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ORIGINAL ARTICLE

Association of Single-Nucleotide Polymorphisms of the *MBL2* with Atopic Dermatitis in Korean Patients

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Background: Human mannose-binding lectin (MBL) is a serum lectin taking part in the innate immunity by opsonizing various microorganisms for phagocytosis. The MBL serum concentration is affected by several single-nucleotide polymorphisms (SNPs) in the promoter region of the *MBL2* gene. **Objective:** The purpose of this study was to examine the relationship between *MBL2* polymorphisms and atopic dermatitis (AD) susceptibility. **Methods:** To examine whether the *MBL2* SNPs are related to AD susceptibility, we examined 237 patients with AD and 94 controls by polymerase chain reaction (PCR)-restriction fragment length polymorphism and PCR-sequence specific primer analyses of four polymorphic loci: two (H/L and X/Y) within the promoter region and the other two (P/Q and A/B) within exon 1. MBL concentrations in the blood were estimated by ELISA. **Results:** The prevalence of haplotype HYPB, leading to MBL deficiency, was significantly decreased in the AD patients compared to the controls ($p=0.002$), while the prevalence of haplotype HYPA was increased with a clear trend toward significance ($p=0.056$). The frequency of *MBL2* LYPB/LXPA (odds ratio, 0.08; 95% confidence interval, 0.009～0.655; $p=0.021$) were significantly decreased in the AD patients. The blood log [total immunoglobulin E, IgE] levels of *MBL2* HYPA/HYPA, HYPA/LYPA, HYPA/LYPB, HYPA/LYQA, and LYQA/LXPA haplotype pairs were significantly increased in the AD patients. **Conclusion:** The frequency of *MBL2* HYPB haplotype was significantly decreased in the AD patients compared to the controls. The frequency of LYPB/LXPA had a possibly protective effect on AD. Moreover, the *MBL2* HYPA haplotype pairs, which were related to higher blood total IgE levels, were possibly associated with extrinsic AD. **(Ann Dermatol 29(5) 571～577, 2017)**

-Keywords-
Atopic dermatitis, Innate immunity, Mannose-binding lectin

INTRODUCTION

Atopic dermatitis (AD) is a type of skin inflammation that is caused by both genetic and environmental factors[1].

Human mannose-binding lectin (MBL) is a serum lectin taking part in the innate immunity by binding various microorganisms and activating the lectin-complement[2,3]. Opsonization defect due to deficiency of MBL is associated with increased susceptibility to infection and stems from the presence of a low efficiency promoter and/or three gene mutations in exon 1 (variants B, C, and D) of *MBL2*[2,3]. The patients with abnormal homozygous *MBL* alleles are susceptible to an immune-deficiency disease that is not related to HIV[4].

MBL deficiency could trigger AD or complications when they are additionally exposed to an infection. The first evidence of MBL involvement in AD was suggested by a family study which showed that children with low plasma MBL levels who were homozygous for allele B of *MBL* were prone to pruritic skin disease and possibly AD, with or without recurring infections[5]. In addition, a report revealed that low MBL levels were clearly associated with the BB *MBL2* haplotype in a Turkish family members who

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also had recurrent skin infections and AD[5]. Moreover, the three exon 1 variants B, C, and D of *MBL* were more frequently observed in Brazilian AD patients than in healthy controls, although the disease severity was not investigated[6]. In this study, children with AD had higher frequency of allele O of *MBL* gene related to low or deficient levels of MBL compared to the control group[6]. Likewise, low or deficient serum MBL levels may result in predisposition to AD[7], although there was a conflicting report that showed no association of the B allele of *MBL* with AD susceptibility in a Japanese population[8].

We hypothesized that the modulation of innate immune defense by *MBL2* variants influenced a wide range of susceptibility to AD. Therefore, we investigated whether single-nucleotide polymorphisms (SNPs) of the *MBL2* gene could be proper genetic diagnostic factors in Korean AD patients by examining the SNPs and haplotypes, including −550 and −221 in the promoter region, +4 in the 5′ UTR and codon 54 in exon 1 of the *MBL2* gene.

