Equally high prevalence 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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Equally High Prevalences of Infection with \textit{cagA}-Positive \textit{Helicobacter pylori} in Chinese Patients with Peptic Ulcer Disease and Those with Chronic Gastritis-Associated Dyspepsia

ZHI-JUN PAN,1,2 RENÉ W. M. VAN DER HULST,3 MONIQUE FELLER,1 SHU-DONG XIAO,2 GUIDO N. J. TYTGAT,3 JACOB DANKERT,3 AND ARIE VAN DER ENDE1

Departments of Medical Microbiology1 and Gastroenterology,3 Academic Medical Center, University of Amsterdam, Amsterdam, The Netherlands, and Shanghai Institute of Digestive Disease, Shanghai Second Medical University, Shanghai, People’s Republic of China2

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Approximately 60% of \textit{Helicobacter pylori} isolates in the Western world possess the cytotoxin-associated gene \textit{A} (\textit{cagA}). \textit{cagA}-positive \textit{H. pylori} is found to be associated with peptic ulcer disease (PUD) and gastric adenocarcinoma. To investigate the \textit{cagA} status of \textit{H. pylori} isolates from Chinese patients with PUD and chronic gastritis (CG), \textit{H. pylori} populations from 83 patients, 48 with PUD and 35 with CG, were assessed by two different \textit{cagA}-specific PCRs, Southern blotting, and colony hybridization. The combined results from PCR, Southern blotting, and colony hybridization indicate a prevalence of \textit{cagA}-positive \textit{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 \textit{cagA}-positive Chinese \textit{H. pylori}, respectively. In contrast, the sensitivity of \textit{cagA}-specific PCR for \textit{cagA}-positive \textit{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 \textit{cagA}-positive \textit{H. pylori} populations in Chinese patients with PUD and CG is almost universally high. Therefore, \textit{cagA} cannot be used as a marker for the presence of PUD in Chinese patients. Our data further suggest that allelic variation in \textit{cagA} may exist and that distinct \textit{H. pylori} genotypes may circulate in China and Western Europe.

**MATERIALS AND METHODS**

**Patient population.** Strains were obtained from 83 consecutive \textit{H. pylori}-infected adults derived from a group of \textit{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, had taken antimicrobial agents within 2 weeks prior to endoscopy, or had active gastrointestinal bleeding were not included in the study. The patient population consisted of 48 males and 35 females with a mean age of 41.0 ± 8.7 years (age range, 27 to 72 years). The patients were classified by endoscopic examination as having duodenal ulcers (\textit{n} = 32), gastric ulcers (\textit{n} = 3), both...
duodenal and gastric ulcers (n = 9), or no evidence of mucosal ulceration but with CG 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 H. pylori cultures. During each endoscopic procedure, two antral and two corpus mucosal biopsy specimens were obtained by 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 mucosal 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 (34,24). Cultures were prepared by smearing biopsy specimens on the surface of horse blood agar plates (7% defibrinated horse blood in Columbia agar base; Oxoid CM 331, Unipath, Basingstoke, England) and horse blood agar plates containing Skirrow supplement (Unipath). H. pylori organisms were identified on the basis of typical colony morphology and characteristic appearance on Gram staining, and positive urease, oxidase, and catalase tests. The H. pylori isolates that grew on the primary culture plates of each of the antrum and corpus biopsy specimens were collected with swabs to obtain separately H. pylori populations from the antrum and the corpus. Each swab was shaken in 1.5 ml of 8% glycerol peptone, and the suspension was stored at -70°C. This bacterial suspension is designated the frozen primary culture. For analysis, an aliquot of the frozen primary culture suspension was thawed and cultured on horse blood agar plates. The H. pylori populations isolated either from the antrum or the corpus biopsy specimens from the 83 patients were assessed for their cagA status.

Preparation of genomic DNA for PCR. After thawing of an aliquot of the frozen primary cultures, bacterial suspensions were inoculated on horse blood agar plates and cultured at 37°C for 3 days in a microaerophilic environment. The bacterial suspensions were harvested, and genomic DNA was extracted by using the InstaGene Matrix (Bio-Rad Laboratories, Hercules, Calif.) according to the manufacturer's instructions.

