

Draft Genome Sequence of *Helicobacter fennelliae* Strain MRY12-0050, Isolated from a Bacteremia Patient

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***Helicobacter fennelliae*, a human enterohepatic pathogen, causes bacteremia and colitis. We isolated *H. fennelliae* strain MRY12-0050 from a female patient; this strain was isolated from 2 other patients from the same hospital during the same period, suggesting human-to-human transmission. This is the first report of an *H. fennelliae* genome sequence.**

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Helicobacter species are Gram-negative, spiral bacteria that are categorized into 2 groups, (i) gastric helicobacters and (ii) enterohepatic helicobacters. *Helicobacter pylori* is a major gastric *Helicobacter*, and the genome sequences of several gastric *Helicobacter* strains have been analyzed so far. On the other hand, analyses of genomic sequences for enterohepatic helicobacters have been limited. *H. fennelliae* is an enterohepatic *Helicobacter* that causes bacteremia mainly in immunocompromised hosts (1–3). In this study, *H. fennelliae* strain MRY12-0050 was isolated from the blood of a female patient with non-Hodgkin lymphoma. At first, the strain was misidentified as *H. cinaedi* because the strains have similar morphologies. It was later identified as *H. fennelliae* by sequencing of both the 16S rRNA and 23S rRNA genes. *H. fennelliae* was isolated from 2 other patients from the same hospital ward. Pulsed-field gel electrophoresis (PFGE) of 3 isolates showed the same PFGE pattern between isolates, suggesting human-to-human transmission (4). Since genome-sequencing data for *H. fennelliae* have not yet been reported, we herein describe a draft genome sequence for *H. fennelliae* MRY 12-0050, which causes nosocomial infection.

H. fennelliae was cultured in brucella agar (Becton Dickinson, NJ) containing 5% horse blood under microaerobic conditions with hydrogen, which was provided by the gas replacement method by using an anaerobic gas mixture (i.e., H₂, 10%; CO₂, 10%; and N₂, 80%). Genomic DNA was prepared, and a Roche 454 Life Sciences genome sequencer junior system was used to generate DNA sequences at 32× coverage. The same genomic DNA was analyzed by the Illumina MiSeq system paired-end sequences, and the resulting sequence represents 127× coverage. Sequences obtained by using the Roche 454 were assembled using Newbler Assembler v2.7, whereas sequences obtained by using the Illumina MiSeq were assembled with Geneious. The assembled sequences were merged by using Geneious to generate 49 contigs. The contig N₅₀ was approximately 157 kb in length, and the largest contig assembled was approximately 300 kb. Finally, the DNA

sequences were annotated by using the RAST (Rapid Annotation using Subsystem Technology) server (5).

The whole genome is 2.15 Mb in size, has a G+C content of 37.9%, and contains 2,507 genes (2,467 protein-coding genes and 40 structural RNAs). RAST annotation showed that *H. cinaedi* strain CCUG 18818 (score 502), *H. hepaticus* strain ATCC 51449 (score 456), and *H. canadensis* strain MIT 98-5491 (score 444) are the closest neighbors of *H. fennelliae* MRY12-0050. Although *H. cinaedi* and *H. hepaticus* have been known to express cytolethal distending toxin (CDT), which causes DNA damage to target cells, a CDT cluster was not identified in *H. fennelliae* MRY12-0050. Because both *H. cinaedi* and *H. fennelliae* are likely to cause a nosocomial infection and bacteremia in humans, further analyses are needed to elucidate the pathogenic factor in *H. fennelliae*.

Nucleotide sequence accession numbers. This whole-genome shotgun project has been deposited at DDBJ/EMBL/GenBank under the accession no. [BASD000000000](https://www.ncbi.nlm.nih.gov/nuccore/BASD000000000). The version described in this paper is the first version, [BASD010000000](https://www.ncbi.nlm.nih.gov/nuccore/BASD010000000).

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