

Genome Sequence of *Thermoactinomyces daqus* H-18, a Novel Thermophilic Species Isolated from High-Temperature Daqu

Su Yao,^{a,b} Youqiang Xu,^a Chunhui Xin,^b Ling Xu,^b Yang Liu,^a Hui Li,^a Jinxia Li,^a Jiwen Zhao,^b Chi Cheng^a

China National Research Institute of Food and Fermentation Industries, Beijing, China^a; Shandong Bandaojing Lt., Co., Shandong, China^b

S.Y. and Y.X. contributed equally to this work.

***Thermoactinomyces daqus* H-18 is a new species of *Thermoactinomyces* isolated from high-temperature Daqu used in the fermentation of Bandongjing sesame-flavor liquor. Its genome was sequenced and assembled (3.44 Mb). The coding sequences (CDSs) that correlated to high-temperature tolerance were annotated. The metabolic pathways for the compounds responsible for flavor were also found.**

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Address correspondence to Jiwen Zhao, 1460369765@qq.com, or Chi Cheng, cheng100027@163.com.

Daqu, a primary microbial source and traditional fermentation starter, has been used to produce certain foods, such as vinegar and Chinese liquor with an attractive flavor for thousands of years (1–3). The production of Bandongjing sesame-flavor liquor occurs through mixed-microbial fermentation, while the high-temperature Daqu provides the microorganisms in this process (4). The high-temperature Daqu plays an important role in the quality of liquor (4). In previous studies, we isolated a series of bacterial strains from the high-temperature Daqu of Bandongjing, Shandong province, China (our unpublished data), and one of the preponderant strains, designated *Thermoactinomyces daqus* H-18, is a novel species of the genus *Thermoactinomyces* (5). The analysis of the mechanism for high-temperature tolerance and the metabolic pathways of the flavor chemicals for strain H-18, combined with the studies of other strains isolated, would contribute to the understanding of the functions of high-temperature Daqu for the fermentation of Bandongjing sesame-flavor liquor. Therefore, the genome of strain H-18 was sequenced.

We announce here the draft genome of strain H-18. The genome sequence was determined by Illumina HiSeq 2000 (6), and a total of 7,513,692 reads for shotgun sequencing and 14,633,180 reads for paired-end sequencing were produced. These reads were assembled using the CLC Genomics Workbench 5.0.1 system (CLC bio, Aarhus, Denmark) into 86 contigs (>500 bp) with a length of 3,441,572 bp and a G+C content of 48.8%. The genome sequence was annotated by the RAST server (7). tRNAs and rRNAs were analyzed by tRNAscan-SE version 1.23 (8) and RNAmmer 1.2 (9), respectively.

The genome sequence of strain H-18 contains 4,024 predicted protein-coding sequences (CDSs). Fifty-eight tRNAs and two rRNAs were identified. The CDSs for DnaK (two), DnaJ (one), and GrpE (two) were annotated, which are chaperones capable of repairing heat-induced protein damage (10). Another six CDSs for heat shock proteins were annotated, which are also responsible for high-temperature tolerance (11). The complete metabolic pathways were annotated for the production of acetate, acetalde-

hyde, propanoate, and butanoate, which contribute to the flavor of Bandongjing liquor. We also annotated 53 CDSs for peptidase and seven CDSs for amino acid dehydrogenase, which can degrade proteins and peptides into amino acids and produce ammonium from amino acids, respectively. Ammonium was found to be the precursor of tetramethylpyrazine (12). Tetramethylpyrazine was reported to have nutty, roasty, and toasty tonalities (13). The genome sequence and annotation of *T. daqus* H-18 might be helpful for improving the understanding of its tolerance to high temperature as well as contributing to the production of Bandongjing sesame-flavor liquor during the fermentation processes.

Nucleotide sequence accession numbers. This whole-genome shotgun project has been deposited at DDBJ/EMBL/GenBank under the accession no. [JPST000000000](https://www.ncbi.nlm.nih.gov/nuccore/JPST000000000). The version described in this paper is version JPST01000000.

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