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GENOME SEQUENCES

# Complete Genome Sequence and Annotation of *Campylobacter jejuni* YH003, Isolated from Retail Chicken

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**ABSTRACT** The complete genome sequence of *Campylobacter jejuni* YH003, isolated from retail chicken, was determined using PacBio and Illumina technologies. The assembled genome is 1,743,985 bp (G+C content of 30.3%). Genome annotation revealed several genes encoding virulence and antibiotic resistance factors, including a type VI secretion system, cytolethal distending toxins, and a multidrug efflux system.

Campylobacteriosis caused by *Campylobacter jejuni* is the most prevalent foodborne illness in the United States and worldwide (1, 2). Wild and domestic birds, especially poultry, are the primary reservoirs, which leads to exposure for humans through contact with raw or undercooked poultry (3–5). While campylobacteriosis is usually self-limiting, treatment with antibiotics, mainly fluoroquinolones, may be necessary in some cases (6). Use of antibiotics in poultry to curtail infections has led to an increase in antibiotic resistance in *Campylobacter* spp., which can have an impact on antibiotic treatment in humans (7, 8). The whole-genome sequence and annotation of *C. jejuni* YH003, isolated from retail chicken, can reveal genetic information related to virulence and antibiotic resistance and thus assist in the identification of pathogenicity and antibiotic susceptibilities of the pathogen.

*C. jejuni* YH003 was recently isolated from chicken drumsticks purchased from a local supermarket. The strain was isolated using a passive filtration method (9, 10). Confirmation of the genus and species was done by 16S rRNA gene sequencing and multiplex real-time PCR targeting the *hipO* and *cdtA* genes (11, 12). The strain was grown in *Brucella* broth (Difco; Becton, Dickinson, Franklin Lakes, NJ) for approximately 40 h under microaerophilic conditions and pelleted by centrifugation, and genomic DNA was extracted using the Genomic tip 100/G (Qiagen, Valencia, CA) and sequenced using both single-molecule real-time (SMRT) sequencing (Pacific Bioscience, Menlo Park, CA) and the MiSeq platform (Illumina, San Diego, CA). The Nextera XT library preparation kit (Illumina) was used to prepare the library for Illumina sequencing. SMRTbell library preparation and PacBio sequencing were performed by the University of Delaware DNA Sequencing and Genotyping Center (Newark, DE). Coverages for the PacBio and Illumina reads were 125× and 506×, respectively. Illumina reads (a total of 1,759,375 reads, with an average length of 251 nucleotides) were quality controlled by FastQC and assembled using SPAdes v.3.7.1 (13), while a total of 17,686 PacBio reads, with an average length of 12,592 nucleotides, were assembled using Canu v.1.3 (14). The two *de novo* assemblies were joined and corrected using Pilon v.1.22 to obtain a single contig. The draft genome was manually edited and oriented. CLC Workbench (Qiagen Bioinformatics, Redwood City, CA) was used to confirm the assembly by mapping the reads back. Default parameter settings were used for all software. Annotation of the final assembly was performed using Rapid Annotation using Subsystem Technology (RAST) (http://rast.nmpdr.org). The NCBI Prokaryotic Genome Annotation Pipeline (PGAP) was also used for genome annotation, and the results are publicly available.

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*C. jejuni* YH003 has a circular chromosome of 1,743,985 bp (G+C content of 30.3%), encoding 1,785 proteins. Based on a BLAST search against all of the available *Campylobacter* genomes in the NCBI database and comparative genome analysis with Mauve alignment using default settings, this strain is most closely related to *C. jejuni* NCTC 11168. Distinctly, *C. jejuni* YH003 contains 16 annotated proteins of the type VI secretion system (T6SS), an important virulence factor exporting cytotoxic molecules to host cells. Strain YH003 also contains the ATP-dependent chaperone ClpB as part of the T6SS. In addition to 86 motility and chemotaxis genes, this strain possesses 65 virulence genes, including *cadF*, *jlpA*, *ciaB*, *pebAC*, *omp, htrA*, and the cytolethal distending toxin genes *cdtCBA*. Interestingly, RAST annotation revealed a type II CRISPR system containing the *cas1*, *cas2*, and *cas9/csn1* genes, a type I restriction-modification system with the *hsdM*, *hsdS*, *rloC*, and *hsdR* genes, a *Campylobacter* multidrug efflux pump consisting of *cmeABCR*, and a 36-kb complete Mu-like phage in the chromosome of *C. jejuni* YH003.

**Data availability.** This complete genome sequence has been deposited in GenBank under accession number CP041584. The raw reads from PacBio RS II and Illumina MiSeq sequencing are available in the NCBI Sequence Read Archive (SRA) under accession numbers SRX7021025 and SRX7021026, respectively. The BioProject accession number is PRJNA553752, and the BioSample accession number is SAMN12249490.

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