ASSOCIATION ANALYSIS BETWEEN POLYMORPHISMS OF GENES AND ALZHEIMER’S DISEASE IN CHINESE POPULATION

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As the development of Chinese economy, the average life span is extended. Chronic and multiple factorial diseases have become one of the wide-spreading and serious problems in aging societies. In China, there are lots of people suffering from neurodegenerative disorder such as Alzheimer’s diseases (AD). The majority of AD cases are late-onset Alzheimer’s disease (LOAD). We still don’t fully understand what causes LOAD, but it is generally agreed that LOAD is multi-factorial disease, having environmental and genetic risk factors. It is widely accepted that APOE-ε4 is a major genetic risk factor of LOAD. However APOE-ε4 can only account for about 50% of the susceptibility to LOAD, which strongly suggests that there are additional risk factor genes, and candidates continue to be identified in this exciting area of researches. Results of case-control studies of candidate genes are found to be different among populations. Some of high risk genes in European are not concerned as risk factors in Asian, indicating that susceptibility genes have population specific effects. Therefore, we focus on genetic association studies between genetic variants and LOAD on a population scale, and trying to identify important polymorphisms or a combination of genes/loci that may determine differences in disease risks to Chinese populations. Based on the biological functions, bio-informative information and results of population studies on LOAD, we selected 14 candidate genes and performed association studies on Chinese population. Clarifying the genetic contribution to the disease in Chinese populations will lead to revolutionize diagnosis, targeted treatments and prevention.