INTERNATIONAL JOURNAL OF MEDICAL SCIENCE AND PUBLIC HEALTH RESEARCH (ISSN – 2771-2265)
VOLUME 04 ISSUE 11 Pages: 60-65
SJIF IMPACT FACTOR (2021: 5.456), (2022: 5.681), (2023: 6.591)
OCLC – 1242424495

International Journal of Medical Science and Public Health Research

Journal Website: https://ijmsphr.com/index.php/ijmsphr

Research Article

COMPARATIVE ANALYSIS OF FREQUENCY OF RS 1805087 2756A> G POLYMORPHISM IN MTR GENE IN COVID -19

Submission Date: October 30, 2023, **Accepted Date:** November 04, 2023,
Published Date: November 09, 2023

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ABSTRACT

At present, the mode of transmission of COVID-19 remains to be determined, but human-to-human transmission has been confirmed. The main source of transmission is patients with symptoms of COVID-19, but recent observations indicate that asymptomatic patients and patients in the incubation period are also carriers and sources of transmission of SARS-CoV-2. The latent period of COVID-19 is estimated to be on average 5 to 6 days, but there is evidence that it can be as long as 14 days, which is currently the generally accepted period for medical observation and quarantine of (potentially) infected people. This epidemiological feature of COVID-19 makes it very difficult to control, because it is difficult to identify and isolate these patients in time, which can lead to the accumulation of SARS-CoV-2 in communities. In addition, it should be proven that patients in the recovery phase are also a potential source of infection.

KEYWORDS

COVID-19 , muco r mycosis, orbital cellulitis , ophthalmoplegia.

INTRODUCTION

The incidence of mucociliary mycosis was not related to age or gender, although this study reported a higher number of men, which may be due to the higher prevalence of COVID-19 among men [3]. Signs and symptoms reported by the majority of patients included in this study included fever, headache, orbital cellulitis with eyelid swelling, ptosis, ophthalmoplegia, unilateral facial swelling, and submandibular and retrobulbar swelling. available [7]. Delaying the treatment of mucormycosis by even one week increases the mortality rate from 35% to 66% and worsens the prognosis [1-4].

Candidiasis is the most common type of superficial purulent infection. Candida species is a permanent inhabitant of the mucous membrane of the oral cavity, but its growth is suppressed by other organisms in the body, which prevents all pathological changes developed by this fungus in the mucous membrane. The most common type of yeast is Candida albicans, followed by Candida glabrata, Candida krusei, Candida tropicalis, and Candida stellatoidea [6]. According to this systematic review, 57 cases of oral candidiasis and one case of candidal retinitis were reported in patients treated for COVID-19 [7].

Coronavirus infection triggers a strong immune response and inflammatory cascade, but the exact mechanism of immune-mediated pathways leading to COVID-19-associated candidiasis is not well defined. Increased neutrophil-to-lymphocyte ratio, monocyte-derived macrophages, and decreased human leukocyte antigen DR expression on monocytes may be indirectly associated with systemic candidiasis infections observed in severe cases of COVID-19 [8-10]. Systemic drugs such as antibiotics, immunodepressants, and anticholinergics, diabetes, eating disorders, endocrinopathies, malignant tumors, or decreased antimicrobial proteins in saliva are not only a compromised immune mechanism, but also classic risk factors that can lead to invasive candidiasis in patients with COVID-19 [11]. Pseudomembranous, hyperplastic and erythematous candidiasis are the three main forms of oral candidiasis.

was manifested in the form of yellowish-white migrating plaques on the mucous membrane of the oral cavity, where the most affected areas were the tongue and palate [12]. Also, the development of pseudomembranous candidiasis was observed in patients about 7-8 days after infection with coronavirus [13]. Also, more cases were observed in elderly patients over 50 years of age. In studies by several authors, oral and retinal candidiasis was observed in patients with diabetes, cardiovascular disease, hypothyroidism, corticosteroids, or intensive care unit patients with COVID-19, consistent with other studies reporting fungal co-infections elsewhere [14].

