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Whole-genome sequence of *Periconia* sp. strain TS-2, an ascomycete fungus isolated from a freshwater outflow and capable of Mn(II) oxidation

Shihori Tsushima,[1] **Robert A. Kanaly,**[1] **Jiro F. Mori**[1]

AUTHOR AFFILIATION See affiliation list on p. 2.

ABSTRACT Members of the genus *Periconia* are commonly found as plant-associated filamentous fungi. Here, the first draft genome sequence of a new *Periconia* strain, TS-2, that was isolated from freshwater outflow sediment and possesses the ability to oxidize dissolved Mn(II), was obtained and has an estimated size of 40.7 Mb.

KEYWORDS manganese-oxidizing fungi, genome sequence, *Periconia*

A new isolate of the fungus *Periconia* (*Ascomycota*, *Dothideomycetes*, *Pleosporales*), strain TS-2, was obtained from the sediment of a natural groundwater outflow in Sakae-ku, Yokohama, Japan, that contained 1.5 mg/L dissolved Mn(II) (by the periodate oxidation method) when the sampling was conducted in May 2021. Through the screening of microorganisms for Mn(II) oxidation capabilities by using a medium which consisted of 40 mg/L $MnSO_4 \cdot 5H_2O$, 50 mg/L yeast extract, and 2% agarose (1), strain TS-2 was obtained as a mycelial colony that accumulated brownish Mn-oxide precipitates and was purified. Members of the fungal genus *Periconia* have been characterized as endophytic fungi known to produce pharmacologically valuable natural products (2–4), and Mn(II) oxidation in *Periconia* has rarely been investigated; Mn(II) oxidation was first reported in *Periconia* in 2023 in strain SM10a2_F1 (5), and the genome of this organism is not sequenced. Consequently, the genome of strain TS-2 was sequenced, and the functional genes were investigated to expand our understanding of the physiology of this fungal genus.

To extract genomic DNA, the mycelium of strain TS-2 that was cultured for 9 days on potato dextrose agar was subjected to cell lysis by adding Lysis Solution F (Nippon Gene, Tokyo, Japan) and homogenizing at 1,500 rpm for 2 minutes. The resulting homogenate was then incubated at 65°C for 10 minutes, followed by centrifugation at 12,000 × *g* for 2 minutes. Genomic DNA was obtained from the supernatant using the MPure-12 system and the MPure Bacterial DNA Extraction Kit (MP Biomedicals, Solon, OH, USA). The genome sequence was obtained through DNBSEQ-G400RS shotgun sequencing (MGI Tech, Shenzhen, China). The DNBseq library was prepared with the MGIEasy FS DNA Library Prep Set (MGI Tech). A total of 22,781,687 reads with 2 × 200-bp paired-end read lengths were obtained and then were trimmed and quality-filtered using Cutadapt (version 4.4) (6) and Sickle (version 1.33) (7), and *de novo* assembly was performed using SPAdes (version 3.15.5) (8). Contaminated contigs were detected and removed through the National Center for Biotechnology Information (NCBI) Contamination Screen, and contigs less than 200 bp in length were excluded. Genome completeness was assessed using BUSCO (version 5.3.2, ascomycota_odb10 data set) (9), revealing 98.1% completeness. All software was used with default settings unless otherwise indicated.

The draft genome sequence of strain TS-2 consisted of 2,189 scaffolds (40,665,975 bp with a scaffold N_{50} value of 870,479 bp, an average depth of 197.0×, and a G + C content of 49.5%), and a total of 14,164 protein-coding genes were predicted using BRAKER2 (version

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Address correspondence to Jiro F. Mori, morij@yokohama-cu.ac.jp.

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2.1.6) (10). Among these genes, 14 genes were identified as putative laccase/multicopper oxidase encoding genes, which were considered to be responsible for Mn(II) oxidation (11, 12). These results suggested that Mn(II) oxidation in the genus *Periconia* may be attributed to the activities of these laccases.

