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Association of IL10, IL10RA, and IL10RB Polymorphisms with Benign Prostate Hyperplasia in Korean Population

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Cytokines such as interleukin 10 (IL10) may play an important role in the process of inflammation. The aim of this study was to analyze the association between *IL10*, *IL10RA* and *IL10RB* single nucleotide polymorphisms (SNPs), and benign prostate hyperplasia (BPH) in Korean population. All patients with BPH were divided into two groups according to international porostate symptom score (IPSS), prostate specific antigen (PSA) level, Q_{max}, and prostate volume. We selected two *IL10* SNPs (rs1518111 and rs1554286), three *IL10RA* SNPs (rs2256111, rs4252243, and rs2228054), and two *IL10RB* SNPs (rs999788 and rs2834167). Genotypes of seven SNPs were determined through direct sequencing. The G/G genotype of *IL10RB* polymorphism (rs2834167) was associated with a high PSA level compared with the A/G + A/A genotypes ($P = 0.009$). Of *IL10* SNP, the A/A genotype of rs1518111 and T/T genotype of rs1554286 were associated with small prostate volume, respectively ($P = 0.011$, $P = 0.014$). Moreover, the T/T genotype of *IL10RB* polymorphism (rs999788) was associated with high prostatic volume compared with the T/C + C/C genotypes ($P = 0.033$). The linkage disequilibrium (LD) blocks were formed in *IL10* and *IL10RA*. However, haplotypes in the LD block were not associated with BPH. It is concluded that there is a strong association between the *IL10* and *IL10RB* SNPs, and BPH in Korean population.

Key Words: Benign Prostatic Hyperplasia; Polymorphism, Single Nucleotide; Interleukin-10

INTRODUCTION

Benign prostatic hyperplasia (BPH) is a common disease and occurs in about one third of men in their sixties. In Korea, the overall prevalence of BPH was 40%, and this result suggests an increasing tendency of BPH prevalence (1). BPH is a complex disease from multiple etiologies and pathogenesis point of view. Recently, several reports revealed that BPH is related with immune-mediated inflammatory response (2, 3). Experimental investigations using prostatitis in mice and rats suggested autoimmune responses and genetic background as etiologic factors (4). Chronic inflammation has been documented for years in BPH, and it becomes evident as a major factor in disease initiation and progression (5).

Cytokines such as interleukin 10 (IL10) and interleukin 2 (IL2) have been found in prostate secretion fluids of chronic prostatitis (6). These cytokines maybe play an important role in the process of inflammation. IL10, which is anti-inflammatory cytokine opposing the inflammatory reaction, leads to increase levels of the regulatory cytokine (IL2) (6). IL10 is produced primarily by monocytes and to a lesser extent by lymphocytes. IL10 is capable of inhibiting synthesis of pro-inflammatory cytokines such as IL2, interleukin 3, tumor necrosis factor alpha and interferon alpha made by macrophages and type 1 T helper cells. The *IL10* gene is located in chromosome 1 and consists of five exons. IL10 has been shown to interact with interleukin 10 receptor, alpha (IL10RA) and IL10 receptor, beta (IL10RB).

Single nucleotide polymorphism (SNP) may regulate the biosynthesis, activations, and inactivation of genes and could influence the pathogenesis of disease initiation and progression. Genetic strategy such as polymorphism has been used to investigate pathogenesis of BPH. Several polymorphisms have been reported to have positive associations with prostatic growth (7). The aim of this study was to analyze the association between *IL10*, *IL10RA* and *IL10RB* SNPs, and BPH in Korean population.

MATERIALS AND METHODS

Study population

The present study consisted of 233 patients with BPH and 214 age-matched normal healthy patients. The patients with BPH were enrolled from Kyung Hee University Hospital between January 2002 and December 2008. All healthy control patients underwent screening and had a normal serum prostate-specific antigen (PSA) level (< 4 ng/mL). The patient with BPH complained of moderate or severe lower urinary tract symptoms.