Aspergillosis is a conditionally pathogenic infection, which ranks second in prevalence among mycoses of the oral cavity and maxillofacial region. In most cases, the infection is caused by Aspergillus fumigatus, followed by Aspergillus niger, Aspergillus flavus and Aspergillus terreus [15]. This fungus damages the vascular tissue, causing thrombosis and infarction. Aspergillosis can be invasive, destructive non-invasive and non-invasive. Invasive aspergillosis is characterized by the invasion of tissues by the yeast in the form of a slowly developing and destructive or extremely aggressive and fatal infection [11]. Aspergillosis of the sinus cavity penetrates the tissues of the oral cavity, causing palatal infarcts, sometimes spreading to the general bloodstream. People with weak immunity have a high risk of developing this infection. Only one case of maxillofacial aspergillosis was reported in an immunocompromised elderly woman with diabetes and receiving corticosteroid therapy who contracted COVID-19 [7].

Early diagnosis and prompt treatment of these maxillofacial fungal infections are essential to improve prognosis and reduce morbidity in patients with COVID-19. Computed tomography (CT) is the main diagnostic method for evaluating mucormycosis affecting the sinuses, and the degree of spread outside the sinuses is confirmed by magnetic resonance imaging (MRI). The final diagnosis is made on the basis of histological examination (hyphae not divided into septa branching at an angle of 90 degrees), culture and examination with KON [4].

RESULTS

rs1805087 in MTR gene in group 1 and control group Prevalence values of alleles and genotypes of the 2756A>G polymorphism are presented in Table 1.

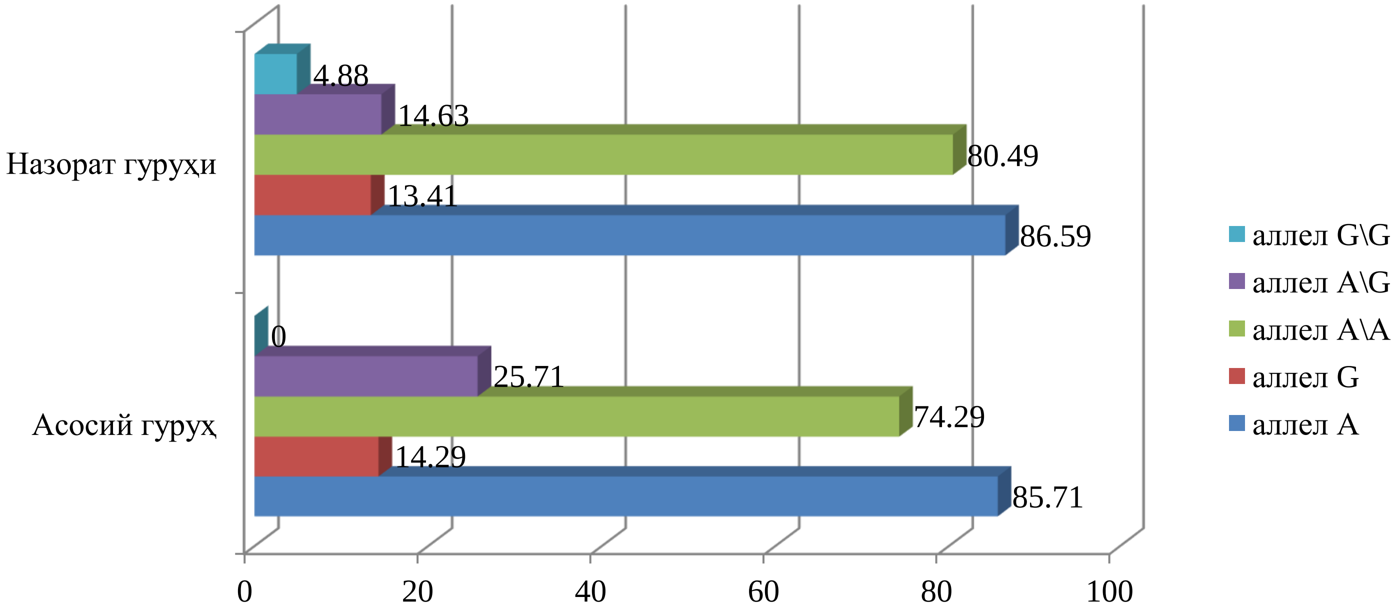
Table 1

In patients and control groups Distribution frequency of alleles and genotypes of 2756A>G polymorphism in MTR gene rs1805087 (gene located on chromosome lp43)

