AMERICAN SOCIETY FOR MICROBIOLOGY | Microbiology Resource Announcements

GENOME SEQUENCES

Draft Genome Sequences of Two *Campylobacter jejuni* Strains That Show Significantly Different Colonization Potentials in Chickens

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ABSTRACT Here, we report the draft genome sequences of robust (A74/C_24-3) and poor (A74/O_2-2) chicken-colonizing *Campylobacter jejuni* isolates. Whole-genome sequence analyses of these isolates will be helpful in facilitating further studies to identify genetic factors used in chicken colonization.

Campylobacter species are considered one of the leading causes of bacterial gastrointestinal disease in humans in the United States and other parts of the globe (1). Among *Campylobacter* species, *Campylobacter jejuni* accounts for 80 to 85% of human infections, while *C. coli* is responsible for 10 to 15% (2). Poultry is a natural reservoir for *C. jejuni*, which is capable of colonizing the chicken intestinal tract, specifically the cecum (3). Handling raw chicken meat or eating insufficiently cooked chicken is believed to be a significant risk factor for *Campylobacter* infection (4). A robust colonizer, A74/C_24-3, and a poor colonizer, A74/O_2-2, exhibiting differing colonization levels were originally isolated after fecal-oral passage through chicks (3). An individual poultry housing challenge model was used to recover *C. jejuni* isolates (5).

Minimal subculture passage (1 at most) for each isolate was performed, and the isolates were stored at −80°C in *Brucella* broth (Thermo Scientific Oxoid, Waltham, MA, USA) containing 15% glycerol. Subsequently, bacteria were subcultured onto Campy-Line agar containing sulfamethoxazole and grown at 42°C in a microaerobic environment (5% O_2, 10% CO_2, and 85% N_2) in a Whitley DG250 microaerophilic work station (Don Whitley Scientific, Ltd., Shipley, UK) (6). Single colonies were inoculated onto Mueller-Hinton agar plates (Millipore Sigma, St. Louis, MO, USA) and grown at 42°C. After overnight incubation, bacterial growth was collected from the plate, and genomic DNA was extracted using the DNeasy blood and tissue kit (Qiagen, Valencia, CA, USA) (7). The NanoDrop spectrophotometer and Qubit double-stranded DNA (dsDNA) broad-range (BR) assay kit were used to measure the quality and quantity of the DNA (Thermo Fisher Scientific, Grand Island, NY, USA). DNA sequencing libraries were constructed using the Nextera XT DNA library preparation kit (Illumina, San Diego, CA, USA). Whole-genome sequencing (WGS) reactions were performed on an Illumina MiSeq instrument in 2 × 300-bp paired-end format (7). The raw sequence data were trimmed and subjected to *de novo* assembly using the CLC Genomics Workbench ver. 9.0 (Qiagen). Sequences were initially annotated using Pathosystems Resource Integration Center (PATRIC) software ver. 3.5.36 (8) and submitted to NCBI for final annotation with the Prokaryotic Genome Annotation Pipeline (PGAP) (9). Default parameters were used for all software unless otherwise specified.

The total numbers of (paired-end) reads for *C. jejuni* A74/O_2-2 and A74/C_24-3 were 2,595,308 and 2,483,699, respectively. The genome coverage for both isolates was approximately 50×. The draft genome sequence of *C. jejuni* A74/C_24-3 was

Citation Sung K, Khajanchi BK, Hiett KL, Line JE, Khan SA. 2020. Draft genome sequences of two *Campylobacter jejuni* strains that show significantly different colonization potentials in chickens. Microbiol Resour Announc 9:e00687-20. https://doi.org/10.1128/MRA.00687-20.

Editor David Rasko, University of Maryland School of Medicine

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Received 15 June 2020
Accepted 16 September 2020
Published 8 October 2020

1,620,931 bp long with a G+C content of 30.49%, which was distributed in 39 contigs (N_{50}, 186,429 bp) with 1,625 coding sequences, 4 rRNAs, and 40 tRNAs. The draft genome sequence of *C. jejuni* A74/O_2-2 was 1,616,776 bp long with a G+C content of 30.52%, which was distributed in 104 contigs (N_{50}, 58,541 bp) with 1,652 coding sequences, 6 rRNAs, and 39 tRNAs.

Data availability. This whole-genome shotgun project was deposited at DDBJ/EMBL/GenBank under the accession numbers JAAAVH000000000 and JAAAVG000000000 for A74/C_24-3 and A74/O_2-2, respectively. The FASTQ sequences were deposited in the Sequence Read Archive (SRA) under the accession number PRJNA593216.

ACKNOWLEDGMENTS

We recognize Jing Han and Jinshan Jin for their critical review of the manuscript.

This project was supported by the National Center for Toxicological Research and the U.S. Food and Drug Administration. The opinions expressed in this article are solely the authors' and do not necessarily represent the official views and policy of the Food and Drug Administration or Department of Health and Human Services. Reference to any commercial material, equipment, or process does not in any way constitute approval, endorsement, or recommendation by the Food and Drug Administration.

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