

Frequency of CagA in *Helicobacter Pylori* Isolates of Patients with Peptic Ulcer Diseases (PUD) and Non-ulcer Dyspepsia (NUD) at Namazi Hospital, Shiraz, Iran

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ABSTRACT

Background

Data concerning the information on the prevalence and association of the *Helicobacter pylori* cytotoxin-associated gene A (CagA) with disease is still controversial. The aim of this study was to isolate and identify *H. pylori* by culture method from biopsy specimens and its relationship with associated diseases by molecular techniques (PCR).

Materials and Methods

Gastric biopsy specimens obtained from 220 patients (aged 18 to 68 years) were evaluated for presence of *H. pylori* using PCR assay on isolates for CagA gene.

Results

From 220 patients that included in this study, 120 patients, 51 from PUD (38 duodenal ulcer and 13 gastric ulcer) and 69 from NUD patients (35 gastritis, 18 reflux disease without and 16 with esophagitis) yielded positive for *H. pylori* culture. Frequency of CagA gene in *H. pylori* isolated from patients with peptic ulcer diseases (PUD) and non-ulcer dyspepsia (NUD) was 82.3% and 59.4%, respectively.

Conclusions

Our data confirmed that CagA gene in *H. pylori* is a virulence factor with high frequency in PUD. Therefore, we suggest that detection of *H. pylori* gene expression may contribute in improving the diagnosis and understanding the pathogenesis of *H. pylori* infections.

Keywords: *Helicobacter pylori*, Peptic ulcer diseases, Non-ulcer dyspepsia, Cytotoxin associated gene A (CagA)

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BACKGROUND

H. pylori is now accepted as the most important cause of gastritis in human being, as an essential factor in the etiopathogenesis of peptic ulcer diseases (an important cause of morbidity), and as a risk factor for gastric cancer, a very common malignancy all over the world.(1), *H. pylori* is one of the most genetically diverse bacteria, as demonstrated by DNA fingerprinting and other

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genotyping and DNA sequencing techniques.(2-3), There is also evidence of important geographic differences among *H. pylori* strains.(4-5), Attempt to identify virulent strain of *H. pylori* which are more likely to result in clinically important outcomes, have focused on two groups of potential bacterial virulence factors, the cytotoxin associated gene pathogenicity island (CagPAI), and vacuolation cytotoxin, VacA.(6), The CagPAI contains 31 genes, including six genes named Cag. CagA gene represents a putative virulence marker and present in 60-70% of *H. pylori* strains, which codes for 96 to 138 kDa protein that is associated with the production of toxin. In vitro studies has