Draft Genome Sequence of *Dysgonomonas macrotermitis* Strain JCM 19375\(^T\), Isolated from the Gut of a Termite

Xinxin Sun, Yingjie Yang, Ning Zhang, Yulong Shen, Jinfeng Ni
State Key Laboratory of Microbial Technology, Shandong University, Jinan, Shandong, China

Here, we report the draft genome sequence of *Dysgonomonas macrotermitis* strain JCM 19375\(^T\), which was isolated from the hindgut of a fungus-growing termite, *Macrotermes barneyi*. The genome information reveals the role of this strain in lignocellulose degradation and adaptation to the gut environment.

The termite contains various microorganisms that symbiotically exist in the hindgut. Metagenomic analysis has revealed a large diverse set of glycoside hydrolase (GH) genes present in the hindgut of a higher termite, which may play an important role in lignocellulose degradation (1). The genus *Dysgonomonas* comprises seven species with validly published names: *D. gadei*, *D. capnocytophagoides*, *D. mossii*, *D. hofstadii*, *D. oryzarvi*, *D. termitidis*, and *D. macrotermitis* (2–8). The first four species are all from humans, and the latter three are from microbial fuel cell and termite guts. *D. macrotermitis*, a novel species of the genus *Dysgonomonas*, is the second most dominant bacterium in the hindgut of a fungus-growing termite, *Macrotermes barneyi* (8). To investigate the symbiotic roles of the strain, its genome sequence was analyzed.

The genome of the strain was sequenced using Illumina MiSeq. A total of 2,809,508 reads were assembled into 78 contigs, with an average length of 149,547 bp, and the largest contig length was 790,807 bp. This assembly resulted in a draft genome sequence of 4,655,756 bp and a G+C content of 38.54%. Together, they contain 3,870 coding sequences (CDSs), 44 tRNA genes, and 3 complete rRNA operons.

We assessed the potential role of *D. macrotermitis* in lignocellulose digestion by screening the CDSs against the CAZy database (9). Preliminary analyses revealed the presence of genes for cellulolytic and hemicellulolytic enzymes in the genome sequence of *D. macrotermitis*. There were various genes encoding glucosidase of glycoside hydrolase 2 (GH2), GH3, and GH97; genes encoding glucanase of GH5, -16, and -26; genes encoding xylanases of the glycoside hydrolase 2 (GH2), GH3, and GH97; genes encoding *N*.-galactosidase of GH2, -27, -35, -36, -42, -43, -53, and -97. In addition, the genome had several genes coding *α*.- and *β*.-glucuronidase, arabinofuranosidase, arabinosidase, and amylase. These results suggest the potential role of the strain in decomposing lignocellulose and providing nutrition to the host termite in the hindguts of fungus-growing termites.

Nucleotide sequence accession numbers. This whole-genome shotgun project has been deposited in DDBJ under the accession numbers BBXL01000001 to BBXL01000078.

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