### Abstract

Background/objective: The aim of this study was to determine the relation among the cytotoxin associated gene (cagA) status of Helicobacter pylori isolates, the associated clinical diseases, and histopathological features of gastric disease in Iranian populations.

Methods: DNA was extracted from paraffin embedded gastric biopsies obtained from dyspeptic patients, and the cagA status determined by the PCR. The prevalence of cagA gene in three clinical groups, gastritis, gastric ulcer, and gastric malignancies was compared. The histological features in sections from antral and corpus biopsies were graded according to Sydney classification system criteria. The grades were compared with cagA gene status, and with clinical outcomes.

Results: Isolates from 84 patients were included. 72 samples were positive for 16sRRNA. form positive samples, forty six (63.9%) were cagA positive. The prevalence of cagA+ strains in peptic ulcer patients (43.5%) was rather greater than in those with gastritis (30%). Chronic inflammation, activity if gastritis, H. pylori density were all significantly more severe in the cagA+ than in the cagA− group.

Conclusions: Helicobacter pylori strains showing cagA positivity genotype are associated with infiltration of inflammatory cells in to gastric mucosa and accumulation of bacteria in infected area. but this virulence factor do not appear to determine the overall pattern. The pattern is closely linked to clinical disease. Therefore, the nature of the disease is determined by host, environmental factors, and bacterial factors determine the risk of developing such disease.

### Keywords

Helicobacter pylori; cagA; peptic ulcer; H. pylori density; gastritis; gastric diseases

Presentation: Poster