Ethnicity association of Helicobacter pylori virulence genotype and metronidazole susceptibility

ABSTRACT

AIM: To characterise the cag pathogenicity island in Helicobacter pylori (H. pylori) isolates by analysing the strains’ vacA alleles and metronidazole susceptibilities in light of patient ethnicity and clinical outcome. METHODS: Ninety-five H. pylori clinical isolates obtained from patients with dyspepsia living in Malaysia were analysed in this study. Six genes in the cagPAI region (cagE, cagM, cagT, cag13, cag10 and cag67) and vacA alleles of the H. pylori isolates were identified by polymerase chain reaction. The isolates’ metronidazole susceptibility was also determined using the E-test method, and the resistant gene was characterised by sequencing. RESULTS: More than 90% of the tested isolates had at least one gene in the cagPAI region, and cag67 was predominantly detected in the strains isolated from the Chinese patients, compared with the Malay and Indian patients (P < 0.0001). The majority of the isolates (88%) exhibited partial deletion (rearrangement) in the cagPAI region, with nineteen different patterns observed. Strains with intact or deleted cagPAI regions were detected in 3.2% and 8.4% of isolates, respectively. The prevalence of vacA s1m1 was significantly higher in the Malay and Indian isolates, whereas the isolates from the Chinese patients were predominantly genotyped as vacA s1m2 (P = 0.018). Additionally, the isolates from the Chinese patients were more sensitive to metronidazole than the isolates from the Malay and Indian patients (P = 0.047). Although we attempted to relate the cagPAI genotypes, vacA alleles and metronidazole susceptibilities to disease outcome, no association was observed. The vacA alleles were distributed evenly among the strains with intact, partially deleted or deleted cagPAI regions. Interestingly, the strains exhibiting an intact cagPAI region were sensitive to metronidazole, whereas the strains with a deleted cagPAI were more resistant. CONCLUSION: Successful colonisation by different H. pylori genotypes is dependent on the host’s genetic makeup and may play an important role in the clinical outcome.

Keyword: Helicobacter pylori; Cag pathogenicity island; VacA alleles; Metronidazole susceptibility