Ethiopian International Journal of Multidisciplinary Research

pISSN:2349-5707 Volume:13,Issue 4, April -2026 eISSN:2349-5715

UDK 616.322-002.289

STUDY OF THE ASSOCIATION OF GENETIC POLYMORPHISM OF SOD2 (Ala16Val) WITH THE DEVELOPMENT OF CHRONIC TONSILLITIS

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Annotation

This study is devoted to investigating the role of the SOD2 (Ala16Val) gene polymorphism in the development of chronic tonsillitis and its association with different clinical forms of the disease. The study included 94 patients aged 3 to 55 years diagnosed with chronic tonsillitis, as well as 90 conditionally healthy individuals examined in the Khorezm region between 2021 and 2025. Depending on the clinical presentation, patients were divided into groups with simple, toxic-allergic form I, and toxic-allergic form II.

Molecular genetic analysis was performed using real-time polymerase chain reaction (PCR). Statistical analysis was carried out using the chi-square (χ^2) test and odds ratio (OR).

The results demonstrated that the presence of the minor Val allele and the Val/Val genotype of the SOD2 (Ala16Val) polymorphism is significantly associated with an increased risk of developing chronic tonsillitis. Specifically, the Val allele increases the risk by 1.7 times, while the Val/Val genotype increases it by 2.3 times. Furthermore, this genetic marker was found to play a significant role in the development of both simple and toxic-allergic forms of the disease.

In conclusion, the SOD2 (Ala16Val) gene polymorphism can be considered an important genetic marker for predicting the risk of chronic tonsillitis and may be useful in selecting individualized treatment strategies.

Key words

chronic tonsillitis, genetic polymorphism, SOD2 (Ala16Val), allele, genotype, risk of development.

INTRODUCTION

Despite the accumulated experience, the problem of tonsillar pathology remains unresolved [1]. The prevalence of chronic tonsillitis (CT) not only remains high, but also shows no tendency to decrease [9,13]. According to some data, the prevalence may reach 37-63% [7,14].

Despite the constant improvement of diagnostic and treatment methods for chronic tonsillitis, this pathology continues to occupy a leading place in the structure of pharyngeal diseases [6 , 15]. According to a number of authors, the prevalence of chronic diseases of the tonsils and adenoids is 1,154.4 per 100,000 population [11, 16].

The relevance of developing new methods for diagnosing diseases, including chemotherapy, is determined not only by the increase in local purulent-inflammatory complications of chemotherapy, but also by the importance of focal infection in the development of tonsillogenic complications from internal organs [2,10,17] .

In this regard, the study of molecular genetic mechanisms plays an important role in determining the risk of developing diseases, including CT (simple, toxic-allergic (TAF)) and choosing the optimal treatment tactics [5,8,12].

Target. Study of the degree of association of the SOD2 gene polymorphism (Ala16Val) with the development of chronic tonsillitis.

MATERIAL AND METHODS

The study was based on the voluntary participation of 94 patients with chronic tonsillitis aged 3 to 55 (median age 29.27 ± 1.7 years). Patients were randomly selected upon admission for diagnosis and treatment at the Khorezm Regional Multidisciplinary Medical Center and the private clinic "Khorezm LOR Shifo" (P. Makhmud Street, Urgench, Uzbekistan) from 2021 to 2025. The diagnosis was established taking into account diagnostic standards based on diagnostic criteria for the nature of clinical manifestations and instrumental data.

Depending on the form of chronic tonsillitis (CT), the selected patients (n=94) were divided into the following groups:

- 1st main group (n=94) – patients with chronic tonsillitis;
- 2nd group (n=39) – patients with a simple form of CT;
- 3rd group (n=32) – patients with toxic-allergic form I (TAF I),
- 4th group (n = 23) – patients with toxic-allergic form II (TAF II),
- 5th control group (CG) (n=90) – included conditionally healthy individuals without ENT diseases.

