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TAP1 and *TAP2* Gene Polymorphisms in Korean Patients with Allergic Rhinitis

Antigen peptides are actively transported across the endoplasmic reticulum by the transporters associated with antigen presentation (TAP). TAP genes polymorphism could influence the selection process that determines which antigen peptides play a role in the pathogenesis of allergic rhinitis. The aim of this study was to investigate the association of TAP genes polymorphism with allergic rhinitis. *TAP1* and *TAP2* genotyping were performed on 110 allergic rhinitis patients and 107 healthy controls. *TAP1* polymorphic residues at codons 333 and 637, and *TAP2* polymorphic residues at codons 379, 565, 651, and 665 were analyzed by the amplification refractory mutation system-polymerase chain reaction (ARMS-PCR). Analysis of *TAP1* gene polymorphism demonstrated decreased frequencies of Ile/Val genotype at codon 333, Asp/Gly genotype at codon 637, and haplotype A and B in allergic rhinitis patients when compared to controls ($p<0.05$). However, there was no significant difference in the genotype, phenotype, or allele frequencies at four *TAP2* codons between controls and allergic rhinitis patients. In conclusion, *TAP1* gene polymorphism may be an important factor contributing to the genetic susceptibility in the development of allergic rhinitis in the Korean population.

Key Words : *Allergic Rhinitis; TAP1; TAP2; Polymorphism*

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INTRODUCTION

Allergic rhinitis (AR) is an immunologic nasal response, primarily mediated by immunoglobulin E (IgE). It is considered as a heterogenous state, determined by genetic and environmental interactions. Previous studies have shown the relationships between allergies and polymorphisms in many candidate genes such as IgE, transporters associated with antigen processing (TAP), T cell receptors, and cytokines and their receptors (1-5).

The inhalent antigens are presented to $CD4^+$ T cell by MHC class II in AR (6). However, it was suggested that exogenous antigens can be channeled into the endogenous pathway (MHC class I) by TAP molecules (7). Therefore, it would be very interesting to determine the other possible antigenic presentation pathway, mediated by TAP in AR.

TAP1 and *TAP2* genes encode heterodimeric molecules involved in endogenous antigen processing. Antigen peptides are degraded from cytosolic proteins, assembled with MHC class I heavy chain and β2-microglobulin in the endoplasmic reticulum, and actively transported across the endoplasmic reticulum membrane by TAP (8, 9). It is possible that TAP gene polymorphisms can influence the antigen peptide selection and transport process and alter immune response regulation (2).

The TAP gene is considered to be one of the candidates for disease susceptibility gene or one of the additional genes conferring susceptibility. Polymorphisms of the TAP gene have been investigated in several HLA-associated diseases such as atopic dermatitis, asthma, rheumatoid arthritis, and systemic lupus erythematosus (10, 11). There have been few studies on the relationship between AR and TAP genes polymorphism, and it still remained controversial. Ismail et al. (2) reported evidence of a strong association between *TAP1* polymorphism and atopy in a Tunisian population. However, Tacheuchi et al. (12) reported no association between *TAP1* gene polymorphism and AR in a Japanese population.

Until now, there has been no study on the TAP genes polymorphism in Korean patients with AR. Therefore, we designed a case-control study to investigate the *TAP1* and *TAP2* polymorphisms and their association with AR in a Korean population.

MATERIALS AND METHODS

Subjects

One hundred and ten consecutive and unrelated patients

with AR were included in this study. They consisted of 40 females and 70 males, ranging in age from 5 to 72 yr old (mean, 24.1 yr). All patients had nasal symptoms such as watery rhinorrhea, sneezing, itching and/or nasal obstruction, and positive skin prick tests (Allergopharma®, Hamburg, Germany) for one or more inhalant allergens including house dust mites. There was no co-morbid condition such as allergic asthma or atopic dermatitis. The control group consisted of 107 healthy subjects with no personal or family history of allergic diseases, cancers or genetic diseases. There were 40 females and 67 males ranging from 7-65 yr old (mean, 26.2 yr). All control subjects were negative for all nasal symptoms and skin prick tests. Prior to the experiment, informed consents were obtained from all patients and controls.

DNA extraction

Heparinized peripheral venous blood (about 10 mL) was drawn from each individual and stored at -70˚C before being used in the experiment. Genomic DNA was extracted from leukocytes in the collected blood with the Wizard™ Genomic DNA purification kit (Promega, Madison, WI, U.S.A.).

