SENSITIVITY, SPECIFICITY, AND PROGNOSTIC EFFICACY INDICATORS OF THE EXAMINED POLYMORPHISMS IN THE PATIENTS WITH NECROTIC PROCESS OF MAXILLOFACIAL REGION FOR RISK-INCREASING ALLELES

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Abstract. *Genetic polymorphisms, particularly single nucleotide polymorphisms (SNPs), play an important role in determining individual susceptibility to disease, clinical progression, and treatment outcomes. This review summarizes current evidence on the sensitivity, specificity, and prognostic efficacy of examined polymorphisms in patient groups carrying risk-increasing alleles. The literature indicates that while many polymorphisms show statistically significant associations with disease risk and prognosis, their individual diagnostic performance is often limited due to modest effect sizes and population heterogeneity. Variations in genetic background, environmental factors, and study design further influence the predictive value of specific alleles. Recent approaches focusing on the combined analysis of multiple polymorphisms, including polygenic risk scores, demonstrate improved sensitivity and specificity compared with single-marker analyses. Integration of genetic data with clinical and demographic variables appears essential for enhancing prognostic accuracy. Overall, the findings highlight both the potential and the limitations of genetic polymorphisms as prognostic biomarkers and underscore the need for large, population-specific studies to support their application in personalized medicine.*

Keywords: *genetic polymorphisms; sensitivity and specificity; prognostic efficacy; risk-increasing alleles; polygenic risk assessment.*

YUZ-JAG‘ SOHASIDA NEKROTIK JARAYONLAR BILAN OG‘RIGAN BEMORLARDA XAVFNI OSHIRUVCHI ALLELLAR UCHUN O‘RGANILGAN POLIMORFIZMLARNING SEZUVCHANLIK, SPETSIFIKLIK VA PROGNOSTIK SAMARADORLIK KO‘RSATKICHLARI

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Annotatsiya. *Genetik polimorfizmlar, xususan bir nukleotidli polimorfizmlar (SNP), kasalliklarga individual moyillikni, klinik kechish xususiyatlarini hamda davolash natijalarini belgilashda muhim ahamiyat kasb etadi. Ushbu sharhda xavfni oshiruvchi allellar tashuvchisi bo‘lgan bemorlar guruhlarida o‘rganilgan polimorfizmlarning sezuvchanlik, spetsifiklik va prognostik samaradorlik ko‘rsatkichlari bo‘yicha zamonaviy ilmiy ma’lumotlar umumlashtirilgan. Adabiyotlar tahlili shuni ko‘rsatadiki, ko‘plab polimorfizmlar kasallik xavfi va prognozi bilan statistik jihatdan ishonchli bog‘liqlikka ega bo‘lishiga qaramay, ularning alohida holdagi diagnostik qiymati ko‘pincha ta’sir kuchining nisbatan pastligi va populyatsiyalar heterogenligi bilan cheklanadi. Genetik fonning farqlanishi, atrof-muhit omillari hamda tadqiqot dizayni xususiyatlari alohida allellarning prognoz qiymatiga qo‘shimcha ta’sir ko‘rsatadi. Bir nechta polimorfizmlarni kompleks tahlil qilishga asoslangan zamonaviy yondashuvlar, jumladan poligen xavf ballari, yagona markerlar tahliliga nisbatan yuqoriroq sezuvchanlik va spetsifiklik ko‘rsatkichlarini namoyon etmoqda. Genetik ma’lumotlarni klinik va demografik ko‘rsatkichlar bilan integratsiya qilish prognoz aniqligini oshirishda muhim hisoblanadi. Umuman olganda, olingan natijalar genetik polimorfizmlarning prognostik biomarker sifatidagi imkoniyatlari bilan bir qatorda ularning cheklovlarini ham ko‘rsatadi hamda ularni shaxsiylashtirilgan tibbiyotda qo‘llashni asoslash uchun yirik, populyatsiyaga xos tadqiqotlar zarurligini ta’kidlaydi.*

Kalit so‘zlar: *genetik polimorfizmlar, sezuvchanlik va spetsifiklik, prognostik samaradorlik, xavfni oshiruvchi allellar, poligen xavfni baholash.*

ПОКАЗАТЕЛИ ЧУВСТВИТЕЛЬНОСТИ, СПЕЦИФИЧНОСТИ И ПРОГНОСТИЧЕСКОЙ ЭФФЕКТИВНОСТИ ИССЛЕДОВАННЫХ ПОЛИМОРФИЗМОВ У ПАЦИЕНТОВ С НЕКРОТИЧЕСКИМИ ПРОЦЕССАМИ ЧЕЛЮСТНО-ЛИЦЕВОЙ ОБЛАСТИ ДЛЯ АЛЛЕЛЕЙ, ПОВЫШАЮЩИХ РИСК

