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THE IMPORTANCE OF THE ALA16VAL POLYMORPHIC LOCUS IN THE SOD2 GENE IN THE PROGRESS OF PROSTATE CANCER

Tursunov Doniyor Muxammadjon ugli
Republic Cancer Center of Uzbekistan, Andijan branch

Abstract

Diagnosis and prognostic stratification of prostate cancer (PC) are traditionally based on three pillars: serum prostate-specific antigen (PSA) levels, clinical staging according to the TNM system, and the Gleason score according to biopsy data. Despite their widespread use and inclusion in international guidelines, these tools have significant limitations that lead to problems of overdiagnosis, overtreatment, and, in some cases, underestimation of disease aggressiveness. In modern urological oncology, there is an urgent need to integrate new, more accurate biomarkers for a personalized approach to patient management.

The SOD2 gene (superoxide dismutase 2) encodes an enzyme that protects cells from damage caused by oxidative stress and converts toxic reactive oxygen species (ROS) into safer molecules. It is a major protein in the mitochondrial matrix, where it detoxifies byproducts of energy metabolism. Mutations in SOD2 may be associated with a variety of diseases, including cancer, as well as accelerated aging.

Keywords: Prostate cancer screening, SOD2 gene polymorphism, prostate cancer development, aggressive prostate cancer.

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Introduction

Relevance of the problem

Prostate cancer (PC) is a classic example of an oncological disease with pronounced clinicopathological heterogeneity. This means that a single term encompasses a spectrum of diseases with radically different biological behavior, prognosis, and treatment approaches [4]. Understanding this heterogeneity is a central problem of modern oncology, as it is directly related to two main problems: on the one hand, hyperdiagnosis and treatment of clinically insignificant tumors, and on the other hand, the need for timely and aggressive treatment of life-threatening forms [2]. The diagnosis and prognostic stratification of prostate cancer is traditionally based on three pillars: serum prostate-specific antigen (PSA) level, clinical stage according to the TNM system, and biopsy-based Gleason score [1]. Despite their widespread use and inclusion in international guidelines, these tools have significant limitations that lead to problems of overdiagnosis, overtreatment, and in some cases, underestimation of disease aggressiveness [3]. In modern oncology, there is a need to integrate new, more accurate biomarkers for a personalized approach to patients [5].

Results and Discussion

Analysis of the allele distribution among the main group of patients showed that the Ala allele was transmitted at a frequency of 0.52, and the Val allele at a frequency of 0.48. In the genotype structure, the Ala/Ala homozygous genotype was observed at a frequency of 0.34, and the Ala/Val and Val/Val genotypes at a frequency of 0.36 and 0.30, respectively. The expected values corresponding to Hardy-Weinberg equilibrium were 0.27, 0.5 and 0.23, respectively.

In the control group, the frequency of the Ala allele was 0.65, and the frequency of the Val allele was 0.35. The genotype distribution was observed in the ratio

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Ala/Ala - 0.46, Ala/Val-0.39, and Val/Val - 0.16, respectively. The expected values according to Hardy-Weinberg equilibrium were 0.42, 0.46, and 0.12.
The observed heterozygosity in the main group was 0.36, while the expected one was 0.5, and the difference between the two was D=-0.27. The observed heterozygosity in the control group was also 0.39, while the expected one was 0.46, and the difference between the two was D=-0.15. This indicates a slight decrease in heterozygosity, but the differences are not significant (Table 1).

Table 1 Distribution of alleles and genotypes of the Ala16Val polymorphism in the SOD2 gene according to Hardy-Weinberg equilibrium in the main and control groups.

Main group					
Alleles	Allele frequency				
Ala	0.52				
Val	0.48				
Genotypes	Genotype frequency		χ^2	p	df
	Observed	Expected			
Ala/ Ala	0.34	0.27	1.81		
Ala/ Val	0.36	0.5	3.89		
Val/ Val	0.3	0.23	2.1		
Vsego	1	1	7.8	-0.004	1
Control group					
Alleles	Allele frequency				
Ala	0.65				
Val	0.35				
Genotypes	Genotype frequency		χ^2	p	df
	Observed	Expected			
Ala/ Ala	0.46	0.42	0.23		
Ala/ Val	0.39	0.46	0.86		
Val/ Val	0.16	0.12	0.8		
Total	1	1	1.9	0.167	1
Groups	Ho	He		D*	
Main group	0.36	0.5		-0.27	
Control group	0.39	0.46		-0.15	

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Comparative analysis of the prevalence of alleles and genotypes of the Ala16Val genetic marker in the SOD2 gene in samples from the main and comparison groups and their role in the development of prostate cancer.

