

VacAm, vacAs and cagA Helicobacter pylori multiple variants genes genotype determination in patients with peptic ulcer: study in Belarus

Introduction:

Frequency of Heticobacter pylori (H.pylori) strains with vacAs, vacAm and cagA alleles varies in populations of different geographical regions. It may be suggested that there is a greater number of patients with multiple strains of this microorganism in the regions with the high spread of H.pylori than it has been reported in West Europe. Belarus is located in the region with high prevalence of H.pylori infection. That is why in Belarusian patients with peptic ulcer it is possible to study the regularities of multiple strains spreading in conditions of high prevalence of H.pylori infection. The aim of this study was to investigate the prevalence of multiple H.pylori strains in patients with peptic ulcer.

Method:

87 patients residents of Belarus underwent upper endoscopy. All patients had history of peptic ulcer and did not use nonsteroidal anti-inflammatory drugs. Gastric biopsy specimens and serum samples were obtained from these patients.

Biopsy specimens for histopathological examinations were stained with hematoxylin-eosin and modified Giemsa procedure. The vacAs1s2, vacAm1m2 and cagA status of H.pylori was determined by PCR method (Lytech, Russia, Helicopol VA, Helicopol NA, Exp. Date: July 2003).

Results:

In 47 out of 62 (75,8%) patients with peptic ulcer multiple vacAm1 and vacAm2 genotypes were detected and in 45 out of 63 (71,4%) patients multiple vacAs1 and vacAs2 genotypes were observed. After eradication cagA-positive strains often disappeared and cagA-negative strains were determined.

Conclusion:

The majority of patients with peptic ulcer have multiple H.pylori strains. The determination of these genes and its subtypes in future may be exclusively important for long-term prognosis H.pylori infection in peptic ulcer patients taking nonsteroidal anti-inflammatory drugs.

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