

Association among dupA, cagA and vacA Helicobacter pylori virulence markers and their distribution in gastritis patients.

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It is estimated that Helicobacter pylori colonizes the stomachs of half the world's population and cagA-positive strains are present in 60–70% of infections in Western countries. Our aim was to determine the prevalence of the cagA, vacA and dupA in H. pylori isolates among patients with gasteric disease in Tehran, Iran. A total of 437 non repeated gastric biopsies obtained from patients undergoing endoscopy in Laleh and Emam Khomeini hospital endoscopy center. The presence of cagA, vacA and dupA genes were determined by PCR method. Of 437 gastric biopsies, 200 (45.76%) samples were positive for various H. pylori virulence genes. Molecular analysis of these virulence factors showed that the frequency of cagA, vacA and dupA were 178 (89%), 147(73.5%) and 82 (41%), respectively. The PCR assay developed herein was able to genotype H. pylori isolates based on the main virulence genes. The ability to detect H. pylori and most of its virulence genes using PCR is helpful in early detection of this disease.

Biography

Shahrooz Konjedi has completed his B.S of Microbiology at the age 24 years from Tonekabon University and M.S of Genetic at the age of 28 years from Arsanjan University . He is the supervisor of Sarv saadat Laboratory in Tehran, a medical, educatioanal and reaserch laboratory center. He has supervised more than 25 pharmacy ,M.S of microbiology and genetic student reaserch projects.

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