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# COMPARATIVE DESCRIPTION OF FREQUENCIES OF DETERMINATION OF ALLELES AND GENOTYPES OF GENE POLYMORPHISMS IN PATIENTS WITH ACUTE SENSONEURAL HEARING LOSS

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**Abstract.** Our data confirm the complexity of the genetic mechanism of the development of ASNHL in patients with acute sensorineural hearing loss of vascular genesis and demonstrate the need and importance of understanding the complex interaction of genes in analyzing the development and clinical stage of the pathology under study. By analyzing the distribution of genotypic variants of this polymorphism, we determined that the C-634G rs2010963 polymorphism in the VEGF-A gene is associated with the development of ASNHL of the G/G monogenotype. In group 1 of patients with vascular ASNHL, a tendency for an increase in the frequency of the minor genotype of the C-634G rs2010963 polymorphism in the VEGF-A gene ( $\chi$ 2=4.6; P=0.30; RR=2.15; OR=1.1; 95%CI: 2.174-6.69) was observed in comparison with the control group. In this case, the indicators of patients in group 1 were separated and compared with the control group, and the OR and RR indicators increased, and the level of reliability in the G/G genotypes increased significantly ( $\chi$ 2 =0.39; P=0.29; RR=2.35; OR=2.4; 95% CI: 37.929- 36.50).

Keywords: gene polymorphism, sensorineural hearing loss, audiometry.

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# O'TKIR SENSONEVRAL ESHITISH ZAIFLIGI BO'LGAN BEMORLARDA ALLELLAR VA GEN POLIMORFIZMLARINING GENOTIPLARINI ANIQLASH CHASTOTLARINING QIYOSIY TA'RIFI

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**Annotatsiya.** Bizning ma'lumotlarimiz qon tomir genezisning o'tkir sensorinöral eshitish qobiliyatini yo'qotgan bemorlarda O'SNEZ rivojlanishining genetik mexanizmining murakkabligini tasdiqlaydi va o'rganilayotgan patologiyaning rivojlanishi va klinik bosqichini tahlil qilishda genlarning murakkab o'zaro ta'sirini tushunish zarurati va ahamiyatini ko'rsatadi. Ushbu polimorfizming genotipik variantlarining tarqalishini tahlil qilib, VEGF-A genidagi C-634G rs2010963 polimorfizmi G/G monogenotipining O'SNEZ rivojlanishi bilan bog'liqligini aniqladik. Qon tomir O'SNEZ bilan og'rigan bemorlarning 1-guruhida VEGF-A genida C-634G rs2010963 polimorfizmining kichik genotipining chastotasini oshirish tendentsiyasi mavjud (ch2 = 4,6; P = 0,30; RR = 2,15; OR = 1,1). 95% CI: 2.174-6.69) nazorat guruhi bilan solishtirganda kuzatildi. Bunday holda, 1-guruhdagi bemorlarning ko'rsatkichlari ajratilib, nazorat guruhi bilan taqqoslandi va OR va RR ko'rsatkichlari ortdi va G/G genotiplarida ishonchlilik darajasi sezilarli darajada oshdi (ch2 =0,39; P=0,29; RR=2,35; OR=2,4; 95% CI: 37,929-36,50).

Kalit so'zlar: gen polimorfizmi, sensonevral eshitish pasayishi, audiometriya.

#### Iqtiboslik uchun:

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### **INTRODUCTION**

The problem of acute sensorineural hearing loss is of both medical and social importance, as it is a widespread disease that leads to disability among young people and people of working age. Current statistics show a steady increase in cases of acute sensorineural hearing loss worldwide [2]. Information on how to apply for medical care according to the frequency of acute sensorineural hearing loss It varies depending on the age of the patients and hearing 0.8% of the total number of patients with pathology does [5].

Acute sensorineural hearing loss is caused by many factors. There are about a hundred of them [1-4]. Currently, infectious diseases (influenza, infectious parotitis, typhoid fever, wounds), sound and mechanical injuries, vascular diseases (hypertension, neurocirculatory dystonia, atherosclerosis, industrial substances and a number of drugs (antibiotics - aminoglycosides, ethacrine acid, furosemide) proved the role of etiological factors such as ototoxic effect [6].

