Protective Effect of 5-HTTLPR (S) and VNTR (10) Allele Combinations of 5-HTT Gene Against Adenotonsillary Hypertrophy

INTRODUCTION: Serotonin transporter protein which is coded by 5HTT gene is responsible for presynaptic reuptake of serotonin. In this study, we investigated the relationship between polymorphisms in the promoter region (5HTTLPR) and in the second intron (VNTR) in the 5-HTT gene and adenotonsillar hypertrophy (ATH) in pediatric cases.

METHODS: Genotyped of the 5-HT gene promoter 5HTTLPR and intronic VNTR of in 197 children were analyzed using Snap Shot, Multifactor Dimensionality Reduction (MDR) software and carried out to assess the interactions among two polymorphisms and phenotype.

RESULTS: A total of 119 children with ATH (48 girls, 71 boys age range: 3-10 years; mean age: 5.38 years) and 78 healthy children (27 girls, 51 boys, age range: 4-13 years; mean age: 6.76 years) were included in this study. The frequencies of the genotype in all of inheritance models of the 5-HTTLPR and the VNTR (10) allele showed no significant differences between ATH patient and healthy controls (for all P>0.05). However, frequency of the 5-HTTLPR (S) allele and VNTR-5HTTLPR (10/S) haplotype and (10/10+S/S) diplotype were significantly higher in the control group compared to ATH cases (P=0.048, P=0.041, P=0.13).

DISCUSSION AND CONCLUSION: In this study, we observed that S/S genotype, 10/S haplotype and 10/10 + S/S diplotype of 5-HTT gene could have protective effect against ATH.

Keywords: adenotonsillar hypertrophy, serotonin transporter, VNTR, 5-HTTLPR, snap-shot

Öz

GİRİŞ ve AMAC: 5HTT geni tarafından kodlanan serotonin taşıyıcı protein, serotoninin presinaptik geri alınmadan sorumludur. Bu çalışmada pediatrik olgularda 5HTT genindeki promotör (5-HTTLPR) ve ikinci intron (VNTR) polimorfizmler ile adenotonsilller hipertrofisi (ATH) arasındaki ilişki araştırıldı.

YÖNTEMLER ve GERECİLER: 197 çocuğun 5-HTT gen promotör 5-HTTLPR ve intron VNTR’si Snap Shot ile genotiplendirilerek, polimorfizmlerin birbiri ve fenotip arasındaki etkileşimleri Çok Faktörlü Boyut Azaltma (Multifactor Dimensionality Reduction; MDR) programı ile analiz edildi.

BULGULAR: Çalışmamızda ATH tanısı alınmış 119 hasta (48 kız, 71 erkek yaş aralığı: 3-10 yıl; ortalaması yaş: 5.38 yıl) ve 78 sağlıklı çocuk (27 kız, 51 erkek, yaş aralığı: 4-13 yıl; ortalaması yaş: 6.76 yıl) dahil edildi. 5-HTTLPR (S) ve VNTR (10) alelleri tüm kalıtım modellerinde genotipik frekanslar açısından, ATH’lı ile kontrol grubu arasında anlamlı bir fark gözlemmedi (tüüm için P>0.05). Bununla birlikte, 5-HTTLPR (S) allele ve VNTR-5-HTTLPR (10/S) haplotipi ve (10/10 + S/S) diplotipinin sıklığı ATH olgularına göre kontrol grubunda anlamlı olarak daha yüksek idi (s rasaysyla, $P = 0.048$, $P = 0.041$, $P = 0.13$).

TARTIŞMA ve SONUC: 5-HTT geninin S / S genotipi, 10 / S haplotipi ve 10/10 + S / S diplotipinin ATH’ye karşı koruyucu etkisi olabilir.

Anahtar Kelimeler: adenotonsiller hipertrofi, serotonin taşıyıcı, VNTR, 5-HTTLPR, snap-shot
INTRODUCTION

Adenoids and tonsils are located at the entrance of respiratory tract and are important components lymphoid tissues known as Waldeyer’s ring. Adenotonsillar hypertrophy (ATH) is the result of chronic inflammation of the adenoid and/or tonsil tissue however, the pathophysiology of this inflammation remains unclear (1). ATH is frequently seen in pediatric population and can cause obstructive sleep apnea (OSA) by airway obstruction that can lead to growth failure, academic learning difficulties, and behavioral problems (2, 3).

