

Infectious Diseases

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Detection of *Helicobacter pylori* *vacA*, *cagA* and *iceA1* virulence genes associated with gastric diseases in Egyptian patients

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Helicobacter pylori (*H. pylori*) virulence markers would be useful to predict peptic ulcer disease (PUD) or gastric cancer. In Egypt, since inadequate data are present regarding *H. pylori* virulence-related genes in different age group patients with gastro-duodenal diseases, it becomes crucial to study the clinical status of *cagA*, *vacA* and *iceA1* genotypes of *H. pylori* strains recovered from patients with dyspepsia. The study included 113 dyspeptic patients who were exposed to upper gastrointestinal endoscopic examination. Four antral biopsies were obtained from each patient for the analysis of *H. pylori* infection by rapid urease test and detection of 16S rRNA. 60 (53.1%) patient were confirmed to be infected with *H. pylori*. Upon endoscopy gastritis was revealed in 27 (45%) and 10 (16.7%) had PUD. Of the 60 *H. pylori* strains, 39 (65%) had at least one virulence gene. Six different genotypic forms were recognized; *vacA* (9/60), *iceA1* (1/60), *vacA/cagA* (7/60), *vacA/iceA1* (13/60), *vacA/cagA/iceA1* (8/60), only one *cagA/iceA1* type and we could not detect *cagA*. The overall *vacA*, *iceA1* and *cagA* genes were identified (61.6%, 38.8%, 26.6% respectively) by PCR-based molecular testing. The *vacA* gene status was highly significant related to gastritis patient ($P \leq 0.036$). The *vacA* s1m1 and s2m2 alleles were significantly found in 50% of *H. pylori* infected patients with PUD and with gastritis 57.1% respectively ($P \leq 0.01$). In conclusion, the main genotype combinations in the studied Egyptian patients were; *vacAs2m2/iceA1*, *vacAs1m1/cagA*, mostly associated with gastritis, and *vacAs1/cagA/iceA1*, mainly in PUD. The less virulent (s2, s2m2) *H. pylori* genotypes were found in patients aged over 43 years.

Biography

Dalia Salem is a Lecturer of Medical Microbiology at Theodor Bilharz Research Institute- Egypt. Her special research interest and expertise is in "Detection of emerging mechanisms of multi-drug-resistant bacteria and their susceptibility patterns to novel antibiotics in addition to antimicrobial resistant genes and virulence markers in *Helicobacter pylori*-related infections".

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