Acute sensorineural hearing loss requires urgent treatment, which is sometimes only etiological, and often empirical, polypragmatic, and carried out without sufficient scientific and theoretical foundations [10]. First, this search for pathogenetic therapy is due to the fact that it is carried out in relation to diseases with different etiological and clinical manifestations. In this regard, there is a need to more clearly and reasonably distinguish individual forms of acute sensorineural hearing loss as an independent nosological unit based on etiological, anamnestic, clinical - audiological, immuno-allergological and other characteristics. Developing a classification based on clear clinical and etiopathogenetic approaches is important in solving the problem of sensorineural hearing loss. Therefore, further investigation of etiopathogenesis and comprehensive treatment of ASNHL seems to be an area that has not yet been fully explored [7].

Studying the factors (triggers) that trigger the development of pathological processes in the sound-receiving part of the auditory analyzer, as well as concomitant diseases (predictors) that affect the frequency of ASNHL development with similar pathogenetic mechanisms, is of great importance for a more rational approach to early diagnosis, as well as ensuring the effectiveness of treatment and pnjreventive measures [8]. However, the importance and scope of research on the possibilities of early diagnosis of hearing function disorders and elimination of disorders in the auditory analyzer at the stage of socially adapted forms is associated not only with general medical aspects, but also with interest in the aspects of communicative socialization of patients with ASNHL from a general medical point of view [9]. The development of permanent hearing loss is known to lead to disability for patients and corresponding economic costs for the state.

The above allows not only to determine the nature of damage to the auditory analyzer, but also to determine the cause of certain disorders of hearing function, the mechanism of their development, as well as to develop pathogenetic therapy for acute sensorineural hearing loss. All of the above has predetermined the goals and objectives of this study.

# RESULTS

A study of the frequencies of alleles and genotypes of the C-634G rs2010963 polymorphism in the VEGF-A gene (Figure 1) showed that there were differences in their distribution between groups 1-2 and the control group (Table 1).

During the study, it was possible to determine that the G allele was detected 9.3 times more frequently in group 1, 3.2 times more frequently in group 2, and 3.5 times more frequently in the control group. Compared with the C/G and G/G genotypes, the C/C genotype was detected 4.16 times more frequently in group 1, 1.84 times more frequently in group 2, and 5.53 times more frequently in the population.

The results of a comparative analysis of the frequencies of alleles and genotypes of the C-634G rs2010963 polymorphism in the VEGF-A gene in the 1st and control groups are presented in Table 2.

The frequency of the C allele of the C-634G rs2010963 polymorphism in the VEGF-A gene is statistically insignificant, being 1.19 times higher among conditionally healthy people ( $\chi 2=9.3$ ; p=0.002; RR=0.83; OR=0.31; 95%CI: 1.675-0.65), and the G allele is 2.6 times higher in patients with ASNHL in group 2 (x2=9.37; p=0.002; RR=1.19; OR=3.18; 95%Cl: 2.77-6.69). The C/C genotype was detected 1.39 times more often in the population group than in patients in group 1, which was a statistically insignificant difference ( $\chi 2=7.6$ ; p=0.006; RR=0.71; OR=0.29; 95% CI: 1.79-0.69). The frequency of detection of the C/G genotype was statistically slightly higher, 1.9 times higher among patients in group 2 than in healthy controls ( $\chi$ 2=4.69; p=0.03; RR=2.15; OR=2.71; 95%CI: 5.57-6.69). Comparative analysis of the occurrence of the G/G genotype showed an increased frequency of its detection among patients with ASNHL compared to the population group (Fig. 4), its value was 7.5% and 1.37%, respectively, and among patients in the 2

Table 1

Prevalence of alleles and genotypes of the C-634G rs2010963 polymorphism in the VEGF-A gene in groups of patients with ASNHL

N⁰	Group	Allele frequency				Distribution frequency of genotypes					
		С		G		C\C		C\G		G\G	
		n	%	n	%	n	%	n	%	Ν	%
1	ASNHL with	61	76.25	19	23.75	24	60	13	32.5	3	7.5
	vascular genesis n=40										
2	ASNHL with	56	90.32	6	9.67	25	80.64	6	19.35	0	0
	infection genesis n=31										
3	Control group n=23	41	89,13	5	10,87	39	84,78	6	13,04	1	2,17

Table 2

Differences in the frequency of allele and genotype variants of the C-634G rs2010963 polymorphism in the VEGF-A gene in patients with ASNHL of vascular origin and in healthy controls

	Quanti	ty of tested alle	eles and ge							
Alleles and	ASNHL with		Control		Xi2	р	RR	+ 95%Cl	OR	+95%Cl
genotypes	vascular genesis n=40		n=23							1 23 /001
	n	%	n	%						
С	61	76,25	42	91,3	9,372	0,002	0,837	1,675	0,314	0,659
G	19	23,75	4	8,69	9,372	0,002	1,195	2,773	3,187	6,694
C/C	24	60	39	84,78	7,697	0,006	0,718	1,792	0,295	0,699
C/G	13	32,5	8	17,39	4,694	0,030	2,157	5,572	2,714	6,697
G/G	3	7,5	1	2,17	2,844	0,092	5,475	18,579	5,838	45,379