The material for the molecular genetic study was lymphocytes obtained from peripheral blood using a standard method.

The molecular genetic study included genotyping of the SOD2 (Ala16Val) gene SNP using a real-time PCR system and software (Applied Biosystems, USA). Fragments of the SOD2 (Ala16Val) gene SNP were amplified on a programmable thermal cycler from Applied . Biosystems » (USA) with preliminary denaturation at 95 ^{0}C (7 min), amplification for 40 cycles, subsequent denaturation at 95 ^{0}C (1 min), primer annealing at 59 ^{0}C (1 min), elongation at 72 ^{0}C (1 min) and final synthesis at 72 ^{0}C (3 min).

Mathematical analysis and statistical processing of the obtained research results were carried out using a statistical software package using methods for calculating the $\chi^{2\ \text{criteria.}}$ and the odds ratio (OR) . The distribution of genotype variants of the studied SOD2 gene (Ala16Val) was matched according to the Hardy-Weinberg equilibrium (HWE) and analyzed using the GenePop (Genetics of Population) program for analyzing genetic data.

Using the OpenEpi 2009, Version 2.9 statistical software package, the 95% CI (confidence interval) and P-values were calculated in addition to $^{\text{the}}\chi2$ and OR . Comparisons of the observation groups were made using the Student's t-test, which yields a probability (P) estimate of the significance of differences between the compared groups, with a significance level of $P < 0.05$.

RESULTS AND DISCUSSION

A study of the genotype distribution of the SOD2 (Ala16Val) polymorphic gene in the main group of patients with CT and CG revealed no deviation from the Hardy-Weinberg equilibrium (HWE, P>0.05).

When analyzing the distribution of the polymorphic gene SOD 2 (Ala 16 Val) in the control group and groups of patients with CT, all three genotype variations were found among all those examined, i.e. Ala / Ala , Ala / Val and Val / Val (Table 1).

Table 1

Analysis of the structure of the SOD 2 gene polymorphism (Ala 16 Val) among patients with chronic tonsillitis depending on the form and healthy

Group	Frequency of alleles and genotypes									
	Ala		Val		Ala/Ala		Ala/Val		Val/Val	
	n	%	n	%	n	%	n	%	n	%
1st MG of patients with chronic tonsillitis (n = 94)	87	46.3	101	53.7	26	27.7	35	37.2	33	35.1
2nd group with a simple form of CT, (n = 39)	37	47.4	41	52.6	11	28.2	15	38.5	13	33.3
3rd group with TAF I , (n = 32)	29	45.3	35	54.7	9	28.1	11	34.4	12	37.5
4th group with TAF II , (n = 23)	21	45.6	25	54.4	6	26.1	9	39.1	8	34.8
5th CG - healthy, (n=90)	108	60.0	72	40.0	35	38.9	38	42.2	17	18.9

Comparative statistical analyses of the differences identified in the 1st MG of patients with CT compared to the CG showed a statistically significant increase in the frequencies of the minor Val allele ^{by} 1.7 times ($\chi 2 = 7.0$; P = 0.01; O R = 1.7; 95% CI : 1.15 - 2.63) and the Val / Val genotype by 2.3 times ($\chi 2 = {}^{6.1}$; P = 0.03; O ^{R} = 2.3; 95% CI : 1.19 - 4.53), simultaneously accompanied by a statistically significant decrease in the protective Ala allele ($\chi 2 = 7.0$; P = 0.01; O R = 0.6; 95% CI : 0.38 - 0.87).

Meanwhile, in terms of frequencies, the frequencies of the wild genotype Ala / Ala ($\chi^2 = 2.6$; P = 0.2; 0 R = 0.6; 95% CI : 0.32 - 1.11) and heterozygote Ala / Val ($\chi^2 = 0.5$; P = 0.5; 0 R = 0.8; 95% CI : 0.45 - 1.47) in the group of patients compared to the control group did not reach a statistically significant level (Table 2).

