Molecular detection and identification of virulence factors of *Helicobacter* pylori strains isolated from gastric biopsy specimens

Abstract

27.14% respectively.

Background: Helicobacter pylori colonizes the human gastric mucosa and is classified as a level 1 carcinogen. In this regards, this study aimed to isolation and detection major virulence factors in related strains which is isolated from gastric biopsy in patients reefed to Aras Clinique in Ardabil, northwest of Iran (2019-2021).

Materials and Methods: In this cross-sectional descriptive study, 287 patients with gastrointestinal symptoms were enrolled during the years 2021-2019. After obtaining written consent, each patient underwent endoscopy and two antral biopsy specimens were taken. Urease, catalase and oxidase assays and 16srRNA amplification (accession number: 2419628) were mainly used to detect *H. pylori* strains. Uniplex PCR technique was used to identify virulence factors.

Results: 70 patients (24.39%) had *H. pylori*, of them , 9 patients (12.857%) and 2 patients (2.875%) had peptic ulcer and gastric cancer, respectively. Frequencies of oipA, dupA, iceA1, iceA2, sabA, ureC, vacAs1, vacAs2, hopQ1, cagA, vacAm1, vacAm2, tnpA, hom, hopQ2, tnpB genes were 67.14%, 15.71%, 22.85%, 14.28%, 14.28%, 14.28%, and

In this study, 57 different patterns of virulence factors were identified, the most common of which were (3. 4, n =28%) *oipA-vacAs1-vacAm2* and (3. 4, n =28%)

oipA-vacAs1-vacAs2-vacAm2. Simultaneous presence of vacAS2, vacAm2 and hopQ2 genes was observed in both patients with gastric cancer. Frequency of virulence factors in people with peptic ulcer were

oipA (n = 5.62.5%), vacAsI (n = 6.75%), vacAs2 (n = 6.75%), vacAmI (n = 3.37.5%), vacAm2 (n = 7.87.5%), cagA (n = 4.50%), hopQ2 (n = 4.50%), hopQI (n = 2.25%), iceAI (n = 3.37.5%), iceA2 (n = 2.25%), tmpB (n = 5.62.5%), tmpB (n = 5.62.5%), tmpB (n = 2.25%), tmpB (n = 5.62.5%), tmpB (n = 5.62.5%), tmpB (n = 2.25%), tmpB (n = 5.62.5%), tmpB (n = 5.62.5%), tmpB (n = 2.25%), tmpB (n = 5.62.5%), tmpB (n = 5.62.5%), tmpB (n = 2.25%), tmpB (n = 5.62.5%), tmpB (n = 2.25%), tmpB (n = 5.62.5%), tmpB (n = 2.25%), tmpB (n = 2.25%), tmpB (n = 5.62.5%), tmpB (n = 2.25%), tm

Conclusion: This study investigated the prevalence of different virulence factors of *H. pylori* infected individuals. The results of this study showed that *vacAs1*, *vacAs2*, *vacAm2*, *oipA* genes are very prevalent in isolates taken from patients with peptic ulcer.

Key words: H.pylori, Gastric biopsy, Urease, Peptic ulcer, Gastric cancer.