MATERIALS AND METHODS

Subjects

In this study, we included 237 unrelated Korean AD patients (132 males and 105 females; mean age 32.5±18.0 years; age range 5∼90 years) who were registered in the Department of Dermatology, Uijeongbu St. Mary's Hospital in Korea. All patients showed moderate to severe AD according to the Hanifin's criteria[9]. Controls were 94 healthy persons without a personal or family history of AD. For genetic studies, blood was collected by venipuncture, and genomic DNA was prepared using QIAamp blood kit (QIAGEN, Hilden, Germany). Blood [total immunoglobulin E, IgE] was measured by LPIA-200 system (Iatron Corp., Tokyo, Japan). Blood IgE levels were in the range of 2∼50,000 IU/ml (median [25th percentiles∼75th percentiles], 282.5 [87.1∼954.0]). Assays for specific IgE antibodies to *Dermatophagoides pteronyssinus* (*Dp*) and *Dermatophagoides farina* (*Df*) were performed with the Pharmacia CAP FEIA immunoassay on a UniCAP 100 automatic analyzer (Pharmacia and Upjohn, Uppsala, Sweden) according to the manufacturer's directions. An antigen-specific IgE value of over 0.35 kU/L was classified as increased. The clinical data are presented in Table 1. This study was carried out from March 3, 2003 to December 25, 2004 in compliance with the principles of the Declaration of Helsinki. Since there was no statutory law during that time, only verbal consent was obtained from the patients and healthy persons after explaining the purpose of our study and their rights. In case of children were included in the study, the parent or guardian was informed orally and they agreed to the purpose and procedure of our study. The coded research data obtained from March 3, 2003 to December 25, 2004 were reanalyzed and the Institutional Review Board (IRB) of Uijeongbu St. Mary's Hospital approved this study on November 12, 2015 (IRB no. UC15RISI0160).

Molecular methods

Primer sets were designed for the four polymorphic sites: H/L at −550, X/Y at −221, P/Q at +4, and A/B at codon 54 (Fig. 1A), and used for differential PCR analysis. Genotyping of the promoter region at position −550 (rs-11003125) of the *MBL2* gene and codon 54 (rs1800450) of exon 1 was carried out by the polymerase chain reaction (PCR)-restriction fragment length polymorphism (RFLP) analysis as described before[10,11]. Genotyping of the promoter region at position −221 (rs7096206) of the *MBL2* gene was performed by the PCR-sequence specific primer method, as described by Steffensen et al.[12]. DNAs with one point mutation in the 5′ UTR at position +4 (P/Q variants) of the *MBL2* gene were amplified by site-directed mutagenesis (SDM)-PCR[13]. The P and Q alleles were detected by RFLP performed on the SDM-PCR products using a mutated 5′-primer (Table 2)[10-13]. *AccI* cleaved the 261 bp PCR product specific for the L allele into two fragments (239 bp and 22 bp), while *BanI* cleaved the A and B alleles. *SacI* and *HindIII* cleaved the 136 bp PCR products specific for the P and Q alleles into 110 bp and 26 bp fragments, respectively. PCR restriction fragments were separated by 8% polyacrylamide gel electrophoresis.

Assay for blood MBL levels

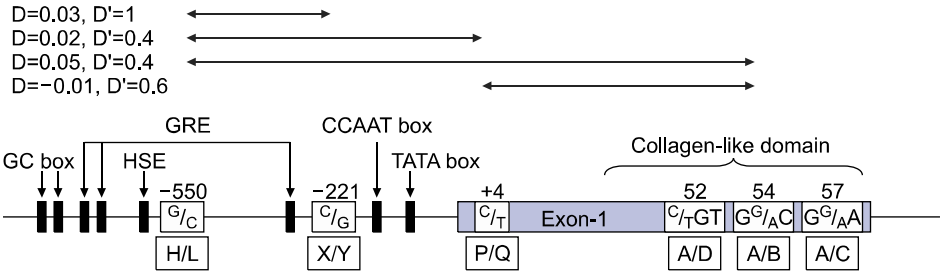
Blood MBL levels were measured in a double-enzyme immunoassay with an anti-MBL mAb (clone HYB-131; State Serum Institute, Copenhagen, Denmark)[4,14].

