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Risk assessment of pathological conditions caused by circulating H. pylori strains

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In recent years, there has been an increase in the prevalence of inflammatory and destructive diseases of the gastroduodenal zone, which is primarily explained by *Helicobacter pylori (H. pylori)* infection. One of the main factors of *H. pylori* pathogenicity is presence of cytotoxin-associated gene — *CagA*. It is known that CagA-positive *H. pylori* strains are associated with the development of atrophy, tumor invasion and rapid metastasis. A number of recently published studies have revealed that *CagA* is a polymorphic gene which contains a different number of repetitive sequences located in the 3' region. Each repetitive region of *CagA* contains Glu-Pro-Ile-Tyr-Ala (EPIYA) profiles including tyrosine phosphorylation. Depending on the sequence of the EPIYA profile, there are 4 segments: EPIYA-A, EPIYA-B, EPIYA-C, EPIYA-D, each containing a repetitive region. Geographical features of the prevalence of *H. pylori* strains depending on the sequence of EPIYA have been revealed: EPIYA-A region of the western isolates of this bacterium is associated with EPIYA-A, EPIYA-B, EPIYA-C segments, while the eastern CagA-positive *H. pylori* isolates are characterized by the A-B-D type of the *CagA* gene. Data illustrating the strong correlation between the western CagA-positive *H. pylori* strains, which have a repeating EPIYA-C segment, and the development of precancerous states, as well as gastric cancer, are presented. *H. pylori* strains containing simultaneously A-B motives of EPIYA or one C-type of the CagA gene are associated with a 7-fold increase of risk of gastric cancer compared to CagA-negative strains; presence of two or more EPIYA-C motives is associated with a 30-fold increase of this risk.