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Sample processing

Lower urinary tract symptoms were quantified using international prostate symptom score (IPSS). Uroflowmetry was done to measure peak urinary flow rate (Q_{max}) for all patients. Serum PSA levels were checked in all BPH patients. The patients with a serum PSA level more than 4 ng/mL underwent transrectal ultrasound-guided prostate biopsy to rule out prostate cancer. Prostate size was assessed with transrectal ultrasound. Exclusion criteria for this study were prostate cancer, neurogenic bladder, urinary tract infection, uncontrolled diabetes mellitus, and cardiovascular disease. All patients with BPH were divided into two groups according to several multicenter studies; low (0-19) and high (≥ 20) IPSS group, low (< 1.5 ng/mL) and high (≥ 1.5 ng/mL) PSA level, low (< 10 mL/sec) and high (≥ 10 mL/sec) Q_{max}, and small (< 30 mL) and large (≥ 30 mL) prostate volume (8, 9). Genomic DNA was extracted from blood samples collected in EDTA using the Qiagen DNA Extraction kit (Qiagen, Tokyo, Japan).

SNP selection

We selected two *IL10* SNPs (rs1518111 and rs1554286), three *IL10RA* SNPs (rs2256111, rs4252243, and rs2228054), and two *IL10RB* SNPs (rs999788 and rs2834167) with greater than 0.3 heterozygosity among SNPs located in the exon and promoter region (http://www.ncbi.nlm.nih.gov/SNP, BUILD 130) for analysis (Fig. 1).

Direct sequencing

Genotypes of two *IL10* SNPs (rs1518111 and rs1554286), three *IL10RA* SNPs (rs2256111, rs4252243, and rs2228054), and two *IL10RB* SNPs (rs999788 and rs2834167) were determined through direct sequencing. Genomic DNA was amplified using PCR primers (Table 1). PCR consisted of 35 cycles at 94°C for 30 sec, 58°C for 30 sec, 72°C for 1 min, and 1 cycle at 72°C for 7 min to terminate the reaction. For automated direct sequencing, the PCR products were amplified using internal forward and reverse primers and a PRISM BigDye Terminator v3.1 Cycle sequencing Kit. The DNA samples containing extension products were added to Hi-Di formamide (Applied Biosystems, Foster City, CA, USA). The mixture was incubated at 95°C for 5 min, followed by 5 min on ice, and then analyzed by the ABI Prism 3730XL DNA analyzer (Applied Biosystems). Sequence data were analyzed using SeqManII software (v2.3; DNAATAR Inc., Madison, WI, USA).

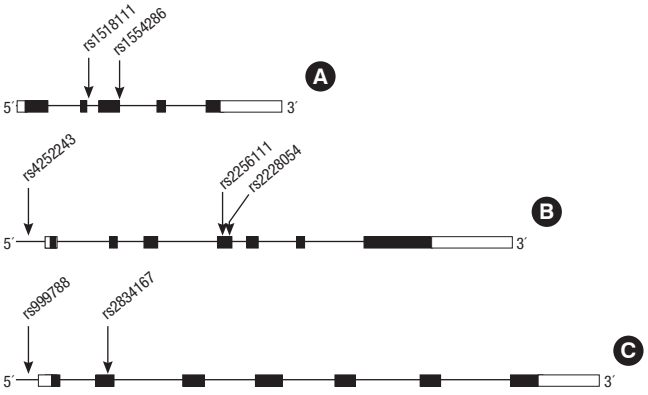

Fig. 1. Gene map and single nucleotide polymorphisms in the *IL10* (**A**), *IL10RA* (**B**), and *IL10RB* (**C**) genes. Exons are marked with black boxes, and 5′-untranslated regions are marked with white boxes. The first nucleotide is denoted as + 1. Arrows indicate the location of each SNP.