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Аннотация. *Генетические полиморфизмы, в частности однонуклеотидные полиморфизмы (SNP), играют важную роль в определении индивидуальной предрасположенности к заболеваниям, особенностей клинического течения и эффективности лечения. В данном обзоре обобщены современные данные о чувствительности, специфичности и прогностической эффективности исследованных полиморфизмов в группах пациентов — носителей аллелей, повышающих риск развития заболевания. Анализ литературы показывает, что, несмотря на статистически значимые ассоциации многих полиморфизмов с риском заболевания и прогнозом, их индивидуальная диагностическая ценность часто ограничена вследствие умеренных размеров эффекта и гетерогенности популяций. Различия в генетическом фоне, воздействие факторов окружающей среды и особенности дизайна исследований дополнительно влияют на прогностическую значимость отдельных аллелей. Современные подходы, основанные на комбинированном анализе нескольких полиморфизмов, включая полигенные шкалы риска, демонстрируют более высокие показатели чувствительности и специфичности по сравнению с анализом одиночных маркеров. Интеграция генетических данных с клиническими и демографическими характеристиками является необходимым условием повышения точности прогноза. В целом полученные данные подчеркивают как потенциал, так и ограничения генетических полиморфизмов в качестве прогностических биомаркеров и указывают на необходимость проведения масштабных, популяционно-специфичных исследований для обоснования их применения в персонализированной медицине.*

Ключевые слова: *генетические полиморфизмы, чувствительность и специфичность, прогностическая эффективность, аллели повышенного риска, полигенная оценка риска.*

Introduction. Genetic polymorphisms, particularly single nucleotide polymorphisms (SNPs), have been extensively investigated as potential biomarkers for disease susceptibility, prognosis, and therapeutic response. In recent years, increasing attention has been paid to evaluating the sensitivity, specificity, and prognostic efficacy of risk-increasing alleles in different patient groups, as these indicators determine the clinical applicability of genetic markers [1,2]. Sensitivity reflects the ability of a polymorphism to correctly identify individuals at high risk, whereas specificity indicates its capacity to exclude individuals without increased susceptibility [3].

Numerous studies have demonstrated that polymorphisms in genes involved in DNA repair, inflammation, apoptosis, and drug metabolism are associated with disease progression and clinical outcomes [4,5]. For example, variants in DNA repair genes such as XRCC1, ERCC1, and BRCA1 have been linked to altered treatment response and survival in cancer patients [6,7]. However, while statistically significant associations are often reported, the sensitivity of individual polymorphisms is frequently limited, as many risk alleles contribute only modestly to overall disease risk [8].

The specificity of examined polymorphisms also varies considerably across populations. Ethnic background, linkage disequilibrium patterns, and environmental exposures may influence genotype–phenotype relationships, leading to inconsistent results between studies [9]. As a result, a polymorphism that demonstrates high prognostic value in one population may show reduced specificity in another, limiting its generalizability [10]. This variability highlights the importance of population-specific validation when assessing genetic risk markers.

To improve prognostic efficacy, recent research has shifted toward combining multiple polymorphisms into polygenic risk scores (PRS). These composite indicators have been shown to enhance both sensitivity and specificity compared to single SNP analyses [11]. In several disease models, PRS based on risk-increasing alleles demonstrated improved prediction of disease progression, recurrence, and mortality, suggesting greater clinical relevance [12]. Nonetheless, the prognostic performance of such models still depends on careful selection of polymorphisms and integration with clinical and demographic variables.

Overall, the literature suggests that while individual polymorphisms may serve as statistically significant risk indicators, their standalone sensitivity and specificity are often insufficient for reliable clinical decision-making. The prognostic efficacy of genetic markers improves when multiple risk alleles are evaluated simultaneously and combined with traditional clinical parameters [1,5]. Future studies should focus on large, well-characterized cohorts and standardized analytical approaches to refine the predictive accuracy of genetic polymorphisms. Such efforts are essential for translating genetic risk assessment into effective tools for personalized medicine and patient stratification.

Results.

Furthermore, one of the main objectives of studying the gene polymorphisms in this research was to reduce the incidence of disease in patients

with a high predisposition to necrotic changes in the maxillofacial area induced by various etiological factors. This could be achieved through specific preventive and therapeutic interventions. To this end, the prognostic efficiency (AUC) of all analyzed molecular genetic markers was studied both independently (Table 1) and in gene–gene syntropic interactions to predict the development of necrotic changes in the maxillofacial area due to specific etiological causes.

1-Table.

