Characterizing helicobacter pylori cagA in Myanmar

Type: Article

Abstract:

Background/Aims: Differences in the Helicobacter pylori infection rate are not sufficient to clarify the dissimilarity of gastric cancer incidence between Myanmar and its neighboring countries. To better understand this trend, the H. pylori virulence gene cagA was characterized in Myanmar. Methods: Glutamate-proline-isoleucine-Tyrosine-Alanine (EPIYA) patterns and CagA multimerization (CM) motifs of cagA genotypes were examined by performing polymerase chain reactions and DNA sequencing. Results: Of 69 tested H. pylori strains, cagA-positive patients had significantly more severe histological scores in their antrum than cagA-negative patients. Sequence analysis revealed that 94.1% of strains had Western-Type cagA containing an EPIYA motif (92.6%) or EPIYT motif (6.4%). The intestinal metaplasia scores in the antral of patients infected with the ABC and ABCC types of cagA were significantly higher than those of patients with AB-Type cagA. Interestingly, in patients infected with H. pylori, 46.3% of strains with three EPIYA motifs contained two identical Western-Typical CM motifs, and these patients showed significantly higher antrum inflammation scores than patients infected with two identical nontypical-CM motif strains (p=0.02). Conclusions: In Myanmarese strains, Western-Type cagA was predominant. The presence of CM motifs and the proportion of multiple EPIYA-C segments might partially explain the intermediate gastric cancer risk found in Myanmar.

Author	a) Myint T. b) Miftahussurur M. c) Vilaichone R.-K. d) Ni N., Aye T.T. e) Subsomwong P. f) Uchida T. g) Mahachai V. h) Yamaoka Y.
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