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Research Article

INDICATORS OF FREQUENCY OF MTHFR GENE RS 1801131 1298 A>C POLYMORPHISM IN COVID-19

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ABSTRACT

Mucormycosis is a rare and aggressive form caused by the Mucoraceae family . less a deep fungal infection that can be observed and fatal , and is very difficult to diagnose . This fungus is a common commensal of the nasal mucosa . After entering the host's tissues, the fungal spores transform into hyphae, causing clinical symptoms and phagocytic functions causes infection in people with weak immunity . Disturbance of phagocytic function and level of gifs Thrombosis, ischemia, infarction and necrosis in tissues causes. In patients with diabetic ketoacidosis, severe burns, tumors, organ transplants , or corticosteroids, fungal spores can grow in the nasal cavity, paranasal sinuses , palate, orbit, and even the brain, sometimes causing death. Among the clinical forms of mycomycosis, the rhinoceros - orbital form is the most common (44-48), followed by the skin form (10-19), then the pulmonary form (10-11), the diffuse form (6-10%), the last place is the gastrointestinal form (2-11%).

KEYWORDS

mucormycosis, thrombosis, paranasal cavities.

INTRODUCTION

Treatment of patients with purulent-inflammatory diseases of the maxillofacial region remains one of the main tasks of maxillofacial surgery clinics. This pathology is the most common form of septic inflammation in our country. However, not only the severity of the course and the possibility of the development of serious complications forces researchers to deal with the issues of improving the quality of treatment and reducing the duration of treatment . Purulent-inflammatory diseases of the face-jaw area affect the working class of the population, cause patients to stay in the stages of inpatient and outpatient treatment for a long time, and therefore have socio-economic importance [11].

Despite the established measures to prevent this pathology, the number of patients still remains high, and according to experts, it is 23-38% of all patients who turn to a maxillofacial surgeon [1-5].

Complications such as sepsis, mediastinitis, and pneumonia often occur when inflammatory diseases of the face and jaw are severe [4].

C. albicans, C. Glabrata, C. Tropicalis, and C. Krusei , are normal commensals living on the skin, respiratory tract, urinary tract, or digestive tract mucosa in humans. Mucous candidiasis develops in patients with weak immunity or long-term pharmacotherapy. Oropharyngeal candidiasis (OFC), mainly caused by C.albicans colonization, may be the cause of disease in these patients [6-10]. Invasive candidiasis has a mortality rate of 19-40% , and can rise to approximately 70% in intensive care unit patients [11-16].

In recent years , the repeated occurrence of this maxillofacial fungal infection in patients with COVID-19 is considered urgent . Such The group with a high risk of developing fungal infections includes diabetics, immunocompromised people, patients receiving corticosteroids, and patients with hematological deficiency . Every day new cases are detected but not reported. In this study , we , clinicians and laboratory experts, to understand the nature of the disease and carefully monitor these comorbidities , in patients infected with COVID- 19 maxillofacial. We systematically reviewed invasive fungal infections affecting the field [14].

Results. MTHFR gene gi rs 1801131 among patients with post-covid complications of UJS and among conditionally healthy individuals 1298 A>C distribution of polymorphism alleles and genotypes was studied, the results are presented in Table 1.

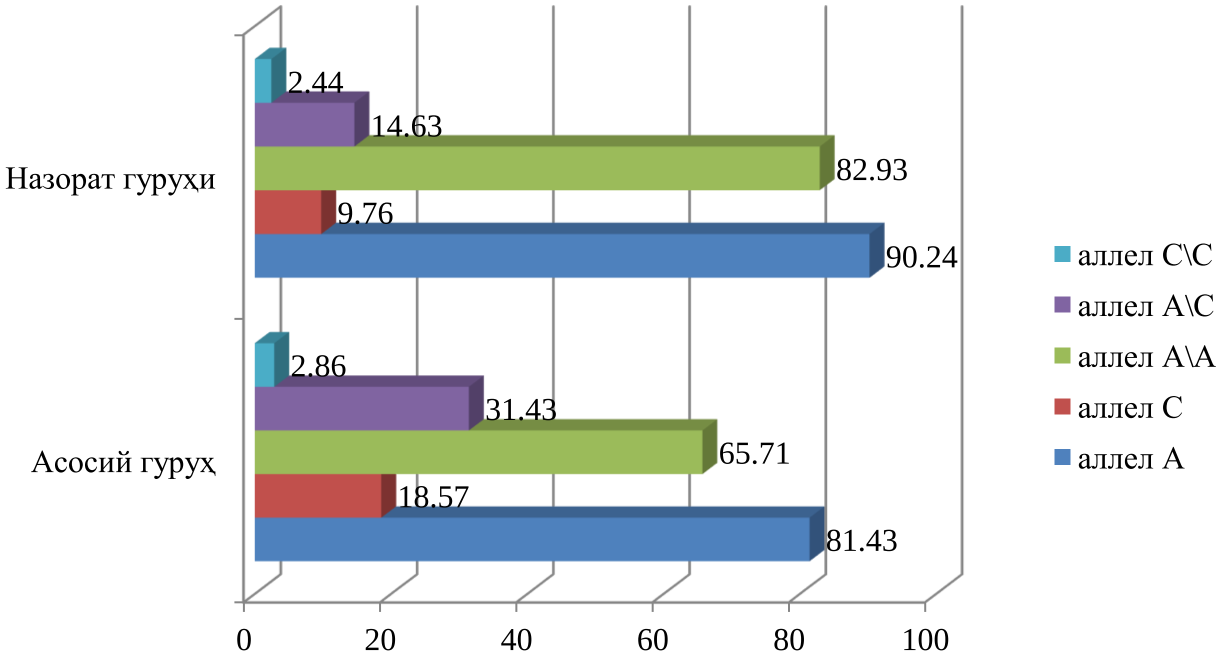
Table 1

MTHFR gene rs 1801131 in patient group and control group Distribution frequency of allelic and genotypic variants of 1298 A>C polymorphism

