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Equally high prevalences of infection with cagA-positive *Helicobacter pylori* in Chinese patients with peptic ulcer disease and those with chronic gastritis-associated dyspepsia
Chapter 7

Eradicating high prevalence of infection with caput-positi Helicobacter pylori in Chinese patients with hepatic failure: a case series.

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Equally High Prevalences of Infection with cagA-Positive Helicobacter pylori in Chinese Patients with Peptic Ulcer Disease and Those with Chronic Gastritis-Associated Dyspepsia

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Approximately 60% of Helicobacter pylori isolates in the Western world possess the cytotoxin-associated gene A (cagA). cagA-positive H. pylori is found to be associated with peptic ulcer disease (PUD) and gastric adenocarcinoma. To investigate the cagA status of H. pylori isolates from Chinese patients with PUD and chronic gastritis (CG), H. pylori populations from 83 patients, 48 with PUD and 35 with CG, were assessed by two different cagA-specific PCRs, Southern blotting, and colony hybridization. The combined results from PCR, Southern blotting, and colony hybridization indicate a prevalence of cagA-positive H. pylori isolates of 98% (47 of 48) among Chinese PUD patients and 100% (35 of 35) among Chinese CG patients. Amplification with primer sets 1 and 2 yielded 52 and 95% of the 82 cagA-positive Chinese H. pylori, respectively. In contrast, the sensitivity of cagA-specific PCR for cagA-positive H. pylori isolates from Dutch patients with primer set 1 was 92% (112 of 122) and that with primer set 2 was 91% (50 of 55). The prevalence of cagA-positive H. pylori populations in Chinese patients with PUD and CG is almost universally high. Therefore, cagA cannot be used as a marker for the presence of PUD in Chinese patients. Our data further suggest that allelic variation in cagA may exist and that distinct H. pylori genotypes may circulate in China and Western Europe.

Since the initial identification and successful culture of Helicobacter pylori from human gastric biopsy specimens by Marshall and Warren (11, 12), it has become accepted that this gram-negative spiral bacterium is a major cause of gastroduodenal diseases (7, 9, 25, 27). Although nearly all H. pylori-infected persons develop gastritis (8, 20), it remains unclear whether bacterial, host, or dietary factors determine the differences in the extent of the mucosal lesions induced by H. pylori among them. Only a proportion of H. pylori-colonized subjects develop peptic ulceration, and few of them have an increased risk of developing gastric cancer. Differences among bacterial strains may induce the divergent clinical or pathologic effects of H. pylori infection. Two phenotypic characteristics among H. pylori strains, the vacuolating cytotoxin (3) and the high-molecular-weight protein (6) encoded by the cytotoxin-associated gene A (cagA), have been found to be associated with distinct gastrointestinal disorders. The cagA gene has been cloned and its sequence has been determined (2, 23). Although the gene encoding the vacuolating toxin is present in nearly all strains, the activity of this cytotoxin is found in only 40 to 60% of the H. pylori strains (3, 26). A total of 40 to 60% of the H. pylori strains from patients with peptic ulcer disease (PUD) and 30% of the strains from patients with chronic gastritis are cagA positive (21, 26). About 60 to 80% of H. pylori strains express the 120- to 140-kDa CagA product (1, 6).

Various studies in the United States (3), Great Britain (6), Italy (2), and The Netherlands (26) have demonstrated a strong association between the presence of antibodies to CagA and PUD. An association between infection with cagA-positive H. pylori and PUD was also observed (26). In contrast, only in 50 to 60% of patients with chronic superficial gastritis were antibodies to CagA found (3). However, the data about the correlation between cagA and the cytotoxicity of H. pylori and gastroduodenal disease are mainly obtained from the North American and Western European populations (4, 19, 22, 26).

China is one of the countries with a high prevalence of H. pylori infection and a high incidence of gastroduodenal diseases. In China about 40% of children have acquired infection with H. pylori by 10 years of age, and the prevalence rises with age to about 70% in those over 30 years old (18, 28). In a previous study that used the Western immunoblot technique to determine the antibody response to H. pylori in 167 Chinese patients with gastric cancer, PUD, or chronic gastritis (CG), we showed that 97% of them had antibodies against a 138-kDa protein band, most probably the CagA protein (17). However, the characteristics of the infecting H. pylori strains remained unknown and the nature of this protein could not be assessed.

Therefore, in the study described in this report we determined the prevalence of cagA-positive H. pylori strains among Chinese patients in relation to the occurrence of PUD and CG. The results of a study about the vacuolating cytotoxic properties of these strains will be dealt with in another report.