ARMS-PCR

Polymorphic residues at codons 333 and 637 in *TAP1*, and codons 379, 565, 651 and 665 in *TAP2* were analyzed. The dimorphic sites were: $TAP1^{333}$ (A→G, Ile→Val, exon 4), $TAP1^{637}$ (A→G, Asp→Gly, exon 10), $TAP2^{379}$ (G→A, Val→Ile), $TAP2^{565}$ (G→A, Ala→Thr), $TAP2^{651}$ (C→T, Arg→Cys) and $TAP2^{665}$ (A→G, Thr→Ala) (13). *TAP1* and *TAP2* polymorphism analyses were performed by the amplification refractory mutation system-polymerase chain reaction (ARMS-PCR), described by Newton et al. (14). Four primers were used for each dimorphic site (Table 1). Two of these were complementary to one of the dimorphic sites, while the other two allele-nonspecific primers were used as an internal control. The $TAP1^{333}$, $TAP1^{637}$, $TAP2^{379}$, $TAP2^{565}$ and $TAP2^{665}$ primers were designed as described by Powis et al. (15). The $TAP2^{651}$ primers were designed as described by Jackson et al. (16).

Genomic DNA samples (1 μL) were amplified in a 20 μL reaction mixture containing 1 μL each of all four oligonucleotide primers, 2 μL dNTPs mix (Cat. No. BIO-39029, London, U.K.), 1 μL DNA template, and 13 μL of distilled water. A thermal cycler (GeneAmp PCR system 2400, Perkin Elmer, MA, U.S.A.) was used with the following specifications: 94˚C for 6 min; 35 cycles of 94˚C for 1 min, 62˚C for 1 min and 72˚C for 1 min; there was a final 72˚C incubation for 7 min. The reaction products were separated on a 2% agarose gel stained with ethidium bromide.

Determination of genotypes and haplotypes

Genotyping of the $TAP1^{333}$ was done as follows: Ile/Val if 241, 351 and 533 bp bands were visible, Ile/Ile if 241 and 533 bp bands were visible, and Val/Val if 351 and 533 bp bands were visible (Fig. 1). Genotyping of the $TAP1^{637}$ was

Table 1. Oligonucleotide primers used for ARMS-PCR *TAP1* and *TAP2* typing

Codon	Sequence (5′ to 3′)	Specificity	Size (bp)
$TAP1^{333}$	CCCTGCACTGAGATTTGCAGACCTCTGGAG	5′ flanking	Control; 533
	GATCAGTGTCCCTCACCATGGTCACCCGGA	Ile-333	Ile-333; 241
	GGGCAGAAGGAAAAGCAGAGGCAGGGTCAC	Val-333	Val-333; 351
	ACCTGGGAACATGGACCACAGGGACAGGGT	3′ flanking	
$TAP1^{637}$	CATCTTCCCAGAATCTCCCCTATCCAGCTA	5′ flanking	Control; 429
	CATCTTGGCCCTTTGCTCTGCAGAGGTACA	Asp-637	Asp-637; 307
	ACCCCCTGACAGCTGGCTCCCAGCCTCCC	Gly-637	Gly-637; 180
	TGGGGAGGCATCCAATGGAACTGGATTTGG	3′ flanking	
$TAP2^{379}$	TTGGAGGGCTGCAGACCGTTCGCAGTTTTG	5′ flanking	Control; 427
	GAGACCTGGAACGCGCCTTGTACCTGCGCG	Val-379	Val-379; 328
	ACAACCACTCTGGTATCTTACCCTCCTGAT	Ile-379	Ile-379; 158
	ACATAGCTCCCCACGCTCTCCTGGTAGATC	3′ flanking	
$TAP2^{565}$	CTCACAGTATGAACACTGCTACCTGCACAG	5′ flanking	Control; 400
	TGTTCTCCGGTTCTGTGAGGAACAACAGTA	Thr-565	Thr-565; 161
	ATCATCTTCGCAGCTCTGCAGCCCATAAAC	Ala-565	Ala-565; 298
	GGAGCAAGCTTACAATTTGTAGAAGATACC	3′ flanking	
$TAP2^{651}$	AGAGGGAGGACGAAGGACCTACTAGTGGAA	5′ flanking	Control; 471
	CACCCCTTCAGCTGCAGGACTGGAATTACC	Arg-651	Arg-651; 195
	AGCAATCACCAGCACTGTGCGATCCCCTCA	Cys-651	Cys-651; 335
	GGCCTCAGTCCATCAGCCGCTGCTGCACCA	3′ flanking	
$TAP2^{665}$	TTGGGGAATGGAATCCGGTGGTGTGAGGGC	5′ flanking	Control; 408
	CAGTGCTGGTGATTGCTCACAGGCTGCAAA	Thr-665	Thr-665; 141
	CACCAGGATCTGGTGGGCGCGCTGAACTAC	Ala-665	Ala-665; 326
	TCAGCCGCTGCTGCACCAGGCGGGAATAGA	3′ flanking	