According to the results of the analysis of the genetic marker Ala16Val in the SOD2 gene, significant differences were observed in the frequency of alleles and genotypes between the main and control groups. The frequency of the Ala allele in the main group was 51.9%, which was significantly lower than in the control group, while in the control group this allele was 65.0%, respectively ($\chi2$=6.9; p=0.01; OR=0.6; 95%CI:0.39-0.87). (Table 1). In contrast, the Val allele was recorded in 48.1% of cases among the main group, while in the control group the frequency of this allele was significantly lower than in the main group and was 35.0%, respectively. This indicates that the Val minor allele may be associated with the development of these diseases ($\chi2$=6.9; p=0.01; OR=1.7; 95%CI:1.15-2.59). (Table 2).

Genotype analysis also revealed similar results. The prevalence of the Val/Val negative homozygous genotype in the main group was 29.9%, which is almost 2 times higher than 15.6% in the control group. The presence of this genotype indicates a 2.3-fold increase in the risk of developing the disease ($\chi2$=5.6; p=0.03; OR=2.3; 95%CI:1.16-4.64). (Table 2).

Table 2 Comparative analysis of the prevalence of alleles and genotypes of the Ala16Val polymorphism in the SOD2 gene in the main and comparison group samples.

Alleles and genotypes	Amount of alleles and genotypes tested				$\chi2$	p	OR	95%CI
	Main group		Comparison group					
	n	%	n	%				
Ala	111	51.9	117	65.0	6.9	0.01	0.6	0.39 - 0.87
Val	103	48.1	63	35.0	6.9	0.01	1.7	1.15 - 2.59
Ala/ Ala	36	33.6	41	45.6	2.9	0.10	0.6	0.34 - 1.08
Ala/ Val	39	36.4	35	38.9	0.1	0.80	0.9	0.51 - 1.61
Val/ Val	32	29.9	14	15.6	5.6	0.03	2.3	1.16 - 4.64

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No statistically significant differences were found between the groups tested for the Ala/Ala homozygous and Ala/Val heterozygous genotypes. However, the fact that the Ala/Ala homozygous positive genotype had a higher incidence rate in the comparison group does not exclude a tendency for a possible protective role of this genotype (33.6% vs. 45.6%; $\chi 2=2.9$; p=0.1; OR=0.6; 95%CI:0.34-1.08) (Table 2).

In the next stage of our research, conducted to study the significance of the Ala16Val polymorphism of the SOD2 gene in the pathogenesis of prostate cancer, examinations conducted in a group of 65 patients with this disease showed that the distribution of alleles in this polymorphism was 79.2% for the Ala allele, and 50.8% for the Val allele (Table 3).

Table 3 Comparative analysis of the prevalence of alleles and genotypes of the Ala16Val polymorphism in the SOD2 gene in prostate cancer and benign prostatic hyperplasia group samples.

Alleles and genotypes	Amount of alleles and genotypes tested				$\chi 2$	p	OR	95%CI
	Prostate cancer		Benign prostatic hyperplasia					
	n	%	n	%				
Ala	64	49.2	47	56.0	0.9	0.40	0.8	0.44 - 1.32
Val	66	50.8	37	44.0	0.9	0.40	1.3	0.76 - 2.27
Ala/ Ala	20	30.8	16	38.1	0.6	0.50	0.7	0.32 - 1.63
Ala/ Val	24	36.9	15	35.7	0.0	0.90	1.1	0.47 - 2.36
Val/ Val	21	32.3	11	26.2	0.5	0.50	1.3	0.57 - 3.18

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As a result of observation, in the second subgroup, which included 42 patients with benign prostatic hyperplasia, the Ala allele was found in 56.0% of cases, while the Val allele was found in 44.0%. However, the differences in the prevalence of alleles of the SOD2 gene Ala16Val polymorphism between the studied groups were not statistically significant (Ala allele - $\chi 2$=0.9; r=0.4; OR-0.8; 95%CI:0.44 - 1.32 and Val allele - $\chi 2$=0.9; r=0.4; OR-1.3; 95%CI:0.76 - 2.27) (Table 3). Comparative assessment of the differences in the frequency of homozygous genotypes of the Ala16Val polymorphism of the SOD2 gene Ala/Ala allowed us to determine the absence of statistically significant differences between the two groups of patients studied (30.8% vs. 38.1%; $\chi 2$=0.6; R=0.5; OR=0.7; 95%CI:0.32-1.63) (Table 3).

It was also observed that the frequency of homozygous Val/Val genotypes was significantly higher in the group of patients with PBS compared to individuals with PBXG (52.4% vs. 53.1%; $\chi 2$=0.0; R=0.9; OR=1.0; 95%CI:0.56-1.7) (Figure 1).

