Diversity of Helicobacter pylori vacA and cagA Genes and Relationship to VacA and CagA Protein Expression, Cytotoxin Production, and Associated Diseases

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The vacuolating cytotoxin and the cytotoxin-associated protein, encoded by vacA and cagA, respectively, are important virulence determinants of Helicobacter pylori. Sixty-five H. pylori strains were isolated from dyspeptic patients (19 with peptic ulcer disease, 43 with chronic gastritis, and 3 with gastric cancer) and studied for differences in the vacA and cagA genes and their relationship to VacA and CagA expression, cytotoxin activity, and the clinical outcome of infection. By PCR, fifty-four (83.1%) of 65 strains had the vacA signal sequence genotype s1 and only 10 (15.4%) had the type s2. After primer modification, the vacA middle-region types m1 and m2 were detected in 24 (36.9%) and 41 (63.1%) strains, respectively. The combinations s1-m2 (31 [47.7%]) and s1-m1 (23 [35.4%]) occurred more frequently than s2-m2 (10 [15.4%]) (P = 0.01). No strain with the combination s2-m1 was found. All-19 patients with peptic ulcers harbored type s1 strains, in contrast to 32 (74.4%) of 43 patients with gastritis (P = 0.02). The vacA genotype s1 was associated with the presence of cagA (P < 0.0001), VacA expression (P < 0.0001), and cytotoxin activity (P = 0.003). The cagA gene was detectable in 48 (73.8%) of 65 isolates and present in 16 (84.2%) of 19 ulcer patients and 29 (67.4%) of 43 patients with gastritis (P = 0.17). The vacA genotypes of German H. pylori isolates are identical to those previously reported. H. pylori strains of vacA type s1 are associated with the occurrence of peptic ulceration and the presence of cagA, cytotoxin activity, and VacA expression.

Helicobacter pylori, a spiral-shaped, microaerophilic bacterium that colonizes the stomach in humans has been identified as the cause of chronic gastritis, peptic ulcer disease (PUD), gastric cancer, and mucosa-associated lymphoid tissue lymphoma (15, 18, 25, 27). Once established, it may reside in the gastric mucosa for years, possibly for the life of the host (21), because the immunological defense mechanisms of the host fail to eliminate it.

There are specific virulence determinants in H. pylori strains, apart from immunological factors in the host, that influence the clinical outcome of infection. Virulence factors found in a subset of clinical isolates, such as the vacuolating cytotoxin (VacA) and the cytotoxin-associated protein (CagA), have been recently identified (4, 6, 11, 12, 16).

Only 50 to 65% of strains produce an 87-kDa cytotoxin that induces vacuolation of HeLa or primary gastric epithelial cells in vitro (4, 8, 12, 14, 16, 20). Infection with VacA-producing strains is associated with the presence of PUD (5, 12, 13). Recently, specific vacA genotypes, which are characterized by differences in the signal sequence and middle-region of the gene, have been identified in isolates obtained from U.S. subjects (1, 2). The vacA signal sequence type s1, but not type s2, was closely associated with in vitro cytotoxin activity, PUD, and the presence of the cagA gene. It is unknown whether H. pylori isolates from Europe have identical vacA genotypes or carry vacA alleles different from strains isolated in the United States.

The cagA gene is present in about 60 to 70% of H. pylori strains and encodes a high-molecular-weight protein (120 to 140 kDa) (4, 22). CagA-producing H. pylori strains have been detected in patients with PUD more frequently than in patients with chronic gastritis alone (4, 6, 10, 29). Sequencing of the cagA gene in H. pylori revealed a region of internal duplications which may be responsible for CagA size heterogeneity (4). However, no information is available on the influence on the clinical outcome with respect to diversity at the cagA gene level.

The objectives of this study were (i) to characterize the vacA alleles and analyze differences in the cagA gene that are present in German H. pylori strains and (ii) to correlate differences found within these genes with VacA and CagA protein expression, in vitro cytotoxicity, and clinical outcome.

MATERIALS AND METHODS

Patients, biopsy sampling, and cultivation of H. pylori strains. Sixty-five H. pylori isolates from a consecutive series of patients with H. pylori infection undergoing upper gastrointestinal endoscopy and two reference strains, H. pylori 60190 (ATCC 49503) (cytotoxin producing, cagA+) and Tx30a (non-cytotoxin-producing, cagA negative) were used in this study (4, 16). Endoscopic and histological diagnoses were recorded for all patients. An ulcer was defined as an excavated mucosal break with a diameter of >5 mm. All patients gave informed consent to biopsy sampling. The study was approved by the Ethics Committee of the University of Heidelberg.