Statistical analysis

We analyzed genetic data in control and BPH subjects. SNPStats (http://bioinfo.iconcologia.net/index.php), HelixTree (Golden Helix Inc., MT, USA), and SNPAnalyzer (ISTECH Inc., Goyang, Korea) software were used to analyze genetic data. The Hardy-Weinberg equilibrium (HWE) was assessed by SNPStats in control and BPH cases. Multiple logistic regression models (codominant, dominant and recessive model) were used to calculate odds ratio (OR), 95% confidence interval (CI), and corresponding *P* values with Bonferroni correction, while controlling for age as a covariable (10). A linkage disequilibrium (LD) block of polymorphisms was tested using Haploview version 4.02 (11). A $P < 0.05$ was considered significant.

Ethics statement

The institutional review board at Kyung Hee University Hospital approved this study (KMC IRB 0913-03). All patients with BPH provided informed consent for the use of their clinical data and samples.

RESULTS

The clinical characteristics of the study subject with BPH at baseline were given in Table 2. The median age of the BPH subjects was 66.0 yr. A total of 233 BPH subjects and 214 age-matched control subjects were genotyped to analyze associations between SNPs and BPH.

Table 1. Primer sequences of seven polymorphisms

Gene symbol	SNP		Sequence (5′-3′)	Size (bp)
IL10	rs1554286	Forward	CCAATCTCTCACTCACCTTTGG	359
		Reverse	TGCTCAAAGAGAAATGAGCAAG	
IL10	rs1518111	Forward	CCAAACCTCAAGTTCATTCTCC	385
		Reverse	GAGCCAAAGGTGAGTGAGAGAT	
IL10RA	rs4252243	Forward	CAGCAAACAATTCCACTCTTCA	373
		Reverse	GCCTTACGCACGTTTATTTACC	
IL10RA	rs2256111	Forward	GCCCTCAAGTCTCATGGTATTC	368
		Reverse	GGTGGTTTCTACTCCCTCCTCT	
IL10RA	rs2228054	Forward	CCCCAACTCCATTTAGTGACTC	339
		Reverse	GGTGGTTTCTACTCCCTCCTCT	
IL10RB	rs999788	Forward	TCTATGGCTGTGAGTGTGTGTG	319
		Reverse	GCTGTCCAGTGTCTTGGGTAAT	
IL10RB	rs2834167	Forward	GGGCTTTTTCATGGGCATCTGT	404
		Reverse	CAAATCGTCAACCATCACAACT	

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Genotype distributions of SNPs in this study were in Hardy-Weinberg equilibrium in control subjects (*IL10* SNPs [rs1518111, $P = 0.64$ and rs1554286, $P = 0.54$], *IL10RA* SNPs [rs2256111, $P = 0.18$; rs4252243, $P = 1.00$; and rs2228054, $P = 0.51$], and *IL10RB* SNPs [rs999788, $P = 0.49$ and rs2834167, $P = 0.34$]). Genotype distributions of seven SNPs for control and BPH subjects are analyzed. There were no associations between control and BPH subjects, maybe, due to high prevalence in Korean population (*IL10* SNPs [rs1518111, $P = 0.70$ and rs1554286, $P = 0.69$], *IL10RA* SNPs [rs2256111, $P = 0.91$; rs4252243, $P = 0.26$; and rs2228054, $P = 0.83$], and *IL10RB* SNPs [rs999788, $P = 0.22$ and rs2834167, $P = 0.80$]). The genotype distributions of seven SNPs were analyzed according to low (0-19) and high (≥ 20) IPSS scores. No significant associations were found between IPSS score (*IL10* SNPs [rs1518111, $P = 0.64$ and rs1554286, $P = 0.54$], *IL10RA* SNPs [rs2256111, $P = 0.18$; rs4252243, $P = 1.00$; and rs2228054, $P = 0.51$], and *IL10RB* SNPs [rs999788, $P = 0.49$ and rs2834167, $P = 0.34$]). In allele analysis, there were no significant differences according to IPSS score. Table 3 shows genotype distributions of seven SNPs for low (< 1.5 ng/mL) and high (≥ 1.5 ng/mL) PSA level. The T/T genotype of *IL10RB* polymorphism (rs999788) was associated with a high PSA level compared with the T/C + C/C genotypes (95% CI 0.28-0.95, $P = 0.031$). Moreover, the G/G genotype of *IL10RB* polymorphism (rs2834167) was associated with a high PSA level compared with the A/G + A/A genotypes (95% CI 0.23-0.83, $P = 0.009$). In allele analysis, however, there were no significant differences. The genotype distributions of SNPs were analyzed according to low (< 10 mL/sec) and high (≥ 10 mL/sec) Q_{max}. There were no significant associations between low and high Q_{max}. In allele analysis, there were no significant differences according to Q_{max}.

