Specific Detection and Prevalence of Helicobacter heilmannii-Like Organisms in the Human Gastric Mucosa by Fluorescent In Situ Hybridization and Partial 16S Ribosomal DNA Sequencing

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Gastric infection with Helicobacter heilmannii (previously known as Gastrospirillum hominis) is invariably linked with the presence of chronic gastritis and the risk of developing low-grade mucosa-associated lymphoid tissue lymphoma in humans. In contrast to Helicobacter pylori, various H. heilmannii species colonize the stomachs of domestic animals, which might be a reservoir for transmission to humans (zoonosis). To identify the number and prevalence of different H. heilmannii types in humans, we analyzed 89 gastric biopsy samples histologically identified as H. heilmannii positive by fluorescence in situ hybridization. Of these gastric specimens, 84 (94.4%) contained a single H. heilmannii type. In five samples, however, two different H. heilmannii types were detected. The most prevalent species in monoinfected samples is H. heilmannii type 1, found in 78.5% (66 of 84) of the specimens, followed by a novel H. heilmannii-like organism (HHLO), HHLO type 4, identified in 9.6% (8 of 84) of tissue sections. H. heilmannii type 2 and a further HHLO type not described before, type 3, were found in 8.3% (7 of 84) and 1.2% (1 of 84) of the monoinfected samples, respectively. Additionally, HHLO type 5 with a 16S ribosomal DNA sequence identical to that of Helicobacter salomonis was found with a prevalence of 2.4% (2 of 89). Thirteen of these biopsy samples were also investigated by a PCR approach developed for this study that allows a Helicobacter-specific amplification of a variable portion of the 16S rRNA gene and subsequent sequencing. In total, five different types of HHLOs could be identified within these samples. We conclude that humans can be infected by at least five different HHLO types, which presumably have their origin in animal species like dogs, cats, and pigs.

Chronic Helicobacter infections of the stomach are increasingly recognized as a major risk factor for development of gastroduodenal disease. Helicobacter pylori is the major stomach-colonizing bacterium of humans that causes gastritis and peptic ulcer disease and is considered a risk factor for gastric adenocarcinoma (15) and malignant mucosa-associated lymphoid tissue lymphoma (MALT) lymphoma (20, 23). Helicobacter heilmannii (17), previously known as Gastrospirillum hominis, infects humans to a much lower extent than H. pylori, with frequencies ranging between 0.25 and 1.7% (10, 24). Most of those infected suffer from chronic active gastritis (24), but sporadic cases of gastric erosions (9) and gastric cancer have also been reported for such patients (13, 24). More important, H. heilmannii infection is associated with the development of primary gastric MALT lymphoma in humans as well as in experimental animal infections (11). Eradication of H. heilmannii by antibiotic treatment of patients resulted in complete remission of the MALT lymphoma (14), indicating a causal relationship between H. heilmannii infection and MALT lymphoma.

Spiral microorganisms have regularly been observed in gastric tissue samples obtained from humans and different animals. Nevertheless, it was not until 1987 that Dent and coworkers coined the epithet Gastrospirillum hominis for these corkscrew-shaped bacteria found in human gastric samples (5). Subsequently, sequencing of the 16S ribosomal DNA (rDNA) of these bacteria showed that Gastrospirillum hominis belongs to the genus Helicobacter, and the name Helicobacter heilmannii has been proposed (18).

Unlike H. pylori infections, gastric infections with H. heilmannii or Gastrospirillum-like organisms are not restricted to humans. A broad range of animals, including dogs, cats, pigs, and cattle, are naturally infected, with frequencies ranging from 80 to 100% (4, 6, 8). It has been suggested that H. heilmannii infection in humans is a zoonosis and that animals serve as a reservoir for transmission to humans (6, 12). In humans, at least two closely related but different H. heilmannii isolates (G. hominis 1 and G. hominis 2) were identified (17). One H. heilmannii isolate has been cultivated in vitro (2).

However, evidence is accumulating that suggests that H. heilmannii is an assembly of quite variable subtypes of one species or may even consist of different species. Whereas Andersen and coworkers successfully isolated H. heilmannii from human gastric tissue samples (2), other investigators failed to cultivate this species in vitro. Furthermore, two 16S rDNA sequences were retrieved from clinical samples of this species that differed significantly from each other (17).

Finally, although a correlation between animal contact and colonization with H. heilmannii exists, no particular animal species could be identified as a reservoir for human infection. The proposal of the present study was therefore to clarify whether or not different types of H. heilmannii exist in human gastric tissue samples and to sample data on their prevalence.
Since cultivation of H. heilmannii is not possible for all subtypes yet, cultivation-independent techniques, i.e., rDNA-targeted PCR and fluorescent in situ hybridization (FISH), have been applied.

