



Positive association between PPARD rs2016520 polymorphism and coronary heart disease in a Han Chinese population

H.D. Ye^{1*}, Y.R. Li^{1*}, Q.X. Hong^{1*}, A.N. Zhou¹, Q.L. Zhao², L.M. Xu¹, M.Q. Xu³, X.T. Xu¹, L.L. Tang¹, D.J. Dai¹, D.J. Jiang¹, Y. Huang¹, D.W. Wang⁴ and S.W. Duan¹

¹Zhejiang Provincial Key Laboratory of Pathophysiology, School of Medicine, Ningbo University, Ningbo, Zhejiang, China

²Yinzhou People's Hospital, Ningbo University, Ningbo, Zhejiang, China

³Bio-X Institutes, Key Laboratory for the Genetics of Developmental and Neuropsychiatric Disorders, Ministry of Education, Shanghai Jiao Tong University, Shanghai, China

⁴Institute of Hypertension and Department of Internal Medicine, Tongji Hospital, Tongji Medical College, Huazhong University of Science and Technology, Wuhan, China

*These authors contributed equally to this study.

Corresponding author: S.W. Duan

E-mail: duanshiwei@nbu.edu.cn

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ABSTRACT. PPARD encodes peroxisome proliferator-activated receptor delta, which has been shown to play an important role in controlling lipid metabolism and atherosclerosis. In this case-control study, we explored the relationship between PPARD rs2016520 polymorphism and coronary heart disease (CHD) in a Han Chinese population. A total of 657 CHD cases and 640 controls were included in the association study. rs2016520 polymorphism genotyping was performed using the melting temperature-shift polymerase chain reaction method. The PPARD rs2016520-G allele reduced CHD risk by 17.9% ($\chi^2 = 5.061$,

P = 0.025, OR = 0.821, 95%CI = 0.692-0.975). Furthermore, a significant difference in CHD risk was observed for the PPARD rs2016520 polymorphism in the dominant model (AG + GG vs AA: $\chi^2 = 4.751$, degrees of freedom (df) = 1, P = 0.029, OR = 0.784, 95%CI = 0.631-0.976). Analysis by age suggested that the G-allele decreased CHD risk by 14.8% in ages greater than 65 years ($\chi^2 = 4.446$, P = 0.035, OR = 0.852, 95%CI = 0.684-1.060). In contrast, meta-analysis of PPARD rs2016520 among 3732 cases and 5042 controls revealed no association between PPARD rs2016520 and CHD (P = 0.19). We found that the PPARD rs2016520-GG genotype decreased CHD risk in a Han Chinese population. Moreover, we found an association between serum high-density lipoprotein cholesterol level and PPARD rs2016520 in senior individuals aged ≥ 65 years. The meta-analysis revealed no association between PPARD rs2016520 and CHD, suggesting ethnic differences in the association between the PPARD locus and CHD.

Key words: Coronary heart disease; Meta-analysis; PPARD; Polymorphism; rs2016520