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Short communication

Polymorphisms in *SP110* are not associated with pulmonary tuberculosis in Indonesians

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ABSTRACT

Despite being high transmissible, *Mycobacterium tuberculosis* (*M. tuberculosis*) infection causes active disease in only 5–10% of disease-susceptible individuals. This has instigated interest in studying potentially underlying genetic host factors and mechanisms in tuberculosis (TB). The recent identification of the Intracellular pathogen resistance 1 (*Ipr1*) gene, which plays a major role in controlling *M. tuberculosis* susceptibility and infection severity in mice (Pan et al., 2005), has prompted studies on its human homolog; *SP110* in humans. Association of *SP110* SNPs with pulmonary TB were first reported in a study on West African families (Tosh et al., 2006). Subsequent attempts to replicate these findings in other populations, including another West African (Ghanaian) cohort (Thye et al., 2006), however, were unsuccessful. Here we have genotyped 20 SNPs located in the *SP110* gene, including the previously TB associated variants; rs2114592 and rs3948464, for the first time in a South East Asian cohort from Indonesia. Our study did not reveal any statistically significant associations between *SP110* SNPs and pulmonary TB. In addition, a meta-analysis of the two previously TB associated SNPs revealed that these are not associated with TB, further confirming the lack of convincing evidence for *SP110* to be implicated in TB susceptibility, as yet in humans.

1. Introduction

Pulmonary tuberculosis (TB) is primarily an infection of the lung that is spread by inhaling droplets from coughing or sneezing of affected individuals. Even though TB is treatable, it remains one of the top infectious causes of mortality, with close to 9 million new cases and a high fatality rate of 1.7 million, annually. In order to be able to stop TB from spreading and claiming additional lives, there is a need for enhanced knowledge on how to control host infection and disease development (North and Jung, 2004; Ottenhoff et al., 2005). Studies on TB heredity in twins and other forms of familial aggregation (Baghdadi et al., 2006; Bellamy et al., 2000; Jepson et al., 2001; Kallmann and Reisner, 1943), have yielded significant evidence for genetic influences on TB susceptibility (Alcais and Abel, 2004; Rieder, 2003), and encouraged further host genetic studies to decipher mechanism of TB susceptibility and pathogenesis.

Abbreviations: TB, tuberculosis; SNP, single nucleotide polymorphism; HIV, Human immunodeficiency virus; Ct, cycle threshold; d.f., degree freedom; MAF, minor allele frequency; HWE, Hardy Weinberg equilibrium; QC, quality control; WHO, World Health Organization; OPA, oligo pool assay; MH, Mantel–Haenszel; LD, linkage disequilibrium; D', D prime; OR, Odds ratio; C.I., confidence interval; GWAS, genome wide association scan.

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