Table 2

Evaluation of differences in the distribution of the polymorphic gene SOD 2 (Ala 16 Val) between the main and control groups

Alleles and genotypes	Frequency				χ^2	R	R R	95% CI	O R	95% CI
	MG (n=94)		CG (n=90)							
	n	%	n	%						
Ala	87	46.3	108	60.0	7.0	0.01	0.8	0.52 - 1.14	0.6	0.38 - 0.87
Val	101	53.7	72	40.0	7.0	0.01	1.3	0.85 - 1.98	1.7	1.15 - 2.63
Ala/Ala	26	27.7	35	38.9	2.6	0.20	0.7	0.37 - 1.36	0.6	0.32 - 1.11

Ala/Val	35	37.2	38	42.2	0.5	0.50	0.9	0.49 - 1.58	0.8	0.45 - 1.47
Val/Val	33	35.1	17	18.9	6.1	0.03	1.9	1.09 - 3.17	2.3	1.19 - 4.53

The presence of statistically significant differences in the frequencies of the minor Val allele and the Val / Val genotype for the genetic marker SOD 2 (Ala 16 Val) between the MG and CG proves their role in increasing the risk of developing CT by 1.7 (χ^{2} = 4.4; P = 0.05) and 2.3 times (χ^{2} = 6.1; P = 0.03) due to a decrease in the activity of the protective Ala allele (χ^{2} = 7.0; P = 0.01).

Comparing the results of the distribution of the polymorphic gene SOD 2 (Ala 16 Val) in the 2nd group of patients with a simple form of CT in relation to the control group, a pronounced tendency was found to increase the unfavorable effect of the minor allele Val by 1.7 times ($\chi^{2 =}$ $^{3.5}$; P = 0.1; O R = 1.7; 95% CI : 0.98-2.83) and the minor homozygote Val / Val by 2.1 times (χ^{2} = 3.2; P = 0.1; O R = 2.1; 95% CI : 0.93 - 4.97), accompanied by a pronounced tendency to decrease the protective activity of the wild allele Ala (χ^{2} = 3.5; P = 0.1; O R = 0.6; 95% CI : 0.35 - 1.03).

The differences in the groups between the frequencies of the wild genotype Ala / Ala (χ^{2} = 1.4; P = 0.3; 0 R = 0.6; 95% CI : 0.27 - 1.39) and the heterozygote Ala / Val (χ^{2} = 0.2; P = 0.7; 0 R = 0.9; 95% CI : 0.4 - 1.84) were not statistically significant.

Analyzing and evaluating the distribution pattern of the SOD 2 (Ala 16 Val) genetic polymorphism in the 2nd group of patients with a simple form of CT and in the control group, a pronounced tendency was observed to increase the unfavorable effect of the minor Val allele (χ^{2} = 3.5; P = 0.1) and decrease the protective activity of the major wild allele Ala (χ^{2} = 3.2; P = 0.1) and the Val / Val genotype (χ^{2} = 6.1; P = 0.03) which contributes to an increase in the chance of developing a simple form of CT by 1.8 and 2.3 times, respectively, which emphasizes their role in the mechanism of CT onset.

Analyzing the results of the study of the polymorphic gene SOD 2 (Ala 16 Val) in the 3rd group of patients with CT and TAF I compared to the control group, a statistically significant increase in the frequencies of the minor allele Val by 1.8 times (χ^{2} = 4.1; P = 0.05; O R = 1.8; 95% CI : 1.02 - 3.21) and the genotype Val / Val by 2.6 times (χ^{2} = 4.5; P = 0.05; O R = 2.6; 95% CI : 1.08 - 6.17) was found in the gene structure , simultaneously accompanied by a significant decrease in the protective effect of the wild allele Ala (χ^{2} = 4.1; P = 0.05; O R = 0.6; 95% CI : 0.31 - 0.98). As for the wild genotype Ala / Ala ($\chi 2 = {}^{1.2}$; P=0.3; O R =0.6; 95% CI : 0.21 - 1.48) and the heterozygote Ala / Val ($\chi 2 = {}^{0.6}$; P=0.5; O R =0.7; 95% CI : 0.31 - 1.66), no significant differences in their frequencies were found between the groups (Table 3).

