

Association of *TIRAP* (*MAL*) gene polymorhisms with susceptibility to tuberculosis in a Chinese population

Y.X. Zhang¹, Y. Xue^{1,5}, J.Y. Liu^{1,6}, M.Y. Zhao¹, F.J. Li², J.M. Zhou³, H.J. Wang⁴ and J.C. Li¹

¹Institute of Cell Biology, Zhejiang University, Zhejiang, China

Corresponding author: J.C. Li E-mail: lijichen@zju.edu.cn

Genet. Mol. Res. 10 (1): 7-15 (2011) Received November 20, 2010 Accepted December 19, 2010 Published January 4, 2011 DOI 10.4238/vol10-1gmr980

ABSTRACT. Toll-interleukin 1 receptor (TIR) domain containing adaptor protein (TIRAP; also known as MAL) is an essential adaptor molecule in Toll-like receptor signaling, involved in activating the innate immune response during infection. Genetic variations in the *TIRAP* gene may influence human susceptibility to infectious disease. To date, in the Chinese population, a possible predisposition of *TIRAP* gene variants to tuberculosis has not been reported. We investigated whether *TIRAP* gene polymorphisms are associated with the development of tuberculosis in a Chinese population. We investigated all the single-nucleotide polymorphisms (SNPs) within the *TIRAP* exon 5 in a case-control study of 212 patients with tuberculosis and 215 controls in a Chinese population. Genotyping was performed to identify the polymorphisms of *TIRAP* gene by PCR-DNA sequencing method. Haplotypes for the *TIRAP* gene variants were constructed using Haplo-

²Hangzhou Red Cross Hospital, Hangzhou, China

³Jilin Academy of Traditional Chinese Medicine Sciences, Changchun, China

⁴The Sixth Hospital of Shaoxing, Shaoxing, China

⁵Henan University of Science and Technology, Luoyang, China

⁶Department of Cell Biology, Hangzhou Normal University, Hangzhou, China

view version 4.2. Six polymorphisms of the SNPs listed in the National Center for Biotechnology Information database were detected in these Chinese tuberculosis patients. It was found that both the frequency of the 286A allele (odds ratio (OR) = 13.37; 95% confidence interval (CI) = 0.75-238.3; P < 0.01) and the frequency of 286AG genotype (OR = 13.57; 95%CI = 0.76-242.5; P < 0.01) were significantly higher in patients than in healthy controls. However, two other SNPs, C539T and C558T, reported to be associated with tuberculosis in other populations, were found not to be associated with tuberculosis in this Chinese population. We conclude that TIRAP G286A (D96N) polymorphism is associated with susceptibility to tuberculosis and may be a new risk factor for the development of tuberculosis in China.

Key words: Innate immunity; Single-nucleotide polymorphisms; Toll-interleukin 1 receptor domain containing adaptor protein; Disease susceptibility; Tuberculosis