Increased immunologic activity results with ATH which is one of the most common indications for adenotonsillectomy. The immunological responses, may change the progress and severity of the inflammatory processes may result in structural changes in the airway such as fibrosis, increased thickness of the airway smooth muscle layer, hyperplasia of mucus-secreting cells, and new vessel formation (4).

Serotonin (5-hydroxytryptamine 5HT) is a neurotransmitter which contributes regulation of visceral and physiologic functions in human body and causes bronchoconstriction in most animal. Functional alterations in serotonin receptors and serotonin transporters are thought to be associated with neuropsychiatric and visceral diseases. Serotonin acts through several receptor types located on postsynaptic membranes. Presynaptic reuptake is the mechanism of inactivation of synaptic serotonin in which serotonin transporters (SERT or 5HTT) are responsible. The serotonin transporter proteins are coded by 5-HTT gene located on chromosome 17q12. Two polymorphisms, VNTR (variable-number-tandem repeats of 17 bp sequence in the second intron) and 5-HTTLPR (5-HTT gene-linked polymorphic region which is a deletion/insertion polymorphism in the promoter), have been described for 5-HTT gene. VNTR has five alleles (STin 2.7, STin 2.9, STin2.10, STin 2.11 and STin 2.12). 5-HTTLPR has two alleles (S for short and L for long) (5).

Various genetic polymorphisms and their combinations can change the severity of the chronic inflammatory diseases through changing the level of expression of genes (6, 7). Recently some studies focused on the relation between VNTR and 5-HTTLPR polymorphisms of 5-HTT gene and obstructive sleep apnea (OSA) (8). Significant association was observed between 5-HTTLPR L allele and severity of OSA in older adults (9). Also, plasma serotonin levels are reported to be elevated in asthma and are significantly related to asthma severity (10, 11). OSA is characterized by repetitive pauses in breathing during sleep despite the effort to breathe, caused by obstruction of the airway. Serotonin delivery is reduced to upper airway dilator neurons in sleep, leading to sleep related reductions in dilator muscle activity and upper airway obstruction (11). Muscle tone of nasopharynx, palate, oropharynx and tongue also contribute to patency of upper airway and pooling of secretions due to reduced dilator muscle activity may lead an increase in frequency of upper airway infections. We suggested that polymorphisms of 5-HTT gene could play a role in ATH formation either as contributing agents or biomarkers.

The aim of this study is to investigate the relationship between VNTR and 5-HTTLPR polymorphisms of the serotonin transporter gene and adenoid hypertrophy in pediatric patients.

MATERIALS AND METHODS

Subject and Recruitment

This case-control study involved 197 children (119 patients with ATH and 78 healthy children) under 18 years of age who were admitted to Department of Otolaryngology between January 2014 September 2015. The study was approved by the local ethics committee (ID No: 99950669/137), and written informed consent was obtained from all of the participants and/or their parents/guardians.

The patient group was comprised of 119 pediatric patients with the diagnosis of ATH who underwent either a total tonsillectomy, a tonsillectomy with adenoidectomy, or an adenoidectomy. The diagnosis of ATH was based on history, ototorhinolaryngologic examination and flexible fiberoptic nasopharyngoscopy and/or direct adenoid X-ray.

For determining whether to perform each tonsillectomy was made according to the diagnostic criteria for tonsillectomy defined by the American Otolaryngology and Head Neck Surgery Academy (12). Adenoidectomy were performed in the symptomatic patients with upper respiratory tract infections 4-5 times per year combined with nasal congestion, snoring, mouth breathing, sleeping with their mouths open, irritable sleeping, and sleep apnea, the degree of obstruction for diagnose is determined to have 75% or above choanal obstruction in the nasopharynx with adenoid tissue by endoscopic examination. We excluded all patients with proven immunodeficiency, diabetes mellitus, renal failure, sinonasal diseases, chronic periodontal disease, inflammatory bowel disease, congenital or genetic disorder, known malignancy or other pathological diseases.