**MATERIALS AND METHODS**

**Strains and cultivation conditions.** The following bacterial strains were used to evaluate specificity of PCR primers and hybridization probes developed for this study: H. pylori (NCTC 11637), Helicobacter acinonychis (CCUG11284), Helicobacter bibersteinii (ATCC 45936), Helicobacter salomonis (CCUG37845), Helicobacter felis C51 (ATCC 49179), Helicobacter mustelae (NCTC 12032), Helicobacter bilis (ATCC 51630), Helicobacter canis (CCUG 32756), Helicobacter muridarum (CCUG29262), Helicobacter fennelliae (LMG1746), Helicobacter cinaedi (LMG13991), Helicobacter pullorum (NCTC 12824), Campylobacter rectus (DSM3266), Campylobacter jejuni (ATCC 33560) and Campylobacter coli (TU Munich). More distantly related species tested were: Wollabela succinogenes (ATCC 29543), Arcobacter cryaerophilus (LMG6622), Arcobacter butleri (LMG6620), and Proteus vulgaris (ATCC 13315). Helicobacter strains, C. jejuni, C. coli, and Arcobacter strains were grown on GC agar plates (Difco) supplemented with horse serum (8%), vancomycin (10 mg liter⁻¹), trimethoprim (5 mg liter⁻¹), and nystatin (1 mg liter⁻¹) (serum plates) and incubated for 2 to 3 days in a microaerophilic atmosphere (85% N₂, 10% CO₂, 5% O₃) at 37°C. Bacteria were transferred with an inoculation loop to a phosphate-buffered saline solution and were thoroughly suspended. Proteus vulgaris and Pseudomonas aeruginosa were grown aerobically in Luria-Bertani broth. Cell bacterial suspicions were fixed with 3 volumes of freshly prepared 4% paraformaldehyde solution as described by Amann et al. (1). W. succinogenes and C. rectus were grown by the Deutsche Sammlung von Mikroorganismen und Zellkulturen as active cultures and were directly fixed by inoculation loop to a phosphate-buffered saline solution and were air dried. Hybridization of the slides was performed according to secondary structure data delivered by the program.

**Patient material.** Gastric biopsy specimens of nonulcer dyspepsia patients without cases of ulcers, carcinoma, or MALT lymphoma taken during diagnostic endoscopies from 1988 to 1998 in Germany were included in this study. In total, 543 H. heilmannii gastritis samples were collected in that time frame at the Institute for Pathology in Bayreuth, which corresponded to 0.2% of the H. pylori-induced gastritis cases diagnosed at the same time. From those, 89 biopsy samples were taken for this study. To guarantee optimal performance of the test, fixation of the biopsies should immediately follow sampling. Biopsies were fixed in 10% freshly prepared buffered formalin solution (incubation time in formalin should not exceed 48 h), paraffin embedded, and cut into 4-μm sections. Gastritis was histologically diagnosed with hematoxylin and eosin staining according to the updated Sydney System (7), and Warthin-Starney-stained sections (22) were used to detect H. heilmannii.

**PCR primers and probes for in situ hybridization.** Comparative analysis of more than 10,000 16S rRNA sequences was performed with the probe design tool of the ARB program to develop specific probes for the different HHLO types. Furthermore, a heminested PCR system was developed suitable for a sensitive detection of all bacterial species assigned to the genus Helicobacter (forward primer HelF and two reverse primers, HelR1 and HelR2). Probe and primer names and specifications are listed in Table 1. All probe and primer sequences were subjected to a BLAST search and were compared to a comprehensive database comprising all published 16S rRNA sequences of the ε subdivision of the Proteobacteria (16). Probes and primers were provided by Metabion GmbH (Munich, Germany). Probes were 5' labeled either with Cy3 or with 5 (and 6)-carboxyfluorescein by the supplier.

**PCR amplification and sequencing of DNA.** For preparation of DNA from biopsy specimens, six paraffin-embedded tissue sections of each of the 13 patient samples were chosen. The sections were placed in a microcentrifuge tube, and paraffin was extracted from the tissue sections by two 30-min incubations in hexane and two subsequent 15-min incubations in 96% ethanol. After air drying, DNA was extracted from the samples with the QiAmp DNA minikit (Qiagen GmbH, Hilden, Germany) according to the instructions of the manufacturer. Five microliters of the obtained DNA solution was applied to a 50-μl PCR solution. The first PCR was performed employing primers HelF and HelR1 (Table 1) with 2.5 U Taq Gold polymerase (Perkin Elmer) in a PCR buffer supplied by Perkin Elmer. After 10 min of denaturation at 94°C, 30 cycles (30 s at 94°C, 30 s at 58°C, and 30 s at 72°C) were performed on a 9700 thermocycler (Perkin Elmer). Five microliters of the obtained PCR product was transferred to a new Eppendorf tube, and a second PCR with primers HelF and HelR2 was performed under the same conditions as the first PCR. Five microliters of each PCR product was analyzed by electrophoresis on 2% agarose gels. Both strands of the amplified 16S rDNA portions were sequenced with primers HelF and HelR2 using the cycle sequencing protocol and an ABI Prism 373A automatic sequencer (Applied Biosystems, Weiterstadt, Germany).

