

# Association of CTLA4 Gene Polymorphisms with Susceptibility and Pathology Correlation to Pulmonary Tuberculosis in Southern Han Chinese

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## Abstract :

The cytotoxic T lymphocyte antigen-4 (*CTLA4*) gene is a key negative regulator of the T lymphocyte immune response. It has been found that *CTLA4* +49A>G (rs231775), +6230G>A (rs3087243), and 11430G>A (rs11571319) polymorphisms are associated with susceptibility to many autoimmune diseases, and can down-regulate the inhibition of cellular immune response of *CTLA4*. Three SNPs in *CTLA4* were genotyped by using the PCR and DNA sequencing methods in order to reveal the susceptibility and pathology correlation to pulmonary tuberculosis in Southern Han Chinese. We found that the frequency of *CTLA4* +49AG genotype in the pulmonary tuberculosis patients (38.42%) was significantly lower than that of the healthy controls (49.77%), ( $P_{\text{cor}}=0.038$ , OR 0.653, 95% CI 0.436-0.978). But, no associations were found between the other 2 SNPs (+6230G>A, 11430G>A) and tuberculosis ( $P>0.05$ ). Haplotype analysis showed that the frequency of haplotype AGG in the healthy controls group (6.9%) was significantly higher than the pulmonary tuberculosis patients group (1.4%), (global  $P=0.005$ ,  $P_{\text{cor}}=0.0002$ , OR 0.183, 95% CI 0.072-0.468). In addition, haplotype GGA was found to be significantly related to tuberculosis with double lung lesion rather than single lung lesion ( $P_{\text{cor}}=0.042$ ). This study is the first to report that genetic variants in the *CTLA4* gene can be associated with pulmonary tuberculosis in Southern Han Chinese, and *CTLA4* +49AG genotype as well as haplotype AGG may reduce the risk of being infected with pulmonary tuberculosis. The GGA haplotype was related to tuberculosis with double lung lesion, which provides a new experimental basis to clarify the pathogenesis of pulmonary tuberculosis.

## Key Word :

Pulmonary Tuberculosis, Single-nucleotide polymorphism, CTLA4 gene, Southern Han Chinese, Lung lesion.

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