Control group was comprised of 78 healthy volunteers and selected among children who were known as being healthy for more than one year by our outpatient clinic follow-up. Children who have high mallampati grade, unilateral choanal atresia, chronic disease such as asthma and obesity and history of adenotonsillectomy, craniofacial abnormalities, neuromuscular disease and chronic tonsillitis or symptoms/signs of acute, recurrent respiratory tract infection were excluded from the control group.

The presence of witnessed sleep apnea, open-mouth sleeping, snoring and allergy in children were primarily based on clinical history with the help of parents (13). The presence of asthma was based on the children’ medical history or examinations in the department of pulmonology (14).

DNA Isolation

DNA was extracted from peripheral blood samples (200 μL) collected from each patient and healthy subject. QIAamp DNA Blood Mini Kit (Qiagen Inc.) was used for DNA extraction and
extracted DNA was kept under -20°C.

**PCR Analysis**

A repetitive region of 44-base pair (bp) located in the promoter region (5-HTTLPR) of the 5-HTT gene was amplified by PCR. The PCR reaction mixture constituted of 0.5 μL dNTP (10 μM concentration), 1 μL of forward primer 5’-CACCTAAACCCCTAATGCCTACTGC-3’ (5 μM) and 1 μL of reverser primer 5’-AGAGGGACTGAGCTGGAACACCAC-3’ (5 μM), 0.2 μL of SuperHotTaq DNA polymerase (Bioron Inc.), 5 μL of Taq buffer and 20-50 ng/μL of template DNA. PCR thermal conditions comprised of an initial denaturation at 95°C for 10 minutes, followed by denaturation for 45 seconds at 95°C (35 cycles/minute), annealing for 45 seconds at 60°C (35 cycle/minute), extension for 45 seconds at 72°C (35 cycle/minute) and final extension for 10 minutes at 72°C. The amplified DNA fragments were analyzed by 2% agarose gel electrophoresis. Ethidium bromide was used to stain DNA fragments in the gel for visualization. Alleles were classified as S for short (463-bp) and L for long (507-bp).

Repetitive region of 17-bp located in the second intron (VNTR) of the 5-HTT gene was also amplified by PCR. The PCR reaction mixture constituted of 0.5 μL dNTP (10 μM concentration), 1 μL of forward primer 5’-CCTCAGTGATTGGCTATGCTGTGG (5 μM) and 1 μL of reverse primer 5’-CATCATGTTCCTAGTCTTACGCCAGTG (5 μM), 0.2 μL of SuperHotTaq DNA polymerase (Bioron Inc.), 5 μL of Taq buffer and 20-50 ng/μL of template DNA. Same thermal cycle was used and the amplified DNA fragments were analyzed by 2% agarose gel electrophoresis. Alleles were classified as 12 for 380-bp and 10 for 346-bp.

**In the literature, several types of serotonin transporter protein gene polymorphisms have been described. Due to economic reasons, we could only work on 5-HTTLPR and VNTR.**

**Statistical analysis**

All the statistical analyses were implemented with the SPSS 16.0 package program (Statistical Package for Social Sciences; version 11.0, SSPS Inc, Chicago, IL, USA). The χ² test or Fisher’s exact test were used to assess the difference between the genotypes and clinical phenotypes. Also, genotypes and haplotypes analysis were detected using a regressed logistic model, expressed as the odds ratio (OR) and 95% confidence interval (95% CI) (http://bioinfo.iconcologia.net/index.php?module=SNPstats) Multifactor Dimensionality Reduction (MDR) software package (version 1.0.0, available at www.epistasis.org) was used to evaluate possible relationship between genotype–genotype and genotype–phenotype (15). All statistical analyses were considered significant at P< 0.05.

**RESULTS**

**Characteristics of Study Participants**

A total of 119 children with ATH (48 girls, 71 boys age range: 3-10 years; mean age: 5.38 years) and 78 healthy children (27 girls, 51 boys, age range: 4-13 years; mean age: 6.76 years) were included in this study. There was no significant age and gender difference between the patient and control groups (P > 0.05) (Table 1). The frequency of asthma, allergy witnessed sleep apnea, open-mouth sleeping and snoring in the children with ATH were significantly higher (P= 0.017, P= 0.037, P=

