Draft Genome Sequence of an Obligate Psychrophilic Yeast, *Candida psychrophila* NRRL Y-17665<sup>T</sup>

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**ABSTRACT** *Candida psychrophila* is an obligate psychrophilic yeast classified into the family *Debaryomycetaceae* (*Saccharomycotina*). Here, we report the draft genome sequence of the type strain, NRRL Y-17665. The genome sequence is 11.2 Mb long and codes for 5,827 predicted proteins.

The yeast *Candida psychrophila* was originally isolated from penguin dung at Cape Royds, Ross Island (Antarctica) (1). Later studies showed its affiliation with the genus *Debaryomyces* belonging to the CTG clade of *Saccharomycotina* (2, 3). *C. psychrophila* is an obligate aerobe and psychrophile that does not grow at temperatures above 17°C (4). Its adaptation to cold environments is mediated by lipidome enrichment for unsaturated fatty acyl moieties (5, 6) and stress proteins, which are induced at a mild heat shock (25°C) (7).

In this work, the genome sequence of *C. psychrophila* was determined using Illumina HiSeq2500 technology. Genomic DNA was isolated from a clonal culture of the type strain grown overnight in YPD medium (1% [wt/vol] yeast extract, 2% [wt/vol] peptone, 2% [wt/vol] glucose) at 7°C with constant shaking. The DNA was extracted essentially as described previously (8) and purified using DNeasy minispin columns (Qiagen). The sequencing of a paired-end (2 × 101 nucleotides) TruSeq PCR-free DNA library was performed by Macrogen (South Korea). In total, 51,320,288 reads were generated. The low-quality ends of reads were trimmed by Trimmomatic (9), and the assembly was done by SPAdes version 3.9.1 (10) with K = 67. The mitochondrial genome and ribosomal DNA (rDNA) repeat were manually adjusted in Geneious version 5.6.6 (11).

Contigs with coverage less than 10× or length less than 200 bp were discarded. The assembly was further polished with Pilon (12). The resulting assembly has a length of 11,241,723 bp in 193 contigs; the *N*<sub>50</sub> is 487,949 bp, and the longest contig has a length of 1,179,685 bp. The GC content is 36.74%. Ten contigs terminate on one side with an array of telomeric repeats (TTATGAGGTGTCTGGATG). The sequence complementary to this motif was also found in the template domain of putative telomerase RNA (TER1).

To annotate the nuclear genome, protein-coding genes were predicted using ExonHunter (13) (with custom parameter training) and Augustus (14) (with model for *Debaryomyces hansenii*). ExonHunter reported 5,827 protein-coding genes, and Augustus 5,502. According to tRNAscan-SE version 1.3 (15), the genome contains 192 nuclear tRNAs, including 2 pseudogenes. The genome statistics are comparable to those of *D. hansenii*, which has a genome size of 12 Mb, with 6,284 predicted proteins in the UniProt proteome and 200 tRNAs. The BUSCO pipeline (16), comparing the ExonHunter gene set to 1,711 conserved single-copy orthologs in the order *Saccharomycetales*, reported 3 missing and 33 fragmented genes. Some of these are found in the Augustus...
predictions; combined ExonHunter and Augustus gene predictions are 98.9% complete using the BUSCO approach.

The genome sequence of C. psychrophila together with the genomes of D. hansenii (17) and Debaryomyces fabryi (18) provide a resource for comparative and functional studies, which may elucidate strategies for cold adaptation, including metabolic alterations, membrane composition, and stress responses. Moreover, the genome sequence would allow identification of cold-active enzymes suitable for biotechnology (19).

**Accession number(s).** This whole-genome shotgun sequencing project has been deposited in ENA/DDBJ/GenBank under the accession no. FYBW00000000. The version described in this article is the first version, FYBW01000000.

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