



Association of *LTβR* gene polymorphisms with prostate volume in benign prostatic hyperplasia in the Korean population

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ABSTRACT. The lymphotoxin-β receptor (*LTβR*) gene is involved in autoimmune disease and inflammatory disorder development, but the relationship between *LTβR* and benign prostatic hyperplasia (BPH) is unclear. In total, 222 with BPH were examined for 3 single nucleotide polymorphisms [rs3759333 (-1387C/T), rs3759334 (-1326A/G), and rs2364480 (Ala172Ala)] located in the promoter and coding regions of *LTβR* using direct sequencing. The genotype distributions of rs3759334 were associated with prostate volume larger than 40 g. There were significant differences between the small (<40 g) and large (≥40 g) group subjects [codominant 1 model: odds ratio (OR) = 4.65, 95% confidence interval (CI) = 1.95-11.09, P = 0.001; dominant model: OR = 4.91, 95%CI = 2.07-11.63, P = 0.0002; log-additive model: OR = 4.81, 95%CI = 2.05-11.24, P = 0.0001]. The allele distributions of rs3759334 were significantly associated with BPH (OR = 4.87, 95%CI = 2.16-10.99, P = 0.0001). The distribution of rs2364480 was significantly different between groups (codominant 1 model: OR = 2.17, 95%CI = 1.11-4.26, P = 0.028; dominant model: OR = 2.16, 95%CI = 1.13-4.12, P = 0.019; log-additive model: OR

= 1.86, 95%CI = 1.07-3.24, P = 0.027). The allele distribution of rs2364480 was significantly associated with BPH (OR = 1.88, 95%CI = 1.08-3.30, P = 0.027). We found that *LTβR* polymorphisms caused severe BPH. Thus, *LTβR* may contribute to the risk of BPH development.

Key words: Benign prostatic hyperplasia; Lymphotoxin beta receptor; Polymorphism; Prostate