### Table 1. Characteristics of the study population

| Clinical Features | Patients with ATH (n:119) | Healthy children (n:78) | P≠ | P≠ |
|-------------------|---------------------------|-------------------------|-----|-----|
| Age (years) (mean ± SD) | 5.38 [2.013; 3-10] | 6.76 [3.998; 4-13] | 0.550 | 0.566 |
| Gender, n (%) | | | | |
| Male | 71 (60) | 51 (65) | 0.592 | 0.699 |
| Female | 48 (40) | 27 (35) | | 0.639 |
| Asthma (+), n (%) | 32 (27) | 8 (10) | 0.017 | 0.550 |
| Allergy (+), n (%) | 32 (27) | 9 (12) | 0.037 | 0.504* |
| Witnessed sleep apnea (+), n (%) | 99 (83) | 12 (15) | < 0.001 | < 0.001* |
| Open-mouth sleeping (+), n (%) | 42 (53) | 6 (12) | < 0.001 | 0.102 |
| Snoring (+), n (%) | 57 (72) | 6 (12) | < 0.001 | < 0.001* |
| Tonsillectomy and Adenoidectomy | 65 (55) | 0 (0) | - | - |
| Tonsillectomy | 43 (36) | 0 (0) | - | - |
| Adenoidectomy | 11 (9) | 0 (0) | - | - |

*Derived from two-sided X² test for comparison of discrete variables and paired Student’s t-test for continuous variables.

**Fisher’s Exact Test between cases and controls P≠

value between cases and controls

P≠ value between variables and individual SNPs

Values are presented as median ± SD or numbers (%) unless otherwise specified; SD= Standard deviation; SDB= Sleep disordered-breathing; OMS= Open mouth sleeping
Genotyping

The individual polymorphisms analyses revealed that there was no difference for each individual-polymorphisms frequency of the VNTR and 5-HTTLPR (P= 0.814, P= 0.492). There was no significant difference for the frequency of each individual-polymorphisms of 5-HTTLPR and VNTR in patient group for asthma, allergy and open-mouth sleeping variables. However, in the patient group frequency of VNTR was high for the witnessed sleep apnea and snoring variables (P= 0.001 and P= 0.001) (Table 1).

Table 2. Results from genotyping for 5-HTT gene

| Polymorphism | SNP ID | Locus | Allele change | Allele | Case | Control | Database (HapMap/NCBI/dbSNP) | **Turkey (%) |
|--------------|--------|-------|---------------|--------|------|---------|-------------------------------|-------------|
| VNTR         | STin2  | Intron2 | 12/10         | 10-repeat | 0.30 | 0.30    | 0.24-0.44 (33)               | 0.33 (31)-42 (32) | 0.51 |
| 5-HTTLPR     | rs25531| Promotor | L/S           | S-repeat | 0.42 | 0.50    | 0.46-86 (26-30)             | 0.48 (31)-49 (32) | 0.82 |

5-HTT= 5-Hydroxytryptamine transporter; VNTR= Variable number of tandem repeats; 5-HTTLPR= 5-HTT gene-linked polymorphic region; S= 14-repeat short (486bp); L= 16-repeat long (529bp); SNP ID= Single-nucleotide polymorphism accession number or NCBI dbSNP (http://www.ncbi.nlm.nih.govsnp); MAF= Minor allele frequencies;

*MAF from the HapMap databases (http://www.hapmap.org) or NCBI dbSNP (http://www.ncbi.nlm.nih.govsnp);

**MAF from healthy control groups in independent studies on Turkish population
Table 3. Frequencies of 5-HTT gene SNPs genotype and allele