Table 3

Evaluation of differences in the distribution of the polymorphic gene SOD 2 (Ala 16 Val) between patients with CT with TAF I and healthy individuals

Alleles and genotypes	**Frequency**				**χ^{2}**	**R**	**RR**	**95% CI**	**OR**	**95% CI**
	CT with TAF I (n=32)		**CG (n=90)**							
	n	**%**	**n**	**%**						
Ala	29	45.3	108	60.0	4.1	0.05	0.8	0.33 - 1.73	0.6	0.31 - 0.98

Val	35	54.7	72	40.0	4.1	0.05	1.3	0.97 - 1.8	1.8	1.02 - 3.21
Ala/Ala	9	28.1	35	38.9	1.2	0.30	0.7	0.19 - 2.72	0.6	0.26 - 1.48
Ala/Val	11	34.4	38	42.2	0.6	0.50	0.8	0.24 - 2.82	0.7	0.31 - 1.66
Val/Val	12	37.5	17	18.9	4.5	0.05	2.0	0.63 - 6.21	2.6	1.08 - 6.17

Thus, comparing the distribution of the genetic polymorphism SOD 2 (ALA 16 VAL) in the group of patients with CT with TAF I and CG, statistically significant differences were found in the frequencies of the minor allele Val (χ^2 = 3.4; P = 0.1) and the genotype Val / Val (χ^2 = 4.5; P = 0.05), proving their association with an increase in the risk of developing CT TAF I by 1.8 and 2.6 times.

Similar studies in the 4th group of patients with chemotherapy with TAF II Compared with the control group, in the structure of the polymorphic gene SOD 2 (Ala 16 Val) it was possible to trace the presence of a pronounced tendency to a decrease in the frequency of the Ala allele (χ^2 = 3.1; P = 0.1; O R = 0.6; 95% CI : 0.29-1.07) and an increase in the proportion of the Val allele by 1.8 times (χ^2 = 3.1; P = 0.1; O R = 1.8; 95% CI : 0.93 -3.41). Meanwhile, no statistically significant differences were found between the frequencies of the Ala / Ala (χ^2 = 1.3; P = 0.3; O R = 0.6; 95% CI : 0.2 - 1.53), Ala / Val (χ^2 = 0.1 P = 0.8 ; O R = 0.9; 95% CI : 0.35 - 2.24) and Val / Val (χ^2 = 2.7; P = 0.2; O R = 2.3; 95% CI : 0.85 - 6.17) genotypes.

The presence of a pronounced tendency towards an increase in the proportion of the Val allele ($\chi^{2 = 3.1}$; P = 0.1) and a decrease in the proportion of the Ala allele (χ 2 = $^{3.1 ; P = 0.1)}$ in the structure of the polymorphic gene SOD 2 (Ala 16 Val) in the group of patients with CT TAF II compared to the control shows the possible contribution of the studied marker to an increase in the chance of developing this form of chronic tonsillitis by 1.8 times.

Having assessed the differences revealed in the distribution of the polymorphic gene SOD 2 (Ala 16 Val) taking into account the form of CT between patients with the simple form of HT and HT with TAF I, no statistically significant differences were found for the allelic variants Ala (χ^2 = 0.1; P = 0.9; O R = 1.1; 95% CI : 0.56 - 2.11) and Val (χ^2 = 0.1; P = 0.9; O R = 0.9; 95% CI : 0.47 - 1.78), or for the genotypes Ala / Ala (χ^2 <3.84; P = 0.99; O R = 1.0; 95% CI : 0.36 - 2.84), Ala / Val (χ^2 = 0.1; P = 0.8; O R = 1.2; 95% CI : 0.45 - 3.16) and Val / Val (χ^2 =0.1; P = 0.8; O R =0.8; 95% CI : 0.31 - 2.21).

