

TITLE: DETECTION OF *Helicobacter pylori* AND ITS VIRULENCE GENE *vacA* AMONG PATIENTS WITH GASTRODUODENAL DISEASE IN ACADEMIC HOSPITAL, CENTRAL BRAZIL

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ABSTRACT:

Helicobacter pylori (*H. pylori*) is a bacteria closely associated with the development of gastric pathologies, such as chronic gastritis, peptic ulcer and gastric adenocarcinoma. The microorganism is considered a type I carcinogen for the development of stomach cancer. Approximately eighty percent of cases of stomach cancer are attributed to chronic *H. pylori* infection. The infection caused by this pathogen affects more than 50% of the world population, mainly in developing countries. In Brazil, infection prevalence rates can reach 90%, particularly in the poorest areas, being highest in the north and northeast of the country. The genetic variability of *H. pylori* is associated with different gastric complications and the presence of the Vacuolating Cytotoxin A (*vacA*) gene may contribute to these complications. The present study aimed to detect *H. pylori vacA* genotypes and to correlate them with clinical outcomes and histopathological changes in dyspeptic patients from the Central Region of Brazil. This study was approved from the Research Ethics Committee of the Clinics Hospital of Federal University of Goiás (HC/UFG), under the reference number 2,519,032 (CAAE: 95637418.3.3001.0031). A total of 119 gastric biopsy specimens from dyspeptic patients were collected between in the state of Goiás, Brazil. *H. pylori* was detected by screening of the 16S rRNA gene and *vacA* genotype by polymerase chain reaction (PCR). A total of 75 patients (60♀ / 15♂) were positive for *H. pylori* and 43 had the *vacA* genotype. The results showed that 85% patients had at least one type of confirmed lesion. Gastritis (53.4%) and duodenitis (16%) were the most prevalent lesions in patients infected with *H. pylori vacA* positive strains. Young patients infected with *H. pylori* presented severe gastric pathologies earlier. The *vacA* genotype was found in 40.7% of patients undergoing conventional treatment for bacterial infection. The logistic regression analysis results showed association between *H. pylori vacA* positive and age statistically significant. It was not possible to verify the allelic subtypes of the *vacA* gene to identify the most virulent genotype in the studied population, but it was observed the emergence of strains resistant to conventional treatment. Additional studies with larger numbers of samples are essential to evaluate virulence genotype subtypes as well as the antibiotic resistance profile used in first-line treatment in the strains found.

Keywords: Virulence Factors. Vacuolating Cytotoxin A. Stomach Disease.

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