MATERIALS AND METHODS

Patient population. Strains were obtained from 83 consecutive H. pylori-infected adults derived from a group of H. pylori-positive patients who had undergone gastroduodenoscopy in two hospitals of Shanghai, China, because of dyspeptic complaints. Strains from patients who had a history of gastric surgery, were receiving steroids, had an active infection requiring current antimicrobial therapy, took antacids, or had severe gastrointestinal bleeding were not included in the study. The patient population consisted of 46 males and 35 females with a mean age of 41.1 ± 8.7 years (age range, 17 to 72 years). The patients were classified by endoscopic examination as having duodenal ulcers (n = 27), gastric ulcers (n = 9), both...
duodenal and gastric ulcers (n = 9), or no evidence of mucosal ulceration but with CO as diagnosed by histopathological examination (n = 35). Four patients had no ulceration at the time of endoscopy but had a history of endoscopically diagnosed duodenal ulcers; thus, 48 patients were considered to have PUD and 35 patients were considered to have CG.

Endoscopy, histopathology, and \textit{H. pylori} cultures. During each endoscopic procedure, all patients were given two sets of mucosal biopsy specimens. Both the antrum and corpus biopsy specimens were obtained by the use of biopsy forceps, which were cleaned with a detergent, disinfected with 70% ethanol, and rinsed with sterile water after each examination. One antrum and one corpus biopsy specimen were placed in 2 mL of normal saline at 4°C, and used for bacteriological culturing. The other two specimens were fixed in 10% formalin for histopathological examination. Bacteriological and histological assessments of the mucosal biopsy specimens were carried out as described previously (24). Cultures were prepared by staining biopsy specimens on the surface of horse blood agar plates (22) and incubated at 37°C for 48 hr

Bacteria were harvested, and genomic DNA was extracted using the InstaGene Matrix (Bio-Rad Laboratories, Hercules, Calif) according to the manufacturer's instructions.

\textbf{PCR amplification of cagA}. Two sets of primer were designed on the basis of the published sequence (2). Primer set 1 consists of primer cagA1 (5'-GATAT CGGGCG CGCAAC: positions 1249 to 1270) and primer cagA2 (5'-GGAAAA TCCTTT ATAC TACG CGG CGG: positions 1379 to 1819). Primer set 2 includes primer cagA5 (5'-GGGAAA TTGGTG GTCTC GGAGCG TAGGCG: positions 1495 to 1519) and primer cagA2. These two primer sets were used in a PCR mixture to produce products calculated to be 570 and 324 bp, respectively. Briefly, 10 ng of genomic DNA was used in a PCR mixture of 25 μL containing 10 mM Tris-HCl (pH 8.3), 50 mM KCl, 0.5 mM MgCl₂, and 0.1 mg of bovine serum albumin per ml. The incubation conditions with primer set 1 were as follows: 1 cycle of 1 min at 95°C, and in 55°C, and 1.5 min at 72°C and a final 5-min incubation at 72°C. When primer set 2 was used the number of cycles was 35 and the annealing temperature was 60°C. The PCR products were analyzed by horizontal agarose (1.5%) gel electrophoresis with ethidium bromide staining as described previously (15). Two Dutch \textit{H. pylori} strains with laboratory numbers 348 and 026 were used as the positive and negative controls for \textit{cagA}, respectively (26). Negative and positive control amplifications were performed in every experiment. The genomic DNA from the bacterial species \textit{Helicobacter fenniae} Sweden E8, \textit{Campylobacter fetus} Sweden 7/75, \textit{Campylobacter coli} Linz 46, \textit{Campylobacter jejuni} Linz 2, \textit{Haemophilus influenzae} ATCC 26667, \textit{Nontypeable Haemophilus influenzae} ATCC 14561, \textit{Nontypeable Haemophilus influenzae} ATCC 14561, \textit{Escherichia coli} ATCC 25922 were tested by PCR with either primer set to assess the specificity of the PCR amplification of \textit{cagA}.

\textbf{Southern blotting}. To test the sensitivity and specificity of PCR with primer set 1, all PCR-negative and 20 PCR-positive \textit{H. pylori} populations were analyzed by Southern blotting. The genomic DNA from \textit{H. pylori} was prepared as described previously (10). After digestion of the DNA with HindIII, the fragments were separated by electrophoresis on a 0.7% agarose gel and transferred to Zeta-Probe Membranes (Bio-Rad Laboratories) as described by Sansbrooke et al. (21). The probe used to detect \textit{cagA} was made by PCR amplification with primer set 1 (cagA1-cagA2). The PCR products obtained from four \textit{H. pylori} isolates (positive control strain infected with \textit{CagA}) were used as the positive and negative controls for \textit{cagA}, respectively (26). Negative and positive control amplifications were performed in every experiment. The probe was labelled with digoxigenin (DIG)-UTP by using the random primed labelling kit (Boehringer Mannheim GmbH, Mannheim, Germany). Hybridization conditions were as described previously (26), except that the hybridization temperature was 8°C. Probes were detected with anti-DIG antibodies conjugated to alkaline phosphatase and stained according to the instructions of the manufacturer.

