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Genome Sequence of the Amphotericin B-Resistant *Candida duobushaemulonii* Strain B09383

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ABSTRACT *Candida duobushaemulonii* is a drug-resistant yeast that can cause invasive candidiasis. Here, we report the first genome sequence of *C. duobushaemulonii*, isolate B09383, generated using PacBio sequencing technology. The estimated genome size was 12.5 Mb with a GC content of 46.84%.

First described in 2012, *Candida duobushaemulonii* has been classified as part of the *C. haemulonii* complex that also comprises *C. haemulonii* and *C. haemulonii* var. *vulnera* (1). The yeast has been linked to deep cutaneous infections (2), recurrent vulvovaginal candidiasis (3), and candidemia (4). Additionally, antifungal susceptibility testing has shown that *C. duobushaemulonii* is often resistant to amphotericin B and fluconazole (4, 5). Species identification methods based on biochemical profiles such as the Vitek 2 automated system are unable to distinguish species within the *C. haemulonii* complex and other closely related species such as *C. auris*. Thus, genetic methods including whole-genome sequencing are becoming increasingly important in the proper identification of *C. duobushaemulonii*. In response, we have generated the first genome sequence of *C. duobushaemulonii* from the drug-resistant isolate B09383.

Long fragments of genomic DNA were prepared using a nonenzymatic method, with the MasterPure yeast DNA purification kit (Epicenter, Madison, WI, USA). Single-molecule real-time (SMRT) sequencing was done at the Genome Sequencing Laboratory (CDC, Atlanta, GA, USA) using the PacBio RS II SMRT DNA sequencing system (Pacific Biosciences, Menlo Park, CA, USA). Specifically, 20-kb libraries were generated with the SMRTbell template prep kit 1.0 (Pacific Biosciences). Libraries were bound to polymerase using the DNA/polymerase binding kit P6 v2 (Pacific Biosciences), loaded on two SMRT cells (Pacific Biosciences), and sequenced with C4 v2 chemistry (Pacific Biosciences) for 360-minute movies.

Sequence reads were *de novo* assembled using Canu v1.6 (6). The resultant contigs were checked for further joins and circularity using Circlator v1.5 (7). Contigs were polished using Quiver, part of SMRT analysis suite v2.3 (Pacific Biosciences) (8), and the sequence order was verified using restriction enzyme AflII whole-genome mapping (OpGen, Gaithersburg, MA). Seven contigs ranging from 787,164 bp to 3,440,864 bp and one mitochondrial chromosome of 22,443 bp were identified.

Accession number(s). The whole-genome sequencing project for isolate B09383 has been deposited in DDJ/ENA/GenBank under the accession number PKFP00000000. The version described in this paper is the first version.

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