**RESULTS**

In situ hybridization of 89 human gastric biopsy samples with probes Hhe-1 and Hhe-2. The primary goal of the present study was to evaluate the prevalence of two known H. helman-
nii types in 89 human gastric biopsy samples. Therefore, hybridization probes for these two different types were developed (Table 1). In order to illustrate the strategy of oligonucleotide probe design, which included FISH, genus-specific PCR, and sequencing of the obtained partial 16S rDNA sequences, the complete procedure is summarized in a flow chart in Fig. 1.

The oligonucleotide probe sequences were subjected to an extensive “in silico” analysis at the National Center for Biotechnology Information database, which contains all hitherto-published sequences of Proteobacteria from the ε subdivision, in order to identify putative cross-hybridizing gene sequences. In addition to their original 16S rRNA sequences, the Hhe-1 target sequence is one base moiety different from the 16S rRNA sequence from Candidatus Helicobacter suis (4), and Hhe-2, as expected, picked up H. heilmannii type 2.

The specificity of the oligonucleotide probes was analyzed under experimental conditions by hybridizing 18 different species belonging to the ε subdivision of Proteobacteria to the

FIG. 1. Scheme illustrating the strategy used in this study to analyze 89 human gastric biopsy samples.
developed _H. heilmannii_ probes. Twelve _Helicobacter_ species different from _H. heilmannii_ were included (see Materials and Methods). Neither Hhe-1 nor Hhe-2 hybridized to any of the strains tested. In contrast, Hhe-1 hybridized to 66 monoinfected gastric tissue sections (71 with mixed infections) and Hhe-2 complementary sequences were detected within 15 monoinfected tissue samples (17 with mixed infections) (Table 2; Fig. 2). Two biopsy specimens harbored two distinct cell populations. One population hybridized with Hhe-1, whereas the other population bound to probe Hhe-2. Three gastric tissue samples did not hybridize to Hhe-1 or Hhe-2. However, cells within these specimens strongly hybridized to probe Eub-338 (1). This probe is complementary to a 16S rRNA region conserved in almost all bacteria but not in eukaryotes and _Archaea_, and it was used as a control in our FISH assays to demonstrate the presence of rRNA in the cells. Furthermore, all specimens hybridized to probe Hpy-1 (21), which specifically detects _H. pylori_, but we did not detect _H. pylori_ in the gastric sections.

**PCR-based amplification and sequence analysis of partial 16S rDNA sequences retrieved from formalin-fixed biopsy samples.** Next, a _Helicobacter_ genus-specific PCR approach was developed to specifically amplify a variable portion of _Helicobacter_ rDNA from the human gastric tissue samples. Primers HelF, HelR1, and HelR2 were developed by comparing all available _Helicobacter_ 16S rDNA gene sequences in the database (Table 1). A 250-bp PCR product was obtained from all _Helicobacter_ species enrolled in this study (see Material and Methods). In contrast, no amplification was obtained with DNA preparations of five further _Eubacteriaceae_ species belonging to the genera _Campylobacter_, _Wolinella_, and _Arcobacter_ and from the remotely related genera _Proteus_ and _Pseudomonas_ (see Strains and cultivation conditions in Materials and Methods). As little as 50 fg of DNA (corresponding to 30 _H. pylori_ genomes) prepared from _H. pylori_ and _H. mustelae_ could be successfully amplified.