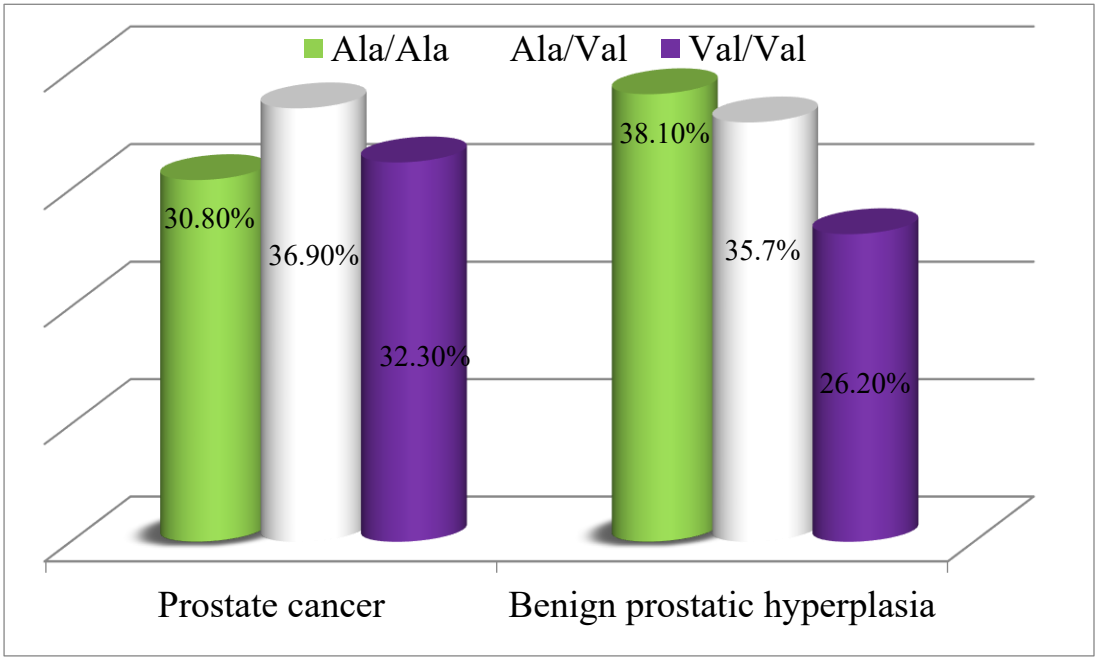

Figure 1. Comparative analysis of the prevalence of genotypes of the SOD2 gene Ala16Val polymorphism among PBS and PBXG samples.

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Among patients with PBS, the Ala/Val heterozygous genotype was slightly more common than in the group of patients with PBXG, accounting for 36.9%. This genotype was detected in 35.7% of cases in the PBXG group, respectively ($\chi2$=0.0; R=0.9; OR=1.1; 95%CI:0.47-2.36) (Figure 1).

In a comparative study of the prevalence of the major Ala allele of the SOD2 gene Ala16Val polymorphism between the subgroup of patients with PBXG and the control group, no significant differences were found, and the OR value was close to 1.0 (56.0% vs. 65.0%; $\chi2$=2.0; r=0.2; OR=0.7; 95% CI:0.4-1.16). Although the differences between the minor Val allele types did not reach reliable values, the OR=1.5 indicated a strong trend towards an increased probability of developing PBXG in patients with this allele compared to the control group (44.0% vs. 35.0%; $\chi2$=2.0; r=0.2; 95%CI:0.86-2.48) (Table 4).

Table 4 Comparison and comparative analysis of the prevalence of alleles and genotypes of the Ala16Val polymorphism in the SOD2 gene in samples from a group of benign prostatic hyperplasia.

Alleles and genotypes	Amount of alleles and genotypes tested				$\chi2$	p	OR	95%CI
	Prostate cancer		Comparison group					
	n	%	n	%				
Ala	47	56.0	117	65.0	2.0	0.20	0.7	0.4 - 1.16
Val	37	44.0	63	35.0	2.0	0.20	1.5	0.86 - 2.48
Ala/ Ala	16	38.1	41	45.6	0.6	0.50	0.7	0.35 - 1.55
Ala/ Val	15	35.7	35	38.9	0.1	0.80	0.9	0.41 - 1.87
Val/ Val	11	26.2	14	15.6	2.1	0.20	1.9	0.8 - 4.67

According to the results of statistical analysis, in the subgroup of patients with PBXG, the Ala/Ala genotype of this gene was detected in 38.1% and the Ala/Val heterozygous genotype in 35.7% and 45.6% and 38.9% of cases, respectively, in

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the group of respondents. The distribution of these genotypes between the studied groups did not differ significantly from each other ($\chi 2<3.84$; $r>0.05$) (Table 4).