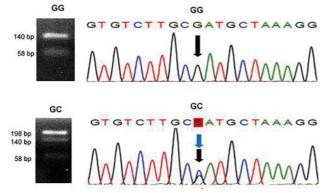


Figure 1. Allele and genotype distribution diagram of the C-634G rs2010963 polymorphism in the VEGF-A gene

groups, its occurrence was 1.39 times higher than in conditionally healthy people ( $\chi 2=1.37$ ; p=0.09; RR=5.4; OR= 5.3; 95% CI: 18.57- 45.37).

Table 3 presents the results of a comparative analysis of the frequency of alleles and genotypes of the C-634G rs2010963 polymorphism in the VEGF-A gene in group 2 and the control group.

In group 2 patients and healthy controls,

#### C vs G



Events	Total	Events	lotal	weight	M-H, Fixed, 95% CI	Year	M-H, Fixed, 95% CI	
9	48	16	100	12.5%	1.21 [0.49, 2.98]	2010		
37	282	37	216	53.9%	0.73 [0.45, 1.20]	2011		
26	193	29	234	33.6%	1.10 [0.62, 1.94]	2018	+	
	523		550	100.0%	0.91 [0.65, 1.29]		+	
72		82						
57. df = 2 (	P = 0.4	(6); I <sup>2</sup> = 09	6					
0.50 (P =	0.61)						0.01 0.1 1 10 100	
							Favours SLE Favours control	
SLE		Contr	ol		Odds Ratio		Odds Ratio	
Events	Total	Events	Total	Weight	M-H, Fixed, 95% Cl	Year	M-H, Fixed, 95% CI	
21	48	35	100	10.6%	1.44 [0.72, 2.92]	2010		
110	000							
110	282	84	216	48.0%	1.00 [0.70, 1.45]	2011		
70	193	84	216	48.0% 41.5%	1.00 [0.70, 1.45] 0.96 [0.65, 1.43]		Ŧ	
							Ŧ	
	193		234	41.5%	0.96 [0.65, 1.43]		Ŧ	
70	193 523	87	234 550	41.5%	0.96 [0.65, 1.43]		0.01 0.1 1 10 100	
	37 26 72 57, df = 2 ( = 0.50 (P = <u>SLE</u> Events 21	9 48 37 282 26 193 523 72 57, df= 2 (P = 0.4 0.50 (P = 0.61) SLE Events Total 21 48	9 46 16 37 282 37 26 193 29 523 72 82 57, df = 2 (P = 0.46); P = 05 0:50 (P = 0.61) SLE Contri Events Total Events 21 48 35	9 48 16 100 37 282 37 216 26 193 29 234 523 550 72 82 57, df = 2 (P = 0.46); P = 0% 0.50 (P = 0.61) SLE Control Events Total Events Total 21 48 35 100	9 48 16 100 12.5%   37 282 37 216 53.9%   26 193 29 234 33.6%   523 550 100.0% 525, df=2 (P=0.46), P=0% 50.00 (P=0.61)   SLE Control Events Total Weightt   21 49 35 100 10.8%	9 48 16 100 12.5% 1.21 [0.4, 2.58] <th 1.21="" 2.5<="" [0.4,="" td=""><td>9 48 16 100 12.5%, 12.1 [0.49,2.99] 2010   37 28.2 37 216 53.9%, 0.73 [0.45,1.20] 2018   26 193 29 234 33.6%, 1.10 [0.62,1.94] 2018   523 550 100.0%, 0.91 [0.65, 1.29] 202   57, df=2 (P=0.46), P= 0% 0 0.91 [0.65, 1.29] 203   0.50 (P= 0.61) 0 0.4%, P= 0% 0   SLE Control Codes Ratio   Codes Ratio   SLE Control Odds Ratio   Codes 7.5 (2 Year   21 48 35 100 10.4%, 7.2, 2.92 2014</td></th>	<td>9 48 16 100 12.5%, 12.1 [0.49,2.99] 2010   37 28.2 37 216 53.9%, 0.73 [0.45,1.20] 2018   26 193 29 234 33.6%, 1.10 [0.62,1.94] 2018   523 550 100.0%, 0.91 [0.65, 1.29] 202   57, df=2 (P=0.46), P= 0% 0 0.91 [0.65, 1.29] 203   0.50 (P= 0.61) 0 0.4%, P= 0% 0   SLE Control Codes Ratio   Codes Ratio   SLE Control Odds Ratio   Codes 7.5 (2 Year   21 48 35 100 10.4%, 7.2, 2.92 2014</td>	9 48 16 100 12.5%, 12.1 [0.49,2.99] 2010   37 28.2 37 216 53.9%, 0.73 [0.45,1.20] 2018   26 193 29 234 33.6%, 1.10 [0.62,1.94] 2018   523 550 100.0%, 0.91 [0.65, 1.29] 202   57, df=2 (P=0.46), P= 0% 0 0.91 [0.65, 1.29] 203   0.50 (P= 0.61) 0 0.4%, P= 0% 0   SLE Control Codes Ratio   Codes Ratio   SLE Control Odds Ratio   Codes 7.5 (2 Year   21 48 35 100 10.4%, 7.2, 2.92 2014

