

Polymorphic Allele of Human MRC1 Confer Protection against Tuberculosis in a Chinese Population

Xing Zhang¹, Feng Jiang², Liliang Wei³, Fujian Li⁴, Jiyan Liu^{1,5}, Chong Wang¹, Menyuan Zhao¹, Tingting Jiang¹, Dandan Xu¹, Dapeng Fan⁴, Xiaojun Sun³, Ji-Cheng Li¹, ?

1. Institute of Cell Biology, Zhejiang University, Hangzhou 310058, P.R.China; 2. Dongzhimen Hospital Affiliated to Beijing University of Chinese Medicine, Beijing 100700, P.R. China; 3. The Sixth Hospital of Shaoxing, Shaoxing 312000, P.R. China; 4. Hangzhou Red Cross Hospital, Hangzhou 310003, P.R. China; 5. Department of Cell Biology, Hangzhou Normal University, Hangzhou 310036, P.R. China.

Abstract :

Mannose receptor is a member of the C-type lectin receptor family involved in pathogen molecular-pattern recognition, and plays a critical role in shaping host immune response. Single nucleotide polymorphisms (SNPs) in the *MRC1* gene may affect expression levels and differences in the structure and function of proteins in different individuals, thereby affecting individual susceptibility to pulmonary tuberculosis. However, to date, *MRC1* polymorphisms associated with susceptibility to pulmonary tuberculosis have not yet been reported. The present study aimed to investigate potential associations of SNPs in the *MRC1* gene with pulmonary tuberculosis in a Chinese population. Six SNPs (G1186A, G1195A, T1212C, C1221G, C1303T and C1323T) in exon 7 of the *MRC1* gene were genotyped using the PCR and DNA sequencing methods in the pulmonary tuberculosis patients and the healthy controls. Linkage disequilibrium analysis was performed between polymorphic sites. The study found that the allele frequency of G1186A (rs34039386) of the *MRC1* gene in a Chinese population was higher in the pulmonary tuberculosis group than the healthy control group. There was a significant difference in frequency distribution between the two groups ($P = 0.037$; OR = 0.76; 95% CI, 0.58-0.98). Genotypic analysis also indicated that the AG genotypes in a Chinese population were significantly correlated with pulmonary tuberculosis ($P < 0.01$; OR = 0.57; 95% CI, 0.37-0.87). After adjustment for age and gender, G1186A sites were found to be dominant ($P < 0.01$; OR = 0.59; 95% CI, 0.40-0.87), over-dominant ($P = 0.045$; OR = 0.69; 95% CI, 0.47-0.99) and additive models ($P = 0.041$; OR = 0.76; 95% CI, 0.59-0.99) in association with pulmonary tuberculosis. But, no association was found between the other 5 SNPs (G1195A, T1212C, C1221G, C1303T and C1323T) and tuberculosis ($P > 0.05$). This study is the first to report that genetic variants in the *MRC1* gene can be associated with pulmonary tuberculosis in a Chinese population, and may reduce the risk of infecting pulmonary tuberculosis. This also provides a new experimental basis to clarify the pathogenesis of pulmonary tuberculosis.

Key Word :

Mannose receptor, MRC1 gene, Tuberculosis, Single-nucleotide polymorphism, Chinese.