Patterns and drivers of fungal community depth stratification in *Sphagnum* peat

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Running title: Controls on fungal community structure in peatlands

Abstract

Peatlands store an immense pool of soil carbon vulnerable to microbial oxidation due to drought and intentional draining. We used amplicon sequencing and quantitative PCR to 1) examine how fungi are influenced by depth in the peat profile, water table (WT) and plant functional group (PFG) at the onset of a multi-year mesocosm experiment, and 2) test if fungi are correlated with abiotic variables of peat and pore water. We hypothesized that each factor influenced fungi, but that depth would have the strongest effect early in the experiment. We found that: 1) communities were strongly depth stratified; fungi were four-times more abundant in the upper (10-20 cm) than the lower (30-40 cm) depth, and dominance shifted from ericoid mycorrhizal fungi to saprotrophs and endophytes with increasing depth; 2) the influence of PFG was depth-dependent, with Ericaceae important in structuring the community in the upper peat only; 3) WT had minor influences; and 4) communities strongly covaried with abiotic variables, including indices of peat and pore water carbon quality. Our results highlight the importance of vertical stratification to peatland fungi, and the depth-dependency of PFG effects, which must be considered when elucidating the role of fungi in peatland carbon dynamics.

40 **Introduction**

41 Northern peatlands are characterized by extremely high soil carbon density, sequestering
42 almost one third of the world's soil organic carbon stocks in ~3% of land area (Page, Rieley and
43 Banks 2011). Carbon accumulates in peatlands because anoxic, phenol-rich, water-saturated
44 conditions depress rates of decomposition relative to primary production (Rydin and Jeglum
45 2013). In many locations around the world, peatlands are experiencing water table (WT) declines
46 due to climate change related droughts, and drainage for forestry and agriculture (Rydin and
47 Jeglum 2013). Such declines in WT expose formerly anoxic peat to oxic conditions favorable to
48 aerobic microbial metabolism and decomposition, and are likely to have important influences on
49 microbial community structure (Freeman, Ostle and Kang 2001; Jaatinen, Laiho and Vuorenmaa
50 2008; Trinder, Johnson and Artz 2008). The switching of large areas of peatlands from net sinks
51 to net sources of carbon may act as a positive feedback to climate change (Bardgett, Freeman
52 and Ostle 2008; Bridgham *et al*. 2008). However, our understanding of the responses of
53 peatlands to drainage and climate-change stresses are incomplete without understanding how
54 altered WT interacts with other factors, including plant functional groups (PFGs) and peat depth,
55 to influence the structure and function of microbial communities involved in decomposition
56 (Andersen, Chapman and Artz 2013).

57 Hydrologically driven shifts in the relative dominance of PFGs may influence communities
58 of microorganisms, such as fungi. Of particular importance, fungal community structure and
59 function could be regulated by differences in root traits among PFGs. At one end of the
60 spectrum, peatland sedge (*Carex* and *Eriophorum* spp.) roots typically lack coevolved
61 mycorrhizal symbionts (e.g. Thormann, Currah and Bayley 1999) but locally oxic conditions
62 created by their aerenchyma (spongy tissues with air channels that permit gas exchange into

63 otherwise anoxic peat) likely have strong influences on free-living fungi. In contrast, ericaceous
64 shrubs (Ericaceae) are sensitive to anoxic conditions due to their lack of aerenchyma, but host
65 ericoid mycorrhizal fungi (ErMF) with extracellular enzymes that enable depolymerization of
66 complex organic molecules to gain access to limiting nutrients (e.g. nitrogen, phosphorous;
67 Cairney and Burke 1998; Cairney and Meharg 2003; Read, Leake and Perez-Moreno 2004).
68 Experimental work indicates that drier peat conditions promote dominance by ericaceous shrubs,
69 whereas sedges can sometimes be favored by more moist conditions (Weltzin *et al*. 2003;
70 Breeuwer *et al*. 2009; Potvin *et al*. 2015). The link between plants and fungi suggests that shifts
71 in the dominance of PFGs due to WT alteration could change the structure and function of
72 peatland fungal communities.
73 Fungal communities can also exhibit vertical stratification within peat profiles (Artz *et al*.
74 2007; Lin *et al*. 2014), and the causes of vertical stratification are likely intertwined with the
75 effects of WT and PFG on fungi. A suite of abiotic variables change between surface and deep
76 peat, including water content, oxygen availability, redox potential, temperature, dissolved
77 organic carbon (DOC), bulk density and peat humification (i.e. the level of decomposition)
78 (Hribljan *et al*. 2014; Lin *et al*. 2014; Tfaily *et al*. 2014; Potvin *et al*. 2015). Depth gradients of
79 many of these chemical and physical characteristics are largely a consequence of water
80 saturation and age, creating a contrast between the more frequently oxic, lower bulk density,
81 fibric peat (acrotelm) and the typically water saturated, anoxic, denser, more sapric deeper peat
82 (catotelm). Plant functional groups also have divergent influences on abiotic properties of peat
83 (Andersen, Chapman and Artz 2013), and different PFGs can thus be expected to modulate the
84 effect of depth in the peat profile on fungal communities. For example, sedge aerenchyma allows
85 living sedge roots to penetrate deeper into a peat profile than roots of Ericaceae, potentially

