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Research Article

IN COVID-19 COMPARATIVE ANALYSIS OF FREQUENCY OF POLYMORPHISM RS 1801133 IN MTHFR GENE

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ABSTRACT

Purulent - necrotic inflammatory diseases of the maxillofacial region are among the most common pathologies in stomatology and maxillofacial surgery , which is associated with the modern environmental situation, the widespread spread of purulent diseases, and a decrease in local and general immunity. All researchers agree that purulent diseases of the maxillofacial area , including purulent - necrotic cases , are increasing in the world in recent years . Epidemiological studies of purulent - necrotic inflammatory diseases of the face - jaw area , which were carried out at 10-year intervals in European countries , show that the prevalence of the disease does not change significantly during the selected time period in each specific region. Due to a number of reasons (ecological condition, pandemic conditions , changes in the functional parameters of the most important homeostatic systems of the human body, etc.), one should not expect a decrease in the incidence of purulent - necrotic inflammatory diseases of the face - jaw area developing after COVID-19.

KEYWORDS

COVID-19, purulent - necrotic inflammation, maxillofacial surgery, purulent diseases of the maxillofacial region.

INTRODUCTION

Severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) is the etiological agent of severe acute respiratory syndrome caused by coronavirus 2019 (COVID-19). Typical clinical symptoms in patients with novel viral pneumonia are fever, cough, and myalgia or fatigue, with sputum production, headache, hemoptysis, and diarrhea being less common symptoms [2].

The epidemiological nature of COVID-19 makes it very difficult to control, because it is difficult to identify and isolate patients in time, which can lead to the accumulation of SARS-CoV-2 in communities [3-5]. In addition, it should be proven that patients in the recovery phase are also a potential source of transmission [1].

Currently, the modes of transmission of COVID-19 remain to be determined, but human-to-human

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transmission has been confirmed [4]. The main source of infection 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 infection for SARS-CoV-2 [6-11]. 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 [7]. 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 [15]. In addition, it should be proven that patients in the recovery phase are also a potential source of transmission [12].

Clinically, most patients with COVID-19 have relatively mild or asymptomatic cases. According to a recent study of hospitals in China by Guan et al. (2020) and data from the National Health Commission of China, the proportion of severe cases among all patients with COVID-19 in China was approximately 15–25%. Typical symptoms are fever and dry cough, and some people have experienced shortness of breath, fatigue, and other atypical symptoms, such as muscle pain, confusion, headache, sore throat, diarrhea, and vomiting [13-17]. A common symptom in patients undergoing chest computed tomography was bilateral pneumonia, which was manifested in the form of "stained glass" and bilateral speckled shadows [16]. In general, older age and the presence of comorbidities (eg, diabetes, hypertension, and cardiovascular disease) have been associated with poor prognosis [18-21].

A combination of epidemiological data (for example, history of travel to or residence in an affected area within 14 days before the onset of symptoms), clinical symptoms, computed tomography and laboratory tests (for example, RT-PCR tests of respiratory samples) World Health Organization or plays an important role in the diagnosis of COVID-19 according to the standards of the National Health Commission of China [21]. Another important point is that in suspected patients, a single negative result of the RT-PCR test does not rule out infection.

Oral signs of mucormycosis in patients with COVID-19 usually appear on the palate and may include varying degrees of mucosal discoloration, palatal swelling, ulcers, superficial necrotic areas, bony dehiscence, and black crustal necrosis formation [19].

Mucormycosis is mainly nasal and oral cavities occur in areas including facial tissues, palate, alveolar bones, and mandibular bones.

Finally, it should be noted that although there has been a recent increase in mucormycosis with COVID-19, a causal relationship between the two conditions cannot be asserted, but rather, it is related to pandemic situations and there are many factors and conditions that predispose to mucormycosis. may be related, making patients with COVID-19 more susceptible to co-infections [15].

The pus formed as a result of the infection disrupts the blood supply under the bone membrane, causing ischemia, which in turn leads to the development of necrosis [12]. The frequency of occurrence of osteomyelitis of the upper jaw is low due to the large blood supply, the presence of thin cortical plates, and the lack of tissue that prevents infection in the bone. As a result of fungal invasion into the bone marrow, fungal organisms multiply, affecting the endothelial lining of the vessels, causing vascular insufficiency, leading to bone necrosis, which eventually turns into

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fungal osteomyelitis [19]. Fungal osteomyelitis is difficult to diagnose and is aggressive .

