Complete Genome Sequence of *Helicobacter cinaedi* Type Strain ATCC BAA-847

Tohru Miyoshi-Akiyama, a Nozomi Takeshita, b Norio Ohmagari, b and Teruo Kirikae a

Department of Infectious Diseases, National Center for Global Health and Medicine, Toyama, Shinjuku-ku, Tokyo, Japan, a and Disease Control and Prevention Center, National Center for Global Health and Medicine, Toyama, Shinjuku-ku, Tokyo, Japan b

Here we report the completely annotated genome sequence of the *Helicobacter cinaedi* type strain (ATCC BAA-847), which is an emerging pathogen that causes cellulitis and bacteremia. The genome sequence will provide new insights into the diagnosis, pathogenic mechanisms, and drug resistance of *H. cinaedi*.

The type strain of *Helicobacter cinaedi*, ATCC BAA-847 (CDC DO148), was isolated in the 1980s (February 1980 to June 1983) from a rectal swab taken from a homosexual man who had attended the Sexually Transmitted Disease Clinic at Harborview Medical Center, Seattle, WA, and it was identified as a novel *Campylobacter* species (7). When the *Campylobacter* genus underwent reclassification in 1991, it was moved into the *Helicobacter* genus (8). *H. cinaedi* causes cellulitis and bacteremia in immunocompromised patients (3), as well as in immunocompetent hosts (4). Nosocomial *H. cinaedi* infections have recently been reported (5). However, the pathogenicity and etiological properties of *H. cinaedi* are poorly understood. Recently, the genome sequence of *H. cinaedi* strain PAGU611, isolated from a case of human bacteremia in Japan, was reported (2).

Here, an 8-kb paired-end library of the *H. cinaedi* ATCC BAA-847 genome was prepared and used for sequence analysis with a GS FLX titanium sequencer (Roche). This generated 567,221 reads, covering 171,999,544 bp (68.8-fold coverage), which were assembled into scaffolds and contigs. Gap filling was then performed by conventional Sanger sequencing of the PCR fragments based on brute force PCR among the contigs and scaffolds. Finally, the Illumina MiSeq 2×150-bp 110,730 paired-end reads were added to the draft genome sequence. Primary coding sequence extraction was performed using MetaGeneAnnotator (6). Initial functional assignment and manual correction were carried out by comparing the genome sequence data of *H. cinaedi* PAGU611 (AP012344 and AP012345) and CCUG18818 (ABQT01000001.1 to ABQT01000096.1) by *in silico* molecular cloning (In Silico Biology, Inc., Yokohama, Japan). Prophage regions were identified by Prophage Finder (1). The *H. cinaedi* ATCC BAA-847 genome consists of a single circular chromosome of 2,240,130 bp with an average GC content of 38.34%. The chromosome was shown to contain a total of 2,322 protein-coding genes, 40 tRNA genes for all amino acids, and 2 rrr operons. In addition, the chromosome harbors 3 prophage-like elements. The genome of *H. cinaedi* ATCC BAA-847 contains two unique regions spanning 1.4 to 1.6 Mbp, the latter half (from 1.54 to 1.56 Mbp) of which corresponds to a putative prophage, in comparison to that of PAGU611.

Nucleotide sequence accession number. The nucleotide sequence of the chromosome of *H. cinaedi* ATCC BAA-847 has been deposited in the DNA Data Bank of Japan under accession no. AP012492.

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