

**TITLE:** *Helicobacter pylori* GENOTYPES AMONG CENTER-WEST BRAZIL PATIENTES WITH GASTRODUODENAL DISORDERS AND THEIR ASSOCIATION WITH CLINICAL OUTCOME.

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**ABSTRACT:**

*Helicobacter pylori* is a gram-negative bacterium that colonizes the human gastric mucosa and has been considered the main cause of gastric pathologies, among them chronic gastritis, peptic ulcer, gastric cancer and lymphoma of lymphoid tissue associated with gastric mucosa (MALT). This study was approved by 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). The present study aimed to evaluate the association among the genotypes of *cagA*, *vacA* and *dupA* *H.pylori* virulence and the severity of gastric pathologies. A total of 117 gastric biopsy specimens from dyspeptic patients were collected and the molecular diagnosis was performed by the detection of the *H. pylori* 16S rRNA gene (*hpx* / *hpx1*) through the Polymerase Chain Reaction. Positive *hpx* samples were subsequently genotyped for virulence genes *cagA*, *vacA* and *dupA*. In analyzing whether the number of virulence genes present in the infecting strain was associated with the patient's clinical outcome, we found that patients with non-severe pathologies had a significantly higher mean ( $p = 0.0199$ ) of virulence genes identified in the infective strain, compared with those who presented severe pathologies. In addition, we also observed that patients with severe pathologies had a higher average age ( $p = 0.0047$ ) and also a higher mean number of gastric diseases ( $p < 0.0001$ ) compared to those with non-severe pathologies. We observed that among *H. pylori* positive patients with severe pathologies, 1/7 (14.2%) had only the *cagA* gene; 2/7 (28.7%) the genotypes *cagA* and *vacA*; 3/7 (42.8%) *cagA* and *dupA*; 1/7 (14.2%) presented the *cagA*, *vacA* and *dupA* genes. This study showed a relationship between *H. pylori* infection and old age in progression to severe pathologies. We identified that patients with *H. pylori*-positive strains with less genes of virulence detected had more severe pathologies. However, the interaction between virulence factors present in *H. pylori* strains may be related to the severity of clinical outcomes.

**Key-words:** cytotoxin associated with gene A (*cagA*), cytotoxin vacuolation A (*vacA*), *dupA*; clinical outcomes.

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