Results. The MTHFR gene is located in the promoter region of chromosome 1 at the 1q36-22 locus and contains 5 exons and 4 introns [5]. Several polymorphisms were found in the gene, the most famous of which is C\T at point 677 transition (rs1801133) . This polymorphism plays an important role in inflammatory and infectious diseases [13] .

This part of the work is devoted to the study of the distribution frequencies of the rs1801133 polymorphism in the MTHFR gene , as well as to the analysis of the contribution of this polymorphism to the formation, development and clinical course of post- covid complications in SCI .

Studying the frequencies of alleles and genotypes of the gi 677C>T polymorphism in the MTHFR gene showed differences in their distribution between the main and control groups (Table 1).

Table 1

677C>T rs1801133 (gene lp36.22) in the MTHFR gene in patients and controls in the chromosome located) distribution frequency of polymorphism alleles and genotypes

No	Group G	Frequency of alleles				The frequency of distribution of genotypes					
		C		T		C/C		C/T		T/T	
		n	%	n	%	n	%	n	%	n	%
1	Main group (n = 70)	105	75	35	25	45	64.29	16	22.86	9	12.86
2	Control group (n = 41)	72	87.8	10	12.2	31	75.61	9	21.95	1	2.44

it was possible to determine the frequency of detection of the S allele, which was 3.0 times higher than the detection frequency of the T allele in the main group and 7.19 times higher than the detection frequency of the T allele in the control group . In the main group, the C\C genotype was detected 2.8 and 4.9 times , respectively, compared to the C\T and T\T genotypes , and in the control group , it was 3.4 and 30.9 times, respectively (chart 1).

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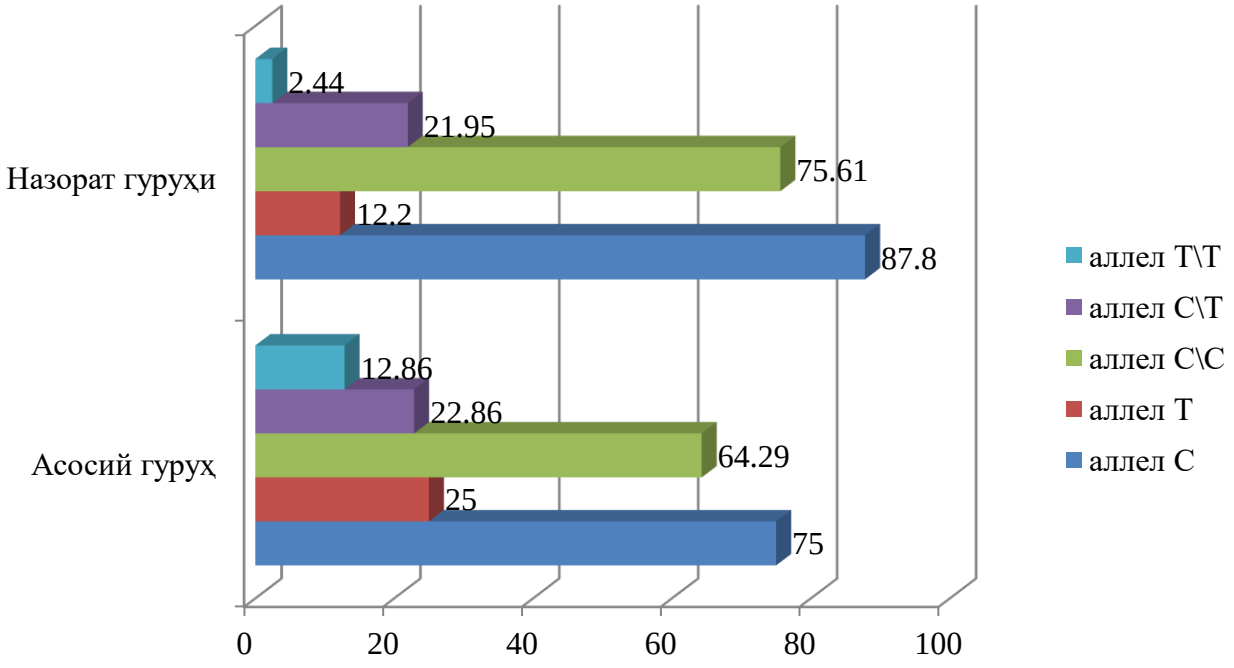

Diagram 1 . _ Prevalence of 677C>T allele and genotypes of rs1801133 (localization of gene on chromosome lp 36.22) in MTHFR gene in patients and control groups

Table 2 presents the results of a comparative analysis of the frequencies of alleles and genotypes of the rs1801133 677C>T polymorphism in the MTHFR gene in the 1st group of patients with post-covid complications of UJS and the control population.

