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Genome Sequence of a Multidrug-Resistant *Candida haemulonii* Isolate from a Patient with Chronic Leg Ulcers in Israel

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ABSTRACT *Candida haemulonii* is an emerging multidrug-resistant yeast that can cause invasive candidiasis. Here, we report the first genome sequence of *C. haemulonii* (isolate B11899) generated using PacBio sequencing technology. The estimated genome size was 13.3 Mb, with a GC content of 45.19%.

Since its first isolation from a clinical specimen in 1984 (1), *Candida haemulonii* (*Candida haemulonis*) has increasingly been linked to invasive candidiasis infections, including candidemia (2–4). With high MICs to both amphotericin B and fluconazole, *C. haemulonii* is often resistant to two major classes of antifungal drugs (5, 6). Its close relative, *C. auris*, has emerged in health care settings globally and, notably, is often misidentified as *C. haemulonii* by phenotypic methods (7). A recent outbreak (May 2014 to May 2015) of both *C. haemulonii* and *C. auris* infections was reported in multiple units within a tertiary-level hospital in Tel Aviv, Israel (8). Investigation of the outbreak revealed that the *C. haemulonii* isolates were recovered from chronic leg ulcers of patients, while the *C. auris* isolates were from patients with bloodstream infection. These reports and plans for future studies prompted us to generate the first genome sequence of *C. haemulonii* from the multidrug-resistant isolate B11899.

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 version 1.0 (Pacific Biosciences). Libraries were bound to polymerase using the DNA/polymerase binding kit P6v2 (Pacific Biosciences), loaded on two SMRTcells (Pacific Biosciences), and sequenced with C4-V2 chemistry (Pacific Biosciences) for 360-min movies.

Sequence reads were *de novo* assembled using Canu version 1.6 (9). The resultant contigs were checked for further joins and circularity using Circlator version 1.5 (10). Contigs were polished using Quiver, part of the SMRT Analysis suite version 2.3 (Pacific Biosciences) (11), and the sequence order was verified using the restriction enzyme AflII for whole-genome mapping (OpGen, Gaithersburg, MD, USA). Eleven contigs, ranging from 96,418 bp to 2,075,488 bp, and one mitochondrial chromosome of 39,519 bp were identified.

Accession number(s). The whole-genome sequencing project for strain B11899 has been deposited in DDBJ/ENA/GenBank under the accession number PKFO00000000. The version described in this paper is the first version.

Received 14 February 2018 **Accepted** 28 February 2018 **Published** 12 April 2018

Citation Chow NA, Gade L, Batra D, Rowe LA, Jueng P, Ben-Ami R, Loparev VN, Litvintseva AP. 2018. Genome sequence of a multidrug-resistant *Candida haemulonii* isolate from a patient with chronic leg ulcers in Israel. Genome Announc 6:e00176-18. https://doi.org/10.1128/genomeA.00176-18.

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