No	Group	Alleles are variable _				Distribution of genotypes _					
		A		G		A/A		A / G		G / G	
		n	%	n	%	n	%	n	%	n	%
1	Main group (n = 70)	120	85.71	20	14.29	52	74.29	18	25.71	0	0
2	Control group (n = 41)	71	86.59	11	13.41	33	80.49	6	14.63	2	4.88

Taking into account that in both groups of the study, the detection of the A allele prevailed (diagram 1), it should be noted that the frequency of detection of the A allele in the control group was slightly higher than in the 1st group. The frequency of detection of G allele, on the contrary, was slightly higher in patients of group 1 compared to the control group.

The study of the distribution of genotypes showed that the A/A genotype with homozygous a was detected in group 1 a little, almost 1.08 times less often, that is , it was 74.29% , while the heterozygous A/ G genotype was less than ng The frequency of detection was 1.75 times higher than that of patients in the 1st group . In the study of the homozygous G / G genotype in the control group, it was possible to observe the opposite situation, its detection rate in the control group was almost 4.8 times higher and was 4.88 % (Table 2).



1 -d diagram. rs1805087 2756 in the MTR gene in patients and controls Distribution frequency of A>G alleles and genotypes

Table 2 presents the results of the analysis of distribution of alleles and genotypes among representatives of the control population and patients in group 1.

Table 2

rs1805087 2756 in the MTR gene in patient groups Differences in frequency of A>G allele and genotypic variants

Alleles and genotypes	Number of tested alleles and genotypes				Xi2	p	RR	95% CI	OR	95% CI
	Main group		Control group							
	n	%	n	%						
A	120	85.71	71	86.59	0.03	0.86	0.99	0.569 - 1.724	0.93	0.425 - 2.035
G	20	14.29	11	13.41	0.03	0.86	1.01	0.372 - 2.74	1.08	0.488 - 2.372
A/A	52	74.29	33	80.49	0.554	0.468	0.923	0.506 - 1.685	0.7	0.274 - 1.791
A / G	18	25.71	6	14.63	1,873	0.178	1,757	0.999 - 3.091	2,019	0.738 - 5.523

The analysis showed that although the detection frequency of the A allele did not have statistically significant differences in the 1st and control groups , however, there was a tendency for its detection to increase in patients with post- covid complications in UJS ($\chi 2 = 0, 03$; R= 0.86 ; RR = 0.99 ; OR = 0.93 ; 95% CI : 0.569 - 1.724), for the G allele , on the contrary, a slight increase in its occurrence was observed in conditionally healthy people ($\chi 2 = 0.03$; R = 0.86 ; RR = 1.01 ; OR = 1.08 ; 95% CI : 0.488 - 2.372).

Summary. The analysis of the frequency of detection of the A/A genotype showed that in conditionally healthy people, this genotype was detected at a statistically significant value , i.e. 1.08 times more often than in patients with post-covid complications in the UJS ($\chi 2 = 0.554$; R= 0.468 ; RR = 0.923 ; OR= 0.7 ; 95% CI: 0.506 - 1.685). The study of the distribution of the A/G genotype also showed the same result , according to which, compared to conditionally healthy people, patients with post-covid complications in the UJS had an insignificant and statistically significant - 1.75 - fold advantage ($\chi 2 = 1.873$; R = 0.178 ; RR= 1.757 ; OR= 2.019 ; 95% CI: 0.999 - 3.091).

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