ARMS-PCR, amplification refractory mutation system-polymerase chain reaction.

done as follows: Asp/Gly if 180, 307 and 429 bp bands were visible, Asp/Asp if 307 and 429 bp bands were visible, and Gly/Gly if 180 and 429 bp bands were visible. The *TAP2* genotypes were also classified using the same methods.

Four possible *TAP1* haplotypes (A-D) were determined by a combination of the dimorphic sites at codons 333 and 637. Eight possible *TAP2* haplotypes (A-H) were determined by combination of four dimorphic sites at codons 379, 565, 651 and 665. We used *TAP1* and *TAP2* haplotype nomenclature as proposed by Powis et al. (15) and Jackson et al. (16) (Table 2).

Statistical analysis

All statistical analyses were performed with SPSS 10.0 (Chicago, IL, U.S.A.). A chi-square test was used to compare the distribution of *TAP1* and *TAP2* genotypes between control and AR groups. Odds ratios (OR) with a 95% confidence interval (CI) were calculated using the Mantel-Haenzel chi-square test. Differences were significant if $p<0.05$.

RESULTS

TAP1 polymorphisms and allergic rhinitis

Three *TAP1* genotypes (Ile/Ile, Ile/Val and Val/Val) were found at codon 333 (Table 3). The Ile/Val genotype was significantly decreased in the AR group when compared to Ile/Ile (OR=0.32, 95% CI=0.17-0.60, p=0.001). The Val phenotype was significantly decreased in the AR group when compared to the Ile phenotype (OR=0.52, 95% CI=0.30-0.92, p=0.016). The Val allele was also significantly decreased in AR patients when compared to the Ile allele (OR=0.48, 95% CI=0.28-0.81, p=0.003).

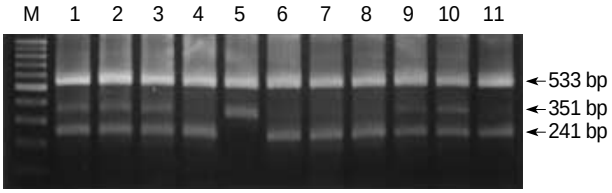

Fig. 1. *TAP1* codon 333 genotyping by ARMS-PCR. Four oligonucleotides were included in each polymerase chain reaction mix. Lanes 4, 6, 7, 8 and 11 consist of one control and one allele-specific 241 bp fragment defining the Ile/Ile homozygote. Lanes 1, 2, 3, 9 and 10 consist of one control and two allele-specific, smaller fragments (241 bp and 351 bp) defining the Ile/Val heterozygote. Lane 5 consists of one control and one allele-specific 351 bp fragment defining the Val/Val homozygote.

Three *TAP1* genotypes (Asp/Asp, Asp/Gly and Gly/Gly) were seen at codon 637 (Table 3). The Asp/Gly genotype was significantly decreased in the AR group when compared to Asp/Asp (OR=0.43, 95% CI=0.24-0.80, p=0.011). In AR patients, the Gly allele was significantly decreased when compared to the Asp (OR=0.62, 95% CI=0.38-1.01, p=0.04). However, there was no difference between the two $TAP1^{637}$ phenotypes, Asp and Gly.

Four possible *TAP1* haplotypes (A-D) were found in this study (Table 4). The C and D haplotypes were significantly less than A in the AR group (phenotype, p=0.006; allele, p=0.0002). By combining the four haplotypes, the following seven genotypes were found: AA, AB, AC, AD, BC, BD, and DD. The AB (OR=0.31), AC (OR=0.08), and AD (OR=0.13) genotypes were significantly decreased in the AR group when compared with the AA genotype.

