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Title
Draft genome sequence of Microdochium bolleyi, a dark septate fungal endophyte of beach grass

Permalink
https://escholarship.org/uc/item/8b98t4kz

Journal
Genome Announcements, 4(2)

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Publication Date
2016

DOI
10.1128/genomeA.00270-16

Peer reviewed
Microdochium bolleyi (syn.: Idrilla bolleyi) is a fungus commonly found growing endophytically within plant roots, particularly those of grasses (1). It is characterized as a dark septate endophyte due to its melanized cell walls and intra- and intercellular growth within the roots of healthy plants (2). In culture, M. bolleyi produces one-celled, crescent-shaped conidia (3). Its hyphae are dark brown and may release an orange pigment (3). M. bolleyi frequently associates with native and invasive beach grasses on coastal dunes of the U.S. Pacific Northwest (4). These dunes present harsh environments for plant and fungal growth due to high winds and salt spray and low soil moisture and nutrients (5, 6), making them important ecosystems for understanding fungal diversity. We sequenced the genome of a strain of M. bolleyi (J235TASD1), isolated from surface-sterilized roots of Ammophila breviligulata in Pacific City, Oregon, USA. To our knowledge, only one previous study has sequenced the genome of M. bolleyi (7), and ours is the first publicly available genome.

We identified J235TASD1 as M. bolleyi based on high similarity of the ITS region to sequences of references strains CBS137.64 (GenBank accession no. AM502264) and CBS172.63 (AM502265) (8), and to sequences (AJ279454, AJ279475) identical to that from a culture identified using morphological characteristics (9). Prior to DNA and RNA extractions, the fungus was grown in 2% malt extract liquid media at room temperature. We extracted DNA using the QiaGen DNEasy plant minikit (Valencia, CA, USA). RNA was extracted using a Trizol and chloroform protocol, and purified using the Ambion PureLink RNA minikit (Austin, TX, USA). Sequencing and annotation followed the U.S. Department of Energy Joint Genome Institute (JGI) pipeline (10). Genomic 2×150–bp reads from a single 300–bp insert library were obtained using Illumina HiSeq2500 and initially assembled using Velvet (11). The resulting assembly was used to simulate long 3-kb mate pairs that were then assembled together with the original reads using AllPathsLG version R49403 (12) and annotated using the JGI Annotation pipeline (10). The transcriptome was de novo assembled using Rnnotator version 3.4.0 (13).

The assembled genome was 38.84 Mbp and consisted of 215 contigs and 173 scaffolds. Sequencing read depth coverage was 136.2×. The assembled transcriptome consisted of 18,493 consensus contigs, of which 99% mapped to the genome assembly to confirm its completeness. Annotation resulted in 13,177 gene models. Median gene length was 1,516 bp and median protein length was 377 amino acids. The estimated haploid genome size was 40.14 Mbp with an estimated genome repeat of 4.0% (25-bp k-mer). The J235TASD1 genome is larger than the M. bolleyi genome reported by Jewell (7) (38.16-Mbp genome, 13,047 predicted genes, 8,060 annotated genes). The genome of our M. bolleyi strain may help illuminate how fungi tolerate stressful environmental conditions.

**Nucleotide sequence accession numbers.** The genome sequences and annotations are available from the JGI fungal genome portal MycoCosm (10). This whole-genome shotgun project has been deposited at DDBJ/EMBL/GenBank under the accession number LSSP00000000. The version described in this paper is the first version, LSSP01000000.

**ACKNOWLEDGMENTS**

This fungus was sequenced as part of the 1000 Fungal Genomes Project at the U.S. Department of Energy Joint Genome Institute, a DOE Office of Science User Facility, supported by the Office of Science of the U.S. Department of Energy under contract no. DE-AC02-05CH11231. Please contact G.M. for strain and DNA requests.

**FUNDING INFORMATION**

This work, including the efforts of Aaron S. David, was funded by the National Science Foundation Graduate Research Fellowship (NSF 00039202). This work, including the efforts of Georgiana May, was funded by National Science Foundation Dimensions of Biodiversity (NSF 1045608). The work by the U.S. Department of Energy Joint Genome Institute, a DOE Office of Science User Facility, was supported by the Office of Science of the U.S. Department of Energy under contract no. DE-AC02-05CH11231.
REFERENCES