Table 1. Clinical profiles of the study subjects

Clinical profile	Atopic dermatitis patient	Control
No. of subjects	237	94
Age (yr)	32.5 (5∼90)	43.2 (13∼62)
Sex (male/female)	132/105	77/17
Log [total IgE]±SD	5.54±1.74*	4.19±1.31
Positive rate of specific IgE (*Dp*)	54%	-
Positive rate of specific IgE (*Df*)	55%	-

Values are presented as number only, mean (range), log [total IgE]±SD, or percent only. IgE: immunoglobulin E, SD: standard deviation, *Dp*: *Dermatophagoides pteronyssinus*, *Df*: *Dermatophagoides farina*. *p-value<0.0001 for the difference between atopic dermatitis patients and normal controls.

A Map of the *MBL* gene located on chromosome 10q11.2-q21



B *MBL* haplotypes

Haplotype	*MBL*−550 *G>C*	*MBL*−221 *G>C*	*MBL*+4 *C>T*	*MBL*+230 *G>A*	Frequency
ht1 (HYPA)	G	G	C	G	0.458
ht2 (LYPA)	C	G	C	G	0.187
ht3 (LYPB)	C	G	C	A	0.159
ht4 (LYQA)	C	G	T	G	0.070
ht5 (LXPA)	C	C	C	G	0.054
ht6 (HYPB)	G	G	C	A	0.038
ht7 (HYQA)	G	G	T	G	0.021
Others					0.014

C LD coefficients |D'|(*p*-value) among *MBL* SNPs

D/D'/r^2

		MBL −550 *G>C*	−221 *G>C*	+4 *C>T*	+230 *G>A*
MBL	−550 *G>C*	-	0.998 (<0.0001)	0.413 (0.003)	0.439 (<0.0001)
			D=0.034	0.021	0.046
			r^2=0.073	0.020	0.052
	−221 *G>C*		-	0.091 (0.063)	0.231 (0.427)
				0.005	−0.003
				0.005	0
	+4 *C>T*			-	0.599 (0.01)
					−0.012
					0.010
	+230 *G>A*				-

Fig. 1. Gene map, haplotypes and linkage disequilibrium (LD) coefficients in *MBL*. (A) Gene map and single-nucleotide polymorphisms (SNPs) in *MBL* located on chromosome 10q11.2-q21. Polymorphic sites within the promoter region and exon-1 are marked by a gray block. Pairwise measures of linkage disequilibrium for the 4 polymorphisms are shown. (B) Haplotypes of *MBL*. Haplotypes with frequency >0.02 are presented. (C) LD coefficient (|D'|) among *MBL* SNP.

Statistics

Hardy-Weinberg equilibrium was analyzed for the gene frequencies obtained by simple gene counting and the chi-square test was performed for comparing the observed and expected values. We examined a widely used measure of linkage disequilibrium (LD) between all pairs of bi-allelic loci, Lewontin's D' (|D'|)[15]. Haplotype frequencies were calculated using the Phase 2.0 program, as described elsewhere[16]. Phase probabilities of each site were also calculated for each individual by the Phase 2.0 program. Individuals with phase probabilities less than 0.987 were excluded from the analysis. Genetic effects of inferred haplotypes were analyzed in the same way as SNPs. Comparison of genotype and haplotype frequencies for each *MBL2* polymorphism was carried out by chi-square test. Odds ratios (ORs) with 95% confidence intervals (CIs) were calculated using SAS ver. 8.1 (SAS Institute, Cary, NC, USA). $p<0.05$ after Bonferroni's adjustment for multiple testing of the four SNPs in the diplotype was considered to be statistically significant throughout the study. An OR provides an effect estimate, whereas a score of <1 is related to a protective effect, and a score of >1 is related to an increased risk. Genotype distribution of *MBL2* SNPs and haplotypes among AD patients and normal controls were analyzed with logistic regression models adjusted for age, sex and log [total blood IgE] levels as covariates.

