

Interleukin-12B & interleukin-10 gene polymorphisms in pulmonary tuberculosis

S. Prabhu Anand, P. Selvaraj, M.S. Jawahar, A.R. Adhilakshmi & P.R. Narayanan

Tuberculosis Research Centre (ICMR), Chennai, India

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Background & objectives: Cytokines play an important role in anti-tuberculosis immune response. Skewing of immunity from protective to pathogenic may involve a shift in Th1-Th2 paradigm. Cytokine gene polymorphism is known to be associated with functional differences in cytokine regulation and altered clinical performance in a variety of diseases. The aim of this study was to know whether Interleukin-12B 3' UTR (Taq1) (A/C) and Interleukin-10 (-1082 G/A) gene polymorphisms were associated with susceptibility to pulmonary tuberculosis.

Methods: IL -10 (-1,082 G/A) and IL-12B gene polymorphisms were studied in 132 pulmonary TB (PTB) patients and 143 normal healthy subjects (NHS), using DNA based polymerase chain reaction (PCR) with sequence specific primers and restriction digestion.

Results: The allelic as well as genotypic frequencies of Interleukin -10 (-1082) and Interleukin -12B (3'UTR Taq 1) did not differ significantly between the patients and controls.

Interpretation & conclusion: Our findings suggested that IL -10 (-1082 G/A) and IL -12B 3'UTR (Taq I) (A/C) gene polymorphisms were not associated either with susceptibility or resistance to pulmonary tuberculosis in the south Indian population.

Key words Cytokine - IL-10 - IL-12B - polymorphism

Mycobacterium tuberculosis is responsible for at least 1.5 million deaths per year worldwide. One third of the world's population is infected with *M. tuberculosis*¹. But development of tuberculosis depends on complex environmental factors and host genetic factors. Case control studies have found significant associations between tuberculosis and gene polymorphisms like human leukocyte antigen (HLA)² and non-HLA genes such as natural resistance associated macrophage protein (NRAMP1)³, vitamin

D receptor (VDR)⁴, mannose binding lectin (MBL)⁵, interleukin-1 (IL-1)⁶, IL-10⁷ and IL-12 receptor⁸. Interaction between the pathogen and host immune response probably determines the development or resistance to tuberculosis. Moreover, cytokines play an important role in anti-tuberculosis immune response⁹. Studies on mouse models have equated Th1 response to protective cell-mediated immunity and Th2 response to disease status^{10,11}. IL-12 is a regulatory cytokine which connects the innate and

adaptive host response to mycobacterium and exerts its effects mainly through induction of interferon gamma (IFN- γ)¹². Deleterious mutations in genes of IL-12B encoding IL-12p40, a subunit of IL-12 and IL-12R have been shown to be associated with susceptibility to infections caused by poorly pathogenic mycobacterium¹³. Studies also have shown that IL-10, a Th2 cytokine is a potent inhibitor of T cell functions, Major histocompatibility complex (MHC) class II expression, antigen specific proliferation and IFN- γ synthesis¹⁴. Moreover, IL-10 is inversely correlated in human tuberculosis¹⁵. Hence allelic variations in the coding as well as regulatory regions of IL-10 and IL-12B genes that are associated with differential cytokine levels might be expected to have an impact on susceptibility to tuberculosis. In this study, we therefore investigated IL-10 (-1082 G/A) and IL-12B (3'UTR, TaqI A/C) gene polymorphisms in pulmonary tuberculosis (PTB) patients and normal healthy subjects in south India.

Material & Methods

Patients attending Tuberculosis Research Centre (TRC), Chennai, from January 2004 to December 2005, with respiratory symptoms and radiographic abnormalities suggestive of PTB and sputum positive for *M. tuberculosis* by both smear and culture were included. Normal healthy subjects (NHS) included were staffs, trainees and students of TRC who volunteered to donate blood, were clinically normal at the time of blood collection. The study group consisted of 132 PTB patients (mean age \pm SD: 35.5 \pm 12.3 yr) and 143 NHS (mean age \pm SD: 29.7 \pm 9.5 yr). Among the 132 patients, 75 were males and in 143 NHS, 84 were males. The patients and the healthy normal subjects were south Indian Tamil speaking

population of Dravidian descent living in and around Chennai, Tamil Nadu. Blood samples were collected after an informed consent was obtained. The study was approved by the ethical committee of the institute.