\textbf{Colony hybridization}. An aliquot from each of the frozen primary culture suspension yielding approximately 200 to 400 colonies was grown on horse blood agar plates for 3 days. Colonies from the plates were transferred onto a nylon membrane (Hybond-N, Amersham Life Sciences, Little Chalfont, England) by replica plating. The colonies were lysed and denatured, and then hybridization for \textit{cagA} was done as described previously (26). The probe used to detect \textit{cagA} in the colony hybridization assay was identical to that used in the Southern blotting mentioned above.

\textbf{Results}. Statistical analysis was performed by using the two-tailed Fisher's exact probability test. A P value of <0.05 was considered statistically significant.

\textbf{Specificity of PCR assay}. The specificity of PCR with either primer set 1 (cagA1-cagA2) or primer set 2 (cagA5-cagA2) targeting \textit{cagA} was determined by testing bacterial strains, including \textit{H. fenniae}, various \textit{Campylobacter} species, and bacterial species which are studied in our laboratory and which may occur as contaminants in our detection system. Only the \textit{cagA}-positive control \textit{H. pylori} strain amplified the expected 570- and 324-bp fragments in the \textit{cagA} PCR with primer set 1 and primer set 2, respectively. For the \textit{cagA}-negative control \textit{H. pylori} strain as well as any of the other bacterial species tested, the \textit{cagA} PCR never yielded an amplification product (data not shown).

\textbf{Sensitivity of \textit{cagA}-specific PCR}. The \textit{cagA}-specific PCR with primer set 1 detected 112 of 122 \textit{cagA}-positive \textit{H. pylori} isolates from Dutch patients (26). So, the sensitivity of this PCR was 93%. This primer set was initially used to assess \textit{cagA} in 10 \textit{H. pylori} isolates from Chinese patients. Only 3 of the 10 isolates appeared to be \textit{cagA} positive. However, when assessed by Southern blotting and colony hybridization, all 10 isolates appeared to be \textit{cagA} positive. Therefore, primer set 2 was designed. Assessment of 55 \textit{cagA}-positive \textit{H. pylori} isolates from Dutch patients by this PCR (primer set 2) yielded \textit{cagA} in 50 isolates (sensitivity, 91%). In order to determine the sensitivity of the PCR with these primers for Chinese strains, confirmation was done by Southern blotting and colony hybridization. PCR amplification yielded the expected 324-bp PCR product in 78 of 83 \textit{H. pylori} from Chinese patients (Fig. 1). Four of these five \textit{H. pylori} populations that were \textit{cagA} negative by PCR were positive by Southern blotting and colony hybridization. In addition, 20 Chinese strains \textit{cagA} positive by PCR were also positive by Southern blotting (Fig. 2). Furthermore, 30 \textit{H. pylori} populations from Chinese patients \textit{cagA} positive by PCR were also found to be \textit{cagA} positive when assessed by colony hybridization. So, the sensitivity of this PCR with primer set 2 was 95% (78 of 82). In contrast, assessment of the 82 \textit{cagA}-positive \textit{H. pylori} isolates from Chinese patients by
PCR with primer set 1 yielded only 43 cagA-positive *H. pylori* strains (sensitivity, 52%). These results indicate sequence variation in the site complementary to primer cagal in cagA of Dutch and Chinese *H. pylori* isolates.

**Prevalence of cagA and relation with clinical outcome.** The combined results from PCR, Southern blotting, and colony hybridization indicated an overall prevalence of cagA-positive *H. pylori* isolates of 99% (82 of 83) from Chinese patients with PUD or CG, cagA was detected in 47 of 48 (98%) *H. pylori* populations isolated from patients with current or previous PUD (of whom 36 had duodenal ulcer, 3 had gastric ulcer, and 9 had both duodenal and gastric ulcers) and in 35 (100%) *H. pylori* populations isolated from patients with CG. There was no significant difference between the prevalence of cagA-positive *H. pylori* isolates from the subgroups of patients with distinct clinical manifestations ($P = 1.0$).

**Discussion**

The aim of this study was to determine the prevalence of cagA among *H. pylori* isolates and its relationship with PUD and CG in 83 Chinese patients. The specificity of the cagA PCR was certified by using DNAs from a cagA-positive and a cagA-negative control *H. pylori* strain and various other bacterial species as templates in the PCR amplification. By PCR with primer set 2, our results indicated that 78 Chinese *H. pylori* populations possessed cagA. Four of five strains cagA negative by PCR were found to be positive when assessed by Southern blotting and colony hybridization with the cagA-specific probe under stringent conditions. In addition, 20 *H. pylori* populations were confirmed to be positive by Southern blotting and 30 *H. pylori* strains positive for cagA by PCR were confirmed to be positive by colony hybridization. The expression of the CagA protein was also assessed in 20 cagA-positive and 1 cagA-negative *H. pylori* populations by the Western blotting (immunoblotting) technique with anti-CagA-positive serum. The results indicated that the CagA protein was expressed by the 20 cagA-positive *H. pylori* strains tested and not by the cagA-negative *H. pylori* strain (data not shown), being consistent with the results obtained by PCR, Southern blotting, and colony hybridization. Together, by using these methods, 82 of 83 (99%) *H. pylori* strains were cagA positive.

