

عنوان مقاله:

Evaluating the Genetic Diversity of *Helicobacter pylori* Isolates in Patients Suffering from Gastritis

محل انتشار:

بیست و چهارمین کنگره بین المللی میکروب شناسی ایران (سال: 1402)

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خلاصه مقاله:

BACKGROUND AND OBJECTIVES *Helicobacter pylori* infections vary in severity and virulence in different populations for various reasons. There are different *H. pylori* strains with varying degrees of virulence. The genetic diversity of *H. pylori* strains in gastritis patients in different areas has not been well understood. This study aimed to evaluate the prevalence rate and different genotypes of *H. pylori* strains in clinical specimens of patients with gastritis in Ilam, Iran. **MATERIALS AND METHOD** Saliva and gastric biopsy samples were collected from 88 patients (55 males and 33 females in the age range of 20 to 90 years) referring to Ilam medical centers. After DNA extraction, the prevalence of *H. pylori* as well as *vacA*, *cagA*, and *ureC* genes was evaluated using PCR, and then each *vacA*-positive sample was further evaluated for *m1m2* and *s1s2* variants. **RESULTS AND DISCUSSION** The *cagA* and *vacA* genes were found in 77 (71%) and 36 (94.7%) *H. pylori*-positive samples, respectively. The *cagA* gene was detected in patients with gastric pain (44.4%) and anorexia (18.51%). Also, the results showed that the *vacA* *s2m2* genotype and *m2* allele were present in 32.9% of *H. pylori* isolates. Moreover, *s2m2* and *s1m2* genotypes were detected in 42.1 and 26.3% of *vacA*-positive samples, respectively. The lowest frequency was related to the *m1* allele (17.18%). **CONCLUSION** This study results indicate a plausible relationship between the presence of some genotypes of *H. pylori* and the progression of gastritis, suggesting these markers as promising biomarkers to predict the disease severity

کلمات کلیدی:

Helicobacter pylori, Gastritis, Genotyping, *vacA*, *cagA*, PCR

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