



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

Introduction:

Frequency of *Helicobacter 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 ÑÄ, 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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