This PCR approach was applied to substantiate the results obtained by in situ hybridization of human gastric samples with probes Hhe-1 and Hhe-2. Five biopsy samples hybridizing to Hhe-1 and five biopsy samples hybridizing to Hhe-2 were chosen. Total chromosomal DNA was extracted and _Helicobacter_ 16S rDNA was amplified by the PCR approach mentioned above. The same procedure was applied to the biopsy samples negative for both probes (three samples) (Fig. 1). The resulting partial 16S rDNA sequences were aligned with the sequences in the 16S rRNA database of the ARB program package, and the most closely related 16S rRNA sequences were determined. All five samples positive for Hhe-1 were completely identical to the sequence of _Candidatus H. suis_ (accession no. AF127028). The published sequence of _H. heilmannii_ type 1 showed one mismatch to the Hhe-1 sequences retrieved in this study. However, Hhe-2-positive sequences could be divided into two different rRNA groups. Two sequences were found to be identical to the _H. heilmannii_ type 2 sequence, as expected. The three remaining Hhe-2-positive sequences, however, showed the expected identity within the probe target region, but they were significantly different throughout the remaining part of the sequence (at least 2.8% difference from any rDNA sequence known) (Fig. 1).

Two of the sequences obtained from samples negative for probes Hhe-1 and -2 were identical and showed 100% identity to _H. salomonis_ and _H. felis_ (accession no. AF103880), both isolated from dogs. The third sequence retrieved from these samples was unique and most closely related (97.2% homology) to an _H. heilmannii_ isolate cultured from human gastric samples (2) (Table 3).

**Prevalence of three HHLOs newly discovered in human gastric tissue samples.** Based on the partial 16S rRNA sequence retrieved in the present study, specific oligonucleotide probes were developed for HHLO types 3, 4, and 5, named Hhe-3, Hhe-4, and Hhe-5, respectively. According to the procedures employed for probes Hhe-1 and Hhe-2, specificity of the probes was tested in vitro with the reference strains mentioned above and in silico in the respective databases. Whereas probe Hhe-3 and Hhe-4 did not hybridize to any of the bacterial species tested, probe Hhe-5 hybridized to _H. felis_. These results were confirmed by in silico analysis. No matching sequences were found for Hhe-3 and Hhe-4. In contrast, 12 matching sequences were found for Hhe-5. Within the probe target region nine sequences were identical to _H. felis_ sequences, two were identical to _Helicobacter bizzozeronii_ sequences, and one was identical to _H. salomonis_ sequences. The newly developed probes Hhe-3 and Hhe-5 hybridized to their respective biopsy samples, as expected, but not to any other tissue sample. As expected from the sequence data, Hhe-4 hybridized to a subset of Hhe-2-positive samples but not to any Hhe-1-, Hhe-3-, or Hhe-5-positive samples.

Since all probes hybridized specifically to their respective target organisms, prevalence studies were extended to the HHLOs newly discovered in human gastric biopsy samples. A single HHLO was observed in 84 biopsy samples (94.4%). _H. heilmannii_ type 1, originally identified by Solnick et al. (17), was found in 78.5% (66 of 84) of samples containing a single HHLO type and thus corresponds to the predominant species in human _H. heilmannii_ infections. The novel HHLO-4 was detected as the sole HHLO type in 9.6% (8 of 84) of biopsy samples, followed in frequency by _H. salomonis_ and _H. felis_ with 8.3% (7 of 89), and HHLO-5, with 2.4% (2 of 84). HHLO-3 was detected only in a single sample (1.2%). The remaining five patients (5.6%) contained two different HHLOs (Table 2).

**DISCUSSION**

In contrast to _H. pylori_, which predominantly colonizes humans, _H. heilmannii_ has often been found in animals, like cats, pigs, and cattle. It has been postulated that upon close contact
with these animals, transmission to humans may occur. However, although a correlation between colonization with *H. heilmannii* and animal contact is obvious (6, 12), a distinct species could not be identified as a reservoir. Also, conflicting results were reported about the ability to grow *H. heilmannii* on artificial media. A probable explanation for these results may be the existence of morphologically similar subtypes of HHLO, differing in animal reservoir and growth requirements. rDNA
sequencing performed by Solnick and coworkers provided the first evidence for such differences (17). They retrieved two different 16S rRNA sequences from human gastric tissue samples with less than 97% homology, which was considered to be the interspecies border (19). Despite this significant difference, Solnick et al. assigned both sequences to one species and proposed the epithet Helicobacter heilmannii for this morphologically defined species.

