

Evaluation of OipA and DupA Genes in Helicobacter Pylori Strains and Their Relationship with Different Gastroduodenal Diseases

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Background & Objectives: *Helicobacter pylori* cause gastroduodenal diseases. Studies suggest that there are geographic variations in the some of its virulence factors such as oipA and dupA genes which may cause more severe diseases. The aim of the current survey was to determine the oipA and dupA genes of *Helicobacter pylori* isolates from west of Iran and find their relationship with the severity of the gastroduodenal diseases.

Methods: This cross-sectional descriptive study was performed on 150 *Helicobacter pylori*-positive isolates obtained from patients with dyspeptic symptoms. DNA was extracted from biopsies and the oipA and dupA status were determined by Polymerase Chain Reaction (PCR). Statistical analyses were performed to find relationship between the virulence factors and diseases.

Results: According to the results, dupA gene was found in 41 (33.33%) of *H.pylori*-positive specimens. There was a reverse correlation between this gene and gastric cancer. The oipA gene was detected in 88 (71.54%) of samples and statistically there was no association between this gene and gastric disorders. As statistical analyses revealed, presence of the dupA were more common in isolates with the oipA negative.

Conclusion: As the results show, dupA gene can be the predictable marker for severity of gastric disorders such as gastric cancer. Extended molecular epidemiology researchers in other populations are recommended.

Keywords: *Helicobacter pylori*; OipA; DupA; Gastroduodenal Diseases