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GENOME SEQUENCES

Complete Genome Sequence of *Campylobacter fetus* subsp. *venerealis* P4531 from a Rhesus Monkey

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ABSTRACT *Campylobacter fetus* subsp. *venerealis* is associated with animal and human infections. We report the circularized 1.8-Mbp complete genome sequence of a multilocus sequence type 43 (MLST43) *C. fetus* subsp. *venerealis* isolate from a rhesus monkey (*Macaca mulatta*).

Campylobacter fetus subsp. *venerealis*, one of three *C. fetus* subspecies, primarily infects mammals, including humans and livestock. However, the origin and pathogenicity of *C. fetus* subsp. *venerealis* are poorly studied and remain unknown. Recently, a whole-genome-based global phylogenetic study suggested that *C. fetus* lineages were likely transmitted from humans to domesticated livestock (1). *C. fetus* subsp. *venerealis* causes sexually transmitted bovine genital campylobacteriosis, which leads to infertility and abortions worldwide (2, 3).

Rhesus monkey fecal samples, collected from a nonhuman primate colony at a research center, were screened for *Campylobacter* species by culturing on *Campylobacter* selective medium (Remel, San Diego, CA) at 42°C for 4 days under microaerobic conditions. A typical curved Gram-negative rod-shaped isolate was identified as *Campylobacter fetus* subsp. *venerealis* using automated bacterial identification methods, a MALDI Biotyper (Bruker, Billerica, MA), and the microbial identification (MIDI) system (MIDI, Newark, DE) and confirmed by 16S rRNA sequence analysis.

Genomic DNA was isolated using a blood and tissue kit (Qiagen, Redwood City, CA), and the quality and quantity of the DNA were determined using a NanoDrop spectrophotometer (Thermo Fisher Scientific, Waltham, MA) and Qubit fluorometer (Thermo Fisher Scientific). Following the manufacturer's protocols, short-read sequencing was performed using the MiSeq platform (Illumina, San Diego, CA) with a Nextera XT library prep kit and a MiSeq v2 reagent kit in 250-bp paired-end mode. Long-read sequencing was performed on a Nanopore MinION instrument (Oxford Nanopore, Oxford, UK) using a NEBNext kit (New England BioLabs, Ipswich, MA), a ligation sequencing kit (SQK-LAK109) and a FLO-MIN107 flow cell (Oxford Nanopore). Default parameters were used for all software unless otherwise noted. After quality checking and trimming using the genomic file manipulation tools in Galaxy, 392,964 short reads and 39,840 long reads (N_{50}, 17,430 bp) were combined using Unicycler v0.4.8 (default normal bridging mode, rotation) in Galaxy (4, 5). One contiguous hybrid genome, 1,799,726 bp long with a G+C content of 33.06%, was assembled, with 96× depth for the short reads and 21× depth for the long reads, and annotated by the NCBI Prokaryotic Genome Annotation Pipeline (PGAP) v4.11 (6). The annotated *C. fetus* subsp. *venerealis* P4531 genome contained 1,741 coding genes, 26 pseudogenes, 44 tRNAs, 9 small RNAs (sRNAs), and 2 CRISPR arrays. The Mash distance between *C. fetus* subsp. *venerealis* P4531 and *C. fetus* subsp. *venerealis* NCTC 10354 (GenBank accession number NZ_CP043435) is 0.022, which equates to an average nucleotide identity (ANI) of 97.8% as estimated using MinHash (7).

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Data availability. The genome sequence has been deposited in GenBank under the accession number CP051880. The raw reads have been deposited in the Sequence Read Archive (SRA) under the accession numbers SRX11506070 and SRX11506071.

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