strength of the association between the three gene polymorphisms and AD was evaluated by the odds ratio and the corresponding 95% confidence interval (CI). Based on the individual OR, a pooled OR was estimated, of which the statistical significance was determined using the Z-test. Where there was heterogeneity in studies, a pooled OR was estimated by the random effects model; otherwise, the fixed effects model was used. Funnel plots were used to investigate publication bias. All analyses were performed with Cochrane RevMan software version 5.0 (Cochrane Library, UK).