Gastric biopsy specimens obtained from the antrum of all patients were homogenized, and ethanol precipitate according to standard protocols. Identical PCR results were obtained from the frozen stocks. All H. pylori isolates were positive for oxidase, catalase, and urease. The strains were numbered, and all analyses were performed without prior knowledge of the clinical diagnosis. Moreover, each analysis was performed by different investigators who were unaware of the other results.

Preparation of samples for PCR amplification. Genomic DNA was isolated from H. pylori cultures by phenol-chloroform-isooamylalcohol extraction and ethanol precipitation according to standard protocols. Identical PCR results were obtained from the frozen stocks. All H. pylori isolates were positive for oxidase, catalase, and urease. The strains were numbered, and all analyses were performed without prior knowledge of the clinical diagnosis. Moreover, each analysis was performed by different investigators who were unaware of the other results.

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were obtained when supernatants from bacterial suspensions in sterile water were directly amplified. Therefore, further analyses were performed without the DNA isolation step.

**PCR amplification and detection of amplified DNA products.** For vacA, primers vacF and vacR were used to amplify the signal sequence region (Table 1) (1). Amplification fragments of 201 and 228 bp were expected from genotype s1 and s2, respectively. The middle region of the vacA gene was analyzed with primers vac3F and vac3R (for m1) and vac4F and vac4R (for m2), which amplified 388-bp fragments for m1 and 346-bp fragments for m2.

For the amplification of cagA4 sequences, two primer sets were used. The first primer set, cag1 and cag3, amplified a fragment of 612 to 615 bp from the hydrophobic region of cagA (Table 1) (4, 22). Primers cag2 and cag4 were derived from a region of internal duplications (4) and amplified DNA with expected fragment lengths of 450 and 558 bp (4, 22).

**PCR amplification was performed as previously described** (17), under the following conditions: initial denaturation at 95°C for 3 min followed by 35 cycles of denaturation at 95°C for 50 s, annealing and extension for 160 s, and final extension at 72°C for 2 min. Annealing temperatures were set at 55°C for vacF-vac1R, at 60°C for vac3F-vac3R and vac4F-vac4R, and at 50°C for primers cag1-cag3 and cag2-cag4. Negative and positive controls (DNA of strain 26695) were assayed in each run. Thirty microliters of each PCR mixture was PCR products of regions s1 and s2 were differentiated on the basis of molecular size and restriction endonuclease digestion with *NlaIII.*

**Results**

**Strain collection.** Sixty-five strains were isolated from *H. pylori*-positive patients with dyspeptic symptoms. Endoscopic and histological examination revealed gastritis in 43 patients, PUD in 19 patients (9 with gastric ulcers of the antrum and 10 with duodenal ulcers), and gastric adenocarcinoma in 3 patients. In all patients with gastric ulcers, moderate to severe antral predominant chronic gastritis was diagnosed histologically. Patients with duodenal ulcers presented with duodenitis and, in some cases, with chronic antral gastritis. In six patients, two isolates were obtained from the antrum and the corpus. For each of these patients, both isolates showed identical features by PCR, Southern blotting, and Western blot analysis.

**Detection of vacA genotypes and relationship to gastrointestinal disease.** The vacA gene was detectable in all *H. pylori* isolates. By using the primers vacF1 and vacR1 to amplify the vacA signal sequences, the predicted PCR products of either 201 or 228 bp were obtained from 64 (98.5%) of 65 isolates. Fifty-four (83.1%) of 65 strains yielded the smaller product, representing genotype s1, and 10 (15.4%) yielded the larger product, representing genotype s2. None of the strains yielded a PCR product of any other size. All amplicons from genotype s1 were directly amplified. Therefore, further analyses were performed without the DNA isolation step.

**Statistical methods.** Analysis of data was performed by using the χ² test with Yates’ correction and Fisher’s exact test. Probability levels (P) of <0.05 were considered statistically significant.
vacAII-vacAIII digestion of the vacA gene and products were obtained with both primer sets or gave PCR products of sizes other than those predicted. Among the 65 isolates studied, vacAII homologs containing three of the four possible combinations of signal sequence and middle-region types were identified. The s1-m1 and s1-m2 combinations were found in 23 (35.4%) and 31 (47.7%) strains, respectively, and the s2-m2 combination was identified in 10 (15.4%) of 65 isolates. The s2-m1 combination was not detectable ($P = 0.01$).

Infection with a type s1 strain was found in all 19 (100%) patients with PUD, compared with 32 (74.4%) of 43 subjects with gastritis ($P = 0.02$). All type s2 strains were isolated from patients with gastritis. The distribution of type s1-m1 and type s1-m2 strains was similar in patients with PUD (s1-m1, 8; s1-m2, 11) and gastritis (s1-m1, 13; s1-m2, 19), indicating that the vacAII middle-region types were not independently associated with the occurrence of PUD.