Table 2

Differences in frequency of allelic and genotypic variants of rs1801133 677C>T polymorphism in MTHFR gene in patient groups

Alleles and genotypes _	Number of tested alleles and genotypes				Xi2	p	RR	95% CI	OR	95% CI
	Main group		Control group							
	n	%	n	%						
C	105	75	72	87.8	5.25	0.02	0.85	0.579 - 1.259	0.42	0.197 - 0.881

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T	35	25	10	12.2	5.25	0.02	1.17	0.38 - 3.612	2.40	1,135 - 5,077
C/C	45	64.29	31	75.61	1,536	0.219	0.85	0.49 - 1.473	0.581	0.246 - 1.371
C/T	16	22.86	9	21.95	0.012	0.916	1,041	0.539 - 2.011	1,053	0.418 - 2.653
T/T	9	12.86	1	2.44	3,423	0.068	5,271	3,166 - 8,774	5,902	0.9 - 38,706

practically healthy people of the studied group 2 of the control group, the S allele was slightly higher frequency (1.17) than in the 1st group . The T allele in study group 1 patients with post-covid complications in UJS had a slightly higher frequency (2.04) than in the control group . In the 1st group with post-covid complications in the UJS It can be noted that the frequency of T-genotype detection is slightly higher . In addition, group 1 with post-covid complications in UJS The frequency of genotype C in patients was found to be 0.9 times higher than the frequency of this genotype in the control group , slightly more significant , but statistically significant (χ 2 = 5.25 ; r = 0.02 ; (RR = 0.85 ; OR = 0.42 ; 95% CI: 0.579 - 1.259). Control rs1801133 677C>T polymorphism in the MTHFR gene in group 1 , the frequency of C/C genotype with post - covid complications in UJS 1.17 times more than patients (χ 2 = 1.536 ; r = 0.219 ; RR= 0.85 ; OR= 0.581 ; 95% CI: 0.49 - 1.473). The frequency of C/T genotype in the 1st group with post-covid complications in UJS in patients i was slightly higher than in the control group and was 1.04 and 22.86%, respectively (χ 2 = 0.012 ; r= 0.916 ; RR= 1.041 ; OR= 1.053 ; 95% CI: 0.539 - 2.011) . Group 1 with post-covid complications in UJS The frequency of detection of the Gln /Gln genotype in patients was 3.23% , which is statistically reliable , because it is 5.27 times higher than in the control population, i.e. , its frequency in the control group was 8.4% (χ 2 = 3.423 ; r= 0.068 ; RR= 5.271 ; OR= 5.902 ; 95% CI: 3.166 - 8.774) (Table 2).

CONCLUSION

Thus, the risk C allele of the rs1801133 677C>T polymorphism in the MTHFR gene is slightly more common in patients with post-covid complications in SCI than in healthy individuals. We found out what happened. A high frequency of this allele with the predominance of T/T variant with homozygous α was noted , especially in the 3rd stage of the disease (from 2.3 times to 5.3 times) . At the same time, differences between 1 - and control group i were noted at the trend level , and the trend was at the threshold level d a for statistical significance . These data allow us to conclude that the C allele and T/T genotype of the gi rs1801133 677C>T polymorphism in the MTHFR gene , associated with a decrease in the production of MTHFR , have a significant predisposing effect on the development and clinical course of post-covid diseases in SCI . Since this polymorphism is located in the promoter region of the gene and includes functional polymorphisms , it can be confirmed that its presence affects the expression rate of the MTHFR gene encoded by i . Inflammatory response gene patterning is capable of altering the immune and inflammatory response towards an inappropriate hyper- inflammatory response, leading to the occurrence and development

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of more severe post-covid complications . According to the odds ratio, the risk of developing post-covid complications of UJS in carriers of this genotype increases by 5.902 times (χ 2 = 3.423 ; R = 0.068 ; RR= 5.271 ; OR= 5.902 ; 95% CI: 3.166 - 8.774).

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