Draft Genome Sequence of *Campylobacter jejuni* 11168H

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ABSTRACT *Campylobacter jejuni* is the most prevalent cause of food-borne gastro-enteritis in the developed world. The reference and original sequenced strain *C. jejuni* NCTC11168 has low levels of motility compared to clinical isolates. Here, we describe the draft genome of the laboratory derived hypermotile variant named 11168H.

*C*ampylobacter jejuni is a Gram-negative, microaerophilic, spiral-shaped enteric pathogenic bacterium and is the leading cause of bacterial food-borne gastroenteritis worldwide (1). *C. jejuni* infection is associated with mild diarrhea to severe inflammatory enteritis. In most cases, *C. jejuni* infection is self-limiting, however, there can be life-threatening postinfection complications such as Guillain-Barré syndrome, an acute autoimmune paralyzing neuropathy (2). *C. jejuni* 11168H is a hypermotile clonal derivative of NCTC 11168 (3, 4). The motility of the original sequenced strain *C. jejuni* 11168 was noted to be significantly lower than that of fresh clinical isolates (4). However, it was noted that there was variable motility ranging from almost nonmotile to hypermotile and that this could readily derive the wild-type parent strain (4). *C. jejuni* 11168H has been used in several studies including *C. jejuni* pathogenesis glycan analysis, colonization of chickens, *Galleria mellonella* larvae, responses to oxidative and aerobic stresses, and the investigation into outer membrane vesicles (5–9).

C. jejuni 11168H was sequenced using an Illumina MiSeq (2 × 151 bp) which generated 1,168,138 reads and 171,157,831 bp. MiSeq reads were polished using Trimmomatic (10) (v0.33). A draft genome was assembled using VelvetOptimiser (http://bioinformatics.net.au/software.velvetoptimiser.shtml). Assembled contigs were further polished using SSPACE (standard v3.0) (11), GapFiller (12) (v1.10), and Pilon (13) (v 1.16). Contigs were ordered with Abacas and Mauve and finally annotated using Prokka (14) (v1.11). The draft genome consisted of 83 contigs, totaling 1,615,620 bp with 30.5% G+C. Prokka identified 44 tRNAs and rRNAs, one clustered regularly interspaced short palindromic repeat (CRISPR), and 1,631 coding sequences (CDS).

Accession number(s). This whole-genome shotgun project has been deposited in the European Nucleotide Archive under the accession no. FPEE01000001 to FPEE01000083. The version described in this paper is the first version, FPEE01000000.

REFERENCES

1. Epps SV, Harvey RB, Hume ME, Phillips TD, Anderson RC, Nisbet DJ. 2013. Foodborne campylobacter: infections, metabolism, pathogenesis and reservoirs. Int J Environ Res Publ Health 10:6292–6304. https://doi.org/10.3390/ijerph10126292.
2. Nyati KK, Nyati R. 2013. Role of *Campylobacter jejuni* infection in the pathogenesis of Guillain-Barre syndrome: an update. BioMed Res Int 2013:852195. https://doi.org/10.1155/2013/852195.
3. Karlyshev AV, McCrossan MV, Wren BW. 2001. Demonstration of poly-saccharide capsule in *Campylobacter jejuni* using electron microscopy. Infect Immun 69:5921–5924. https://doi.org/10.1128/IAI.69.9.5921-5924.2001.
4. Karlyshev AV, Linton D, Gregson NA, Wren BW. 2002. A novel paralogous gene family involved in phase-variable flagella-mediated motility in *Campylobacter jejuni*. Microbiology 148:473–480. https://doi.org/10.1099/00221287-148-2-473.
5. Karlyshev AV, Everest P, Linton D, Cawthraw S, Newell DG, Wren BW.

2004. The *Campylobacter jejuni* general glycosylation system is important for attachment to human epithelial cells and in the colonization of chicks. Microbiology 150:1957–1964. https://doi.org/10.1099/mic.0.26721-0.

6. Jones MA, Marston KL, Woodall CA, Maskell DJ, Linton D, Karlyshev AV, Dorrell N, Wren BW, Barrow PA. 2004. Adaptation of *Campylobacter jejuni* NCTC11168 to high-level colonization of the avian gastrointestinal tract. Infect Immun 72:3769–3776. https://doi.org/10.1128/IAI.72.7.3769-3776.2004.

7. Champion OL, Karlyshev AV, Senior NJ, Woodward M, La Ragione R, Howard SL, Wren BW, Titball RW. 2010. Insect infection model for *Campylobacter jejuni* reveals that O-methyl phosphoramidate has insecticidal activity. J Infect Dis 201:776–782. https://doi.org/10.1086/650494.

8. Elmi A, Nasher F, Jagatia H, Gundogdu O, Bajaj-Elliott M, Wren B, Dorrell N. 2016. *Campylobacter jejuni* outer membrane vesicle-associated proteolytic activity promotes bacterial invasion by mediating cleavage of intestinal epithelial cell E-cadherin and occludin. Cell Microbiol 18: 561–572. https://doi.org/10.1111/cmi.12534.

9. Gundogdu O, da Silva DT, Mohammad B, Elmi A, Mills DC, Wren BW, Dorrell N. 2015. The *Campylobacter jejuni* MarR-like transcriptional reg-

ulators RrpA and RrpB both influence bacterial responses to oxidative and aerobic stresses. Front Microbiol 6:724. https://doi.org/10.3389/fmicb.2015.00724.

10. Bolger AM, Lohse M, Usadel B. 2014. Trimmomatic: a flexible trimmer for Illumina sequence data. Bioinformatics 30:2114–2120. https://doi.org/10.1093/bioinformatics/btu170.

11. Boetzer M, Henkel CV, Jansen HJ, Butler D, Pirovano W. 2011. Scaffolding pre-assembled contigs using SSPACE. Bioinformatics 27:578–579. https://doi.org/10.1093/bioinformatics/btq683.

12. Nadalin F, Vezzi F, Policriti A. 2012. GapFiller: a de novo assembly approach to fill the gap within paired reads. BMC Bioinformatics 13:S8. https://doi.org/10.1186/1471-2105-13-S14-S8.

13. Walker BJ, Abeel T, Shea T, Priest M, Abouelliel A, Sakthikumar S, Cuomo CA, Zeng Q, Wortman J, Young SK, Earl AM. 2014. Pilon: an integrated tool for comprehensive microbial variant detection and genome assembly improvement. PLoS One 9:e112963. https://doi.org/10.1371/journal.pone.0112963.

14. Seemann T. 2014. Prokka: rapid prokaryotic genome annotation. Bioinformatics 30:2068–2069. https://doi.org/10.1093/bioinformatics/btu153.