

THE ROLE OF THE CYP2C9 GEN IN DUODENAL ULCER COMPLICATIONS

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The relevance of the problem. Currently, genetic markers have been identified that largely predetermine the likelihood of developing duodenal ulcer disease complicated by bleeding in a specific individual. These include certain biochemical indicators, as well as specific markers determined by studies at the chromosomal and even molecular levels. As a rule, genetic mechanisms are a very important factor in the development of ulcer disease. The genes whose alterations cause ulcer disease have not yet been identified. The degree of involvement of genetic mechanisms in the development of ulcer disease varies across different patient groups.

Aim. Forecasting the course of the disease in patients with duodenal ulcers complicated by bleeding.

Materials and methods. A targeted scientific study of the CYP2C9 gene frequency was conducted in 119 patients with duodenal ulcer bleeding. The treated patients were divided into 3 groups: Group I - Main group (patients with duodenal ulcers complicated by bleeding): 119 patients; II - Patients with uncomplicated gastric and duodenal ulcers: 20 patients; III - Examined group (practically healthy individuals): 20 people.

Results. In multifactorial analysis, the CYP2C9 T allele persisted as an independent prognostic factor even when evaluating age, gender, history of anti-inflammatory drug use, clinical anamnesis data, and the CYP2C9 genotype ($\beta=1.07$; $p=0.004$).

The association of the T allele and TT genotype of the CYP2C9 gene with the risk of duodenal ulcer bleeding

Genetic indicator	OR	95% CI	p
Carriers of the T allele (CT+TT)	2.94	1.51 - 5.72	0.002
TT genotype	4.76	1.22 - 18.54	0.024

Conclusion. Therefore, the early detection of this genetic marker in patients at risk is considered important in clinical practice for selecting individualized treatment tactics, preventing recurrent bleeding, and improving the patient's prognosis.