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Analysis of *Helicobacter pylori* Genotypes amongst Jordanians' Dental Plaque Samples

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Background & Aims: *Helicobacter pylori* (*H. pylori*) have been associated with gastritis, gastric ulcer, mucosa-associated lymphoid tissue lymphoma and gastric cancer. The prevalence of *H. pylori* virulence genes has been studied in different populations and from different sources of samples but their prevalence has not been studied in dental plaque in Jordanian people; therefore, the aim of this study was to determine the genotypes of *H. pylori* isolated from dental plaque samples.

Methods: Dental plaque samples were collected from 60 Jordanian volunteers. The genotypes of *H. pylori* virulence genes including the cytotoxin-associated

gene (*cagA*) and the vacuolating toxin (*vacA*) were determined using polymerase chain reaction (PCR).

Results and Conclusions: The *cagA* gene was detected in 14 (23.3%) samples, while *vacA* was detected in all volunteers enrolled in this study (100%). The most prevalent *vacA* alleles were m2 and s1 in 54 (90%) and 55 (91.7%) of volunteers, respectively. Compared to the other combinations including the most virulent *vacA* genotype s1/m1 which was detected in 11 (18.2%) of volunteers, the most prevalent *vacA* allelic combinations were s1/m2 and s2/m2 in 56 (93.3%) and 27 (45%) of volunteers, respectively. These results indicate a significant carriage of virulent *H. pylori* strains among Jordanian people in their dental plaques, which increases the possible transmission of these strains among them. In addition, the studying of the genotypic pattern of *H. pylori* virulence genes in the dental plaque could represent an essential tool for infection prevention and predicting the severity and prognosis of *H. pylori* gastric infection.