Prevalence and size variation of the cagA gene in H. pylori isolates. Forty-eight (73.8%) of 65 strains were cagA+. In 47 of 48 isolates and in reference strain H. pylori 60190, PCR products were obtained with both cagA primer sets (Fig. 3). One strain showed an amplicon only with the primer set cag2-cag4 but not with the primer set cag1-cag3. Sixteen (84.2%) of 19 strains isolated from patients with PUD but only 29 (67.4%) of 43 isolates obtained from patients with gastritis carried the cagA gene ($P = 0.17$). All three isolates from patients with gastric cancer were cagA+.

The PCR products of cagA+ strains obtained with primer set cag2-cag4 differed in size, varying from 450 bp in 8 isolates, including H. pylori 60190, to 552 to 558 bp in 22 isolates and 654 to 660 bp in 16 isolates (Fig. 4). NlaIII digestion of the 450-bp product resulted in DNA fragments of 307 to 313 bp and 143 bp. In addition, a fragment of 102 bp was obtained with PCR products of 552 to 558 bp and 654 to 660 bp after NlaIII digestion. Southern blotting with the probe hyb1 identified all fragments of 143 and 102 bp, if present. cagA PCR fragments of 450 bp or 552 to 558 bp were found more frequently in H. pylori strains isolated from patients with PUD (14 of 16 [87.5%]) than in those from patients with only gastritis (15 of 29 [51.7%]; $P = 0.012$).

Relationship between vacA genotypes and presence of cagA gene. Forty-seven (87.0%) of 54 vacA type s1 strains were cagA+ ($P < 0.0001$). Of the 48 cagA+ strains, 47 (97.9%) were found to have the vacAII genotype s1. The signal sequence type could not be determined in one cagA+ strain. None of the 10 type s2 strains carried the cagA+ gene. No association was found between vacAII middle-region type and cagA+ status.

Relationship between vacA genotype and cag4 gene and protein expression and cytotoxin activity. By SDS-PAGE, supernatants of whole-cell sonicates showed the CagA protein band, varying between 120 and 140 kDa, which was recognized by immunoblotting with CagA antiserum in 35 (85.4%) of 41 cagA+ H. pylori strains. In cagA mutant strains, only 1 (5.9%) of 17 isolates was positive by immunoblotting ($P < 0.0001$). VacA protein was detected by VacA antiserum in 44 (75.9%) of 58 H. pylori isolates. Forty-one (87.2%) of 47 strains with the

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genotype s1 were detected by VacA antiserum. In contrast, only 3 (30%) of 10 strains with vacA type s2 showed a weak protein band by Western blotting (P < 0.0001).

Of the 58 H. pylori strains tested, supernatants from 34 (58.6%) induced vacuolation of HeLa cells (Tox'). Seventeen (31%) of 52 strains with the vacA genotype s1-m1 and 16 (61.9%) of 26 strains with s1-m2 genotype were Tox'. In contrast, only 1 (10%) of 10 strains with the genotype s2-m2 induced a weak vacuulation in HeLa cells. Thus, strains possessing the vacA type s1 (33 of 47 [70.2%]) were more frequently associated with vacuolating cytotoxicity than s2 type strains (P = 0.001). Although H. pylori strains isolated from patients with PUD were more likely to be 'Tox' (13 of 17 [76.5%]) than those obtained from patients with gastritis only (21 of 37 [56.8%]), the differences were not significant (P = 0.16). Twenty-seven (67.5%) of 40 vacA* strains and 8 (47.1%) of 17 vacA-negative strains induced vacuolation in HeLa cells (P = 0.147), demonstrating that vacA is not associated with cytotoxin activity.

**DISCUSSION**

In this study, new oligonucleotide primers were established to characterize the vacA genotypes in a consecutive series of isolated H. pylori strains. Using these primers, the vacA genotypes s1 and s2 were identified in all but one of the H. pylori strains. In addition, restriction endonuclease digestion with NlaIII allowed definitive differentiation of genotypes s1 and s2 by cutting only the PCR product of type s1. For determination of the vacA middle-region genotypes, the published oligonucleotide primers vac3R and vac4F were modified, because computer-assisted alignment of the various vacA sequences of European H. pylori strains deposited in the GenBank database revealed single base exchanges at the locations of the original primers (1). Therefore, primer sequences with complete identity next to these locations were selected. By using these primers for PCR, reliable classification of the vacA middle-region genotype was possible in all H. pylori strains. In contrast, use of the originally described primers (1) allowed characterization of middle-region types in only 70% of the H. pylori strains isolated from German patients (18a). This suggests that the mosaicism of the vacA gene described for H. pylori strains from the United States is also found in German H. pylori isolates. However, regional variation in the vacA gene may occur due to the enormous heterogeneity of H. pylori, which would thus require modification of the oligonucleotide primers to characterize the vacA alleles in European H. pylori strains.