Table 2. Primers for *MBL* genotyping by PCR-RFLP, PCR-SSP and SDM-PCR RFLP

Nucleotide position	Sequence (5′~3′)	Annealing temperature	RFLP	Reference
Promoter				
−550 (H/L)	F-ggg gct agg ctg ctg agg ttt c R-ttg ctt ccc ctt ggt gtt gta	64°C, 30 s	*AccI*	Tsutsumi et al.[10] (2001)
Promoter				
−221 (X)	F-cct gcc aga aag tag aga gg R-gga aga cta taa aca tgc ttt cg	64°C, 30 s 2.5 mM $MgCl_2$		Steffensen et al.[12] (2000)
(Y)	F-cct gcc aga aag tag aga gg R-ctg gaa gac tat aaa cat gct ttc c	59°C, 30 s 1.4 mM $MgCl_2$		
5′ UTR				
+4 (P)	F-cag att gta gga cag agg gcg agc t	55°C, 30 s	*SacI*	Madsen et al.[13] (1995)
(Q)	F-cag att gta ggc acg agg gca agc t	55°C, 30 s	*HindIII*	
(P/Q)	R-cac cat act cag gag aag ga			
Exon 1				
Codon 54	F-gta gga cag agg gca tgc tc R-cag gca gtt tcc tct gga agg	64°C, 10 s	*BanI*	Matsushita et al.[11] (1998)

PCR: polymerase chain reaction, RFLP: restriction fragment length polymorphism, PCR-SSP: sequence specific primers for a polymerase chain reaction's ability to determine whether sequence motifs are in cis or trans, SDM: site-directed mutagenesis.

Table 3. Genotype distribution of *MBL* polymorphisms in atopic dermatitis (AD) patients and normal controls (NC) in a Korean population

Locus	Group	Genotype			Frequency*	HW†	*p*-value‡
		GG	CG	CC			
MBL−550 *G>C*	AD	68 (28.7)	111 (46.8)	58 (24.5)	0.479	0.23	0.92
	NC	26 (27.7)	43 (45.7)	25 (26.6)	0.495		
		GG	CG	CC			
−221 *G>C*	AD	210 (88.6)	26 (11)	1 (0.4)	0.060	1	0.38
	NC	79 (84.0)	15 (16.0)	0 (0)	0.080		
		CC	CT	TT			
+4 *C>T*	AD	194 (81.9)	41 (17.3)	2 (0.8)	0.095	1	0.81
	NC	74 (78.7)	19 (20.2)	1 (1.1)	0.112		
		GG	AG	AA			
+230 *G>A*	AD	150 (63.3)	77 (32.5)	10 (4.2)	0.205	0.50	0.54
	NC	62 (66)	26 (27.7)	6 (6.4)	0.202		

Values are presented as number (%). *Minor allele frequencies. †*p*-values of deviation from Hardy-Weinberg (HW) equilibrium in total subjects (n=331). ‡*p*-values for chi-square test.

RESULTS

Characteristics of the study population

The clinical characteristics of 331 subjects are shown in Table 1. Mean age was higher in the controls compared to the patients, and males were predominated in both groups. Around 54% of the patients with AD were positive for *Dp*-specific IgE and 55% of patients were positive for *Df*-specific IgE. Subjects with AD had higher blood log [total IgE] levels (Student's t-test, $p<0.0001$).