At the same time, evaluating the differences revealed in the distribution of the polymorphic gene SOD 2 (Ala 16 Val) between patients with a simple form of CT and CT with TAF II , similarly to the previous comparison, no statistically significant differences in the proportion of alleles and genotypes were revealed (for alleles Ala - χ^2 <3.84; P = 0.9; O R = 1.1; 95% CI : 0.52 - 2.23 and Val - χ^2 <3.84; P = 0.9; O R = 0.9; 95% CI : 0.45 - 1.93, as well as genotypes Ala / Ala - χ^2 <3.84; P = 0.9; O R = 1.1; 95% CI : 0.35 - 3.56, Ala / Val - χ^2 <3.84; P=0.98; O R =1.0; 95% CI : 0.34 - 2.8 and Val / Val - χ^2 <3.84; P=0.95; O R =0.9; 95% CI : 0.32 - 2.78).

Comparative analyses of the distribution of the polymorphic gene SOD 2 (Ala 16 Val) between patients with CT with FAT I and CT with FAT II again failed to reveal statistically significant differences for the alleles Ala (χ^2 <3.84; P=0.98; O R =1.0; 95% CI : 0.46 - 2.11) and Val (χ^2 <3.84; P=0.98; O R =1.0; 95% CI : 0.47 - 2.17), as well as the genotypes Ala / Ala (χ^2 <3.84; P=0.9; O R =1.1; 95% CI : 0.33 - 3.71), Ala / Val (χ^2 =0.1; P = 0.8; O R =0.8; 95% CI : 0.27 - 2.47) and Val / Val (χ^2 <3.84; P = 0.9; O R =1.1; 95% CI : 0.37 - 3.44).

CONCLUSION

Thus, analyzing the results of the study of the distribution features and functional significance of the allelic genetic polymorphism SOD 2 (Ala 16 Val), we can conclude that this marker is associated with the risk of developing CT. In particular, the study results showed that the minor allele Val and the genotype Val / Val for the genetic marker SOD 2 (Ala 16 Val) have a risk effect, increasing the formation of CT by 1.7 ($\chi^2 = 4.4$; $P = 0.05$) and 2.3 times ($\chi^2 = 6.1$; $P = 0.03$). Moreover, it was established that carriage of the minor Val allele and the Val / Val genotype are associated with the development of the simple form and TAF I CT, increasing the risk of their development by 1.8 ($\chi^2 = 3.5$; $P = 0.1$) and 2.3 times ($\chi^2 = 6.1$; $P = 0.03$), respectively, and also by 1.8 ($\chi^2 = 3.4$; $P = 0.1$) and 2.6 times ($\chi^2 = 4.5$; $P = 0.05$), respectively. Along with this, the role of the polymorphic gene SOD 2 (Ala 16 Val) was also traced in relation to the formation of CT TAF II , the risk of which is increased among carriers of the Val allele by 1.8 times ($\chi^2 = 3.1$; $P = 0.1$).

As a result, it is quite obvious that the genetic polymorphism of SOD 2 (Ala 16 Val) is a genetic marker involved in increasing the risk of developing HT and its forms (simple, toxic-allergic forms I and II).

