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GENOME ANNOUNCEMENT

Draft Genome Sequence of *Treponema* sp. Strain JC4, a Novel Spirochete Isolated from the Bovine Rumen

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Morphologically and biochemically diverse members of the *Treponema* genus are present in the gastrointestinal tract of ruminants, yet very little is understood about their functional importance to this microbiome. Here we describe the annotated draft genome sequence of *Treponema* sp. strain JC4, a novel spirochete isolated from a bovine rumen sample.

The genus *Treponema* is comprised of microaerophilic or anaerobic spiral-shaped bacteria residing within the phylum *Spirochetes*. Members of this genus existing as both pathogens and commensals have been cultivated from a variety of host-associated microbiomes (2, 5). This paper describes the draft genome sequence of *Treponema* sp. strain JC4, isolated as part of a larger project to characterize mechanisms of carbohydrate metabolism in the rumen of cattle from the Australian semiarid tropics. Based on comparison of NAST-aligned 16S rRNA genes, the closest cultured representative to strain JC4 is *Treponema bryantii* RUS-1 (91.4% sequence similarity), a saccharolytic spirochaete also isolated from the bovine rumen (7).

Treponema sp. JC4 was isolated from pooled rumen contents collected from six fistulated *Bos indicus* steers consuming Rhodes grass (*Chloris gayana*). Samples were enriched in liquid anaerobic medium 1 (1) supplemented with 10% (wt/vol) powdered Rhodes grass. Glycerol stocks from the initial enrichments were plated on medium 10 agar (4) containing starch, cellobiose, and glucose. Genomic DNA from an anexic culture was extracted using the NML method (6) and sequenced from a shotgun library using the 454 Life Sciences GS FLX Titanium system, generating 3,033,760 bp of sequence data at 15× coverage. Sequence reads were assembled into 147 contigs of >200 bp using Newbler version 2.6. The contig N50 was approximately 71.9 kb and the largest assembled contig was 325.5 kb. The DNA sequence was annotated using the Integrated Microbial Genomes Expert Review (IMG ER) system (3). Carbohydrate active enzymes were further analyzed using dbCAN (8) to identify functional motifs.

The G+C content of the draft genome is 40% and contains 2,614 complete open reading frames (ORFs) (2,570 protein coding genes and 44 structural RNAs). Consistent with the function of many rumen bacteria in coordinating carbohydrate metabolism, we identified an assortment of cellulases, endohemicellulases, and debranching enzymes (glycoside hydrolase [GH] families 5, 10, 51, 53, and 64), oligosaccharide-degrading enzymes (GH families 1, 2, 3, 35, 36, 37, 42, 43, 65, and 94), in addition to members of GH families 13, 16, 18, 23, 46, 57, 73, 77, 109, and 114. Furthermore, we identified a suite of carbohydrate esterases (CE families 1, 2, 4, 7, and 12) responsible for deacteylation of xylans and xylo-oligosaccharides. Prediction of such a wide variety of carbohydrate-active enzymes suggests that *Treponema* sp. JC4 has a broader substrate range than *T. bryantii*, which is capable only of fermenting a restricted subset of the soluble sugars released from cellulose by the action of cellulolytic bacteria (7). Additional sequencing and comparative analysis of genomes from diverse treponemes will provide a greater understanding of their contribution to the function of gastrointestinal microbiomes.

Nucleotide sequence accession numbers. This Whole Genome Shotgun project has been deposited at DDBJ/EMBL/GenBank under accession no. AJGU00000000. The version described here is version 1, AJGU01000000. The near-complete 16S rRNA sequence (derived using Sanger dideoxy sequencing of a PCR product) has been deposited in DDBJ/EMBL/GenBank under accession no. JQ783348. Genome project data are available at GenBank under Genome Project identifier 78730.

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