There were significant associations between *IL10* and *IL10RB* SNPs, and prostatic volume in Table 4. Of *IL10* SNP, rs1518111 (95% CI 1.01-2.31, $P = 0.044$ in codominant model, 95% CI 1.17-3.34, $P = 0.011$ in dominant model) and rs1554286 (95% CI 1.00-2.30, $P = 0.047$ in codominant model, 95% CI 1.16-3.32, $P = 0.014$ in dominant model) were associated with prostatic volume. The G allele of rs1518111 and the C allele of rs1554286 were found to be significantly associated with large prostatic volume and a

Table 2. The clinical characteristics of 233 BPH patients

Parameters	Mean ± SE
Age (yr)	65.85 ± 0.60
IPSS	17.71 ± 0.54
QoL	3.57 ± 0.09
PSA (ng/mL)	4.43 ± 0.35
Free PSA (ng/mL)	0.98 ± 0.08
Q_{max} (mL/sec)	11.34 ± 0.38
Q_{avg} (mL/sec)	6.49 ± 0.25
VV (mL)	209.10 ± 12.11
PVR (mL)	60.09 ± 6.81
Total prostate volume (mL)	38.97 ± 1.39
Inner prostate volume (mL)	18.13 ± 1.23

BPH, benign prostatic hyperplasia; IPSS, international prostate symptom score; QoL, quality of life; PSA, prostate-specific antigen; Q_{max}, peak urinary flow rate; Q_{avg}, average urinary flow rate; VV, voided volume; PVR, postvoid residual urine.

Table 3. Analysis of genotype frequencies in *IL10*, *IL10RA*, and *IL10RB* gene polymorphisms, based on low (< 1.5 ng/mL) and high (≥ 1.5 ng/mL) PSA level, in subjects with BPH

SNP (Locus)	Genotype	Low PSA n = 86 (%)	High PSA n = 146 (%)	Model	OR (95% CI)	*P*
IL10						
rs1518111	A/A	45 (52.3)	61 (41.8)	Codominant	1.17 (0.77-1.78)	0.46
Intron	A/G	31 (36.0)	74 (50.7)	Dominant	1.53 (0.89-2.61)	0.12
	G/G	10 (11.6)	11 (7.5)	Recessive	0.62 (0.25-1.53)	0.30
rs1554286	T/T	43 (50.0)	61 (41.8)	Codominant	1.11 (0.73-1.68)	0.64
Intron	T/C	33 (38.4)	74 (50.7)	Dominant	1.39 (0.82-2.38)	0.22
	C/C	10 (11.6)	11 (7.5)	Recessive	0.62 (0.25-1.53)	0.30
IL10RA						
rs2256111	G/G	36 (41.9)	59 (40.4)	Codominant	1.03 (0.69-1.55)	0.87
Ala153Ala	A/G	40 (46.5)	70 (48.0)	Dominant	1.06 (0.62-1.82)	0.83
	A/A	10 (11.6)	17 (11.6)	Recessive	1.00 (0.44-2.30)	1.00
rs4252243	C/C	74 (86.0)	113 (77.4)	Codominant	1.45 (0.75-2.81)	0.26
-1379C>T	T/C	10 (11.6)	33 (22.6)	Dominant	1.80 (0.87-3.71)	0.10
	T/T	2 (2.3)	0 (0)	Recessive	0.00 (0.00-NA)	
rs2228054	G/G	43 (50.0)	69 (47.3)	Codominant	1.05 (0.68-1.63)	0.82
Pro175Pro	A/G	37 (43.0)	68 (46.6)	Dominant	1.12 (0.65-1.90)	0.69
	A/A	6 (7.0)	9 (6.2)	Recessive	0.88 (0.30-2.55)	0.81
IL10RB						
rs999788	T/T	19 (22.1)	51 (35.4)	Codominant	0.72 (0.49-1.06)	0.097
-641T>C	T/C	48 (55.8)	65 (45.1)	Dominant	0.52 (0.28-0.95)	0.031
	C/C	19 (22.1)	28 (19.4)	Recessive	0.85 (0.44-1.64)	0.63
rs2834167	G/G	16 (18.6)	50 (34.2)	Codominant	0.70 (0.48-1.03)	0.07
Lys47Glu	A/G	51 (59.3)	66 (45.2)	Dominant	0.44 (0.23-0.83)	0.009
	A/A	19 (22.1)	30 (20.6)	Recessive	0.91 (0.48-1.74)	0.78

