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### Permalink

<https://escholarship.org/uc/item/0sp737kb>

### Journal

Microbiology Resource Announcements, 4(6)

### ISSN

2576-098X

### Authors

Weis, Allison M  
Clothier, Kristin A  
Huang, Bihua C  
et al.

### Publication Date

2016-12-29

### DOI

10.1128/genomea.01324-16

Peer reviewed

# Draft Genome Sequences of *Campylobacter jejuni* Strains That Cause Abortion in Livestock

Allison M. Weis,<sup>a,b</sup> Kristin A. Clothier,<sup>c</sup> Bihua C. Huang,<sup>a,b</sup> Nguyet Kong,<sup>a,b</sup>  Bart C. Weimer<sup>a,b</sup>

School of Veterinary Medicine, UC Davis, Davis, California, USA<sup>a</sup>; 100K Pathogen Genome Project, UC Davis, Davis, California, USA<sup>b</sup>; California Animal Health and Food Safety, Davis, California, USA<sup>c</sup>

***Campylobacter jejuni* is an intestinal bacterium that can cause abortion in livestock. This publication announces the public release of 15 *Campylobacter jejuni* genome sequences from isolates linked to abortion in livestock. These isolates are part of the 100K Pathogen Genome Project and are from clinical cases at the University of California (UC) Davis.**

Received 30 September 2016 Accepted 10 October 2016 Published 1 December 2016

**Citation** Weis AM, Clothier KA, Huang BC, Kong N, Weimer BC. 2016. Draft genome sequences of *Campylobacter jejuni* strains that cause abortion in livestock. *Genome Announc* 4(6):e01324-16. doi:10.1128/genomeA.01324-16.

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Address correspondence to Bart C. Weimer, bcweimer@ucdavis.edu.

*Campylobacter jejuni* is transmissible between wildlife, livestock, and humans, often leading to foodborne illness in humans and disease burden among livestock (1–4). Globally, *C. jejuni* is a common foodborne pathogen (5) that infects over 1.3 million people each year in the United States (6), causing gastroenteritis; in rare cases, it may induce Guillain-Barré syndrome, an autoimmune disease (7–10). In addition to human infection, *C. jejuni* infects domesticated livestock, including sheep, cattle, goats, and pigs, most often leading to gastroenteritis in these species (11, 12).

*Campylobacter* spp., specifically, *C. fetus* subsp. *fetus*, are one of the leading causes of abortion in ungulates, characterized by late term abortion, stillbirths, and occasional ewe deaths (13). In recent years, many cases have recovered *C. jejuni* from aborted fetuses with similar disease pathologies (14, 15). Emergence of abortive hypervirulent *C. jejuni* isolates have been observed in various regions of the United States (14, 15). We sequenced 15 *C. jejuni* isolates associated with abortion in sheep, cows, and goats in northern California at an average coverage of 91×, assembled, and annotated (Table 1).

**TABLE 1** Coverage and accession numbers of 15 abortive *C. jejuni* genomes

GenBank accession no.	SRA accession no.	Isolate name	Coverage (×)
<a href="#">MJZI00000000</a>	SRR3619957	BCW_6919	93
<a href="#">MKAC00000000</a>	SRR3619958	BCW_6920	91
<a href="#">MKAD00000000</a>	SRR3619959	BCW_6921	79
<a href="#">MKAE00000000</a>	SRR3619960	BCW_6922	100
<a href="#">MKAF00000000</a>	SRR3619963	BCW_6924	90
<a href="#">MKAG00000000</a>	SRR3619964	BCW_6925	84
<a href="#">MKAR00000000</a>	SRR3619965	BCW_6926	84
<a href="#">MKAS00000000</a>	SRR3619966	BCW_6927	80
<a href="#">MKAT00000000</a>	SRR3619967	BCW_6928	50
<a href="#">MKAU00000000</a>	SRR3619968	BCW_6929	76
<a href="#">MKAV00000000</a>	SRR3619969	BCW_6930	101
<a href="#">MKIC00000000</a>	SRR4020196	BCW_6931	111
<a href="#">MKID00000000</a>	SRR4020197	BCW_6932	70
<a href="#">MKIB00000000</a>	SRR4020198	BCW_6933	81
<a href="#">MKIA00000000</a>	SRR4020199	BCW_6934	182

All *C. jejuni* isolates were cases from the University of California (UC) Davis California Animal Health and Food Safety Laboratory System (CAHFS) and sequenced by the 100K Pathogen Genome Project (<http://www.100kgenomes.org>) in the laboratory of Bart Weimer (UC Davis, Davis, CA). As described (16), isolates were checked for purity (17), genomic DNA (gDNA) was extracted from cultures grown on 5% blood agar plates (UC Davis, VetMed Biological Services) for 1 to 2 days, lysed (18), purified with Qiagen QIAamp DNA minikit, and analyzed on Agilent 2200 TapeStation system using the Genomic DNA ScreenTape assay for integrity of gDNA (19). Isolated gDNA was used to construct libraries using the Kapa HyperPlus kit (KR1145 version 3.16; Kapa Biosystems, Wilmington, MA, USA) with dual-SPRI size selection (20). Libraries were constructed using the PerkinElmer Sciclone next-generation sequencing (NGS) Workstation (PerkinElmer, Hopkinton, MA). Library quantitation was done using the Kapa SYBR Fast quantitative PCR (qPCR) kits (Kapa Biosystems) to ensure the starting concentration of 400 ng and a fragment insert size between 350 and 450 bp (20). Libraries were indexed using Integrated DNA Technologies Weimer 384 TS-LT DNA barcodes, which allowed multiplexing up to 384 isolates. Sequencing was done at the UC Davis Genome Center (Davis, CA, USA) on the HiSeq 3000 instrument using a paired-end 150 protocol (Illumina, Inc., San Diego, CA, USA) (21, 22). Paired-end reads were assembled using ABySS 1.5.2 using  $k = 64$  (23).

**Accession number(s).** These sequences can be found in the 100K Project BioProject at the NCBI SRA BioProject PRJNA186441 and in the NCBI GenBank. Individual GenBank and SRA accession numbers are presented in Table 1.

## ACKNOWLEDGMENTS

We thank all of the collaborators to the 100K Pathogen Genome Project and members of the Weimer lab for helpful discussions. We also thank the staff at CAHFS and all individuals associated with the isolation of each *C. jejuni* strain presented here.

This project was funded by 100K Pathogen Genome Project with ini-

tial funding from the FDA, and Agilent Technologies, to produce these sequences.

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