No	Group G	Frequency of alleles				The frequency of distribution of genotypes					
		A		C		A/A		AC		C/C	
		n	%	n	%	n	%	n	%	n	%
1	Main group (n = 70)	114	81.43	26	18.57	46	65,71	22	31.43	2	2.86
2	Control group (n = 41)	74	90.24	8	9.76	34	82,93	6	14.63	1	2.44

As can be seen from Table 1, in the control group, the frequency of A allele was higher than that of C allele, the frequency of which was 9 , 76% versus 90 , 24% , respectively . Compared to the C allele frequency of 18.57 % in the main

group, the frequency of the A allele with a frequency of 81 , 43% prevailed . In general, the manifestation of differences was high.



1 -d diagram. Distribution frequency of rs 1801131 1298 A>C allele and genotypes in MTHFR gene in patients and control groups (gene lp is located on chromosome 36.22).

As can be seen from diagram 1, homozygous A/A genotype was detected in the highest frequency in group 1 and the control group , its detection rate was 65.71 % . In the study of the frequency of detecting the heterozygous C/C genotype, slightly lower values of this indicator were obtained, i.e. it was 31.43% (Table 4.3). In this In the study of the C/C genotype , a significantly lower incidence rate of 2.86% was found in patients with post-covid complications of UJS , and in the control group, this indicator was slightly lower than in patients with post-covid complications of UJS (2.44%) was recorded .

The study of the distribution of genotypes in the population group revealed small differences between the meeting values of the genotypes characteristic of the 1st group . As in group 1, the highest rate (82.93%) among conditionally healthy individuals was determined in the study of A/A homozygous genotype . A slightly lower meeting value equal to 14.63% was characteristic for the A/C genotype with heterozygous α . As in patients with post-covid complications, the lowest detection rate among conditionally healthy patients - 2.44% was found in the study of C/C homozygous ali genotype (Table 2).

Table 2

1 in the MTHFR gene in patient groups (gen lp is located on chromosome 36.22) Differences in the frequency of allelic and genotypic variants of the 1298A > S polymorphism

Alleles and genotypes	Number of tested alleles and genotypes				Xi2	p	RR	95% CI	OR	95% CI
	Main group		Control group							
	n	%	n	%						
A	114	81.43	74	90.24	3.10	0.08	0.90	0.587 - 1.386	0.47	0.206 - 1.088
C	26	18.57	8	9.76	3.10	0.08	1.11	0.321 - 3.819	2.11	0.919 - 4.846
A/A	46	65,71	34	82,93	3,806	0.052	0.792	0.469 - 1.338	0.395	0.155 - 1.004
AC	22	31.43	6	14.63	3,866	0.05	2,148	1,273 - 3,623	2,674	1,003 - 7,128
C/C	2	2.86	1	2.44	0.017	0.898	1,171	0.238 - 5.762	1,176	0.103 - 13.453

results of the comparative analysis of alleles and genotypes in both the control and the main group are presented in Table 2.

of gi alleles in group 1 and the control group showed that in the control group A It was more statistically significant than the main group (χ 2 = 3.10 ; R= 0.08 ; RR= 0.90 ; OR= 0.47 ; 95% CI: 0.587 - 1.386) (Table 2). When comparing the distribution frequencies of alleles , A allele was statistically significantly more frequent in the main group than in the control group (χ 2 =14.71; R=0.29; RR=1.19; OR=6.76; 95% CI: 6.76-17.98). The A/A genotype was statistically significantly more common in the control group than in the control group of patients with post-covid complications in UJS (χ 2 = 3.806 ; R= 0.052 ; RR= 0.792 ; OR= 0.395 ; 95% CI: 0.469 - 1.338).

Significant differences were found in the frequency of the heterozygous A\C genotype, but the analysis showed that it was detected at a significantly higher frequency in patients with post-covid complications in UJS (χ 2 = 3.866 ; R= 0.05 ; RR= 2.148 ; OR= 2.674 ; 95% CI: 1.273 - 3.623) (Table 2). Genotype C/C was statistically more common in patients with post- covid complications in UJS compared to the control group (χ 2 = 0.017 ; R= 0.898 ; RR= 1.171 ; OR= 1.176 ; 95% CI: 0.238 - 5.762).

CONCLUSION

Summarizing the obtained results, we can conclude that there are significant differences in the detection frequency of rs 1801131 polymorphic locus allele and genotypic variants of the MTHFR gene in the 1st and control groups . In comparison with the control group, an insignificant trend towards an increase in the frequency of the C/C genotype in patients with post-covid complications was revealed . According to the odds ratio, the risk of developing post-covid complications in UJS increased by 1.17 times in carriers of this genotype ($\chi^2 = 0.017$; R = 0.898 ; RR = 1.171 ; OR = 1.176 ; 95% CI: 0.238 - 5.762) . This fact is probably related to the significantly higher anti-inflammatory activity of epithelial matrix metalloproteinases in patients carrying the C/C rs 1801131 genotype in the MTHFR gene compared to patients carrying other genotypic variants.

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