REFERENCES:

1. Abraham ZS et al. Prevalence and bacteriology of tonsillitis among patients attending otorhinolaryngology Department at Muhimbili National Hospital, Dar es Salaam-Tanzania //Medical journal of Zambia. – 2019. – T. 46. – No. 1. – pp. 33-40.
2. Abu Bakar M. et al. Chronic tonsillitis and biofilms: a brief overview of treatment modalities //Journal of inflammation research. – 2018. – S. 329-337.
3. Andreychyn MA et al. Thermographic differential diagnosis of acute tonsillitis and exacerbation of chronic tonsillitis //Wiadomości Lekarskie. – 2020. – T. 73. – No. 3. – pp. 417-422.
4. Esamuratov AI, Ermatov NJ. Features of the occurrence of single-nucleotide polymorphism il10 (c592a) among patients with purulent-inflammatory diseases of the middle ear and assessment of its contribution to the mechanisms of disease formation // British Medical Journal . 2022, Vol. 1 No. 1 : 57-64 . (14.00.00; No. 6).

5. Esamuratov A.I., Zh.F. Shamsiev, M. A. Mirzaeva. Features of the distribution of allelic polymorphisms of inflammatory (TNF (G308A), IL2 (T330G), IL6 (C174G), IL10 (C592A)) cytokine genes in pyoinflammatory diseases of the middle ear // European journal of molecular medicine, Vol. 2 No. 5 (September 2022), P.70-73
6. Esamuratov A.I. , Mirzaeva M.A., Shamsiev Zh.F. Immune and molecular genetic aspects of the formation of chronic reliable otitis media (csom) // Evrosiyo pediatriya akhborotnomasi. - Toshkent . - 2021; 3 (10): -B. 2-6 (ОАК Раёсатининг 2019 йил 31 октябрдаги 270/8.2-сон қарори).
7. Esamuratov AI, Mirzayeva MA, Shamsiyeva JF. Genetic predictors for the formation of chronic purulent otitis media // British Medical Journal . 2021, Vol. 2 No. 1 : 159-164 (14.00.00; No. 6).
8. Esamuratov AI, Ermatov NJ. Features of the occurrence of single-nucleotide polymorphism il10 (c592a) among patients with purulent-inflammatory diseases of the middle ear and assessment of its contribution to the mechanisms of disease formation // British Medical Journal . 2022, Vol. 1 No. 1 : 57-64 . (14.00.00; No. 6).
9. Gaździcka J. et al. Selected SNPs of FCN2 associated with chronic tonsillitis in the adult population //Genes. – 2023. – T. 14. – No. 2. – S. 242.

10. Guntinas-Lichius O. et al. Treatment of recurrent acute tonsillitis—a systematic review and clinical practice recommendations //Frontiers in surgery. – 2023. – T. 10. – P. 1221932.
11. Kostić M. et al. Analysis of tonsil tissues from patients diagnosed with chronic tonsillitis—microbiological profile, biofilm-forming capacity and histology //Antibiotics. – 2022.

– T. 11. – No. 12. – P. 1747.
12. Marlina L., Barreto JCHA, Poluan FH Analysis of Chronic Tonsillitis A Case Study //Asian Journal of Advanced Research and Reports. – 2025. – T. 19. – no. 3. – S. 301-310.
13. Matkarimova D.S., Karimov Kh. Ya., Boboev K.T. Features of the renin-angiotensin system gene polymorphism in patients with immune microthrombovasculitis in Uzbekistan // Bulletin of Hematology. 2022. No. 2.
14. Nimmana BK, Paterek E. Tonsillitis //StatPearls [Internet]. – StatPearls Publishing, 2025.
15. Shukurullayevna BS et al. Modern laboratory diagnostics of tonsillitis //Web of Teachers: Inderscience Research. – 2025. – T. 3. – No. 1. – S. 61-65.
16. Tzelnick S. et al. Long-term outcomes of tonsillectomy for recurrent tonsillitis in adults //The Laryngoscope. – 2020. – T. 130. – No. 2. – pp. 328-331.
17. Yarmukhamedova, N. F., Matkarimova, D. S., Bakieva, S. K., & Salomova, F. I. (2021). Features of the frequency of distribution of alleles and genotypes of polymorphisms of the gene Tnf-A (G-308a) in patients with rhinosinusitis and the assessment of their role in the development of fhis pathology.