BPH, benign prostatic hyperplasia; CI, confidence interval; IL10, interleukin-10; IL10RA, interleukin-10 receptor, alpha; IL10RB, interleukin-10 receptor, beta; OR, odds ratio; PSA, prostate-specific antigen; SNP, single nucleotide polymorphism.

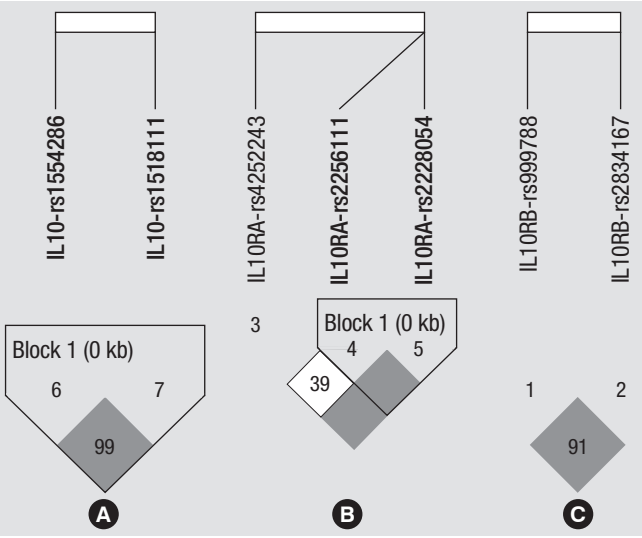

Fig. 2. Linkage disequilibrium (LD) blocks are consisted in *IL10* (**A**) and *IL10RA* (**B**). LD block in *IL10RB* (**C**) is not consisted. IL10, interleukin-10; IL10RA, interleukin-10 receptor, alpha; IL10RB, interleukin-10 receptor, beta.

risk factor for increased prostatic volume in present study. Moreover, the T/T genotype of *IL10RB* polymorphism (rs999788) was associated with high prostatic volume compared with the T/C + C/C genotypes (95% CI 0.30-0.96, $P = 0.033$). In allele analysis, however, there were no significant differences according to prostatic volume.

Seven SNPs were analyzed for LD and haplotypes using Haploview (version 4.2) according to IPSS score, serum PSA level, Q_{max}, and prostatic volume. The LD blocks were formed in *IL10* and *IL10RA* (Fig. 2). The LD block of *IL10* gene consisted of rs1554286 and rs1518111. The LD block of *IL10RA* gene consisted of rs2256111 and rs2228054. However, haplotypes in the LD block of *IL10* and *IL10RA* were not associated within BPH subjects based on prostatic volume (Table 5).

