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GENOME ANNOUNCEMENT

Complete Genome Sequence of *Helicobacter cinaedi* Strain PAGU611, Isolated in a Case of Human Bacteremia

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We report the complete genome sequence of *Helicobacter cinaedi* strain PAGU611, isolated in a case of human bacteremia. The PAGU611 genome comprises a 2,078,348-bp chromosome and a 23,054-bp plasmid. The chromosome contains a unique genomic island, encoding a type VI secretion system and clustered regularly interspaced short palindromic repeat (CRISPR) loci.

Helicobacter cinaedi causes cellulitis, diarrhea, and bacteremia frequently in immunocompromised patients and occasionally in immunocompetent individuals (7, 10, 11, 20). Cases of nosocomial *H. cinaedi* infection (10, 12) and results of epidemiological studies (9) have recently been reported. Despite the clinical importance of *H. cinaedi*, its genome sequence and virulence mechanism have not been completely defined. We report the first complete genome sequence of *H. cinaedi* species.

The genome of PAGU611, an *H. cinaedi* strain isolated in a case of human bacteremia, was sequenced using the Roche 454 GS FLX Titanium system with an 8-kb paired-end library (341,681 reads, 30.8-fold genome coverage). Sequence reads were assembled using Celera Assembler 5.3, and gaps were closed by sequencing PCR products spanning the gaps. Sequence errors were corrected by mapping with Illumina Miseq 150-bp paired-end reads (727,442 reads, 52-fold coverage). The genome sequence was automatically annotated using the Microbial Genome Annotation Pipeline (18) and manually corrected using *in silico* Molecular Cloning Genomics Edition software (In Silico Biology, Inc., Yokohama, Japan) (13).

The PAGU611 genome comprises a 2,078,348-bp chromosome and a 23,054-bp plasmid, pHci1, with average G+C contents of 38.6% and 31.6%, respectively. The chromosome contains 2,096 predicted protein-coding sequences (CDSs), 39 tRNA genes, and 2 rRNA operons. The plasmid encodes 29 predicted CDSs, of which 27 are hypothetical proteins. The genome has no prophage or insertion sequence element.

We performed reciprocal best hit analysis of PAGU611 chromosomal CDSs against 4 sequenced *Helicobacter* species using BLASTP (1) (E value cutoff, 10^{-10}), and significant homology was observed: homologies of 66.1% to *Helicobacter hepaticus* (17), 49.6% to *Helicobacter mustelae* (14), 47.4% to *Helicobacter felis* (2), and 47.3% to *Helicobacter pylori* 26695 (19). Synteny plots of all orthologs indicated that *H. cinaedi* is most similar to *H. hepaticus*.

Synteny plots also identified a unique *H. cinaedi* genomic island—HciGI1. The HciGI1 island (approximately 132 kb, 32.3% G+C content, spanning from HCN_1310 to HCN_1482) contains 173 CDSs, including 147 hypothetical protein genes and 12 genes to assemble a type VI secretion system (T6SS). These T6SS genes are homologous to those of *H. hepaticus* (33.7 to 83.4% amino acid sequence identity), which limit the colonization of *H. hepaticus* to a germfree murine intestine and prevent intestinal inflammation during colonization (6). The *H. cinaedi* chromosome encodes 2 clustered regularly interspaced short palindromic repeats (CRISPR) and CRISPR-associated (Cas) systems (3, 8), which confer immunity to host cells against foreign DNA. Of these, one is encoded on HciGI1. The *H. mustelae* chromosome encodes a CRISPR/Cas system similar to that in HciGI1. However, the 3 other sequenced *Helicobacter* chromosomes have no CRISPR/Cas system.

Additionally, the PAGU611 chromosome encodes 2 known virulence factors, cytolethal distending toxin (16) and alkyl hydroperoxide reductase (4), and several potential virulence-related proteins, such as neutrophil activation protein (5) and a homolog of *Campylobacter jejuni* invasion antigen B (15).

Nucleotide sequence accession numbers. The complete chromosome and plasmid sequences of *H. cinaedi* PAGU611 have been deposited in DDBJ/EMBL/GenBank under accession no. AP012344 and AP012345, respectively.

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