Complete Genome Sequence of *Campylobacter fetus* subsp. *venerealis* Biovar Intermedius, Isolated from the Prepuce of a Bull

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*Campylobacter fetus* subsp. *venerealis* is the causative agent of bovine genital campylobacteriosis, a sexually transmitted disease distributed worldwide. *Campylobacter fetus* subsp. *venerealis* biovar Intermedius strains differ in their biochemical behavior and are prevalent in some countries. We report the first genome sequence for this biovar, isolated from bull prepuce.


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*Campylobacter fetus* is an important veterinary pathogen. This species is currently divided into two subspecies, *Campylobacter fetus* subsp. *fetus*, causative of abortion in sheep, and *Campylobacter fetus* subsp. *venerealis*, the etiologic agent of bovine genital campylobacteriosis (1), a disease that has spread worldwide and causes economic losses mainly in countries where natural breeding is frequent (2). A distinct group of *C. fetus* strains known as *C. fetus* subsp. *venerealis* biovar Intermedius has also been determined; these strains phenotypically resemble *C. fetus* subsp. *venerealis*, but they react positively to the H2S test (typically positive for *C. fetus* subsp. *fetus*) (3). In recent years, an increase in the prevalence of this biovar has been noticed in some countries (e.g., South Africa) (4). However, the lack of genomic information for these atypical strains has hindered the development of molecular diagnostic tools and the study of their genomic evolution. Here we present the first complete genome sequence for *Campylobacter fetus* subsp. *venerealis* biovar Intermedius INTA 99/541, isolated from the prepuce of a naturally infected bull (5).

Sequencing was performed on an Illumina Hi-Seq 2000 platform and generated 13,953,630 paired-end reads (2 × 100 cycles). The resulting library was first corrected using ALLPATHS-LG (6) and then assembled with Velvet (7) software, producing 111 contigs with an average coverage of 130-fold. The assembly quality of this biovar has been noticed in some countries (e.g., South Africa) (4). However, the lack of genomic information for these atypical strains has hindered the development of molecular diagnostic tools and the study of their genomic evolution. Here we present the first complete genome sequence for *Campylobacter fetus* subsp. *venerealis* biovar Intermedius INTA 99/541, isolated from the prepuce of a naturally infected bull (5).

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REFERENCES