Figure 4. Comparative analysis of the incidence of G/G genotype in patients with vascular idiopathic urticaria

the C and G alleles were found at almost the same frequency. Among healthy controls, the C genotype was slightly more frequent ( $\chi$ 2=0.03; p=0.86; RR=0.99; OR=0.91; 95% Cl: 3.891-2.52).

76

Table 3

Differences in the frequency of alleles and genotypic variants of the C-634G rs2010963 polymorphism in the VEGF-A gene in patients with ASNHL of infectious genesis and conditionally healthy people

	Quar	ntity of teste genotyp		and	Xi2	р	RR	+ 95%Cl	OR	+95%CI
Alleles and genotypes	ASNHL is of infectious genesis			ntrol						
	n=									
	n	%	n	%						
С	56	90,32	42 91,3		0,031	0,860	0,992	3,891	0,912	2,528
G	6	9,68	4 8,69		0,031	0,860	1,009	1,886	1,096	3,023
C/C	25	80,65	39 84,78		0,129	0,719	0,965	4,051	0,820	2,419
C/G	6	19,35	8	17,39	0,292	0,589	1,284	5,303	1,353	4,048

Table 4

Differences in the frequency of allelic and genotypic variants of the C-634G rs2010963 polymorphism in the VEGF-A gene between patients in groups 1 and 2

	Quantity o	of tested allele	es and ger	notypes						
Alleles and genotypes	Group 1		Group 2		X2	р	RR	+ 95%CI	OR	+95%Cl
5 71	n=40		n=31							
	n	%	n	%						
С	61	76,25	56	90,32	4,769	0,029	1,185	4,885	2,907	7,576
G	19	23,75	6	9,68	4,769	0,029	0,844	1,462	0,344	0,896
C/C	24	60	25	80,65	3,481	0,062	1,344	5,680	2,778	8,126
C/G	13	32,5	6	19,35	1,540	0,215	0,596	2,442	0,498	1,498
G/G	61	76,25	56	90,32	4,769	0,029	1,185	4,885	2,907	7,576

Compared to the control group, the frequency of the G genotype in the group of patients with ASNHL of infectious genesis was significantly, but not statistically significantly, increased by 1.08 times ( $\chi$ 2=0.3; p=0.86; RR=1.0; OR=1.09; 95% CI: 1.88-3.02). The frequency of detection of the C/C genotype of the C-634G rs2010963 polymorphism in the VEGF-A gene in the control group was significantly higher, 1.03 times, compared to group 2 ( $\chi$ 2=0.12; p=0.719; RR=0.96; OR=0.82; 95% CI: 4.05-2.41). The frequency of the C/G genotype among patients with ASNHL of infectious genesis was 1.28 times higher than in the control group of conditionally healthy people, i.e. 19.35 and 15.07%, respectively ( $\chi$ 2=0.29; p=0.589; RR=1.28; OR=1.35; 95% CI: 5.303-4.04) (Table 3).

Table 4 below presents the results of a comparative analysis of the frequencies of alleles and genotypes of the C-634G rs2010963 polymorphic locus in the VEGF-A gene among patients in groups 1 and 2.

