

Anthropogenic N deposition increases soil C storage by reducing the relative abundance of lignolytic fungi. Elizabeth M. Entwistle, Donald R. Zak, and William A. Argiroff. *Ecological Monographs*.

APPENDIX S2

Table S1. Additional information on the taxa we included in our compilation of highly lignolytic taxa used in our study. This includes the name of the taxa in our taxonomic summary file from mothur (Schloss et al. 2009), the taxonomic assignment for these taxa in the Ribosomal Database Project (RDP) v7 fungal 28S LSU classifier files (Liu et al. 2012), their current known taxonomic assignment, their ecology, and their morphology. Information including justifications for their inclusion and citations may be found in Table 2.

name	assignment with RDP v7 classifier	current known taxonomic placement	ecology	morphology
<i>Marasmius</i>	Agaricales/Marasmiaceae/ <i>Marasmius</i>	Agaricales/Marasmiaceae/ <i>Marasmius</i> (Matheny et al. 2006)	litter decay	gilled mushroom
<i>Amyloflagellula</i>	Agaricales/Tricholomataceae/ <i>Amyloflagellula</i>	Agaricales/Marasmiaceae/ <i>Amyloflagellula</i> (Douanla-Meli and Langer 2008)	litter decay	gilled mushroom
<i>Gymnopus</i>	Agaricales/Tricholomataceae/ <i>Gymnopus</i>	Agaricales/Marasmiaceae/ <i>Gymnopus</i> (Matheny et al. 2006)	litter decay	gilled mushroom
<i>Clitocybe</i>	Agaricales/Tricholomataceae/ <i>Clitocybe</i>	Tricholomataceae/ <i>Clitocybe</i> (Matheny et al. 2006)	litter decay	gilled mushroom
<i>Lepista</i>	Agaricales/Tricholomataceae/ <i>Lepista</i>	Tricholomataceae/ <i>Lepista</i> (Matheny et al. 2006)	litter decay	gilled mushroom
<i>Mycena</i>	Agaricales/Tricholomataceae/ <i>Mycena</i>	Agaricales/Mycenaceae/ <i>Mycena</i> (Moncalvo et al. 2002)	litter decay	gilled mushroom
<i>Poromyce</i>	Agaricales/Tricholomataceae/ <i>Poromyce</i>	Agaricales/Mycenaceae/ <i>Poromyce</i> (Moncalvo et al. 2002)	litter decay	gilled mushroom
Crepidotaceae	Agaricales/Crepidotaceae	Agaricales/Crepidotaceae (Matheny et al. 2006)	white rot of wood and litter decay	gilled "oysterling"
Auriscalpiaceae	Polyporales/Auriscalpiaceae	Russulales/Auriscalpiaceae (Larsson and Larsson 2003, Miller et al. 2006)	white rot of wood and litter decay ^a	tooth and shelf fungi ^a

Lachnocladiaceae	Polyporales/Lachnocladiaceae	Russulales/Lachnocladiaceae (Kirk et al. 2008) ^b	white rot of wood	resupinate
<i>Antrodiella</i>	Polyporales/Coriolaceae/ <i>Antrodiella</i>	Polyporales/Steccherinaceae/ <i>Antrodiella</i> (Miettinen et al. 2012)	white-rot	
Ganodermataceae	Polyporales/Ganodermataceae	Polyporales/Ganodermataceae (Kirk et al. 2008)	White-rot saprotrophs and plant pathogen	shelf fungi
Aphylophorales	Polyporales/Polyporales incertae sedis/Aphylophorales	Aphylophorales is a formerly used morphological taxonomic group for fungi without gills. However, molecular phylogenetics showed that Aphylophorales to be comprised of distantly related taxa (Hibbett and Donoghue 1995). The sequences used to define this group in the RDP v7 classifier ^c now belong to several families in the Polyporales (Binder et al. 2013). In our data set, sequences classified as Aphylophorales were members of the genera <i>Phanerochaete</i> and <i>Scopuloides</i> ^d .		

a All Auriscalpiaceae sequences in our data set classified to the wood-rot genus *Lentinellus*, which are mushrooms with gills.

b Some authors include the genera contained in Lachnocladiaceae in Russulales/Peniophoraceae (Miller et al. 2006, Larsson 2007)

c Searches for the sequences used to define Aphylophorales in the RDP v7 taxonomic classifier returned close matches for sequences identified as *Antrodiella*, *Cerrena*, *Ceriporia*, *Phlebia*, *Bjerkandera*, *Rigidoporus*, *Phanerochaete*, and *Irpex* using the National Center for Biotechnology Information (NCBI) Basic Local Alignment Tool (BLAST®) online portal.

d For sequences classified to Aphylophorales, we obtained an alignment all of the unique sequences classified to this group using mothur 1.31.2 (Schloss et al. 2009). There were 637 unique sequences that had classified to Aphylophorales in our data set. We selected every 50th sequence in the alignment as well as the final two sequences in the alignment and conducted a search using

NCBI BLAST®. *Phanerochaete laevis* (GenBank accession KJ668345) was the top BLAST® result with a 99% identity score for the 14 sequences which we selected from among the first 636 unique sequences in the alignment. *Scopuloides hydnooides* (GenBank accession LN611118) was the top BLAST® match with 99% identity for the final sequence in the alignment. Therefore, we included Aphyllophorales among highly lignolytic taxa as we were confident that sequences classified to this group represented highly lignolytic white-rot Polyporales in our data set.

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