TAP2 polymorphisms and allergic rhinitis

There was no significant difference in the genotype, phenotype, and allele frequencies of *TAP2* at codons 379, 565, 651 and 665 between the AR and control groups (Table 5). The previously reported seven *TAP2* haplotypes (A, B, C, D, E, F, and G) were observed; however haplotype H (Ile^{379}-Thr^{565}-Arg^{651}-Ala^{665}), reported by Tacheuchi et al. (17) was not found in this study. A new haplotype (Val^{379}-Thr^{565}-Arg^{651}-Ala^{665}) was observed in one person (controls), and we named it as haplotype I (Table 2). By combining the eight *TAP2* haplotypes, 18 genotypes could be possible from AA to FG. However, their distributions were not different between the AR and control group (Table 6).

Table 2. Nomenclature of *TAP1* and *TAP2* haplotypes

TAP1	333		637	
	ATC	GTC	GAC	GGC
A	Ile		Asp	
B		Val		Gly
C		Val	Asp	
D	Ile			Gly

TAP2	379		565		651		665	
	GTA	ATA	GTA	ATA	GTA	ATA	GTA	ATA
A	Val		Ala		Arg		Thr	
B	Val		Ala		Arg			Ala
C		Ile	Ala		Arg		Thr	
D		Ile		Thr	Arg		Thr	
E	Val			Thr	Arg		Thr	
F	Val		Ala			Cys	Thr	
G		Ile	Ala		Arg			Ala
H		Ile		Thr	Arg			Ala
I	Val			Thr	Arg			Ala

Table 3. *TAP1* polymorphisms in allergic rhinitis patients and controls

TAP1		Controls		Allergic rhinitis		Odds ratio	CI*	*p* value
Genotype		(n=107)	(%)	(n=110)	(%)			
TAP1^{333}	Ile/Ile	54	50.5	82	74.5			0.001
	Ile/Val	53	49.5	26	23.7	0.32	0.17-0.60	
	Val/Val	0	0	2	1.8			
TAP1^{637}	Asp/Asp	55	51.4	76	69			0.011
	Asp/Gly	50	46.7	30	27.3	0.43	0.24-0.80	
	Gly/Gly	2	1.9	4	3.7	1.45	0.22-11.85	
Phenotype		(n=107)	(%)	(n=110)	(%)			
TAP1^{333}	Ile	107	100	108	98.2			0.016
	Val	53	49.5	28	25.5	0.52	0.30-0.92	
TAP1^{637}	Asp	105	98.1	106	96.4			0.094
	Gly	52	48.6	34	30.9	0.65	0.38-1.11	
Allele		(2n=214)	(%)	(2n=220)	(%)			
TAP1^{333}	Ile	161	75.2	190	86.4			0.003
	Val	53	24.8	30	13.6	0.48	0.28-0.81	
TAP1^{637}	Asp	160	74.8	182	82.7			0.04
	Gly	54	25.2	38	17.3	0.62	0.38-1.01	

*, 95% confidence interval.

Table 4. *TAP1* haplotypes in allergic rhinitis patients and controls

TAP1	Controls		Allergic rhinitis		Odds ratio	CI*	*p* value
Genotype	(n=107)	(%)	(n=110)	(%)			
AA	29	27.1	71	64.5			
AB	28	26.2	21	19.1	0.31	0.14-0.66	
AC	26	24.3	5	4.5	0.08	0.02-0.24	
AD	22	20.6	7	6.4	0.13	0.04-0.37	
BC	0	0	2	1.8			
BD	1	0.9	0	0	0	0.00-7.38	
DD	1	0.9	4	3.7	1.63	0.16-41.08	
Phenotype	(n=107)	(%)	(n=110)	(%)			
A	104	97.2	104	94.5			0.006
B	29	27.1	23	20.9	0.76	0.41-1.52	
C	26	24.3	7	6.4	0.27	0.10-0.69	
D	24	22.4	11	10.0	0.46	0.20-1.04	
Allele	(2n=214)	(%)	(2n=220)	(%)			
A	134	62.6	175	79.5			0.0002
B	29	13.6	23	10.5	0.61	0.32-1.14	
C	26	12.1	7	3.2	0.21	0.08-0.52	
D	25	11.7	15	6.8	0.46	0.22-0.95	

*, 95% confidence interval.