The frequency of the C allele was statistically

almost 1.18 times higher in group 1 patients ( $\chi 2=4.7$ ; p=0.02; RR=4.88; OR=2.90; 95% Cl: 4.88-7.57), while the G allele was detected unreliable frequently among group 2 patients ( $\chi$ 2=4.6; p=0.02; RR=0.84; OR=0.34; 95% CI: 1.462-0.89). The frequency of detection of the C/C genotype was statistically insignificant, i.e., it was 1.34 times higher in patients in group 1 than in patients in group 2 ( $\chi 2=3.4$ ; p=0.06; RR=1.34; OR=2.77; 95% CI: 5.680-8.12). The frequency of detection of the C/G genotype was 1.7 times higher in group 1 patients and amounted to 19.35% and 32.5% (x2=1.54; p=0.215; RR=0.59; OR=0.49; 95% Cl: 2.44-1.49). The differences in the frequency of detection of the G/G genotype in groups 1 and 2 were statistically significant, with the value of this indicator in group 1 patients being 1.18 times higher than in group 2 patients ( $\chi 2=4.7$ ; p=0.02; RR=1.18; OR=2.9; 95% CI: 4.88-7.57).

## CONCLUSION

Thus, the C-negative allele of the C-634G rs2010963 polymorphism in the VEGF-A gene is more common in group 1 patients than in healthy individuals and group 2 patients. The high frequency of this allele was observed with a predominance of the homozygous C/G variant (1.28 times). At the same time, the difference between patients in groups 1 and 2 and the control group was noted at the trend level, and the trend was at the level of statistical significance. These data allow us to conclude that the G/G genotype of the C-634G rs2010963 polymorphism in the VEGF-A gene has a predisposing effect on the development and clinical course of the vascular type of ASNHL. This polymorphism is located in the promoter region of the gene and is a functional polymorphism. The presence of the C allele in group 1 patients is associated with increased expression of the VEGF-A gene in the presence of the G/G genotype, which leads to the development and progression of a more severe form of vascular ASNHL.

### **CONFLICT OF INTERESTS**

The authors declare the absence of obvious and potential conflicts of interest related to the publication of this article.

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## **AVAILABILITY OF DATA AND MATERIALS**

All data generated or analysed during this study are included in this published article.

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All authors contributed to the design and interpretation of the study and to further drafts. All authors read and approved the final manuscript.

### ETHICS APPROVAL AND CONSENT TO PARTICIPATE

All applicable international, national, and/or institutional guidelines for the care and use of animals were followed.

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Все авторы внесли свой вклад в подготовку исследования и толкование его результатов, а также в подготовку последующих редакций. Все авторы прочитали и одобрили итоговый вариант рукописи.

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Не применимо.

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#### ЛИТЕРАТУРА / REFERENCES

- Cadoni G. et al. A case-control study on proinflammatory genetic Polymorphisms on sudden sensorineural hearing loss //The Laryngoscope. – 2015. – T. 125. – №. 1. – C. E28-E32.
- Cao Z. et al. Genetic polymorphisms and susceptibility to sudden sensorineural hearing loss: a systematic review // Audiology and Neurotology. – 2019. – T. 24. – №. 1. – C. 8-19.
- 3. Chien C.Y. et al. Heat shock protein 70 gene polymorphisms in sudden sensorineural hearing loss //Audiology and Neurotology. 2012. T. 17. №. 6. C. 381-385.
- Corazzi V. et al. Genetic polymorphisms in sudden sensorineural hearing loss: an update //Ear, Nose & Throat Journal. – 2021. – T. 100. – №. 3\_suppl. – C. 337S-342S.
- Hiramatsu M. et al. Polymorphisms in genes involved in inflammatory pathways in patients with sudden sensorineural hearing loss //Journal of Neurogenetics. – 2012. – T. 26. – №. 3-4. – C. 387-396.
- Kasztelewicz B. et al. Cytokine gene polymorphism associations with congenital cytomegalovirus infection and sensorineural hearing loss //European Journal of Clinical Microbiology & Infectious Diseases. – 2017. – T. 36. – №. 10. – C. 1811-1818.

- Kitoh R. et al. SOD1 gene polymorphisms in sudden sensorineural hearing loss //Acta Oto-Laryngologica. – 2016. – T. 136. – №. 5. – C. 465-469.
- Teranishi M. et al. Polymorphisms in genes involved in oxidative stress response in patients with sudden sensorineural hearing loss and Meniere's disease in a Japanese population //DNA and cell biology. – 2012. – T. 31. – №. 10. – C. 1555-1562.
- Teranishi M. et al. Polymorphisms in genes involved in the free-radical process in patients with sudden sensorineural hearing loss and Meniere's disease //Free radical research. – 2013. – T. 47. – №. 6-7. – C. 498-506.
- Uchida Y. et al. Endothelin-1 gene polymorphism in sudden sensorineural hearing loss //The Laryngoscope. – 2013. – T. 123. – №. 11. – C. E59-E65.