Allele frequencies of the *MBL* polymorphisms

The *MBL2* gene located on chromosome 10q11.2-q21 consists of four exons with a total size of ~10.0 kb. Four SNPs in the *MBL2* gene (Fig. 1A); three within the upstream of the promoter region (a G-C transversion at position 550, a C-G transversion at position 221, and a C-T transition at position +4 in the 5′ UTR) and one G-A transition at +230 calculated on the codon 54 of exon 1 were genotyped by the single-base extension method. As shown in Fig. 1, *MBL* −550 *G>C*, −221 *G>C*, +4 *C>T* and +230 *G>A* were included in the statistical analysis. All four SNPs were in complete ($|D'|=1$ and $r^2 \neq 1$) or absolute LD ($|D'|=1$ and $r^2=1$). Seven haplotypes were identified without any ambiguous phasing due to LDs among SNPs (Fig. 1B, C).

Allele distributions of the polymorphisms on *MBL2* (*MBL* −550 *G>C*, −221 *G>C*, +4 *C>T*, and +230 *G>A*)

were determined in the study population (Table 3). No significant difference was found in the *MBL2* polymorphism frequencies between AD patients and controls.

When haplotypes with a frequency greater than 0.01 were analyzed among the AD patients and controls, 7 haplotypes were observed at positions −550 and −221 in the promoter region, at +4 in the 5′ UTR, and at codon 54 in exon 1 of the *MBL2*. The frequency of the *MBL2* HYPB haplotype was significantly decreased ($p=0.002$) in the AD patients (Table 4). The frequencies of the heterozygous genotype *MBL2* LYPB/LXPA (OR, 0.08; 95% CI, 0.009∼0.655; $p=0.021$) were also significantly decreased in the AD patients (Table 5).

The blood MBL levels were not significantly different between the AD patients and controls (mean±standard deviation: 3.30±2.40 vs. 3.06±2.05, respectively, $p=0.077$, Student's t-test). Interestingly, the blood MBL level was not detected in both AD patients and controls with the *MBL2* HYPB/HYPB and HYPB/LYPB haplotypes, possibly leading to deficiency of MBL (Table 6).

The blood MBL levels were significantly correlated with total IgE levels in the AD patients (r=0.13, $p=0.048$, Pearson's correlation). In addition, the blood log [total IgE] of *MBL2* HYPA/HYPA, HYPA/LYPA, HYPA/LYPB, HYPA/LYQA, and LYQA/LXPA haplotype pairs were significantly increased in the AD patients compared to controls (Table 7).

Table 4. Comparison of haplotype frequencies of the *MBL* gene between patients with AD and controls

MBL haplotype	AD 2N-474	Control 2N-188	*p*-value
HYPA	0.481 (228)	0.399 (75)	0.056
LYPA	0.173 (82)	0.223 (42)	0.134
LYPB	0.175 (83)	0.117 (22)	0.065
LYQA	0.070 (33)	0.069 (13)	0.983
LXPA	0.049 (23)	0.069 (13)	0.291
HYPB	0.023 (11)	0.075 (14)	0.002
HYQA	0.017 (8)	0.032 (6)	0.225
Others	0.013 (6)	0.013 (3)	0.741

( ): number of cases. AD: atopic dermatitis. *p*-values were calculated by chi-square test.

DISCUSSION

In this study, we found a significant decrease in the frequency of *MBL2* haplotype HYPB, −550G (H), −221G (Y), +4C (P), and codon 54Asp (B) in Korean AD patients. We also found that blood log [total IgE] levels of *MBL2* HYPA/HYPA, HYPA/LYPA, HYPA/LYPB, HYPA/LYQA, LYQA/LXPA haplotype pairs were significantly increased in the AD patients.

In a previous study, higher frequency of point mutation at codon 54 (B) of the *MBL* gene has been implicated as a candidate susceptibility loci in Brazilian AD patients 7. We found that the frequency of *MBL* HYPB/HYPB haplotype was decreased in the AD patients, although the plasma MBL was not detected in both AD patients and controls with this haplotype and the number of subjects was too small for the statistical analysis (Table 6). MBL deficiency would not be a susceptibility factor for the development of certain complications. For example, it was demonstrated that AD patients with Eczema herpeticum (EH), a systemic complication caused by herpes simplex virus infection had similar levels and functional activities of serum MBL as AD patients with no history of EH[17]. Considering the sample size limitations in this study and our study, further research is needed to determine the detailed defects that predispose subjects to viral infection and AD.

