

UC Berkeley

UC Berkeley Previously Published Works

Title

Draft Genome Sequence of *Microdochium bolleyi*, a Dark Septate Fungal Endophyte of Beach Grass

Permalink

<https://escholarship.org/uc/item/8b98t4kz>

Journal

Microbiology Resource Announcements, 4(2)

ISSN

2576-098X

Authors

David, Aaron S
Haridas, Sajeet
LaButti, Kurt
et al.

Publication Date

2016-04-28

DOI

10.1128/genomea.00270-16

Peer reviewed

Draft Genome Sequence of *Microdochium bolleyi*, a Dark Septate Fungal Endophyte of Beach Grass

Aaron S. David,^a Sajeet Haridas,^b Kurt LaButti,^b Joanne Lim,^b Anna Lipzen,^b Mei Wang,^b Kerrie Barry,^b Igor V. Grigoriev,^b Joseph W. Spatafora,^c Georgiana May^{a,d}

Department of Ecology, Evolution and Behavior, University of Minnesota, Saint Paul, Minnesota, USA^a; U.S. Department of Energy Joint Genome Institute, Walnut Creek, California, USA^b; Department of Botany and Plant Pathology, Oregon State University, Corvallis, Oregon, USA^c; Department of Plant Biology, University of Minnesota, Saint Paul, Minnesota, USA^d

Here, we present the genome sequence of the dark septate fungal endophyte *Microdochium bolleyi* (Ascomycota, Sordariomycetes, Xylariales). The assembled genome size was 38.84 Mbp and consisted of 173 scaffolds and 13,177 predicted genes.

Received 8 March 2016 Accepted 8 March 2016 Published 28 April 2016

Citation David AS, Haridas S, LaButti K, Lim J, Lipzen A, Wang M, Barry K, Grigoriev IV, Spatafora JW, May G. 2016. Draft genome sequence of *Microdochium bolleyi*, a dark septate fungal endophyte of beach grass. *Genome Announc* 4(2):e00270-16. doi:10.1128/genomeA.00270-16.

Copyright © 2016 David et al. This is an open-access article distributed under the terms of the [Creative Commons Attribution 4.0 International license](https://creativecommons.org/licenses/by/4.0/).

Address correspondence to Aaron S. David, david250@umn.edu, or Georgiana May, gmay@umn.edu.

Microdochium bolleyi (syn.: *Idriella 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 reference 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 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

1. Mandyam K, Loughin T, Jumpponen A. 2010. Isolation and morphological and metabolic characterization of common endophytes in annually burned tallgrass prairie. *Mycologia* 102:813–821. <http://dx.doi.org/10.3852/09-212>.
2. Jumpponen A, Trappe JM. 1998. Dark septate endophytes: a review of facultative biotrophic root-colonizing fungi. *New Phytol* 140:295–310. <http://dx.doi.org/10.1046/j.1469-8137.1998.00265.x>.
3. De Hoog GS, Hermanides-Nijhof EJ. 1977. *Microdochium bolleyi* (R Sprague). *Stud Mycol* 15:222.
4. David AS, Seabloom EW, May G. 2016. Plant host species and geographic distance affect the structure of aboveground fungal symbiont communities, and environmental filtering affects belowground communities in a coastal dune ecosystem. *Microb Ecol* 71:912–926. <http://dx.doi.org/10.1007/s00248-015-0712-6>.
5. Cooper WS. 1958. Coastal sand dunes. Memoir 72, Geological Society of America, Boulder, Colorado.
6. David AS, Zarnetske PL, Hacker SD, Ruggiero P, Biel RG, Seabloom EW. 2015. Invasive congeners differ in successional impacts across space and Time. *PLoS One* 10:e0117283. <http://dx.doi.org/10.1371/journal.pone.0117283>.
7. Jewel LE. 2013. Genetic and pathogenic differences between *Microdochium nivale* and *Microdochium majus*. PhD dissertation. University of Guelph, Guelph, Ontario, Canada.
8. Ernst M, Neubert K, Mendgen KW, Wirsels SGR. 2011. Niche differentiation of two sympatric species of *Microdochium* colonizing the roots of common reed. *BMC Microbiol* 11:242. <http://dx.doi.org/10.1186/1471-2180-11-242>.
9. Hong SK, Kim WG, Choi HW, Lee SY. 2008. Identification of *Microdochium bolleyi* associated with basal rot of creeping bent grass in Korea. *Mycobiology* 36:77–80. <http://dx.doi.org/10.4489/MYCO.2008.36.2.077>.
10. Grigoriev IV, Nikitin R, Haridas S, Kuo A, Ohm R, Otilar R, Riley R, Salamov A, Zhao X, Korzeniewski F, Smirnova T, Nordberg H, Dubchak I, Shabalov I. 2014. MycoCosm portal: gearing up for 1000 fungal genomes. *Nucleic Acids Res* 42:D699–D704. <http://dx.doi.org/10.1093/nar/gkt1183>.
11. Zerbino DR, Birney E. 2008. Velvet: algorithms for de novo short read assembly using de Bruijn graphs. *Genome Res* 18:821–829. <http://dx.doi.org/10.1101/gr.074492.107>.
12. Gnerre S, MacCallum I, Przybylski D, Ribeiro FJ, Burton JN, Walker BJ, Sharpe T, Hall G, Shea TP, Sykes S, Berlin AM, Aird D, Costello M, Daza R, Williams L, Nicol R, Gnirke A, Nusbaum C, Lander ES, Jaffe DB. 2011. High-quality draft assemblies of mammalian genomes from massively parallel sequence data. *Proc Natl Acad Sci USA* 108:1513–1518. <http://dx.doi.org/10.1073/pnas.1017351108>.
13. Martin J, Bruno VM, Fang Z, Meng X, Blow M, Zhang T, Sherlock G, Snyder M, Wang Z. 2010. Rnnotator: an automated de novo transcriptome assembly pipeline from stranded RNA-Seq reads. *BMC Genomics* 11:663. <http://dx.doi.org/10.1186/1471-2164-11-663>.