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AUTHOR AFFILIATION

[1]Graduate School of Nanobioscience, Yokohama City University, Yokohama, Japan

AUTHOR ORCIDs

Jiro F. Mori http://orcid.org/0000-0002-3311-1511

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AUTHOR CONTRIBUTIONS

Shihori Tsushima, Conceptualization, Data curation, Investigation, Writing – original draft, Writing – review and editing | Robert A. Kanaly, Supervision, Writing – review and editing | Jiro F. Mori, Conceptualization, Data curation, Funding acquisition, Investigation, Supervision, Writing – original draft, Writing – review and editing

DATA AVAILABILITY

The genome sequence of strain TS-2 is available in NCBI GenBank under accession number GCA_030378425.1. The SRA raw sequence data are available as accession number SRX20546969, under BioProject number PRJNA977381 and BioSample number SAMN35523210.

REFERENCES

1. Tyler PA, Marshall KC. 1967. Microbial oxidation of manganese in hydroelectric pipelines. Antonie Van Leeuwenhoek 33:171–183. https://doi.org/10.1007/BF02045548
2. Azhari A, Supratman U. 2021. The chemistry and pharmacology of fungal genus *Periconia*: a review. Sci. Pharm 89:34. https://doi.org/10.3390/scipharm89030034
3. Kim S, Shin D-S, Lee T, Oh K-B. 2004. Periconicins, two new fusicoccane diterpenes produced by an endophytic fungus *Periconia* sp. with antibacterial activity. J Nat Prod 67:448–450. https://doi.org/10.1021/np030384h
4. Li JY, Sidhu RS, Ford EJ, Long DM, Hess WM, Strobel GA. 1998. The induction of taxol production in the endophytic fungus—*Periconia* sp from *Torreya grandifolia*. Journal of Industrial Microbiology and Biotechnology 20:259–264. https://doi.org/10.1038/sj.jim.2900521
5. Xu T, Roepke EW, Flynn ED, Rosenfeld CE, Balgooyen S, Ginder-Vogel M, Schuler CJ, Santelli CM. 2023. Aqueous co removal by mycogenic Mn oxides from simulated mining wastewaters. Chemosphere 327:138467. https://doi.org/10.1016/j.chemosphere.2023.138467
6. Martin M. 2011. Cutadapt removes adapter sequences from high-throughput sequencing reads. EMBnet J 17:10. https://doi.org/10.14806/ej.17.1.200
7. Joshi NA, Fass JN. 2011. Sickle: a sliding-window, adaptive, quality-based trimming tool for fastq files
8. Bankevich A, Nurk S, Antipov D, Gurevich AA, Dvorkin M, Kulikov AS, Lesin VM, Nikolenko SI, Pham S, Prjibelski AD, Pyshkin AV, Sirotkin AV, Vyahhi N, Tesler G, Alekseyev MA, Pevzner PA. 2012. SPAdes: a new genome assembly algorithm and its applications to single-cell sequencing. J Comput Biol 19:455–477. https://doi.org/10.1089/cmb.2012.0021
9. Simão FA, Waterhouse RM, Ioannidis P, Kriventseva EV, Zdobnov EM. 2015. BUSCO: assessing genome assembly and annotation completeness with single-copy orthologs. Bioinformatics 31:3210–3212. https://doi.org/10.1093/bioinformatics/btv351
10. Brůna T, Hoff KJ, Lomsadze A, Stanke M, Borodovsky M. 2021. BRAKER2: automatic eukaryotic genome annotation with GeneMark-EP+ and AUGUSTUS supported by a protein database. NAR Genom Bioinform 3:lqaa108. https://doi.org/10.1093/nargab/lqaa108
11. Janusz G, Kucharzyk KH, Pawlik A, Staszczak M, Paszczynski AJ. 2013. Fungal laccase, manganese peroxidase and lignin peroxidase: gene expression and regulation. Enzyme Microb Technol 52:1–12. https://doi.org/10.1016/j.enzmictec.2012.10.003
12. Tebo BM, Geszvain K, Lee S-W. 2010. The molecular geomicrobiology of bacterial manganese(II) oxidation BT - geomicrobiology: molecular and environmental perspective:285–308. https://doi.org/10.1007/978-90-481-9204-5