DISCUSSION

Cytokines play multiple roles in both immune disorders and

Table 4. Analysis of genotype frequencies in *IL10*, *IL10RA*, and *IL10RB* gene polymorphisms, based on small (< 30 mL) and large (≥ 30 mL) prostatic volume, in subjects with BPH

SNP (Locus)	Genotype	Small volume n = 101 (%)	Large volume n = 132 (%)	Model	OR (95% CI)	*P*
IL10						
rs1518111	A/A	56 (55.5)	51 (38.6)	Codominant	1.52 (1.01-2.31)	0.044
Intron	A/G	36 (35.6)	69 (52.3)	Dominant	1.98 (1.17-3.34)	0.011
	G/G	9 (8.9)	12 (9.1)	Recessive	1.02 (0.41-2.53)	0.96
rs1554286	T/T	55 (54.5)	50 (37.9)	Codominant	1.52 (1.00-2.30)	0.047
Intron	T/C	37 (36.6)	70 (53.0)	Dominant	1.96 (1.16-3.32)	0.014
	C/C	9 (8.9)	12 (9.1)	Recessive	1.02 (0.41-2.53)	0.96
IL10RA						
rs2256111	G/G	38 (37.6)	57 (43.2)	Codominant	1.02 (0.69-1.51)	0.92
Ala153Ala	A/G	55 (54.5)	56 (42.4)	Dominant	0.79 (0.47-1.35)	0.39
	A/A	8 (7.9)	19 (14.4)	Recessive	1.95 (0.82-4.67)	0.12
rs4252243	C/C	86 (85.2)	102 (77.3)	Codominant	1.56 (0.82-2.96)	0.17
-1379C>T	T/C	14 (13.9)	29 (22.0)	Dominant	1.69 (0.85-3.34)	0.13
	T/T	1 (1.0)	1 (0.8)	Recessive	0.76 (0.05-12.35)	0.85
rs2228054	G/G	46 (45.5)	66 (50.0)	Codominant	0.95 (0.62-1.46)	0.82
Pro175Pro	A/G	50 (49.5)	56 (42.4)	Dominant	0.84 (0.50-1.41)	0.50
	A/A	5 (5.0)	10 (7.6)	Recessive	1.57 (0.52-4.76)	0.41
IL10RB						
rs999788	T/T	23 (23.0)	47 (35.9)	Codominant	0.73 (0.50-1.05)	0.091
-641T>C	T/C	55 (55.0)	59 (45.0)	Dominant	0.53 (0.30-0.96)	0.033
	C/C	22 (22.0)	25 (19.1)	Recessive	0.84 (0.44-1.59)	0.59
rs2834167	G/G	22 (21.8)	44 (33.3)	Codominant	0.74 (0.51-1.08)	0.11
Lys47Glu	A/G	56 (55.5)	62 (47.0)	Dominant	0.56 (0.31-1.01)	0.05
	A/A	23 (22.8)	26 (19.7)	Recessive	0.83 (0.44-1.57)	0.57

BPH, benign prostatic hyperplasia; CI, confidence interval; IL10, interleukin-10; IL10RA, interleukin-10 receptor, alpha; IL10RB, interleukin-10 receptor, beta; OR, odds ratio; SNP, single nucleotide polymorphism.

Table 5. Haplotypes in the linkage disequilibrium (LD) block of IL10 and IL10RA based on small (< 30 mL) and large (≥ 30 mL) prostatic volume, in subjects with BPH

Gene	Block	Haplotype	Frequency	Small volume		Large volume		Chi square	*P*
				+	-	+	-		
IL10	Block 1	TA	0.678	147	55	169	95	4.021	0.05
		CG	0.313	54	148	92	172	3.503	0.06
IL10RA	Block 2	GG	0.646	131	71	170	94	0.01	0.92
		AA	0.292	60	142	76	188	0.046	0.83
		AG	0.062	11	191	18	246	0.369	0.54

IL10, interleukin-10; IL10RA, interleukin-10 receptor, alpha; IL10RB, interleukin-10 receptor, beta.

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many complex diseases. Inflammatory processes are strongly influenced by the balance between the effects of pro-inflammatory and anti-inflammatory cytokines. Several cytokines have been suggested for their role in BPH (7). Cytokines are crucial regulators of cellular function and polymorphisms in cytokines related with BPH could be very important, not only for assessing the risk of BPH but also in helping to explain the pathogenesis and progression of disease.