Venous blood (20 ml) was collected, defibrinated and the peripheral blood mononuclear cells (PBMC) were separated by Ficoll-Hypaque density gradient centrifugation¹⁶. DNA was extracted from a portion of lymphocytes as described earlier¹⁷ and the concentration and purity of DNA estimated spectrophotometrically. IL-10 genotyping was studied using amplification refractory mutation system-polymerase chain reaction (PCR) method as described earlier¹⁸. Single nucleotide polymorphism (SNP) at the IL-12B 3'UTR (Taq I) was determined using PCR-RFLP as described previously¹⁹.

Allele and genotype frequencies were calculated by direct allele and genotypic counts and expressed as percentage. Comparison between patients and controls was done using 2x2 contingency tables and χ^2 tests with Yates correction (Stat calc programme, Epi Info Version 6.04, CDC, Atlanta, GA, USA). The allele frequencies were also tested for Hardy-Weinberg equilibrium by calculating allele frequencies using Pearson's χ^2 tests with one degree of freedom²⁰.

Results & Discussion

The allele and genotype frequencies of IL-12B (A/C) polymorphism did not differ significantly between normal healthy subjects (NHS) and pulmonary tuberculosis patients (PTB) ($P=0.98$, 0.95 and 0.59 for genotypes CC, CA and AA respectively). Similarly, the allele and genotype frequencies of IL-10-1082 (G/A) polymorphism did not vary significantly between NHS

Table. Allele and genotype frequencies of IL-12 and IL-10 in normal healthy subjects (NHS) and pulmonary tuberculosis patients (PTB)

IL-12 and IL-10 polymorphisms	Allele frequencies		Genotypes	Genotype frequency % (n)	
	NHS (n=143)	PTB (n=132)		NHS (n=143)	PTB (n=132)
IL-12 p40 3'UTR (A/C)	C - 0.42	0.43	CC	19.60 (28)	18.94 (25)
	A - 0.58	0.57	CA	44.00 (63)	48.48 (64)
			AA	36.40 (52)	32.58 (43)
IL-10 (-1082 G/A)*	A - 0.74	0.77	AA	52.14 (73)	56.06 (74)
	G - 0.26	0.23	AG	43.57 (61)	41.67 (55)
			GG	4.29 (6)	2.27 (3)

n = number of subjects

Number in parentheses represents number of subjects positive in each group

* In case of IL-10 polymorphism, n=140, 3 failed PCR (NHS)

Differences in genotype frequency between PTB and NHS were not significant

and PTB ($P=0.51$, 0.84 and 0.55 for genotypes AA, AG and GG respectively) (Table). The genotypes of both the cytokine polymorphism were within Hardy-Weinberg equilibrium.

Candidate gene-based case-control studies found several single nucleotide polymorphisms (SNPs) with a moderate effect on risk of tuberculosis²¹. We studied the associations of single nucleotide polymorphisms present in two vital cytokine genes namely IL-12B (3'UTR Taq 1) and IL-10 (-1082). The genotypes of IL-12B (3'UTR Taq 1) and IL-10 (-1082) did not differ significantly between patient group and controls. Our results suggested a lack of association of these single nucleotide polymorphisms with tuberculosis. The results were in concordance with a study wherein no association between IL-12B 3'UTR A/C polymorphism and tuberculosis was observed both in whites as well as African American populations²². Similarly, no association between IL-10 (-1082) and tuberculosis in Spanish population has been reported¹⁸. Contrary to our results, association between IL-12B intron 2-repeat marker (ATT) as well as haplotypes composed of IL-12B promoter, intron 2, intron 4 and 3'UTR alleles with tuberculosis has been reported in Hong Kong Chinese population²³. Moreover, heterozygosity for the -1082 polymorphism of the IL-10 promoter has been shown to be associated with tuberculosis susceptibility in a Cambodian population⁷. The apparent inconsistency between these studies could be due to ethnic-specific genetic variations greatly influencing host immunity to tuberculosis, causing differential susceptibility to tuberculosis.

Since human susceptibility to tuberculosis is a complicated polygenic trait, interactive effects between the polymorphism studied and other SNPs in human genes (including those in IFN- γ network), need to be evaluated.

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Reprint requests: Dr P. Selvaraj, Assistant Director , Department of Immunology, Tuberculosis Research Centre (ICMR)
Mayor V.R. Ramanathan Road, Chetput, Chennai 600031, India
e-mail: psraj21@hotmail.com