DISCUSSION

It is well known that the major histocompatibility complex (MHC) class I and II have fundamentally different antigen processing pathways. The exogenous antigens such as bacteria are degraded into antigenic peptides within the lysosomes. Upon fusion with endosomes, these peptides may bind MHC II molecules (18). Finally, peptide-loaded MHC class II molecules are delivered to the cell surface, and presented to $CD4^+$ helper T cells. However, the endogenous antigens such as virus and tumor antigens are degraded within the proteasomes and actively transported across the endoplasmic reticulum membrane by TAP (8, 9). These peptides are then assembled with the MHC class I heavy chain and β2-microglobulin. This complex is expressed on the cell surface, where it is recognized by $CD8^+$ T cells. Suto et al. (7) suggested, however, that exogenous antigens can be channeled into the endogenous pathway where antigen presentation is mediated by MHC class I molecules. Therefore, TAP might participate in both endogenous and exogenous antigen processing.

Because AR is a disease caused by inhalant exogenous antigens such as pollens and house dust mites, the preferential pathway of antigen processing is known to be MHC class II. However, it would be possible that inhalant antigenic peptides can be routed into the MHC class I (endogenous) path-

Table 5. *TAP2* polymorphisms in allergic rhinitis patients and controls

TAP2		Controls		Allergic rhinitis		Odds ratio	CI*	*p* value
Genotype		(n=107)	(%)	(n=110)	(%)			
TAP2^{379}	Val/Val	84	78.5	81	73.6			0.373
	Val/Ile	22	20.6	29	26.4	1.37	0.69-2.70	
	Ile/Ile	1	0.9	0	0			
TAP2^{565}	Ala/Ala	89	83.2	95	86.4			0.513
	Ala/Thr	18	16.8	15	13.6	0.8	0.35-1.74	
	Thr/Thr	0	0	0	0			
TAP2^{651}	Arg/Arg	83	77.6	81	73.6			0.789
	Arg/Cys	23	21.5	28	25.5	1.25	0.63-2.46	
	Cys/Cys	1	0.9	1	0.9	1.02	0.00-3.82	
TAP2^{665}	Thr/Thr	39	36.4	41	37.3			0.548
	Thr/Ala	51	47.7	57	51.8	1.06	0.57-1.98	
	Ala/Ala	17	15.9	12	10.9	0.67	0.26-1.72	
Phenotype		(n=107)	(%)	(n=110)	(%)			
TAP2^{379}	Val	106	99.1	110	100			0.53
	Ile	23	21.5	29	26.4	1.22	0.63-2.33	
TAP2^{565}	Ala	107	100	110	100			0.58
	Thr	18	16.8	15	13.6	1.23	0.56-2.74	
TAP2^{651}	Arg	106	99.1	109	99.1			0.60
	Cys	24	22.4	29	26.4	1.18	0.62-2.24	
TAP2^{665}	Thr	90	84.1	98	89.1			0.75
	Ala	68	63.6	69	62.7	0.93	0.59-1.48	
Allele		(2n=214)	(%)	(2n=220)	(%)			
TAP2^{379}	Val	190	88.8	191	86.8			0.53
	Ile	24	11.2	29	13.2	1.2	0.65-2.22	
TAP2^{565}	Ala	196	91.6	205	93.2			0.53
	Thr	18	8.4	15	6.8	0.8	0.37-1.17	
TAP2^{651}	Arg	189	88.3	190	86.4			0.54
	Cys	25	11.7	30	13.6	1.19	0.65-2.19	
TAP2^{665}	Thr	129	60.3	139	63.2			0.53
	Ala	85	39.7	81	36.8	1.13	0.75-1.70	

*, 95% confidence interval.

way, involving TAP molecules in AR (2). The genes encoding the two TAP subunits (*TAP1* and *TAP2*) are located within the MHC class II region between the DPB1 and DQB1 loci (8, 9). Two *TAP1* dimorphic sites (Ile/Val-333 and Asp/Gly-637) and five *TAP2* dimorphic sites (Val/Ile-379, Ala/Thr-565, Arg/Cys-651, Thr/Ala-665 and Stop/Gln-687) have been widely investigated. It is possible that these genetic variations may modify the TAP molecular structures, influencing antigen peptide selection.

