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Original Article

Assessment of possible association between rs3787016 and prostate cancer risk in Serbian population

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Abstract: Recent study, which included meta-analysis of two genome-wide association studies (GWAS), followed by a replication, identified the association between single nucleotide polymorphism (SNP) rs3787016 at 19p13 and prostate cancer (PCa) risk. Considering possible genetic differences between populations, we conducted the study in order to evaluate the association of this polymorphism with prostate cancer risk in Serbian population. 261 samples of peripheral blood were obtained from the patients with PCa and 257 samples from patients with benign prostatic hyperplasia (BPH). 106 volunteers who gave samples of bucal swabs comprised the control group. For individuals diagnosed with PCa clinicopathological characteristics including serum prostate-specific antigen (PSA) level at diagnosis, Gleason score (GS) and clinical stage were determined. Genotypization of rs3787016 was performed by using Taqman® SNP Genotyping Assay. The differences in alelle and genotype frequencies between analyzed groups of subjects were performed by using PLINK, SPSS 17.0 for Windows and SNPStats statistical software. No significant association of rs3787016 with PCa risk was determined comparing allele and genotype frequencies among group of patients diagnosed with PCa and the control group, as well as among groups of patients with PCa and BPH. Also, no evidence of association of rs3787016 with PCa risk was shown using tests for association under dominant and recessive genetic models. SNP rs3787016 showed no significant association with standard prognostic parameters regarding PCa progression, nor with the risk of disease progression assessed according to two different risk classification systems. (IJCEM1210001).

Keywords: Prostate cancer, association study, single nucleotide polymorphism (SNP)

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