| SNPs | Genotype/Allele | Cases (n:119) n (%) | Controls (n:78) n (%) | Models | Cured OR (95 CI) | Adjusted OR (95 CI)* | P ** value |
|------|----------------|---------------------|-----------------------|--------|-----------------|----------------------|------------|
| VNTR | 12/12          | 56 (47)             | 39 (50)               |        | 1.00            | 1.00 (reference)     |            |
|      | 10/12          | 54 (45)             | 31 (40)               | Codominant | 0.83 (0.40-1.73) | 0.96 (0.42-2.18)     | 0.81       |
|      | 10/10          | 9 (8)               | 8 (10)                |        | 1.19 (0.33-4.30) | 0.90 (0.23-3.57)     |            |
|      | 12/12          | 56 (47)             | 39 (50)               | Dominant | 1.00 (reference) | 1.00 (reference)     | 0.72       |
|      | 10/12-10/10    | 63 (53)             | 39 (50)               |        | 0.88 (0.44-1.78) | 0.95 (0.44-2.06)     |            |
|      | 12/12-12/12    | 110 (92)            | 70 (90)               | Recessive | 1.00 (reference) | 1.00 (reference)     | 0.69       |
|      | 10/10          | 9 (8)               | 8 (10)                |        | 1.29 (0.37-4.48) | 0.92 (0.24-3.47)     |            |
|      | 12/12-10/10    | 65 (55)             | 47 (60)               |        | 1.00 (reference) | 1.00 (reference)     | 0.56       |
|      | 10/12          | 54 (45)             | 31 (40)               | Overdominant | 0.81 (0.40-1.64) | 0.98 (0.44-2.15)     |            |
|      | 10              | 0.30                | 0.30                  |        |                 |                      | 0.92       |

Table 4. Associations between risk of AH and frequencies of haplotypes on the basis of the observed 5-HTT genotypes among cases and controls.

| No | VNTR | 5-HTTLPR | Haplotype frequencies | Cure OR (95% CI)* | **P value |
|----|------|----------|-----------------------|-------------------|-----------|
| 1  | 12   | S        | 0.3535                | 0.3709            | 0.3453    | 1.00 (reference) | ---       |
| 2  | 12   | L        | 0.6985                | 0.3254            | 0.3566    | 1.49 (0.38 - 5.88) | 0.57     |
| 3  | 10   | L        | 0.9032                | 0.2443            | 0.1626    | 0.74 (0.28 - 1.98) | 0.049    |
| 4  | 10   | S        | 0.42                  | 0.50              | 1         | 2.47 (0.51 - 11.85) | 0.040    |

5-HTT= 5-Hydroxytryptamine transporter; VNTR= Variable number of tandem repeats; 5-HTTLPR= 5-HTT gene-linked polymorphic region; S= 14-repeat short (486bp); L= 16-repeat long (529bp); SNP= Single nucleotide polymorphism; OR= Odds ratio; CI= Confidence interval
*Adjusted for age and sex, **χ²-test
Assumed risk alleles;
n (%)= Frequency;
Values are presented as (%)
* In logistic regression model.
**Global haplotype association P-value= 0.048
The single-locus model demonstrating effect of the 5-HTTLPR which is able to correctly predict AH with 43.68 % accuracy. The 5-HTTLPR, L/L and L/S genotypes had a 2-fold and 1.52-fold increased risk of AH, respectively. For each genotype, the number of cases is displayed in the histogram on the left in each cell while the number of controls is displayed by the histogram on the right. Darker shade indicates the high-risk group (TBA: 0.436, CVC 6/10, OR 1.930, CI 0.557-6.6881, P= 0.04).

**Figure 1:** Distribution of the 5-HTTLPR genotypes in cases and controls in application of MDR.

The two-locus model demonstrating effect of VNTR and 5-HTTLPR which are able to correctly predict AH with 52.2 % accuracy. The 5-HTT 10/10+L/S, 12/12+L/L, 12/12+S/S and 10/12+L/S diplotypes had a 3-fold, ∞-fold, ∞-fold and 2.2-fold increased risk of ATH, respectively. For each genotype, the number of cases is displayed in the histogram on the left in each cell while the number of controls is displayed by the histogram on the right. Darker shade indicates those combinations that were classified as high-risk in the original analysis while lighter shade indicates those combinations that were classified as low-risk in the original analysis. Note that the pattern of high and low risk for the 5-HTTLPR differs depending on the value of the VNTR (TBA: 0.522, CVC 10/10, OR 1.203, CI 0.129-11.1888, P= 0.013).

**Figure 2:** Distribution of the VNTR and 5-HTTLPR genotype combinations in cases and controls in application of MDR.

DISCUSSION

In the current study, we investigated the role of 5-HTTLPR and VNTR polymorphisms of 5-HTT gene, which are localized in the promoter and the intronic region, and their functional properties in ATH. While there were no differences between the children with ATH and control group in terms of genotypes of the two SNPs and variant allele frequency at the VNTR polymorphism. The S allele of the 5-HTTLPR and the 10/S haplotype of the VNTR_5-HTTLPR occurred more frequently in the control group than in the children with ATH. However, the frequency of these polymorphisms was similar between the subgroups of children with ATH that underwent tonsillectomy, adenoidectomy and both adenoidectomy and tonsillectomy at the same time. Also, we found that the combinations constructed by minor allele of these polymorphisms and were protective effect against ATH.