The primary goals of the present study were therefore to prove by FISH that the previously retrieved rRNA sequence data really do colocalize with the corkscrew-shaped bacteria within human gastric tissue samples and to determine the prevalence of these two rRNA sequences in 89 human gastric biopsy samples known to harbor H. heilmannii. The results of this study clearly demonstrate that H. heilmannii type 1 is the predominant HHLO type colonizing human gastric tissue samples. In 78.1% of biopsy samples containing only one HHLO corkscrew-shaped bacterium could be assigned to H. heilmannii type 1. Interestingly, De Groote et al. retrieved 16S rRNA sequences from gastric samples of pigs with 99.5% homology to H. heilmannii type 1 (4). Since cultivation of this gastric spiral bacterium failed, they describe a Candidatus Helicobacter suis (4). Data presented by De Groote et al. indicate a close phylogenetic relationship between Candidatus H. suis and H. helimmannii type 2 (4). These authors therefore postulate a possible zoonotic role of Candidatus H. suis. This assumption is further corroborated by the data presented in this study, since the sequence retrieved from gastric biopsy specimens shows one mismatch to the H. helimmannii type 1 sequence but is 100% identical to the sequences available from De Groote and coworkers. Taking into account the prevalence data obtained here with human biopsy specimens, more than 75% of H. helimmannii infections found in humans may be transmitted from pigs. As reported by De Groote et al. and others, this particular HHLO type has never been observed in culture (4).

A second hybridization probe, which was originally developed to detect H. helimmannii type 2, hybridized to two different HHLO types, as revealed by genus-specific PCR and subsequent partial 16S rDNA sequencing. One sequence obtained was identical to the H. helimmannii type 2 sequence reported by Solnick et al. (17). However, a novel, hitherto-unknown 16S rRNA sequence was also found by sequencing, showing 2.8% sequence difference to H. helimmannii type 2. A third probe was developed to allow specific detection of this novel H. helimmannii type within human tissue sections. Use of these probes in FISH not only allowed allocation of the retrieved 16S rRNA data to distinct morphotypes within gastric samples, it also showed for the first time that this new HHLO type was more frequent in human gastric samples (9.6%) than H. helimmannii type 2 (8.3%). Although similar 16S rRNA sequences have already been amplified from feline samples, successful cultivation of Helicobacter strains from these groups have not been described. In contrast, another partial 16S rRNA sequence retrieved during this study showed sequence identity to H. salomonis and to one particular H. felis sequence (Table 3). These species, predominantly isolated from dogs, have all been obtained in pure culture. Therefore, in contrast to H. helimmannii type 1 and type 2, cultivation of this particular HHLO type of H. helimmannii from human gastric tissue samples may be possible if appropriate cultivation conditions are applied. This
assumption was supported by the 16S rRNA data obtained by Andersen and coworkers for a cultivable H. heilmannii isolate from human tissue samples (2). The closest relative of this isolate was H. salmonis (98.9% homology). The sequence difference between the 16S RNA determined by Andersen et al. and the sequence of HHLO-5 retrieved from human gastric tissue during the present study is only 0.04% (Table 3). Another HHLO type (type 3) was only found in one patient sample. Therefore, further HHLO types may be present, however, with low frequencies.

In five biopsy samples more than one H. heilmannii subtype was detected. Different subtypes were found in these mixed colonizations. However, HHLO subtype 5 was found in three of them. Whether HHLO-5 needs H. heilmannii type 1 for efficient colonization of human gastric biopsy samples or whether cocolonized hosts or subsequent infections are responsible for this phenomenon has yet to be addressed. A remarkable fact is that no cocolonization of H. pylori and H. heilmannii has been detected; however, in two of the patients massive duodenal infections with Giardia lamblia were observed. Such a coinfection has also been reported by others (V. Grouls and C. Seidl, Letter, Dtsch. Med. Wochenschr. 124:611, 1999). However, whether this means that H. heilmannii colonization prevents H. pylori infection cannot be answered by the present study.

FISH is a powerful tool for the specific detection of noncultivable Helicobacter species in gastric biopsy specimens. Compared to PCR-based techniques, FISH detects its target in intact bacterial cells, i.e., no liberated DNA released after cell death is detected. Furthermore, H. pylori and H. heilmannii can be detected directly in intact tissue specimens, and information concerning histology can be directly linked to the location of the bacteria. In addition, no inhibition of detection was observed by formalin fixation of tissues routinely used as gastric specimens. Therefore, application of this technique in human and animal samples in future will, in combination with PCR, be an appropriate tool for answering three important questions. First, are HHLO types restricted to specific animal hosts and are these hosts the reservoir for human infection? Second, is there any correlation between severity or type of infection, e.g., development of MALT lymphoma, in humans and a particular HHLO type? Finally, which H. heilmannii types are present in different animals and can these H. heilmannii types be correlated to distinct diseases in these animals?

In conclusion, this study clearly demonstrated that H. heilmannii found in human gastric specimen is a mixture of different subtypes or even different species. Unequivocally, the species H. heilmannii urgently awaits systematic investigation regarding its taxonomic status. H. heilmannii type 1 is by far the most prominent species in human gastric biopsy samples. At least four further subtypes of H. heilmannii with different prevalence rates can be detected, and mixed infections are rare, but they do occur.

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REFERENCES


