High Frequency of vacA s1m2 Genotypes Among Helicobacter pylori Isolates From Patients With Gastroduodenal Disorders in Kermanshah, Iran.

Abstract:
Helicobacter pylori infection and related diseases outcome are mediated by a complex interplay between bacterial, host and environmental factors. Several distinct virulence factors of H. pylori have been shown to be associated with different clinical outcomes. Here we focused on vacA and cagA genotypes of H. pylori strains isolated from patients with gastric disorder. The aim of this study was to determine the frequency of two toxins and genotypes of VacA toxin in patients referred to a central hospital in the west of Iran (Imam Reza hospital, Kermanshah) during 2011 - 2012. Samples were collected from patients infected with H. pylori. Gastric biopsy specimens from the stomach antrum and corpus were cultured. PCR analysis was performed for genotyping H. pylori vacA and cagA genes. Helicobacter pylori was isolated from 48% (96/200) of patients with gastroduodenal disorders. In 81/96 (84%) cases, the cagA gene was present. Among different genotypes of vacA, two s1m2 and s2m2 genotypes were dominant with frequency of 39.5% and 50%, respectively. The frequency of the s1m1 genotype was 7.2% (7/96), which is much lower than elsewhere. H. pylori isolates with positive results for cagA gene and vacA s1m2 genotypes showed statistically
significant correlation with peptic ulcer (s1m2 13/34 [38.2%] P = 0.003). However, isolates of H. pylori infection with cagA gene and vacA s2m2 genotypes were significantly associated with development of gastritis (s2m2 41/42 [97.6%] P = 0.000). About 90% of H. pylori strains potentially contained vacA s2m2 and s1m2 genotypes. Infection with H. pylori strain containing the cagA gene or the vacA s1m1 and s1m2 genotypes was associated with increased incidence of peptic ulcer disease (PUD).