5-HTTLPR and VNTR are the most extensively and best characterized of the non-coding variants of 5-HTT gene. Although there are studies that have investigated the relationship of 5-HTT gene polymorphisms with various diseases, there is its relationship with ATH has not been investigated yet. Polymorphism of 5-HTT is studied as a pathophysiologic mechanism in many diseases but to the date there is no known report exists that evaluate the role in ATH. In the present study, the frequencies of VNTR allele were similar between the two groups in, and a protective effect of minor allele of 5-HTTLPR against ATH was observed. In this study, the frequency of VNTRL allele were similar in both groups but the minor allele of 5-HTTLPR had protective effect against ATH. In addition, the genotype distribution of VNTR and 5-HTTLPR in genotype analysis was similar across the groups in all genetic models; however, the single-locus model in MDR analysis showed that the S/S genotype of 5-HTTLPR had 1.2-fold higher protective effect against ATH.

According to genotype analysis in all genetic models, distribution of VNTR and 5-HTTLPR was similar but in MDR analysis according to single locus model, 1.2-fold increased protective effect of S/S genotype against ATH was observed. The expression of 5-HTT is regulated by complex transcriptional mechanisms. S allele of 5-HTTLPR and genotypes involving 10 alleles of VNTR were reported to cause a decrease at the level of 5-HTT gene expression in lymphoblasts (18). In the present study, the haplotype analysis showed that 10/S haplotype had high frequency in the control group and showed a protective effect (2.47-fold). In addition, according to the double-locus model obtained from the MDR analysis, children carrying the harboring 10/10+S/S diplotype was protected (by 1.2-fold) against ATH. It is, however, interesting that 10/10+S/S diplotype was observed only in the control group and 12/12+S/S and 12/12+L/L diplotypes were observed only in the patient group. Although our study does not include functional analysis we consider that homozygous combinations of minor alleles of the two polymorphisms might provide a protective effect against ATH phenotype by changing the level of 5-HTT gene expression at lymphoblast in adenoid
Figure 3: Distribution of the VNTR and 5-HTTLPR genotypes, and allergy combinations in cases and controls in application of MDR.

A. Three-factors model demonstrating effect of the VNTR and 5-HTTLPR genotypes, and allergy combinations which are able to correctly predict AH with 56.3% accuracy. The 5-HTT 10/10+L/S, 12/12+L/S, 12/12+S/S and 12/10+L/S diplootypes had a ∞-fold, 6-fold, ∞-fold and ∞-fold increased risk of allergic-ATH, respectively. For each genotypes combination, the number of cases with allergy (positive or negative skin prick test) is displayed in the histogram on the left in each cell while the number of controls with allergy (positive or negative skin prick test) is displayed by the histogram on the right. Darker shade indicates the high-risk group. Note that the pattern of high and low risk for the 5-HTTLPR differs depending on the value of the allergy (negative or positive skin prick test (TBA 0.563, CVC 10/10, OR 4.6465, CI 2.1195–10.1861, P= < 0.0001).

B. The dendrogram demonstrates the nature of the interactions between the VNTR, 5-HTTLPR, and allergy included in the genetic classifier obtained by MDR. There was synergistic interaction, with the strongest interaction between the VNTR and 5-HTTLPR and tonsillar tissues that have mucosal lymphoid tissue character. The serotonin, as an immune regulator molecule, plays a role in inflammatory reactions including allergic inflammation in which basophils, platelets, and mast cells are involved (19). Serotonin has important effects on respiratory function. Also, it has been reported that changes in plasma serotonin levels may play important roles in the pathogenesis of ATH, asthma, and allergy that share a common genetic background (20–23). In the present study, the MDR analysis of 5-HTT gene showed an important synergistic interaction between the two polymorphisms and allergy in three-factor interaction model. In addition, 12/12+L/L and 10/10+S/S diplootypes of 5-HTT were not observed in allergic children in the study group. We suggest that children carrying harboring 10/10+L/S, 12/12+L/S, 12/12+S/S, and 12/10+L/S diplootypes may have increased the risk for allergic-ATH.

