



Vitamin D receptor gene *FokI*, *TaqI*, *BsmI*, and *ApaI* polymorphisms and susceptibility to pulmonary tuberculosis: a meta-analysis

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ABSTRACT. The aim of this study was to determine whether vitamin D receptor (*VDR*) genetic polymorphisms are associated with the susceptibility to pulmonary tuberculosis (PTB). MEDLINE and Embase databases and manual literature searches were used. A meta-analysis was conducted on the associations between the *VDR FokI*, *TaqI*, *BsmI*, and *ApaI* polymorphisms and PTB susceptibility. A total of 16 studies comprising 3231 patients and 3670 controls met the study inclusion criteria, consisting of 14 studies on the *VDR FokI* polymorphism, 13 on the *VDR TaqI* polymorphism, 8 on the *VDR BsmI* polymorphism, and 5 on the *VDR ApaI* polymorphism. Meta-analysis of the *VDR FokI* polymorphism showed no association between PTB and the f allele of the *VDR FokI* polymorphism (long variant) in all subjects (OR = 1.070, 95%CI = 0.979-1.169, P = 0.134). In contrast, after stratification by ethnicity, meta-analysis indicated that the *VDR FokI* F allele (short variant) was associated with PTB risk in an East Asian population (OR = 1.507, 95%CI = 1.192-1.906, P = 0.001). Meta-analysis revealed no association between PTB susceptibility and the *VDR TaqI* t allele in all study subjects (OR = 0.986, 95%CI = 0.839-1.159, P = 0.866)

or in individual ethnic populations. Furthermore, a risk of PTB was not associated with the *BsmI* and *ApaI* polymorphisms. This meta-analysis suggested that the VDR *FokI* polymorphism is associated with a susceptibility to PTB in East Asians.

Key words: Vitamin D receptor; Meta-analysis; Polymorphism; Pulmonary tuberculosis