H. pylori strains with the vacA signal sequence type s1 were predominant in the series of German H. pylori isolates, whereas strains with type s2 rarely occurred. However, the percentage of strains with the vacA genotype s2 may have been underestimated, since the strains investigated in this study were obtained from dyspeptic patients. Cytotoxic H. pylori strains with vacA genotype s1 may occur more frequently in such patients. vacA genotype s1 was strongly associated with the presence of cagA and was more frequent in patients with PUD (1, 2). The difference between vacA type s2 and type s1 leader sequences is generated by small insertions totaling 27 bp (1). It has been hypothesized that strains with vacA genotype s2 lack effective secretion of VacA through the cytoplasmic membrane of the bacteria (1, 20). Alternatively, differences in the N-terminal residues of the secreted VacA protein, arising from different signal sequence cleavage sites in VacA for type s1 and type s2, may be responsible for differences in protein function (1). In contrast to strains with vacA type s1, type s2 isolates express the VacA protein only in small amounts (1). This explains why almost all isolates with the vacA type s1 but only 3 of 10 type s2 strains had VacA detectable by immunoblot. Furthermore, cytotoxin activity was observed almost exclusively in type s1 strains. Only one type s2 strain showed weak vacuolation of HeLa cells. However, some strains with genotype s1 and lower cytotoxin activity may not have been identified because of the use of nonconcentrated broth culture supernatants for vacuolation testing (12).

Subgroup analysis demonstrated that the vacA middle-region type was not independently associated with the clinical outcome of H. pylori infection, the presence of cagA, or detectable cytotoxin activity. Almost half of the strains contained the combination s1-m2, a finding which is different from the results found in the United States (1), where the genotypes s1-m1 and s2-m2 are more common. The vacA genotype s2-m1 was not found, suggesting that strains with this genotype suffer from a selective disadvantage or are not viable.

About 74% of all isolates were cagA* by PCR, which is in agreement with the results of previous studies from Europe (10, 26, 28, 29). The majority of the patients with PUD (84%) were infected with cagA* strains in contrast to strains isolated from patients with gastritis only, in whom 67% of the H. pylori strains were cagA* (11, 26, 28). By PCR, size variations of the cagA gene were found within the various H. pylori strains. This may account for the size heterogeneity of CagA detected by immunoblot in recent studies (4, 26, 29). Restriction endonuclease analysis and Southern blotting suggested that these size variations may have been generated by a variable number of internal repeat units located downstream of nucleotide 3406 of the gene (4). Unexpectedly, the fragment length of this region of cagA after PCR was found to be shorter in strains isolated from patients with PUD than in those from patients with gastritis alone. It is unclear whether these differences in the cagA gene actually affect the clinical outcome of H. pylori infection or whether these results are incidental. The exact role of the cagA gene, which codes for the highly immunogenic CagA protein, is not known. The cagA gene represents a putative virulence marker and is included in the cag pathogenicity island, a 40-kb segment with several genes, including picB and picA, involved in cytokine induction (3, 24). It is conceivable that size variation of CagA could affect its antigenic properties and thereby alter the host’s immune system’s ability to recognize the antigen.

The presence of the cagA gene was correlated with the expression of CagA protein as determined by immunoblotting (29). However, cagA was not associated with cytotoxicity in HeLa cells and only 68% of cagA* strains were cytotoxic positive. These results are consistent with other reports that cytotoxin production is derived from the vacA gene but not from the cagA gene (23, 26).

In conclusion, the vacA genotypes in German H. pylori strains were identical to those previously reported and could be characterized by PCR after modification of the reported oligonucleotide primers. H. pylori strains with the vacA signal sequence type s1 and middle-region allele m2 were predominant in German H. pylori isolates. All combinations of these vacA alleles occurred, with the exception of s2-m1. Type s1 strains were associated with peptic ulceration, presence of the cagA gene, VacA expression, and cytotoxin activity. Size variations in a distinct region of cagA are common, but their significance for clinical outcome needs further evaluation. The findings suggest that cagA* H. pylori strains with the vacA genotype s1 increase the risk for PUD. Thus, vacA genotyping may allow identification of infected subjects at different risk levels.
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REFERENCES