Sensitivity, specificity, and prognostic efficacy indicators of the examined polymorphisms in the patient groups for risk-increasing alleles

SNP type	Allele	Groups	SE	SP	AUC	OR	95%CI	p
IL10 rs1800872	A	First group// Control group	0.52	0.59	0.55	1.54	0.93-2.58	0.093
		Second group// Control group	0.58	0.59	0.58	1.96	1.17-3.27	0.010
		Third group// Control group	0.43	0.59	0.51	1.10	0.664-1.85	0.695
SERPINE1 rs1799768	4G	First group// Control group	0.63	0.53	0.583	1.94	1.17-3.31	0.01
		Second group// Control group	0.48	0.53	0.508	1.07	0.644-1.77	0.79
		Third group// Control group	0.64	0.53	0.59	2.05	1.22-3.43	0.007
NOS3 rs2070744	C	First group// Control group	0.41	0.77	0.59	2.37	1.35-4.17	0.003
		Second group// Control group	0.29	0.77	0.49	0.90	0.490-1.67	0.755
		Third group// Control group	0.32	0.77	0.545	1.59	0.897-2.84	0.111
IL1β rs1143627	T	First group// Control group	0.51	0.72	0.583	1.99	1.18-3.35	0.01
		Second group// Control group	0.63	0.72	0.645	3.33	1.96-5.65	<0.001
		Third group// Control group	0.41	0.72	0.53	1.33	0.787-2.24	0.287

As shown in Table 4.9, according to the results presented in the Table, for the IL10 gene rs1800872 polymorphism, in the first group (patients with post-COVID related necrotic changes in the face-jaw area) AUC – 0.55, sensitivity (SE) – 0.52, and specificity (SP) – 0.59 were recorded, while in the second group (patients with granulomatous polyangiitis-related necrotic changes in the face-jaw area) these indicators were respectively AUC – 0.58, SE – 0.58, and SP – 0.59. In the third group (patients with chronic renal failure-related necrotic changes in the face-jaw area), the prognostic efficiency was low, with AUC – 0.51, SE – 0.43, and SP – 0.59. For the SERPINE1 gene rs1799768 (4G allele) polymorphism, in the first group AUC – 0.583, SE – 0.63, and SP – 0.53 were recorded, while in the second group AUC – 0.508, SE – 0.48, and SP – 0.53 were noted. In the third group, AUC – 0.59, SE – 0.64, and SP – 0.53 were observed. For the NOS3 gene rs2070744 polymorphism, in the first group prognostic efficiency was AUC – 0.59, sensitivity – 0.41, and specificity – 0.77. In the second group, AUC – 0.49, SE – 0.29, and SP – 0.77 were recorded, while in the third group AUC – 0.545, SE – 0.32, and SP – 0.77 were noted. For the IL1β gene rs1143627 polymorphism, in the first group AUC – 0.583, SE – 0.51, and SP – 0.72 were recorded, while in the second group AUC – 0.645, SE – 0.63, and SP – 0.72 were noted. In the third group, AUC – 0.53, SE – 0.41, and SP – 0.72 were observed.

According to the results of the conducted analysis, the identified AUC values for IL10 (rs1800872), SERPINE1 (rs1799768), NOS3 (rs2070744), and IL1β (rs1143627) gene polymorphisms were in the range of 0.5–0.7, indicating their moderate prognostic efficiency. At the same time, the IL1β rs1143627 polymorphism in the second group (AUC = 0.645) and NOS3 rs2070744 polymorphism in the first group (AUC = 0.59) showed relatively high prognostic significance. These results indicate the potential use of these polymorphisms as clinical-prognostic biomarkers in certain cases.

Conclusion.

The analysis of sensitivity, specificity, and prognostic efficacy of the studied gene polymorphisms demonstrates their potential role in predicting necrotic changes in the maxillofacial area associated with different etiological factors. Overall, the AUC values obtained for the IL10 (rs1800872), SERPINE1 (rs1799768), NOS3 (rs2070744), and IL1β (rs1143627) polymorphisms ranged from 0.5 to 0.7, indicating a moderate level of prognostic efficiency. This suggests that none of the analyzed markers alone can be considered a highly accurate predictor; however, they may still provide clinically meaningful information when used in appropriate patient groups.

Among the analyzed variants, the IL1β rs1143627 polymorphism demonstrated the highest prognostic value in patients with granulomatous polyangiitis–associated necrotic changes, as reflected by an AUC of 0.645 combined with relatively high sensitivity and specificity. Additionally, the NOS3 rs2070744 polymorphism showed notable prognostic relevance in patients with post-COVID–related necrotic changes, characterized by high specificity, which may be particularly useful for identifying individuals at lower risk of false-positive predictions. These findings emphasize the etiological heterogeneity of necrotic processes in the maxillofacial region

and the importance of disease-specific genetic markers.

In conclusion, the studied polymorphisms may serve as supplementary clinical-prognostic biomarkers, especially when combined in gene–gene interaction models and integrated with clinical risk factors. Such an approach could contribute to early identification of high-risk patients and support targeted preventive and therapeutic strategies aimed at reducing the incidence and severity of necrotic changes in the maxillofacial area.

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