




Draft Genome Sequence of *Saccharomyces cerevisiae* DJJ01, Isolated from Dojoji Temple in Gobo, Wakayama, Japan

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ABSTRACT *Saccharomyces cerevisiae* strain DJJ01 was isolated from Dojoji Temple (Gobo, Wakayama, Japan) for development of local breweries. Here, we report the draft genome sequence of this strain to facilitate comparative genomic studies of yeast strains used for Japanese sake brewing.

Saccharomyces cerevisiae is used in the fermentation of food (such as Japanese sake) and the production of useful materials (1–3). For example, Kyokai yeast no. 7 (strain K7) is the most extensively used industrial sake yeast strain and is employed in numerous genetic and biochemical studies as a model sake yeast and as a parent strain for breeding (4–8). In this project, *S. cerevisiae* DJJ01 was isolated from sakura flowers in the precincts of the Dojoji Temple after inoculation to koji medium. Cultivation was carried out at 20°C for 14 days. *S. cerevisiae* smooth cream colonies could be distinguished morphologically from bacteria and fungi on yeast extract-peptone-dextrose (YPD) plates. PCR results using internal transcribed spacer (ITS) primers (ITS1F, GTAACAAGGTYTCCGT; ITS1R, CGTTCTTCATCGATG) showed good agreement between the amplified sequence of strain DJJ01 and *S. cerevisiae*. Here, we report the draft genome sequence of *S. cerevisiae* DJJ01.

Genomic DNA from strain DJJ01 was purified using the ISOIL for bead beating kit (Nippon Gene, Japan) after culturing at 30°C for 24 h in YPD liquid medium. The genomic DNA was further purified using AMPure beads (Beckman Coulter, Inc., USA). Sequencing libraries were prepared using a Nextera XT DNA library preparation kit (Illumina, USA). The library was subjected to short-read sequencing using the MiSeq platform (Illumina) with 250-bp paired-end reads. Low-quality reads were trimmed, and *de novo* assembly was conducted using SPAdes v.3.9.1 (9). Protein-coding genes were predicted using the Microbial Genome Annotation Pipeline v.2.21 (10), local BLAST, and Geneious v.2020.1.2 (Biomatters, New Zealand) (10). Default parameters were used except where otherwise noted.

The assembled genome size was 8,313,543 bp, with 131 contigs (with the size of the largest contig being 365,610 bp), a GC content of 38.3%, an N_{50} value of 63,462 bp, and sequence depth of 65.4× from 8,790,476 paired-end Illumina short reads. In total, 262 tRNAs, 86 noncoding regions, 167 assembly gaps, 53 miscellaneous features, and 5,495 protein-coding sequences were annotated.

Genome mapping using short reads from strain DJJ01 against reference sequences of 16 chromosomes of strains K7 (GenBank accession number [AP012028](#)) and S288C (GenBank accession number [KP263414](#)) was performed to confirm the genome-wide similarity between DJJ01, K7, and S288C. The differences in the nucleotide sequence of the coding

Editor Vincent Bruno, University of Maryland School of Medicine

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The authors declare no conflict of interest.

Received 9 February 2022

Accepted 23 June 2022

Published 11 July 2022

sequence region of strain S288C were 3 times larger than those of strain K7. This hints at a potential of this strain for sake production that can be enhanced using molecular breeding technology, eventually expanding the diversity of sake production in the future, and the data presented here may help in brewing Japanese sake to enhance its richness and flavor.

Data availability. The draft genome sequence of *Saccharomyces cerevisiae* strain DJJ01 was deposited under BioProject accession number [PRJNA785722](https://www.ncbi.nlm.nih.gov/bioproject/PRJNA785722) and BioSample accession number [SAMN23575053](https://www.ncbi.nlm.nih.gov/biosample/SAMN23575053). The sequence of the ITS1 region of strain DJJ01 was deposited in DDBJ/GenBank under accession number [LC405963](https://www.ncbi.nlm.nih.gov/nuccore/LC405963), and genome assembly information was deposited under GenBank accession number [JAMCCV000000000](https://www.ncbi.nlm.nih.gov/nuccore/JAMCCV000000000).

ACKNOWLEDGMENTS

We acknowledge the help of the Industrial Technology Center of Wakayama Prefecture and Dojoji Temple.

This research was funded by the Nate Brewing Co.

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