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Data Article

Data on strains of fungi cultured from baldcypress leaves and gall tissue

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ABSTRACT

We show the distribution of fungal operational taxonomic units (OTUs) cultured from leaves and galls of baldcypress (*Taxodium distichum*) trees (Washburn and Van Bael, 2017) [1]. We include putative names when possible, guided by the nearest match in the NCBI databank. This data table shows only one representative of each OTU group and it's nearest match in the NCBI databank, along with information about coverage and percent match of the reads. In total there were 144 fungal cultures sequenced, and all sequences were deposited in the NCBI database under accession numbers KY765150–KY765293 (Washburn and Van Bael, 2017) [1].

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Specifications Table

Subject area	Biology
More specific subject area	Fungal ecology
Type of data	Table
How data was acquired	Sanger sequencing of the nuclear ribosomal internal transcribed spacer (nrITS) and partial large subunit using primers s ITS1F (5′-CTTGGTCAT TTAGAGGAAGTAA) or ITS5 (5′-GGAAGTAAAAGTCGTAACAAGG) for the forward

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	reaction and LR3 (5′-GGTCCGTGTTTCAAGAC) or ITS4 (5′-TCCTCCGCTTATT GATATGC) for the reverse reaction.
Data format	analyzed
Experimental factors	Comparison of galls that had an insect emerge to galls without insect emergence. Comparison fungi cultured from galls and leaves.
Experimental features	Galls over-wintered and we collected them to analyze their fungal communities and compare them with fungi in leaves.
Data source location	Southeastern Louisiana
Data accessibility	This article, and also in the NCBI database under accession numbers KY765150–KY765293.

Value of the data

- These data are the first observations of fungi living in galls of baldcypress midges.
- The sequences and putative identifications can be used for future comparisons in other regions.
- Some of the fungi may be pathogenic on the midges, which may be pests.

1. Data

Table 1 describes the number of sequences from fungi isolated from galls and leaves. We compare the fungi isolated from galls with and without insect emergence, as well as displaying their totals. One representative from our 144 cultures for each OTU group is listed in Table 1. We include the percent coverage and match with the nearest match in the NCBI Genbank, along with our matching accession number.

2. Experimental design, materials and methods

We amplified the nuclear ribosomal internal transcribed spacer (nrITS) and partial large subunit using primers s ITS1F (5′-CTTGGTCAT TTAGAGGAAGTAA) or ITS5 (5′-GGAAGTAAAAGTCGTAACAAGG) for the forward reaction and LR3 (5′-GGTCCGTGTTTCAAGAC) or ITS4 (5′-TCCTCCGCTTATT GATATGC) for the reverse reaction. Our cycling protocol for amplification followed [2].

After visualization confirmation with SYBR on 1% agarose gels, we sent the PCR products to Beckman Coulter Genomics (Boston, MA) for Sanger sequencing. We sent 164 PCR products from individual cultures of gall or foliar fungi. Due to low quality in the sequences, 20 samples were removed before analyses, leaving 144 sequences. The sequences were assembled and edited in Sequencher v5.0 (Gene Codes Corp., Ann Arbor, MI) with support from Mesquite. Operational taxonomic units (OTUs) were formed from sequences assembled based on 97% similarity (Table 1). These OTUs were compared to the NCBI archives through BLAST searches to assign putative taxonomic identities based on the sequence similarity. For each OTU described in Table 1 of [1], we include the accession and strain number of a representative strain from our collection, the accession number of the nearest match in the NCBI databank, percent identity and query cover information. Voucher cultures were archived in the Van Bael laboratory at Tulane University and are available from the author by request.

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