

TITLE: PREVALENCE OF THE *Helicobacter pylori cagA* VIRULENCE GENE AND ITS ASSOCIATION WITH GASTROINTESTINAL DISEASE.

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ABSTRACT:

Helicobacter pylori is the most significant pathogen associated with gastric diseases, including gastric cancer. Patients infected with strains *CagA*-positive generally have worse results than those infected with strains negative for *CagA*. The presente study aimed to estimate the prevalence of *CagA*-positive *H. pylori* strains in samples of gastric specimes from dyspeptic patients in Goiânia, Goiás, Brazil. We evaluated 117 patients with gastrointestinal symptoms submitted to upper digestive endoscopy. The DNA was extracted from gastric samples and tested for the presence of *H. pylori* using PCR for the ribosomal gene (rRNA 16S). When *H. pylori* was found, the presence of *CagA*-positive strains was research by PCR. The molecular analysis was positive for *H. pylori* infection in 71/117 patients (60,68%). Among the patients with the infection, 62/71 (87,32%) had *CagA*-positive strains. The *cagA* virulence gene was presente in 47/62 (75,8%) of female patients and 15/62 (24,2%) of male patients. The patient's age's ranged from 18 to 74 years, with a mean of 45,7 years. According to endoscopic diagnosis, there are two or more diagnoses (n=97) could be identified, 11/97 (11,3%) did not present gastric pathologies, 47/97 (48,4%) gastritis, 2/97 (2,0%) peptic ulcer, 8/97 (8,2%) duodenitis, 4/97 (4,1%) atrophy, 2/97 (2,0%) gastric cancer, 10 (10,3%) other pathologies and 17 (17,5%) more than one pathology called de mixed group. In this sample of patients, was possible to estimate a high prevalence of *CagA*-positive *H. pylori* strains. The results evidenced the relationship between the presence of *cagA*-positive strain and gastric disorders, and could be used as a marker for the severity of the infection. In addition, it results may help identify the genetic variability among the strains *cagA*-positive found in central Brazil and associated with neoplastic development.

Keywords: Bacterial; Molecular Epidemiology; Virulence fator.

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