Abstract

Introduction. It is known that polymorphisms in C-terminal region of CagA influence gastric disease development on Helicobacter pylori infection. Additionally, the geographic distribution of these polymorphisms has been associated with the appearance of more severe gastroduodenal pathologies. Objective. To determine the CagA phosphorylation motifs pattern (EPIYA pattern) in Cuban H. pylori isolates, and to study its association with patient's pathologies. Materials and methods. DNAs from 95 H. pylori cagA-positive strains were used to amplify the 3' variable region of cagA gene by PCR using two different strategies. Additionally, new primers were designed to identify either Western or Eastern CagA EPIYA motif type by PCR. To confirm the PCR results, PCR products from 14 representative isolates were purified and sequenced Results. The distribution of the EPIYA motif found was, 2 AB (2.1 %), 1 AC (1.1 %), 1 BC (1.1 %), 70 ABC (73.6 %), 19 ABCC (20 %), and 2 ABCCC (2.1 %). Sequencing analysis confirmed the PCR classification in the 14 studied strains and showed three strains with unusual nucleotide sequences, not reported before. Distribution of the EPIYA-ABC pattern was equivalent in all pathologies (78.9 % in gastric ulcer, 72.5 % in duodenal ulcer and 72.2 % in non-ulcer dyspepsia). Conclusion. The PCR results using the new primers confirmed that all studied strains carried the Western CagA type. No specific EPIYA motif was associated with peptic ulcer. This is the first report that shows EPIYA motif distribution in H. pylori isolates from the Caribbean region.

Keywords

Helicobacter pylori, gastric neoplasms, virulence factors, Cuba.