ABSTRACT

A case-control study on a relationship between genetic variation of glutathione S-transferase class pi (GSTP) and individual susceptibility to gastric ulceration in dyspeptic patients was undertaken. Initially, a distribution of a GSTP gene frequency (Ile105Val and Ala114Val) was determined in 100 Thais by the Polymerase Chain Reaction-Restriction Fragment Length Polymorphism (PCR-RFLP) technique. The result revealed that the gene frequencies of the Ile105 and Val105 were 0.84 and 0.16 while those of Ala114 and Val114 were 0.98 and 0.02, respectively. The distribution of the genotypes at codons 105 and 114 were in good agreement with those expected in a Hardy-Weinberg equilibrium. However, the heterozygous Ala114Val genotype was less common and the homozygous Val114 genotype was not found. Thus, in the later study, the investigation was focused only on the genotype at codon 105 of the dyspeptic patients (both ulcer and non-ulcer dyspepsia) who were Ala114 homozygotes. To compare the genotype frequency at codon 105 of the ulcer dyspeptic patients (cases, n = 105) to those of the non-ulcer dyspeptic patients (controls, n = 194), the PCR-RFLP technique was performed as mentioned above. The result demonstrated that the frequency of the genotype at codon 105 from cases and controls appeared to be significantly different. The patients who were homozygous Val105 seemed to have higher risk to peptic ulceration [OR = 4.290 (95% CI, 1.100-16.722), p = 0.030]. In contrast, the Ile105Val genotype appeared to act as a protective genotype [OR = 0.563 (95% CI, 0.333-0.952), p = 0.031]. However, other confounded factors such as sex, age, and *H. pylori* infection may involve this difference. Therefore, stratified analysis was carried out. Screening for *H. pylori* infection was done by a gene amplification of the bacterial *phosphoglucosamine mutase* (*hpglm*M) gene. The result of the analysis revealed that sex and age were not the confounders but the *H. pylori* infection exhibited the influence on the association. This was demonstrated by an increased odds ratio in homozygous Val105 *H. pylori* infected patients. This result confirmed many previous studies that *H. pylori* infection involved peptic ulceration. Thus, besides the genetic factors, the environmental factors could be taken into an account when genotype susceptibility to disease was studied.

KEY WORDS: asssociation, glutathione S-transferease, polymorphism, peptic ulceration, *Helicobacter pylori* infection