IL10 is a multifunctional cytokine with anti-inflammatory and anti-angiogenic properties (12-14). IL10 has been reported to reduce tumor growth and angiogenesis (15-17). IL10 mediates tumor promoting and tumor suppressive activities such as apoptosis (18). A large number of polymorphisms have been identified in the *IL10* gene promoter (19). Low IL10 producing genotypes were associated with increased susceptibility and advanced stage of several diseases such as malignant melanoma and renal cell carcinoma. However, high IL10 producing genotypes were associated with poor outcome of cervical cancer, gastric cancer, and hepatocellular carcinoma (19).

Several studies were reported in *IL10* polymorphism related with prostate cancer and BPH (18, 20-24). Two of these studies found significant results. McCarron et al. (20) reported a significant association of the homozygous variant at -1082 with prostate cancer risk. Both the A/G and A/A genotype at -1082 have been associated with low IL10 production. The T allele at the -819 has been associated with low IL10 production. They concluded that SNP associated with differential production of IL10 are risk factor for prostate cancer acting via their influence on angiogenesis. Faupel-Badger et al. (24) examined the hypothesis that genotypes correlated with low IL10 production may be associated with increased prostate cancer risk among Finnish male participants from the Alpha-tocopherol Beta-carotene Cancer Prevention Study. The -819 T/T and -592 A/A low expression genotypes were highly correlated. These two genotypes also were associated with increased prostate cancer susceptibility and high grade tumors. These data revealed that genotypes correlated with low IL10 production are associated with increased risk of prostate cancer and with high-grade disease in Finnish male (24). Mullan et al. (18) reported the associations between BPH and polymorphism in genes that encode growth factor, cytokines, and vitamin D and receptor. The C/C genotype of the transforming growth factor-beta 1 gene was inversely associated with treatment for BPH. The presence of at least one allele with 17 or more CA repeats of the epidermal growth factor receptor gene was positively associated with high IPSS score. However, *IL10* SNP (rs1800896) was not significantly associated with BPH.

In our study, G/G genotype of rs2834167 had a significant association with high PSA level. Moreover, the G allele of rs1518111 and the C allele of rs1554286 were found to be significantly associated with large prostate volume. We suggest that IL10 may be linked to reduce tumor growth and angiogenesis. He et al. (6) reported that the IL10 levels of expressed prostate secretion were higher in type II and type IIIa chronic prostatitis patients than in controls. They concluded that IL10 presumably play an important role in the process of prostate inflammation.

The limitation of our study was small sample number used for comparison within BPH group. But we have performed the first genetic examination of the relationships between *IL10*, *IL-10RA* and *IL10RB* SNPs, and BPH, using standard diagnostic tools. Our results revealed a strong association between rs1518111, rs1554286, rs999788, and rs2834167 SNPs and BPH.

In conclusion, there is a strong association between the *IL10* SNPs (rs1518111, rs1554286) and *IL10RB* SNPs (rs999788, rs2834167), and BPH in Korean population. Although our results have confirmed an association of *IL10* and *IL10RB* SNP and BPH, additional investigation is needed for understanding protein expression in BPH.

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AUTHOR SUMMARY

Association of IL10, IL10RA, and IL10RB Polymorphisms with Benign Prostate Hyperplasia in Korean Population

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Inflammation has been documented in benign prostatic hyperplasia (BPH). Cytokines such as interleukin 10 (IL10) may play an important role in the process of inflammation. Therefore we analyzed the association between the BPH and single nucleotide polymorphisms (SNPs) of *IL10*, *IL10RA* and *IL10RB* in Korean population (233 BPH subjects and 214 age-matched healthy subjects). All patients with BPH were divided into two groups according to IPSS, PSA level, Q_{max}, and prostate volume. Genotypes of seven SNPs were determined through direct sequencing. The T/T genotype of rs999788 and the G/G genotype of rs2834167 were associated with a high PSA level. Of *IL10* SNP, the A/A genotype of rs1518111 and the T/T genotype of rs1554286 were associated with small prostatic volume. Moreover, the T/T genotype of rs999788 was associated with high prostatic volume. We conclude that there is a strong association between the *IL10* and *IL10RB* SNPs, and BPH in Korean population.

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