This high prevalence of cagA-positive *H. pylori* (99%) among Chinese patients with PUD and CG is almost completely consistent with our previous study in which 97% of serum samples from 167 Chinese patients with PUD and gastric cancer had antibodies against a 138-kDa protein, most probably CagA (17). In previous studies with populations from Europe and the United States, the prevalence of cagA-positive *H. pylori* varied between 69 and 79% (4, 16, 26). Thus, the prevalence of cagA-positive *H. pylori* among Chinese patients with PUD or CG is much higher than that among North American and European *H. pylori*-infected patients. The only other study regarding a population outside Europe and the United States showed a similarly high prevalence of cagA-positive *H. pylori*-isolates among *H. pylori*-infected patients (13). Recently, Mielke et al. (12) found that cagA could be identified in 98% (59 of 60) of *H. pylori* isolates from Korean patients with duodenal ulcer and gastric carcinoma. On the other hand, the prevalence of cagA-positive *H. pylori* isolates from 16 patients of Moroccan ethnicity (most of whom emigrated to Belgium 20 to 30 years ago and who are currently living there) was significantly lower (31.3%) than that among 57 Belgian patients (73.6%) or 23 non-Belgian, non-Morocco patients (82.6%) (4). One possible explanation for the difference between the prevalence of cagA may be that a specific genotype may exist within a particular geographic area or within a particular ethnic group.

The association between cagA-positive *H. pylori* and clinical gastrointestinal disorders, especially PUD, has been shown in a number of studies. Using combined serological and genetic detection methods, Cover et al. (4) found a strong correlation between the presence of antibodies to CagA in serum and the isolation of a cagA-positive strain from a patient. In both nonulcer disease and gastric cancer patients and nonulcer disease patients with functional dyspepsia, evidence of the association of cagA-positive *H. pylori* with peptic ulceration has been provided by reverse transcription PCR applied to stomach biopsy specimens (19). Recently, studying 155 *H. pylori*-infected Dutch patients, we found that the occurrence of cagA-positive *H. pylori* among 76 (93%) patients with PUD was higher than that among 79 (65%) patients with functional dyspepsia, also indicating that cagA is associated with PUD (26). However, our present study together with previous results (17) indicated that almost all of the *H. pylori* populations (99%) isolated from Chinese patients possessed cagA, whereas the prevalence of cagA-positive *H. pylori* isolates from patients with PUD and CG was similar. Therefore, cagA cannot be used as a marker for PUD in *H. pylori*-infected Chinese patients. This is consistent with a recent report by Mitchell et al. (14), in which the seroprevalence of anti-CagA antibodies among Chinese *H. pylori*-infected gastric cancer patients and *H. pylori*-infected asymptomatic subjects was examined by Western blotting. An equally high prevalence of antibodies to CagA in both groups (83 versus 86%) was observed. On the other hand, because cagA and its product, the 128- to 140-kDa protein, exist in almost all *H. pylori* populations from Chinese patients with symptoms of dyspepsia and because of its strong immunogenicity, the CagA protein may be used as an antigen for the serodiagnosis of *H. pylori* infection and the candidate antigen for immunization against *H. pylori* in Chinese patients instead of being a marker for PUD.

When primer set 1 (cagA-caga2) was used to detect cagA by PCR amplification, the expected 570-bp product was observed in only 52% of cagA-positive *H. pylori* populations from Chinese patients. In contrast, 92% (112 of 122) of the cagA-positive *H. pylori* populations were cagA positive by PCR amplification with this primer set when a collection of 155 *H. pylori* populations from Dutch patients with PUD and functional dyspepsia was assessed (26). Assessment of the prevalence of cagA among 55 Dutch cagA-positive *H. pylori* populations by PCR with primer set 2 yielded an equally high sensitivity (91%; 50 of 55). The difference in the detection between *H. pylori* populations from Chinese patients and those from Dutch pa-
tients with primer set 1 was highly significant ($P < 0.001$). These results indicate that the sequence of cagA differs between Dutch and Chinese H. pylori isolates, at least at the site complementary to primer cag1. However, sequencing of cagA is necessary for full elucidation of this observation. In this case if it is confirmed, it would indicate that allelic variation of the cagA gene of H. pylori strains from Chinese patients and H. pylori strains from Dutch patients has occurred.

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REFERENCES


