Genome Sequence of *Helicobacter bizzozeronii* Strain CIII-1, an Isolate from Human Gastric Mucosa

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The canine-adapted *Helicobacter bizzozeronii* is the only nonpylori *Helicobacter* species isolated from human gastric biopsy tissue. Here we present the genome sequence of strain CIII-1, isolated from a 45-year-old female patient with severe gastric symptoms. This is the first genome sequence of nonpylori *Helicobacter* isolated from human gastritis.

*Helicobacter pylori* has been established as the primary cause of gastritis and peptic ulceration in humans and has been recognized as a major risk factor for mucosa-associated lymphoid-tissue lymphoma and adenocarcinoma (3). However, in gastric biopsy tissues of a minority of patients (0.17 to 2.3%) with upper gastrointestinal symptoms, long, tightly coiled spiral bacteria, ascribed to nonpylori *Helicobacter* spp., can be observed (2). Among the five nonpylori gastric *Helicobacter* species reported to be associated with human infections (5), only *Helicobacter bizzozeronii* has been successfully cultivated from gastric biopsy tissues of human patients (7, 8). Humans potentially acquire the infections as a consequence of direct contact with dogs and cats (10), which are normally colonized by *H. bizzozeronii* (6). However, although virtually all cats and dogs carry this *Helicobacter* species, its pathogenic significance in these animals remains unknown (5). Here we present the genome sequence of the Finnish human *H. bizzozeronii* strain CIII-1, isolated in March 2008 from corpus biopsy tissue of a 45-year-old female patient with severe gastric symptoms (8). To our knowledge, this is the first genome sequence of nonpylori gastric *Helicobacter* isolated from humans.

The draft genome sequence of *H. bizzozeronii* CIII-1 was determined using a combination of 454 Titanium (43× genome coverage, 8-kb mate pair library; performed by LGC Genomics GmbH, Berlin, Germany) and Solexa (50 cycles, 132× coverage, 5-kb mate pair library; performed by BaseClear BV, Leiden, The Netherlands) sequencing. Genomic data were processed using MIRA 3.2.1 assembler (4), SSAKE (12), and the Staden package (11). Resulting contigs were merged into two scaffolds, representing a circular chromosome 1,755,458 bp in length and a 52,076-bp circular plasmid. The assembly of the chromosome was validated by mapping to an MluI optical map produced by OpGen, Inc. (Gaithersburg, MD). Gene finding and automatic annotation were done using the RAST server (1; http://rast.nmpdr.org/).

The chromosome of *H. bizzozeronii* is similar in size and GC content (46%) to other sequenced gastric *Helicobacter* species. There are 1,894 protein-coding sequences (CDSs) in a coding area of 93%, with an average length of 851 bp (1,079 genes per kilobase). We detected 36 transfer RNAs using the tRNAscan-SE program (9) and two rRNA loci. A putative function could be predicted for 1,280 (67.7%) CDSs, whereas 614 (32.4%) of the CDSs were annotated as hypothetical proteins. The plasmid contains 77 CDSs, to 21 of which (27.3%) a putative function was assigned.

The role of *H. bizzozeronii* in human gastric disease is limited compared to that of *H. pylori*; however, both species persistently colonize the same niche and possibly exploit similar mechanisms to interact with the host, evade the immune system, and induce gastritis. Detailed studies of the molecular mechanisms of *H. bizzozeronii* infections, including comparative genome analysis, will broaden our knowledge of the biology of gastric *Helicobacter* spp., providing new insights into the understanding of the pathogenesis of human gastritis.

**Nucleotide sequence accession numbers.** The sequences of the chromosome of *H. bizzozeronii* CIII-1 and the plasmid pHBZ1 have been deposited in EMBL under accession numbers FR871757 and FR871758, respectively (project identification number 65019).

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