A Probable New *Helicobacter* Species Isolated from a Patient with Bacteremia

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A probable new *Helicobacter* species was isolated from the blood of a 14-month-old aboriginal child who presented with vomiting, diarrhea, fever, and dry cough. The most similar 16S rRNA gene sequence was that of *Helicobacter fennelliae* CCUG 18820T but the new sequence differed from it by at least 32 base substitutions and by the presence of a large (353-nucleotide) intervening sequence.

**Case report.** A 14-month-old aboriginal child presented with a 1-week history of vomiting, diarrhea, fever, and dry cough. On admission, his temperature was 38°C and he had shortness of breath, rhinorrhea, a discharge from the right ear, and crepitations on the left base of the lung. An ear swab grew *Pseudomonas aeruginosa* and *Streptococcus faecalis*. Lumbar puncture showed the cerebrospinal fluid was clear, and culture was negative. Urine collected from the patient was consistent with *Enterococcus faecalis* urinary tract infection. Hematological investigations showed eosinophilia, neutrophil leukocytosis, and atypical lymphocytosis. A blood culture taken on admission grew a spiral gram-negative rod resembling *Campylobacter* species. X-rays taken at admission suggested a left lower lobe pneumonia. The organism was not isolated from the patient’s feces or from his sputum (although incubation conditions may not have been ideal for the isolation of this organism). The patient was treated with intravenous ceftriaxone for 3 days (500 mg daily), with clinical improvement, and was discharged with a 1-week supply of oral amoxicillin (125 mg three times a day).

The organism was recovered from the inoculated aerobic bottle of the BACTEC Blood Culture System (Becton Dickinson Microbiology Systems, Cockeysville, Md.) after 6 days of incubation. Since the Gram stain indicated a *Campylobacter* sp., the bottle fluid was plated onto 6% sheep blood agar, chocolate agar, and a *Campylobacter* selective medium (Oxoid, Basingstoke, Hampshire, England). Plates were incubated in a microaerobic atmosphere (Campy Pak; Oxoid). The isolate branched within the helicobacter group (epsilon class) of phylogenetic tree reconstructions (PAUP version 4.04b4a) (30) using the 16S rRNA gene sequences are shown in Fig. 1. The isolate branched within the helicobacter group (epsilon subdivision of *Proteobacteria*) and formed part of a statistically well-supported clade that included two other organisms, both originally isolated from AIDS patients. It was most closely related to a partial sequence of *Helicobacter fennelliae* (CCUG 18820T) but differed from it by at least 32 base substitutions as well as by the presence of the IVS. This is a minimum estimate because the *H. fennelliae* sequence (accession number M88154) has 42 unresolved nucleotides, including one region where the number of bases is uncertain. The next closest 16S rRNA sequence (*Helicobacter* sp. strain Mainz) was less than 97% similar. Neither the *H. fennelliae* nor the *Helicobacter* sp. strain Mainz sequence contained an IVS. Using the guidelines proposed by Devereux et al. (6) and Stackebrandt and Goebel (26), a level of 97% or less sequence similarity in the 16S rRNA genes of two organisms would indicate they belong to separate species. We believe the evidence favors the classification of our isolate as a novel species of *Helicobacter*.

The IVS showed significant similarity to an IVS in a 23S rRNA sequence of *Helicobacter canis* NCTC 12743, a species that belongs to a separate clade (Fig. 1). The orientations of the two IVSs differed with respect to their surrounding rRNA.
genes. Secondary-structure predictions (mfold) (38) indicated that the new IVS can form a highly stable cloverleaf structure ($\Delta G = -128$ kcal/mol) with a primary stem of 16 nt (formed between the inverted terminal repeats of the IVS) and considerable base pairing elsewhere. The presence of an IVS in the 16S rRNA gene of this isolate is not surprising, as these elements occur in the 16S and 23S rRNA genes of many other bacteria (references 13 and 18 and references cited therein). We believe that our isolate shows the first example of an IVS that has a homologue in a different rRNA gene (of another organism) and where the two are in opposite orientations with respect to their surrounding genes. It is difficult to imagine a simple model of IVS transfer between organisms that would account for this pattern (18).

On the basis of the type of disease, Helicobacter spp. can be divided into three distinct groups. The first consists of gastric helicobacters such as Helicobacter pylori and Helicobacter heilmannii, which cause upper gastrointestinal tract diseases in humans. The second group consists of Helicobacter spp. that are isolated mainly from animals such as ferrets (11), rodents (16),
dogs (10, 28), cats (9, 27), cheetahs (7), monkeys (3), and other mammals and have been found to cause disease in their respective hosts. The third group consists of helicobacters that cause enteric and systemic diseases in humans, such as *H. cinaedi* (4, 19–22, 32, 34), *H. fennelliae* (19, 34), “*H. westmeadii*” (35), *H. rappini* (1, 23, 24, 31), *Helicobacter* sp. strain Mainz (8, 14), *H. pullorum* (5, 27, 29), *Helicobacter* sp. strain CLO3 (21), and a number of unnamed species in GenBank, such as two strains isolated from AIDS patients in North America (36). All were recovered from the blood of patients except *H. pullorum*, and most were isolated from immunosuppressed persons. The reservoir in this group is unknown. Poultry are a likely source of food-borne enteritis in humans (2, 27), and *H. cinaedi* has been found in hamsters (12). Domestic animals like dogs and cats are also possible sources, and recently, two reports implied that dogs might be the reservoir for *H. rappini* infection (23, 31). Dogs are commonly found in and live in close proximity with aboriginal communities in Australia.

**Nucleotide sequence accession number.** The sequence determined in this study has been deposited in GenBank under accession number AF237612.

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**REFERENCES**


