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The Role of CYP1A1 Gene Polymorphism in Patients with Erysipelas

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Abstract The research aims are to study the role of CYP1A1 gene polymorphism in predisposition to erysipelas and reveal connections with the clinical course of the disease. We used the standard techniques of molecular genetic analysis. The DNA samples used in genotyping were extracted from leukocytes of venous blood by deproteinization with a phenol-chloroform mixture. Genotyping was performed by polymerase chain reaction (PCR). Statistical data relating to the investigated polymorphic markers were estimated at a 95% confidence level (CL). Genotype frequencies were compared using either the standard Pearson's chi-squared test or the two-sided Fisher's exact test. This study presents a comparative analysis of the distribution of gene polymorphisms of cytochrome P450 CYP1A1 (Ile462Val, rs1048943) of phase I detoxification (microsomal oxidation) in the experimental group of 71 patients with erysipelas and a control group of 71 healthy individuals. We also analyzed these relationships of CYP1A1 (Ile462Val) gene polymorphisms with the sex of the patients, the severity and multiplicity of the disease, and the nature of the local process in patients with erysipelas. The results of the investigation indicate the presence of a relationship between cytochrome P450 CYP1A1 (Ile462Val, rs1048943) gene polymorphism and the development of erysipelas. Analysis of these relationships of CYP1A1 (Ile462Val) gene polymorphism with the sex of the patients, the severity and multiplicity of the disease, and the nature of the process in the examined group of patients with erysipelas did not reveal any statistically significant differences.

Keywords Erysipelas · CYP1A1 gene · Polymorphism

1 Introduction

The incidence rate of erysipelas due to *Streptococcus pyogenes* remains persistently high. It is the fourth most common infectious disease and has a considerable social and economic impact. The incidence rate of erysipelas (*S. erysipelas*) in Russia is 10 to 12 per 10,000 people [1, 2]. There has been an increase in cases of severe and recurrent forms of the disease [3].

Many studies have identified frequent background (comorbid) pathologies in patients with erysipelas. It has been shown that local factors (dermatophytosis, trophic ulcers, varicosities, phlebitis) and general factors (obesity, diabetes, heart failure) increase the risk of erysipelas [4–6]. Erysipelas development, as other multifactorial diseases, is determined by a complex combination of genetic factors and unfavorable environmental factors [4, 6, 7]. The wide variability in the clinical course of the disease is characterized by its multiplicity and the nature of the local process, and suggests the need for the study of common genetic risk factors for erysipelas and factors predisposing the development of certain forms of this disease [4–6, 8, 9]. In that regard, the identification of risk factors for erysipelas which predict the probability of the disease, its clinical course, and the development of preventive

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