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Impact of Vitamin D Receptor Gene Polymorphisms on the Susceptibility to Tuberculosis among Iraqi Patients

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Abstract: Tuberculosisis a cosmopolitan disease caused by *Mycobacterium tuberculosis*. Even within similar environmental conditions there is obvious variation in the incidence of this disease which suggests genetic factor effects. This study aimed to assess the effect of vitamin D receptorgene polymorphisms on the susceptibility for tuberculosis among Iraqi patients. A total of 62 patients with tuberculosis and 48 apparently healthy controls were recruited for this case/control study. DNA was extracted from peripheral blood, and vitamin D receptor gene regions corresponding the FokI, BsmI and TaqI polymorphisms were amplified with specific primers using PCR. Genotyping was achieved by restriction fragment length polymorphisms. A significant association was found between homozygote mutant genotype of FokI (ff) and susceptibility to TB (ff vs. FF: OR=10.452, 95%CI=1.253-87.167, P=0.03). Allele f of this polymorphism was more prevalent among patients compared to controls (OR=3.333, 95%CI=1.635-6.797, P=0.001). On the other hand, allele t of TaqI polymorphism seems to have a protective role against TB as it had significantly higher frequency in controls compared to TB patients (OR=0.317, 95%CI=0.136-0.738, *P*=0.008). Therefore, the homozygote mutant genotype of FokI could be considered as a risk factor for tuberculosis, while allele t of TaqI has a protective role against the disease.

Keywords: tuberculosis, vitamin D receptor, FokI, BsmI and TagI polymorphisms.

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