moderating the depth gradient in oxygen and root-derived labile resources. In contrast, shallowly rooted Ericaceae, with enzymatically active ErMF symbionts, may be expected to sharpen the distinction between upper and lower depths in a peat profile. These interactive effects of PFG with peat depth should be further modified by WT, because the WT level defines the major environmental context within which plant roots interact with peat and fungi. When WTs are low, oxygen is available to a greater fraction of the peat profile, which should reduce the importance of oxygenation by sedge aerenchyma on the rhizosphere and be less limiting to the growth of ericaceous roots, associated symbionts and aerobic free-living fungi. Because they are intertwined, the individual and interactive effects of depth in the peat profile, WT and PFG are difficult to understand without direct experimental manipulation.

Here, we characterize the fungal community during the first year of a peatland mesocosm experiment, PEATcosm (Potvin *et al.* 2015). The experiment is aimed at understanding how peatland community and ecosystem processes are influenced by PFG and WT level, and how depth in the peat profile modulates the effects of these factors. Our primary objective with this sampling was to characterize the change in fungal community structure with depth in the peat profile. We hypothesized that, **H1)** the steep physical, chemical and biological gradients associated with depth in the peat profile cause fungal community structure to be vertically stratified. Specifically, we predicted that surface peat has the greatest overall fungal abundance and is dominated by ErMF fungi, whereas deeper in the peat profile fungal abundance declines and saprotrophic fungi become increasingly important. Our next objective was to test for a rapid response of fungi to PFG removal and WT decline. Relative to the effect of peat depth, we expected the effects of these factors to be small during the first season of the experiment. Nevertheless, when they do occur, we hypothesized that, **H2)** contrasting traits between plant

Comment [LL1]:
The last paragraph in the intro was completely revised.

Here is the original hypothesis paragraph, before I revised it:

Here, we characterize the fungal community during the first year of a peatland mesocosm experiment, PEATcosm (Potvin *et al.* 2015). The experiment is aimed at understanding how peatland community and ecosystem processes are influenced by PFG and WT level, and how depth in the peat profile modulates the effects of these factors. Our primary objective with this sampling was to characterize the change in fungal community structure with depth in the peat profile. Due to the steep physical, chemical, and biological gradients associated with depth, we expected this factor to be the strongest force structuring fungal communities. We hypothesized that **H1)** fungal communities differ between depths in the peat profile. Specifically, we predicted that surface peat has the greatest overall fungal abundance and is dominated by ErMF fungi, whereas deeper in the peat profile fungal abundance declines and saprotrophic fungi become increasingly important. Our second objective was to test for a rapid response of fungi to PFG removal and WT decline. We expected the effects of these factors to be relatively small during the first season of the experiment. Nevertheless, when they do occur, we hypothesized that, **H2)** plant functional group manipulation alters fungal community structure. In particular, the distinction in communities between upper and lower peat depths should be greatest in the presence of Ericaceae and the absence of sedges; this is likely, due to the influence of Ericaceae roots and ErMF symbionts in the upper peat, and the potential ability of sedges to homogenize fungal communities along depth gradients by bringing oxygen to deep peat. Furthermore, we hypothesized that **H3)** a lowered WT alters fungal communities, with increases in relative abundance of ErMF and overall fungal abundance as the WT decline ...

Comment [LL2]: From the reviewer:

"lines 103, 109, 114, 120: strictly speaking these are predictions, not hypotheses. A hypothesis should invoke a mechanism that, if correct, lead to a prediction that can be compared to an observation. But this should only take some minor rewording to address because the mechanisms are presented in the sentences leading up to these statements. The more detailed predictions that follow most of these statements are suitably precise and well-written."

functional groups have differential effects on fungal community structure. Experimental removal of different plant functional groups should therefore alter fungal community structure in different ways. In particular, the distinction in community structure between upper and lower peat depths should be greatest in the presence of Ericaceae and the absence of sedges; this is likely, due to the influence of Ericaceae roots and ErMF symbionts in the upper peat, and the potential ability of sedges to homogenize fungal communities along depth gradients by bringing oxygen to deep peat. Furthermore, we hypothesized that, **H3)** WT level influences fungal community structure, due to WT effects on abiotic characteristics of peat and the plant community. We specifically predicted that the relative abundance of ErMF and overall fungal abundance should increase as WT declines with experimentally simulated drought conditions. Our final objective was to test the relationship between fungal community structures and abiotic characteristics of peat and pore water (e.g. humification, carbon quality, temperature). We hypothesized that, **H4)** fungal community variation is coupled with variation in abiotic characteristics of peat and pore water, because these abiotic characteristics are influenced by the activities of fungi (e.g., decomposition), and some represent important resources for, or constraints on, fungi. In particular, variation in abiotic peat and pore water characteristics should mirror changes in fungal community structure between depths in the peat profile, and exhibit corresponding shifts with experimental manipulations of WT and PFG.

