Investigation of the Association of Vitamin D Receptor Gene Polymorphism in Female Genital: Tuberculosis Cases

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Abstract: Objective: To elucidate the role of (ApaI&TaqI) VDR gene polymorphism in the pathogenesis of female genital tuberculosis (FGTB) cases. Background: Female genital TB represents about 15-20% of total extra-pulmonary TB (EPTB). Female subjects with vitamin D deficiency have been shown to be at higher risk of pulmonary TB as well as FGTB. In same context few functional polymorphism in vitamin D receptor (VDR) gene has been considered as an important genetic risk factor that modulate the development of FGTB. Therefore we aimed, to elucidate the role of (ApaI&TaqI) VDR gene polymorphism in the pathogenesis of FGTB. Study design: Case-Control study. Sample size: Cases (60) and Controls (60). Study site: Department of Obstetrics & Gynecology & Department of Microbiology, K.G.M.U. Lucknow, (UP). Inclusion criteria: Cases: Women with age group 20-35 years, premenstrual endometrial aspiration collected and included in the study, those were positive with acid-fast bacilli (AFB)/ TB-PCR/ LJ culture/ liquid culture. Controls: Women with age group 20-35 years having no history of ATT and all test negative for TB recruited as control. Exclusion criteria: -Women with endometriosis, polycystic ovaries (PCOD), positive on Chlamydia & gonorrhea, already on anti-tubercular therapy (ATT) excluded. Materials and Methods: Blood samples were collected in EDTA tubes from cases and controls stored at -20°C. Genomic DNA extraction was carried out by salting-out method. Genotyping of VDR gene (ApaI&TaqI) polymorphism was performed by using single amplification refractory mutation system (ARMS) PCR technique. PCR products were analyzed by electrophoresis on 2% agarose gel. Statistical analysis was done by SPSS16.3 software & computing odds ratio (OR) with 95% CI. Results: Increased risk of female genital tuberculosis was observed in AA genotype (OR =1.1419-6.212 95% CI, P*<0.036) and A allele (OR =1.255-3.518, 95% CI, P* < 0.006) in FGTB as compared to controls. Moreover A allele was found more frequent in FGTB patients. No significant difference was observed in TaqI gene polymorphism of VDR gene. Conclusion: The ApaI polymorphism is significantly associated with etiology of FGTB and plays an important role as a genetic risk factor in FGTB women.

Keywords: ARMS, ATT, EPTB, FGTB, VDR

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