TAP gene polymorphisms have been investigated in several MHC-associated diseases (multiple sclerosis, Grave's disease, and insulin-dependent diabetes mellitus), mostly in Caucasian patients (19-21). Until now, there have been few studies on AR in an Asian population. Ismail et al. (2) provided evidence of a strong association between *TAP1* polymorphism and atopy in a Tunisian population. Tacheuchi et al. (12) reported no association between *TAP1* gene polymorphism and AR in a Japanese population. Therefore, we believe that it is one of the controversial issues in the pathogenetic mechanism of the AR. In this study, we demonstrated a strong association between AR and *TAP1* polymorphism, but not *TAP2*. In the AR group, Ile/Val at *TAP1*^{333}, Asp/Gly at *TAP1*^{637}, and *TAP1* haplotypes C and D were significantly decreased when compared to controls. These results are different from those of previous studies. To find any causes of such discrepancy, we compared the results of controls in different ethnics. In our study, a decreased *TAP1* haplotype A frequency and increased haplotype C and D frequencies were observed when compared to the Tunisian (2) and Japanese (12) controls. *TAP1* haplotype D also deserves to be mentioned. In control groups, *TAP1* haplotype D was found in 5% of Tunisians (2), 7.3% of Japanese (12). However, in our study, *TAP1* haplotype D was found in 11.7% of controls. There might be the various spectrums of genetic pools among different ethnic groups, and therefore, it may be not meaningful to simply compare the results of genetic polymorphisms that have been done in different ethnic groups. Other possible reasons for such discrepancies might be due to multiple factors such as different phenotypic characteristics, heterogeneity within groups of patients and controls, and different genotyping methods.

In this study, we also analyzed the relationships between *TAP1* gene polymorphisms and the results of allergy tests such as total serum IgE, and the strength and the multiplic-

Table 6. *TAP2* haplotypes in allergic rhinitis patients and controls

TAP2	Controls		Allergic rhinitis		Odds ratio	CI*	*p* value
Genotype	(N=107)	(%)	(N=110)	(%)			
AA	13	12.1	11	10.0			
AB	23	21.5	28	25.5	1.44	0.49-4.27	
AC	6	5.7	5	4.5	0.98	0.19-5.16	
AD	2	1.9	5	4.5	2.95	0.38-27.84	
AE	5	4.7	3	2.7	0.71	0.10-4.68	
AF	5	4.7	10	9.1	2.36	0.51-11.29	
BB	16	15.0	12	10.9	0.89	0.26-3.06	
BC	8	7.5	11	10.0	1.63	0.41-6.56	
BD	0	0	2	1.9			
BE	8	7.5	4	3.7	0.59	0.11-3.08	
BF	11	10.3	11	10.0	1.18	0.32-4.43	
BI	1	0.9	0	0	0	0.00-23.81	
CC	1	0.9	0	0	0	0.00-23.81	
CF	4	3.7	5	4.5	1.48	0.25-8.98	
DF	1	0.9	0	0	0	0.00-23.81	
EF	1	0.9	1	0.9	1.18	0.00-50.21	
FF	1	0.9	1	0.9	1.18	0.00-50.21	
FG	1	0.9	1	0.9	1.18	0.00-50.21	
Phenotype	(n=107)	(%)	(n=110)	(%)			
A	53	49.5	62	56.4	1		0.892
B	67	62.6	68	61.8	0.87	0.51-1.47	
C	19	17.8	21	19.1	0.94	0.43-2.07	
D	3	2.8	7	6.4	9.0	0.43-10.31	
E	14	13.1	8	7.3	0.49	0.17-1.37	
F	23	21.5	29	26.4	1.08	0.53-2.20	
G	1	0.9	1	0.9	0.85	0.02-3.21	
I	1	0.9	0	0	0	0.00-1.52	
Allele	(2n=214)	(%)	(2n=220)	(%)			
A	67	31.3	73	33.2	1		0.864
B	83	38.8	80	36.4	0.88	0.55-1.43	
C	20	9.3	21	9.5	0.96	0.45-2.05	
D	3	1.4	7	3.2	2.14	0.47-10.95	
E	14	6.5	8	3.6	0.52	0.19-1.44	
F	25	11.7	30	13.6	1.1	0.56-2.16	
G	1	0.5	1	0.5	0.92	0.02-34.35	
I	1	0.5	0	0	0	0.00-16.26	

*, 95% confidence interval.

ity of positive allergens in skin prick tests; however, there was no association between them (data not shown).

In conclusion, this study showed a meaningful association between AR and a *TAP1* polymorphism, but not *TAP2*. Therefore, it is suggested that a *TAP1* gene polymorphism may be an important factor in AR pathogenesis in a Korean population.

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