

Original Paper

Prevalence of s1, s2, m1 and m2 alleles of *vacA* *Helicobacter pylori* gene isolated from clinical specimen

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Abstract

Background and Objective: *Helicobacter pylori* infection is a pathogenic agent of many stomach disorders, including peptic ulcer disease, stomach cancer and stomach lymphoma. The reasons for the variety of the outcomes of the infection resulting from *Helicobacter pylori* may be related to difference in genotype or expression of pathogenic bacterial-related factors, as well as environmental and host factors. This study was conducted to determine the frequency of s1, s2, m1 and m2 alleles of the *vacA* *Helicobacter pylori* gene isolated from clinical samples.

Methods: This descriptive-analytic study was conducted on 183 patients whom suffering from digestive disorders which referring to the endoscopic department of Kordkuy's Amiralmomenin hospital in Golestan province, north of Iran during 2016. Two samples of biopsy from antrum region were taken from each patient. The first sample was evaluated by urease test and the second one was done with saline buffer phosphate solution. Urease test of 50 positive samples and DNA extraction was performed. The polymerase chain reaction was performed for *vacA* alleles and then the relationship between toxin secretion with the symptoms such as abdominal pain, stomachache, reflux, nausea, gastritis, bleeding, stomach ulcers, burning, anemia, and weight loss were evaluated.

Results: Frequency of s1, s2, m1, m2 *vacA* alleles of isolated strains was 88%, 6%, 38% and 70%, respectively. Also, the s1 / m1, s1 / m2, s2 / m1 and s2 / m2 genotypes of *vacA* *Helicobacter pylori* gene were determined 36%, 58%, 0% and 6%, respectively. Toxin secretion did not have significant relationship with digestive symptoms.

Conclusion: The dominant genotype of the patients with digestive disorders (58%) in this study was s1 / m2 and s2 / m1 genotype did not observe in clinical samples.

Keywords: Digestive diseases, *Helicobacter pylori*, *vacA* gene alleles

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