In the group of patients with PBXG, a slight increase in the frequency of the Val/Val variant of the SOD2 gene polymorphism was noted compared with the group of respondents. According to the calculated OR, it was observed that carriers of the negative Val/Val genotype had a tendency to have a 1.9-fold higher risk of developing PBXG diseases than patients without this genotype (26.2% vs. 15.6%; $\chi 2=2.1$; $r=0.2$; OR=1.9; 95%CI:0.8-4.67) (Table 4).

In the main group of patients with PBS, a significant increase in the negative Val allele of the Ala16Val polymorphism of the SOD2 gene was observed, which was 1.9 times higher than in the control group ($\chi 2=7.7$; $r=0.01$; OR=1.9; 95%CI: 1.21-3.03). At the same time, a significant decrease in the positive Ala allele was found in the patient group compared to the control group, indicating a possible protective effect of this allele in the development of PBS ($\chi 2=7.7$; $r=0.01$; OR=0.5; 95%CI:0.33-0.83) (Table 5).

According to the results of the study, insignificant differences were observed in the frequencies of positive homozygous Ala/Ala and heterozygous Ala/Val genotypes in both groups of patients. The incidence of this genotype was 45.6% and 38.9% in the comparison group, and 30.8% and 36.9% in the patient group (Table 5).

It was also found that there was a direct relationship between the functionally unfavorable Val/Val genotype of this polymorphism and the small group of participants with PBS, the incidence of this factor in this group was statistically significantly increased compared to the control group, with a relative risk of OR=2.6. In this case, when the negative Val/Val genotype of the Ala16Val polymorphic locus of the SOD2 gene was detected, the risk of developing PBS was significantly higher than in patients without this genotype (Table 5).

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Table 5 Comparison and comparative analysis of the prevalence of alleles and genotypes of the Ala16Val polymorphism in the SOD2 gene in prostate cancer group samples.

Alleles and genotypes	Amount of alleles and genotypes tested				χ2	p	OR	95%CI
	Prostate cancer		Comparison group					
	n	%	n	%				
Ala	64	49.2	117	65.0	7.7	0.01	0.5	0.33 - 0.83
Val	66	50.8	63	35.0	7.7	0.01	1.9	1.21 - 3.03
Ala/ Ala	20	30.8	41	45.6	3.5	0.10	0.5	0.27 - 1.03
Ala/ Val	24	36.9	35	38.9	0.1	0.90	0.9	0.48 - 1.78
Val/ Val	21	32.3	14	15.6	6.1	0.03	2.6	1.21 - 5.53

Conclusion

In the main group of patients with diagnosed PBS, a significant increase in the negative Val allele of the SOD2 gene Ala16Val polymorphism was observed, which was OR=1.9 times higher than in the control group (χ2=7.7; r=0.01; OR=1.9; 95%CI: 1.21-3.03). At the same time, a significant decrease in the positive Ala allele was found in the patient group compared to the control group, indicating a possible protective effect of this allele in the development of PBS (χ2=7.7; r=0.01; OR=0.5; 95%CI:0.33-0.83).

According to the results of the study, there were insignificant differences in the frequencies of positive homozygous Ala/Ala and heterozygous Ala/Val genotypes in both groups of patients. The incidence of this genotype was 45.6% and 38.9% in the comparison group, and 30.8% and 36.9% in the patient group.

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References

1. Ahmed, H. U., et al. "Diagnostic accuracy of multi-parametric MRI and TRUS biopsy in prostate cancer (PROMIS): a paired validating confirmatory study." The Lancet (2017)
2. Cybulski, C., et al. (2004). CHEK2 is a multiorgan cancer susceptibility gene. American Journal of Human Genetics, 75(6), 1131–1135.
3. Franklin, R. B., & Costello, L. C. (2009). The important role of mitochondrial citrate and citrate export in prostate cancer. Molecular and Cellular Biochemistry, 328(1-2), 177–183.
4. Kasivisvanathan, V., Rannikko, A. S., Borghi, M., et al. (2018). MRI-Targeted or Standard Biopsy for Prostate-Cancer Diagnosis. NewEnglandJournalofMedicine, 378(19), 1767–1777. (Issledovanie PRECISION).
5. Loeb, S., &Bjurlin, M. A. (2014). Overdiagnosis and Overtreatment of Prostate Cancer. EuropeanUrology, 65(6), 1046–1055.