Previous studies have demonstrated that there are large differences in the frequencies of exon 1 variant and haplotypes of *MBL2* in various ethnic groups. For example, the codon 54 (B) mutant was found with a higher frequency in in Caucasians (0.22∼0.28) and in Asians including Japanese and Korean patients (0.11∼0.26), but very rare in Africans (0.0∼0.03)[11,12,18,19]. In addition, the

Table 5. Comparison of frequencies of *MBL* haplotype pairs between patients with AD and controls

MBL haplotype pair	AD (n=237)	Control (n=94)	*p*-value	OR (95% CI)
HYPA/LYPB	51 (21.5)	9 (9.6)	0.077	
LYPA/LYPB	9 (3.8)	5 (5.3)	>0.999	
LYPB/LYPB	4 (1.7)	0	>0.999	
LYPB/LYQA	6 (2.5)	1 (1.1)	>0.999	
LYPB/LXPA	1 (0.4)	5 (5.3)	0.021	0.08 (0.009∼0.655)
HYPB/LYPB	2 (0.8)	1 (1.1)	>0.999	
HYQA/LYPB	1 (0.4)	0	>0.999	

Values are presented as number (%). AD: atopic dermatitis, OR: odds ratio, 95% CI: 95% confidence interval. *p*-values were calculated by chi-square test after Bonferroni's adjustment for multiple testing.

Table 6. Comparison of plasma MBL levels in *MBL* haplotype pairs between patients with AD and controls

MBL haplotype pair	AD (mg/L, n=237)	Control (mg/L, n=94)	*p*-value
HYPA/HYPA	5,154.7±2,106.1 (54)	4,500.2±1,439.2 (14)	0.277
HYPA/LYPA	4,519.2±1,933.6 (41)	3,862.0±1,434.5 (23)	0.160
HYPA/LYPB	1,413.7±1,561.3 (51)	1,159.1±1,414.3 (9)	0.650
HYPA/LYQA	4,084.4±1,384.2 (16)	4,847.3±1,512.3 (9)	0.213
HYPA/HYPB	444.6±2,166.0 (6)	3,031.7±2,619.7 (3)	0.414
HYPA/HYQA	5,489.9±1,245.8 (6)	5,172.2±1,689.4 (3)	0.756
LYPA/LYPA	2,189±1,688.4 (6)	3,128.2±2,000.4 (4)	0.445
LYPA/LYPB	1,234.5±1,557.8 (9)	1,051.5±1,049.1 (5)	0.820
LYPA/LXPA	2,885.5±1,608.4 (16)	2,961.1±245.0 (6)	0.858
LYPB/LYQA	1,037.3±975.5 (6)	869.5±UD (1)	0.880
LYPB/LXPA	878.3±UD (1)	761.1±1,240.3 (5)	0.936
LYPB/Others	289.1±512.5 (5)	673.6±UD (1)	0.531
LYQA/LXPA	2,912.3±1,710.8 (4)	2,749.8±440.6 (2)	0.906
HYPB/LYPB	0 (2)	0 (1)	UD
HYPB/HYPB	0 (1)	0 (4)	UD
HYPB/HYQA	5,607.7±UD (1)	2,971.9±2,572.8 (2)	0.557

Values are presented as mean±standard deviation (number of cases). AD: atopic dermatitis, UD: undetectable. *p*-value was calculated by t-test.

