

Draft Genome Sequence of *Clostridium straminisolvens* Strain JCM 21531^T, Isolated from a Cellulose-Degrading Bacterial Community

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Here, we report the draft genome sequence of a fibrolytic bacterium, *Clostridium straminisolvens* JCM 21531^T, isolated from a cellulose-degrading bacterial community. The genome information of this strain will be useful for studies on the degradation enzymes and functional interactions with other members in the community.

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Lignocellulosic biomass, which is a mixture of cellulose, hemicellulose, and lignin, is the most abundant biopolymer in the Earth. In nature, lignocellulosic biomass is degraded by a set of synergistically acting enzymes of various microorganisms. Strain CSK1^T (deposited as IAM 15070 and now available from Japan Collection of Microorganisms as JCM 21531^T) was isolated from a cellulose-degrading bacterial community and described as the type strain of a novel species, *Clostridium straminisolvens* (1, 2). The 16S rRNA gene sequence analysis indicated that *C. straminisolvens* is related to anaerobic cellulolytic bacteria *Clostridium thermocellum* and *Clostridium aldrichii*. *C. straminisolvens* JCM 21531^T grows optimally at 50 to 55°C and shows aerotolerance for growth and an ability to ferment cellulose and cellobiose (1). The cellulose-degrading efficiency in pure culture of *C. straminisolvens* JCM 21531^T is remarkably lower than that in coculture with aerobic noncellulolytic bacteria, suggesting their synergistic relationships (3, 4).

The genome of *C. straminisolvens* JCM 21531^T was sequenced using the Ion Torrent PGM system. The 367,174 sequence reads were assembled using Newbler version 2.8 (Roche) into 195 contigs, with an N₅₀ length of 48,174 bp. This assembly resulted in the draft genome sequence of 3,907,117 bp, with 18.7× redundancy and a G+C content of 38.3%. A total of 4,383 protein-coding genes and 53 RNA-coding sequences were identified using the RAST server (5) and with the manual inspections detailed below.

RAST annotations and the following CAZy database analyses (6) revealed that *C. straminisolvens* JCM 21531^T has various genes encoding endoglucanases classified in the glycoside hydrolase 5 (GH5), GH8, GH9, GH48, GH74, and GH124 families, genes encoding GH5 and GH9 of cellobiohydrolases, which degrade crystalline cellulose, and genes encoding β-glucosidases of GH1 and GH3. In addition, *C. straminisolvens* JCM 21531^T also has several genes encoding xylanases of GH10. The presence of genes encoding nitrogenase and enzymes for the reductive acetyl-coenzyme A (CoA) pathway indicated the potentials of this strain of a di-

azotrophic and homoacetogenic nature, respectively. Detailed analyses of the genome of this strain, including comparisons with published genome sequences of *C. thermocellum* strains (7–10), will facilitate studies on the nature of cellulose degradation of *C. straminisolvens* JCM 21531^T and its synergistic relationships with other bacteria in the cellulose-degrading community.

Nucleotide sequence accession numbers. The genome sequence of *C. straminisolvens* JCM 21531^T has been deposited in the DDBJ/EMBL/GenBank database under the accession no. BAVR01000001 to BAVR01000195.

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