In contrast to single-gene disorders, many genetic and environmental factors including gene polymorphisms are combined to produce a cumulative effect that creates the disease phenotype in complex diseases (24). In complex diseases as ATH, in other words, in the absence of a primary effect influencing the disease phenotype MDR analysis acts as a data mining approach to determine and characterize interactions of the parameters, which cannot be determined using other models, and endeavor to explain disease pathogenesis (15, 25, 26). In the present study, MDR analysis showed the best single (5-HTTLPR), double-locus (5-HTTLPR_VNTR), and three-factor interactions by setting the level of statistical significance as P= 0.001. These observed interactions were considered as the best MDR models among other models in the study. In the present study, the data obtained with MDR are consistent with the data obtained from genotype, haplotype, and regression analyses. Besides, new and specific data that cannot be determined with these analysis methods were
obtained with MDR analysis, and it was realized that these data imply more than a simple SNP+SNP or SNP+phenotype (1+1=3). The obtained data with this analysis method supported the hypothesis that the 5-HTT gene is important in determining the risk of ATH (25).

Although the studies investigating the 5-HTT gene reported many polymorphisms of this gene, 5-HTTLPR in promoter and VNTR variations in the secondary intronic region are the most studied polymorphism. Besides, the frequencies of these variations in healthy population were published on international web-based databases (www.hapmap.org and http://www.ncbi.nlm.nih.govsnp).

The most common alleles of the 5-HTTLPR are the S allele (14 repeats) and the L allele (16 repeats). Also, a number of less common alleles of the polymorphism are the minor XS (17–24 repeats) and XL (11–13 repeats) allele variants and these alleles were not observed in this study (5). In our study, the frequency of S allele of 5-HTTLPR in healthy control group was reported to be 46% in Caucasians (27), 66% in Native Americans (28), 86% in Chinese (29), 70% in Japanese (30), and 48.1-49% in Turks (31, 32). In the present study, frequency of the S allele of 5-HTTLPR was 50% in controls that was different than the reports in populations in other parts of the world but consistent with the data on our population. Among VNTR polymorphisms located in the second intron of the 5-HTT gene, 12 and 10 are the most frequently observed alleles, and alleles 7 and 9 may not be found in certain populations due to their very low frequencies (5).

In previous studies, frequency of the allele 10 in healthy controls was reported to be 44.5% in Germany, 32.1% in Spain, 34% in Americans of European origin, 24% in African decent individuals (33, 34) and 33.4–42% in Turkey (31). In the present study, Alleles 7 and 9 of the VNTR were not found in the study group, and the frequency of allele 10 was 30% in healthy controls. The frequency for VNTR minor allele detected in the present study is consistent with the reports from other regions of the world and reports on our population. The deviations in minor allele frequency might have been caused by different parameters such ethnicity, geographic area, and the sample size (35). Although the present study included individuals residing in similar geographic regions in the province of our city and its vicinity, lack of data on ethnic origin of the patients is an important limitation of the study.

There are some potential limitations of the present study. The sample size is small to obtain an accurate and reliable data in such a population-based genetic study (35). Therefore, the sample size is one of our important limitations. The present study also did not evaluate the relationship between these polymorphisms and the expression level of 5-HTT protein. In addition to this, phenotypic classification was not used in the patient group due to strict inclusion criteria for ATH. Besides, the study group is hospital-based and may not actually represent the normal population. Serotonin transporter gene polymorphisms has relation with OSA and asthma severity and adenoid enlargement may have resulted with a multifactorial interaction of these polymorphisms. Despite these limitations, the present study showed protective effects of S/S genotype, 10/S haplotype, and 10/10+S/S diptotype of the 5-HTT gene against ATH. We consider that nucleotide changes in non-coding promoter and intronic regions of the gene may affect transcriptional capacity of the gene and this may change the extent of inflammatory response by affecting the level of gene expression.

We believe that the present study accumulated a preliminary data in an attempt to develop a gene-based diagnosis and treatment strategies in patients with ATH. Nevertheless, the relationship between 5-HTT gene polymorphisms and ATH must be elucidated in advanced functional studies conducted with larger sample size of patients in population-based studies.

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