



Draft Genome Sequences of the Antarctic Endolithic Fungi *Rachicladosporium antarcticum* CCFEE 5527 and *Rachicladosporium* sp. CCFEE 5018

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ABSTRACT The draft genome sequences of *Rachicladosporium antarcticum* CCFEE 5527 and *Rachicladosporium* sp. CCFEE 5018 are the first sequenced genomes from this genus, which comprises rock-inhabiting fungi. These endolithic strains were isolated from inside rocks collected from the Antarctic Peninsula and Battleship Promontory (McMurdo Dry Valleys), Antarctica, respectively.

The past decade has revealed an unexpected fungal diversity associated with rocks, which serves as a primary substrate colonized by microorganisms in extreme dry and cold or hot environments. Under these harsh conditions, active growth is rare on exposed surfaces, and endolithism is a necessary ecological adaptation for survival (1). Black meristematic fungi are a morpho-ecological group of ascomycetes with a peculiar tendency to the extremes and are characterized by melanin pigmentation. They are typical and abundant members of Antarctic cryptoendolithic communities (2). These fungi are equally named black yeasts or microcolonial fungi and rock inhabitant fungi when found growing within rocks (3–7). We produced draft genome sequences of the Antarctic fungi *Rachicladosporium antarcticum* CCFEE 5527 Onofri & Egidi (2) and *Rachicladosporium* sp. strain CCFEE 5018 to provide genome resources to study fungal adaptation to extreme environments and endolithic lifestyles. These genomic resources may give clues for studying the evolution of extremophiles and stress adaptation in these enigmatic fungi.

Rachicladosporium strains were obtained from the Culture Collection of Fungi from Extreme Environments (Viterbo, Italy) and were cultured from inside Antarctic rocks. Species designation of *Rachicladosporium* sp. strain CCFEE 5018 is still being determined, and the internal transcribed spacer sequence is 98.6% identical to *Rachicladosporium monterosium* strain CBS 137178 Isola & Zucconi (2). Cultures were grown on 2% malt extract agar. DNA was extracted using a cetyltrimethylammonium bromide (CTAB)-based protocol (8). Two phenol-chloroform purification steps were used to eliminate melanin from the DNA. Total genomic DNA was sheared with a Covaris S220 ultrasonicator. Sequencing libraries were constructed using NeoPrep TruSeq Nano DNA sample prep (Illumina, Inc., San Diego, CA). Libraries were normalized, pooled, and sequenced on an Illumina MiSeq with 2 × 300 paired-end reads. *R. antarcticum* was sequenced to a depth of 41× and *Rachicladosporium* sp. CCFEE 5018 to 175× to improve assembly quality.

Genome assembly with MaSuRCA version 2.3.2 (9) was followed by vector sequence filtering with Sequin (<https://www.ncbi.nlm.nih.gov/Sequin/>). Redundant contigs which

Received 3 April 2017 Accepted 8 May 2017 Published 6 July 2017

Citation Coleine C, Masonjones S, Selbmann L, Zucconi L, Onofri S, Pacelli C, Stajich JE. 2017. Draft genome sequences of the Antarctic endolithic fungi *Rachicladosporium antarcticum* CCFEE 5527 and *Rachicladosporium* sp. CCFEE 5018. *Genome Announc* 5:e00397-17. <https://doi.org/10.1128/genomeA.00397-17>.

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aligned by MUMmer (10) at 95% across their entire length were removed. The *R. antarcticum* genome assembly was 47.4 Mb (number of contigs, 267; N_{50} , 896 kb; L_{50} , 20). The initial *Rachicladosporium* sp. CCFEE 5018 assembly was fragmented (2,099 contigs) but was scaffolded by synteny to *R. antarcticum* with Satsuma2 (11) and Mercator (12) into 233 scaffolds (N_{50} , 1.35 Mb; L_{50} , 12). The genomes were annotated with Funannotate utilizing Augustus (13), GeneMark.hmm-ES (14), and EVM (15) and prepared for GenBank with Genome Annotation Generator (16). Gene function predictions were assigned by matches to the Pfam (17), MEROPS (18), CAZy (19), InterProScan (20), and Swiss-Prot databases (21). Product descriptions were transferred from homologs with 60% similar alignments across 60% of the protein length. A total of 18,781 protein-coding genes were predicted in *R. antarcticum* and 18,892 in *Rachicladosporium* sp. CCFEE 5018.

Accession number(s). These whole-genome shotgun projects have been deposited at DDBJ/ENA/GenBank under the accession numbers [NAJO00000000](https://doi.org/10.1093/nar/naj000) and [NAEU00000000](https://doi.org/10.1093/nar/naeu00000000). The versions described in this paper are the first versions, NAJO01000000 and NAEU01000000.

ACKNOWLEDGMENTS

We thank the Italian National Program for Antarctic Researches for funding sampling campaigns and research in the frame of project 2013/AZ-17. The Italian National Museum of Antarctica (MNA) is acknowledged for financial support to the Culture Collection of Fungi from Extreme Environments (CCFEE), the mycological section of the MNA, and for kindly providing the strains. This work was partially supported by the USDA Agriculture Experimental Station at the University of California, Riverside and NIFA Hatch project CA-R-PPA-5062-H to J.E.S., and high-performance computing resources in the Institute for Integrative Genome Biology (IIGB) at UC Riverside supported by grants NSF DBI-1429826 and NIH S10-OD016290.

Genome sequencing was performed in the Genomics Core Facility of the IIGB at University of California, Riverside.

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