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Draft Genome Sequence of *Saccharomycopsis fermentans* CBS 7830, a Predacious Yeast Belonging to the *Saccharomycetales*

Ana Hesselbart,[a] Klara Junker,[a] Jürgen Wendland[a,b]

[a]Carlsberg Research Laboratory, Yeast & Fermentation, Copenhagen, Denmark
[b]Vrije Universiteit Brussel, Functional Yeast Genomics, Brussels, Belgium

ABSTRACT *Saccharomycopsis fermentans* is an ascomycetous necrotrophic fungal pathogen that penetrates and kills fungal prey cells via targeted penetration pegs. Here, we report the draft genome sequence and scaffold assembly of this mycoparasite.

Saccharomycopsis is the sole genus of the family *Saccharomycopsidaceae* (1). One member of this genus, the starch-degrading yeast *S. fibuligera*, is known for its contributions to rice wine fermentation (2). The role of *S. fibuligera* as an enzyme producer also spurred interest in using this yeast for bioethanol production (3). Recently, whole-genome sequencing studies revealed that the genome of *S. fibuligera* encompasses seven chromosomes with about 18 Mb (4). Other members of the genus *Saccharomycopsis*, including *S. fermentans*, have been described as predacious yeasts that generate penetration pegs with which they kill other fungal cells utilizing prey cell content (5). *S. fermentans* (formerly classified as *Arthroascus fermentans*) was isolated in 1994 from the soil of a Taiwanese orchard and was shown to ferment glucose (references 6 and 7 and references therein). *Saccharomycopsis* species are natural auxotrophs for organic sulfur (8). In *S. fibuligera*, the absence of genes involved in sulfate assimilation has been observed (4).

The usefulness of non-*S. cerevisiae* yeasts in fermentation and biotechnology depends on detailed characterization of the microbial genomes. Thus, additional draft genome sequences are required to not only provide species-specific markers for identification but also initiate pathway analyses and enable targeted strain improvements. Furthermore, a deeper understanding of the molecular biology of *Saccharomycopsis* species—specifically of their predacious behavior—is warranted. To this end, we recently established the draft genome of another predacious *Saccharomycopsis* yeast, *S. fodiens* strain CBS 8332 (9). We confirmed that, just like *S. fibuligera*, *S. fodiens* also lacks the genes in the sulfate assimilation pathway.

Here, we report the draft genome sequence of *S. fermentans*, obtained using Illumina MiSeq paired-end read sequencing. *S. fermentans* was grown in complex medium (1% [wt/vol] yeast extract-peptone-dextrose [YPD], 2% [wt/vol] peptone, and 2% [wt/vol] dextrose) at 30°C with constant shaking. DNA extraction and sequencing were performed at LGC Genomics (Berlin, Germany). Two paired-end libraries were sequenced, producing 10,363,062 raw reads. These were quality trimmed, resulting in 4,807,796 high-quality reads with the short fragment library and 4,521,208 high-quality reads with an 8-kb mate pair library. These were assembled using Bowtie2 version 2.1.0. The initial assembly generated 160 contigs with a total content of 14,266,439 bp and a contig N_{50} of 265,725 bp. The contigs were then further assembled into 33 scaffolds harboring 14,461,413 bp, with an N_{50} of 2,146,288 bp. The longest scaffold contains 3,513,907 bp, with 13 scaffolds larger than 20 kb. The overall GC content is 35.1%.

For a draft annotation of the nuclear genome, open reading frames (ORFs) with a size of >300 nt were predicted and compared using blastx to translated proteins in the

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Address correspondence to Jürgen Wendland, jurgen.wendland@vub.be.

Saccharomyces cerevisiae genome. In all, 5,917 nonoverlapping ORFs were detected in *S. fermentans*, and of those, 3,882 genes produced hits with *S. cerevisiae*. An additional blast search against other organisms in the nonredundant database at NCBI (https://blast.ncbi.nlm.nih.gov/Blast.cgi) generated a further 263 hits (E values, $<10^{-10}$). We could also verify the absence of genes required for sulfate assimilation in *S. fermentans*. Additionally, we identified 149 tRNA genes in the *S. fermentans* genome using tRNAscan-SE (10).

Accession number(s). This whole-genome shotgun project has been deposited in DDBJ/ENA/GenBank under the accession no. JNFW00000000. The version described in this paper is the first version, JNFW01000000.

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