PCR amplification of cagA. Two primer sets were designed on the basis of the published sequence (2). Primer set 1 consists of primer caga1 (5′-GATTAT ACA TAC CTGAC CCAC CGG-3′; positions 1249 to 1270) (26) and primer caga2 (5′-GGAAA TCTTT AATCT CAGTT CGG-3′; positions 1797 to 1819). Set 2 includes primer caga5 (5′-GGCAA TGGTG GTCTC GGAG CAGG-TGC-3′; positions 1495 to 1519) and primer caga2. These two primer sets were used in a standard PCR mixture to produce products calculated to be 570 and 324 bp, respectively. Briefly, 10 ng of DNA was used in a PCR mixture of 25 µl containing 10 mM Tris-HCl (pH 8.8), 50 mM KCl, 3.0 mM MgCl2, and 0.1 mg of Taq DNA polymerase. The PCR conditions were as follows: 40 cycles of 1 min at 95°C, 1 min at 55°C, and 1.5 min at 72°C, followed by 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 H. pylori strains with laboratory numbers 348 and 628 were used as the positive and negative controls for cagA staining, and positive urease, oxidase, and catalase tests. The other two specimens were fixed in 10% formalin by use of biopsy forceps, which were cleansed with a detergent, disinfected with 70% ethanol, and rinsed with sterile water after each examination. One antrum and one corpus mucosal 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 (34,24). Cultures were prepared by smearing biopsy specimens on the surface of horse blood agar plates (7% defibrinated horse blood in Columbia agar base; Oxoid CM 331, Unipath, Basingstoke, England) and horse blood agar plates containing Skirrow supplement (Unipath).

Statistical analysis. Statistical analysis was performed by using the two-tailed Fisher’s exact probability test. A P value of <0.05 was considered statistically significant.

RESULTS

Specificity of PCR assay. The specificity of PCR with either primer set 1 (caga1-caga2) or primer set 2 (caga5-caga2) targeting cagA was determined by testing bacterial strains, including H. fennelliae, various Campylobacter species, and bacterial species which are studied in our laboratory and which may occur as contaminants in our detection system. Only the cagA-positive control H. pylori strain amplified the expected 570- and 324-bp fragments in the cagA PCR with primer set 1 and primer set 2, respectively. For the cagA-negative control H. pylori strain as well as any of the other bacterial species tested, the cagA PCR never yielded an amplification product (data not shown).

Sensitivity of cagA-specific PCR. The cagA-specific PCR with primer set 1 detected 112 of 122 cagA-positive H. pylori isolates from Dutch patients (26). So, the sensitivity of this PCR was 92%. This primer set was initially used to assess cagA in 10 H. pylori isolates from Chinese patients. Only 3 of the 10 isolates appeared to be cagA positive. However, when assessed by Southern blotting and colony hybridization, all 10 isolates appeared to be cagA positive. Therefore, primer set 2 was designed. Assessment of 55 cagA-positive H. pylori isolates from Dutch patients by this PCR (primer set 2) yielded 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 H. pylori from Chinese patients (Fig. 1). Four of these five H. pylori populations that were cagA negative by PCR were positive by Southern blotting and colony hybridization. In addition, 20 Chinese strains cagA positive by PCR were also positive by Southern blotting (Fig. 2). Furthermore, 30 H. pylori populations from Chinese patients cagA positive by PCR were also found to be 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 cagA-positive 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 caga1 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 caga4. Four of five strains caga4 negative by PCR were found to be positive when assessed by Southern blotting and colony hybridization with the caga4-specific probe under stringent conditions. In addition, 20 H. pylori strains positive for cagA by PCR 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 CG, 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, Miehlke et al. (13) found that caga4 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-Moroccan 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 addition, the prevalence of cagA-positive H. pylori was higher among patients with duodenal ulcer disease than among patients with nonulcer 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 caga4, 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 in 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 (cagA1-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 caga1. However, sequencing of cagA is necessary for full elucidation of this observation. If it is true and 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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