

Complete Genome Sequence of Type Strain *Campylobacter fetus* subsp. *venerealis* NCTC 10354^T

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***Campylobacter fetus* subsp. *venerealis* is the etiologic agent of bovine genital campylobacteriosis, a sexually transmitted disease of cattle that is of worldwide importance. The complete sequencing and annotation of the genome of the type strain *C. fetus* subsp. *venerealis* NCTC 10354^T are reported.**

Campylobacter fetus is divided into two important veterinary pathogens, *C. fetus* subsp. *fetus*, causing sporadic abortion in cattle and sheep, and *C. fetus* subsp. *venerealis*, the etiologic agent of bovine genital campylobacteriosis (BGC) (5), characterized by repeat breeding and abortion (2, 14). Economic losses due to sexually transmitted BGC are important in regions using reproduction by natural breeding (14), such as Brazil, where it is widespread (2) and highly prevalent (16). Due to the fastidiousness and restriction of the microorganism to the genital tract (5), which elicits mainly a mucosal immune response (17), routine diagnosis of BGC is based on a direct fluorescent-antibody test (7) or molecular techniques (6, 14), which could lack specificity (14, 20). Vaccination is the main BGC control strategy (4), but it shows low efficacy in bulls (8). Despite the importance of *C. fetus* subsp. *venerealis* to the cattle industry, only an incomplete genome sequence is available (13).

The complete genome of *C. fetus* subsp. *venerealis* NCTC 10354^T (LMG 6443^T, ATCC 19438^T, Park X/161/5), the type strain of the subspecies (19), isolated from the vaginal mucus of a heifer inseminated with semen from a bull responsible for

infectious infertility in the United Kingdom (11, 15), is reported.

Sequencing was performed on a FLX system (Roche Diagnostics) with approximately 24-fold coverage. Initial assembly was based on 115,459 reads and used the Newbler Assembler software, generating 30 contigs. Contigs were organized and aligned using the genome sequence of *C. fetus* subsp. *fetus* 82-40 (NC_008599) as the scaffold. Structural annotation was performed by the following predictors: for genes, FgenesB (SoftBerry); for rRNA, RNAmmer (10); for tRNA, tRNAscan-SE (12); and for repetitive DNA, Tandem Repeats Finder (<http://tandem.bu.edu/trf/trf.html>). Functional annotation was accomplished by similarity analysis using BLAST (1) and InterProScan (21), and manual annotation was accomplished with Artemis (18). Identification and confirmation of putative pseudogenes were done by using Consed and manual analysis based on the Phred quality of bases in the frameshift area (9).

The circular genome of *C. fetus* subsp. *venerealis* NCTC 10354^T is composed of 1,874,244 bp with a G+C content of 33.23% and includes 1,905 putative protein-coding genes or open reading frames, 3 rRNA operons, 35 tRNA operons, and 185 pseudogenes. The gene density was 0.917 gene/kb, the average length was 826 bp/gene, and the G+C content of gene sequences was 34.09%. BLAST analysis against all of the plasmid sequences in GenBank showed no evidence of plasmid presence in the genome assembly.

Comparison of the *C. fetus* subsp. *venerealis* NCTC 10354^T genome will provide information on conserved and unique

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genes that could be important for adaptation to its host. Initial genomic comparisons with *C. fetus* subsp. *fetus* 82-40 using BLAST (1) and the Artemis comparison tool (3) showed high levels of sequence conservation and synteny.

Therefore, the complete genome sequence of the *C. fetus* subsp. *venerealis* type strain will be inestimable for improving our understanding of microbial physiology and host-pathogen interactions, which could be useful for the development of new diagnostic methods and vaccines.

Nucleotide sequence accession numbers. The *C. fetus* subsp. *venerealis* type strain NCTC 10354^T Whole Genome Shotgun project has been deposited at DDBJ/EMBL/GenBank under accession number AFGH00000000. The version described in this paper is the first version, AFGH01000000.

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