Table 7. Comparison of log [total immunoglobulin E] levels in *MBL* haplotype pairs between patients with AD and controls

MBL haplotype pair	AD (n=237)	Control (n=94)	*p*-value
HYPA/HYPA	5.36±1.94 (54)	4.32±1.15 (14)	0.014
HYPA/LYPA	5.49±1.79 (41)	4.16±1.45 (23)	0.004
HYPA/LYPB	5.82±1.80 (51)	4.08±1.01 (9)	0.007
HYPA/LYQA	5.74±1.54 (16)	4.21±1.02 (9)	0.014
HYPA/HYPB	5.59±2.00 (6)	2.56±1.76 (3)	0.064
HYPA/HYQA	6.34±1.31 (6)	4.57±0.62 (3)	0.061
LYPA/LYPA	5.19±1.68 (6)	4.41±1.44 (4)	0.468
LYPA/LYPB	5.33±1.49 (9)	4.36±0.93 (5)	0.217
LYPA/LXPA	5.11±1.49 (16)	3.80±1.53 (6)	0.083
LYPB/LYQA	5.95±1.65 (6)	4.63±UD (1)	0.491
LYPB/LXPA	3.31±UD (1)	4.94±2.18 (5)	0.531
LYPB/Others	5.04±1.46 (5)	1.63±UD(1)	0.10
LYQA/LXPA	7.27±1.31 (4)	4.04±1.13 (2)	0.042
HYPB/LYPB	6.74±1.48 (2)	4.42±UD (1)	0.423
HYPB/HYPB	4.76±UD (1)	4.15±1.27 (4)	0.698
HYPB/HYQA	4.90±UD (1)	5.90±1.18 (2)	0.614

Values are presented as mean±standard deviation (number of cases). AD: atopic dermatitis, UD: undetectable. *p*-value was calculated by t-test.

HYPA haplotype, the most effective MBL-producing haplotype, was found in Asians including Koreans (0.44～0.47) and Caucasians (0.25～0.34) and commonly in Eskimos (0.81). In contrast, the LXPA haplotype was found rarely in Asians including Koreans (0.07～0.10) and Eskimos (0.03), but it was found more commonly in Caucasians (0.18～0.26)[3,11,12,18].

Various genetic polymorphisms in the *MBL* gene have been reported as risk factors for the development of a certain clinical subtype and severity. The susceptibility to Behcet's disease (BD) is related to a higher frequency of the *MBL2* HYPA haplotype, which may cause increased acute or chronic hyper-inflammatory responses and influence the severity of BD[19]. A significantly higher percentage of patients with BD showed high serum MBL levels (≥500 ng/ml) compared to controls and were associated with skin lesions in Korean patients[20]. In addition, the progression of systemic lupus erythematosus is associated with *MBL* gene polymorphism and serum MBL concentration[21].

In our study, the blood MBL levels were significantly correlated with total IgE levels in the AD patients. In addition, blood log [total IgE] levels of *MBL2* HYPA/HYPA, HYPA/LYPA, HYPA/LYPB, HYPA/LYQA, and LYQA/LXPA haplotype pairs were significantly increased in the AD patients. Extrinsic AD shows high total plasma IgE levels and has specific IgE for environmental and food allergens, whereas intrinsic AD shows normal total IgE levels and the absence of specific IgE[22]. Our previous study demonstrated that the polymorphisms of the macrophage migration inhibitory factor (*MIF*) promoter related to innate immunity were significantly associated with an increased risk for AD. Especially, the −794 7-CATT locus and the *MIF* C/7-CATT haplotype were significantly associated with decrease of total IgE levels in the blood, suggesting that these polymorphisms might be a marker for intrinsic AD[23]. Therefore, the HYPA haplotype pair of the *MBL2* gene, which is related to higher total blood IgE levels, would be a possible marker for extrinsic AD.

In conclusion, we investigated the SNPs and the hap-

lotypes of the *MBL2* gene, which might be proper genetic diagnostic factors in Korean AD patients. The frequency of *MBL2* LYPB/LXPA had a possibly protective effect in Korean AD patients.

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CONFLICTS OF INTEREST

The authors have nothing to disclose.

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