



Draft genome sequences of 12 fungi occurring in cyanobacteria-dominated biotic soil crusts in the Sonoran Desert

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ABSTRACT We present draft genome sequences for 12 fungal isolates, including two isolates each of *Trichoderma*, *Exophiala*, and *Cladosporium*, and one isolate each of *Fusarium*, *Cladorrhinum*, *Epicoccum*, Chaetomiaceae, Didymellaceae, and Pleosporales, from cyanobacteria-dominated biological soil crusts in the Sonoran Desert (Arizona, USA), sequenced on a NovaSeq 6000 at $\geq 40\times$ coverage.

KEYWORDS arid lands, Ascomycota, biological soil crust, desert, fungi

Biological soil crusts (BSCs) are communities of cyanobacteria, algae, fungi, lichens, liverworts, mosses, and other microbes that form cohesive surface layers in arid and semiarid ecosystems. They stabilize soil, promote water retention, facilitate carbon and nitrogen cycling, and support the establishment and growth of vascular plants (1–3). Cyanobacteria-dominated BSCs in the Sonoran Desert harbor diverse fungi for which genomic resources remain limited (4). Here, we report the draft genome sequences of 12 fungal isolates recovered from cyanobacteria-dominated BSCs collected near Tucson, AZ, USA, in an area with upland Sonoran Desert vegetation (32.230662° N, 111.037208° W).

To isolate the fungi, we macerated small fragments of BSC (0.5 cm²) in 750 μ L of sterile water. Aliquots of the resulting suspension (each 20 μ L) were spread onto 2% malt extract agar (MEA). Cultures were incubated at room temperature for up to 3 weeks, with morphologically distinct isolates transferred to axenic culture on 2% MEA.

Isolates were characterized by colony morphology and sequencing of the internal transcribed spacers, the 5.8S gene, and partial nuclear large subunit rDNA (5). They were identified as species of *Trichoderma*, *Fusarium*, *Cladorrhinum*, *Cladosporium*, *Exophiala*, *Epicoccum*, and members of Chaetomiaceae, Didymellaceae, and Pleosporales (Table 1). Some isolates were maintained on antibiotic-amended MEA (kanamycin, chloramphenicol, ampicillin, and tetracycline; see reference 5). Voucher cultures are maintained at the University of Arizona's Robert L. Gilbertson Mycological Herbarium (Table 1).

For DNA extraction, strains were grown on 2% MEA amended with 0.5% yeast extract for 14 days at 25°C. Mycelia were harvested, frozen at -80°C , lyophilized, and homogenized by bead beating (6). Genomic DNA was extracted with the ZymoBIOMICS Soil Kit (Zymo Research, Irvine, CA, USA). For library preparation, 25 ng of total genomic DNA was processed with the KAPA HyperPlus Kit (Roche, Switzerland), amplified for eight cycles, pooled, size-selected (350–900 bp) via the Zymo Select-a-Size Clean & Concentrator Kit and gel purification.

Whole genomes were sequenced using the NovaSeq 6000 platform (Illumina, San Diego, CA, USA), generating 151 bp paired-end reads at $\geq 40\times$ coverage. Adapter trimming and low-quality reads were filtered with fastp (v0.21.0) (7). Genomes were assembled with SPAdes (v3.15.4) with default parameters (8). For taxonomic identification, assembled genomes were compared against the NCBI fungal genome database via BLASTn (v2.17.0) with default parameters, and the top-scoring alignments were used for species assignments. Annotations were completed with BRAKER3 (v3.0.8) (9, 10) with

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TABLE 1 Summary of genome assembly statistics for fungi isolated from cyanobacteria-dominated biocrusts in the Sonoran Desert

Fungal isolate	Accession no.	NCBI assembly	Genome size (Mb)	GC content (%)	No. of genes	Coverage	Contigs	N50 (bp)	Total reads (bp)	Genome completeness (%)
<i>Trichoderma</i> sp.	444A_sa34508	JBYJVV000000000	39.9	48.0	11,235	124.9×	559	256,671	16,739,005	99.6
<i>Fusarium</i> sp.	UA_444B_sa91877	JBYJVX000000000	39.6	48.0	12,175	43.1×	246	915,415	11,455,829	99.5
<i>Cladorrhinum</i> sp.	445A_sa34509	JBYJVV000000000	35.9	50.8	10,573	153.3×	941	64,232	18,815,361	99.6
<i>Trichoderma</i> sp.	UA_446A_sa91860	JBYJVZ000000000	38.2	49.2	11,075	44.0×	672	134,157	11,476,384	99.8
<i>Cladosporium</i> sp.	UA_447A_sa155827	JBYJWA000000000	33.5	54.1	10,445	168.4×	132	444,406	38,584,594	99.8
<i>Exophiala</i> sp.	448A_sa27466	JBYJWB000000000	36.8	50.6	16,128	83.3×	462	291,622	11,730,147	99.5
<i>Exophiala</i> sp.	449A_sa34510	JBYJWC000000000	32.5	50.3	12,155	159.4×	234	223,311	17,297,610	99.7
<i>Cladosporium</i> sp.	UA_450A_sa91895	JBYJWD000000000	54.0	50.6	16,418	194.1×	1592	447,552	73,635,417	99.7
<i>Epicoccum</i> sp.	537A_sa34541	JBYJWE000000000	33.1	52.5	11,294	159.4×	355	229,003	17,615,266	99.1
Chaetomiaceae sp.	UA_537B_sa91975	JBYJWF000000000	28.9	49.1	10,408	45.3×	346	274,997	8,912,106	99.9
Didymellaceae sp.	UA_537F_sa91762	JBYJWG000000000	33.1	50.7	10,712	54.7×	484	453,504	12,195,236	99.9
Pleosporales sp.	UA_538A_sa91976	JBYJWH000000000	31.1	49.6	10,185	75.7×	500	137,612	16,440,456	99.7

only protein models from the closest relatives available in the Joint Genome Institute MycoCosm database. Assembly completeness was assessed using BUSCO (v6.1.0) with the fungi_odb10 lineage data set (11). We predicted secondary metabolite biosynthetic gene clusters (BGCs) using antiSMASH (v8.0.4) (12).

Genome assembly statistics for the 12 strains are summarized in Table 1. Based on antiSMASH ClusterBlast comparisons against the MIBiG database, predicted BGCs were similar to metachelin C/A/B/dimeric acid siderophore BGCs and several previously characterized BGCs associated with metabolites implicated in UV protection, oxidative stress tolerance, and adaptation to nutrient-limited environments (13, 14). BRAKER3 annotation (.gff) and antiSMASH output files are available at <https://doi.org/10.5281/zenodo.19137085>.

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DATA AVAILABILITY

Genome sequence data are available at GenBank under BioProject accession number [PRJNA1425102](https://ncbi.nlm.nih.gov/bioproject/PRJNA1425102) and BioSample accession numbers [SAMN55406242](https://ncbi.nlm.nih.gov/biosample/SAMN55406242)–[SAMN55406253](https://ncbi.nlm.nih.gov/biosample/SAMN55406253). Individual genome assemblies are available under accession numbers [JBYJVW000000000](https://ncbi.nlm.nih.gov/bioproject/JBYJVW000000000)–[JBYJWH000000000](https://ncbi.nlm.nih.gov/bioproject/JBYJWH000000000) (see Table 1). Raw sequencing reads are available in the Sequence Read Archive under accession number [PRJNA1425102](https://ncbi.nlm.nih.gov/bioproject/PRJNA1425102). Additional data on BGCs are available at <https://doi.org/10.5281/zenodo.19137085>.

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