Draft Genome Assemblies of Xylose-Utilizing Candida tropicalis and Candida boidinii with Potential Application in Biochemical and Biofuel Production

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ABSTRACT Non-albicans Candida species are growing in prominence in industrial biotechnology due to their ability to utilize hemicellulose. Here, we present the draft genome sequences of an inhibitor-tolerant Candida tropicalis strain (Y6604) and Candida boidinii NCAIM Y01308T.

Manufacturing higher-value commodities from hemicellulosic sugars (e.g., xylose) is crucial for environmental and bioeconomic sustainability of lignocellulosic biorefineries. Candida tropicalis has been widely investigated in the bioconversion of xylose into the higher-value sweetener xylitol and/or into bioethanol (1, 2), while the methylotroph Candida boidinii is well established for heterologous gene expression and enzyme/biochemical production (3, 4). In this study, we report the draft genome sequences of an environmentally derived inhibitor-tolerant C. tropicalis isolate (Y6604) and C. boidinii NCAIM Y01308T (NCAIM, Budapest, Hungary). Strain Y6604 has high tolerance to lignocellulose-derived inhibitors (up to 3 g/liter furfural and 4 g/liter 5-hydroxymethylfurfural), and metabolically engineered variants have improved xylose-to-xylitol bioconversions in lignocellulosic hydrolysates (data not shown).

Genomic DNA (1 μg) (YeaStar; Zymo Research, USA) was extracted, and Illumina TruSeq libraries were size selected with AMPure beads for an average insert size of ~700 bp. Prior to sequencing on an Illumina HiSeq 2500 platform, paired-end reads were produced for both species, with additional mate pair reads for C. boidinii NCAIM Y01308T. Overlapping paired-end sequence reads were merged using FLASH (5). The quality control suite FastQC (http://www.bioinformatics.babraham.ac.uk/projects/fastqc/) identified some initial 5 base bias, low-quality 3 bases, and Illumina adaptors, which were removed using Trimmomatic (6). NxTrim (7) was used for adaptor trimming of raw C. boidinii mate pair sequences. All sequences were error corrected and assembled using SOAPdenovo (8). Following genome masking, coding genes predicted by AUGUSTUS (9) and trained for C. tropicalis were submitted to a BLASTp search. Candidate hits (E value, ≤1 × 10^-10) were assigned names, Gene Ontology (GO) and Kyoto Encyclopaedia of Genes and Genomes (KEGG) annotations using Blast2GO (10).

A total of 51,470,621 paired-end reads for Y6604 gave an assembly length of 14,318,547 bp, with 296× coverage of 563 scaffolds (N50, 51,027), and 10,177 contigs. Scaffolds with more than 50% “N” calls and <300 coding bases were removed, giving 533 scaffolds and 688 contigs. The combined C. boidinii assembly from both paired-end and mate pair reads had high coverage depths (259× and 523×, respectively) and a total length of 19,266,739 bases. Scaffolds with <1,000 coding bases and/or more than 50% N calls were removed, giving 79 scaffolds (N50 606,681) and 61 contigs. The overall GC content in Y6604 was 34%, while that in C. boidinii was lower (31%). De novo annotation with AUGUSTUS yielded 6,772 proteins in Y6604 (8,270 exons and 1,498...
introns) and 6,067 proteins (6,951 exons and 884 introns) in C. boidinii NCAIM Y01308T. Reciprocal best BLAST hits (maximum E value, $1 \times 10^{-10}$) for Y6604 proteins compared with the 6,254 proteins in the reference C. tropicalis (strain MYA-3404) assembly (11) identified 5,487 matching proteins, with 1,285 and 767 proteins unique to Y6604 and MYA-3404, respectively. A BUSCO (v3.0.1) (11) comparison between the 1,711 profiles within the order Saccharomycetales and the proteins predicted by AUGUSTUS suggested that the strain Y6604 and C. boidinii NCAIM Y01308T gene sets were largely complete, with only 6% and 7% (96 and 112 genes, respectively) of the conserved orthologs, respectively, deemed missing.

**Accession number(s).** The C. tropicalis strain Y6604 and C. boidinii NCAIM Y01308T whole-genome shotgun projects have been deposited in DDBJ/ENA/GenBank under the accession numbers PKKZ00000000 and PKKY00000000, respectively. The versions described in this paper are the first versions.

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**REFERENCES**