Materials and methods

Experimental study system

PEATcosm is a multifactorial peatland mesocosm experiment located at the Houghton Mesocosm Facility, USDA Forest Service, Northern Research Station, Forestry Sciences

Laboratory in Houghton, Michigan (N47.11469°, W88.54787°). The experiment includes 24 mesocosms, each composed of a single ~1 m^3 intact peat monolith excavated from an oligotrophic peatland in Meadowlands, MN, USA (N47.07278°, W92.73167°) in May 2010, and installed in the Houghton Mesocosm Facility. Monoliths were obtained from lawn habitat, with existing vegetation dominated by the ericaceous shrubs *Chamaedaphne calyculata* (L.) Moench., *Kalmia polifolia* Wangenh., and *Vaccinium oxycoccus* L, and the sedge *Carex oligosperma* Michx., above a moss layer of *Sphagnum* species and *Polytrichum strictum* Brid. (Potvin *et al.* 2015). No experimental treatments were imposed during the 2010 growing season. The experiment included a two level WT treatment, and a three level PFG treatment, with four replicate spatial blocks representing each of the six unique factor-level combinations. In June 2011 PFG manipulation was initiated with clipping of ericaceous shrubs (Sedge treatment), sedges (Ericaceae treatment), or unclipped as a PFG control (Unmanipulated treatment; n = 8 for each treatment). Ericaceae and Sedge treatments were subsequently maintained by clipping new growth of excluded species as needed on a weekly basis. WT manipulations were also initiated in June 2011 (12 mesocosm bins with high and 12 with low water tables; hereafter referred to as High and Low, respectively). WT manipulation was designed to match typical seasonal WT dynamics for average (High) and summer drought (Low) years, and was carried out using rain-out shelters, artificial rainwater addition and drainage in the spring at the acrotelm-catotelm boundary (~25 cm depth). In 2011, WT manipulation was minimal but distinct between treatments, to avoid stress to mosses after initiation of the PFG treatment; High and Low WT treatments differed by ~5 cm through the season, with the High averaging ~7 cm and the Low ~12 cm below the peat surface during the peat sampling period (Fig. S1, Supporting Information). See Potvin *et al*. (2015) for additional details on design and treatments.

155

156 *Fungal sampling and molecular methods*

157 One core per mesocosm was collected between August 31 and September 13, 2011,
158 approximately three months after initiation of experimental manipulations. Peat cores were
159 extracted using a 2.54 cm diameter aluminum corer sharpened at the leading edge and fitted to an
160 electric drill. The 10-20 cm (acrotelm) and 30-40 cm (catotelm) depth increments from each core
161 were split length-wise and one half (for DNA analysis) was immediately flash frozen in liquid
162 nitrogen, then stored at -80 ºC. Each sample was pulverized in a mortar and pestle under liquid
163 nitrogen, and then ground to a fine powder with liquid N in an electric coffee grinder. Total soil
164 DNA was isolated from 0.5 g of ground, wet peat using a PowerSoil DNA Isolation kit followed
165 by purification with a PowerClean DNA Clean-Up kit (MoBio Laboratories Inc., Carlsbad,
166 California, USA). To enable wet to dry-mass conversion, a subsample of ground peat from each
167 core was weighed wet and again after oven drying for 36 hours at 60 ºC.

168 Fungal abundance was estimated in each sample using quantitative PCR (qPCR) following
169 Lau and Lennon (2011). Briefly, the first internal transcribed spacer region (ITS1) was amplified
170 with the primers ITS1f and 5.8S (Fierer, Vilgalys and Jackson 2005). Each 30 µL reaction
171 included 1 µL of DNA template, 0.5 µL of each primer (10 µmol), 14.5 µL of DNase-free water,
172 and 13.5 µL of 5 PRIME 2.5x Real-MasterMix SYBR ROX (5 Prime, Inc. Gaithersburg,
173 Maryland, USA). PCR assays were performed with an Eppendorf Mastercycler realplex^2 system
174 using the thermal cycle conditions of Fierer, Vilgalys and Jackson (2005). Standards were
175 generated from a *Trichosporon* sp. isolate using the TOPO TA Cloning Kit (Invitrogen;
176 Carlsbad, California, USA). Plasmids were extracted from transformed cells (Sambrook and
177 Russell, 2001), and the M13 forward and reverse primers from the cloning kit were used to

generate PCR products for a standard curve. The standard curve ranged from 10^2–10^7 copies per µL, with coefficients of determination (R^2) of 0.96–0.99 and amplification efficiencies of 0.93–0.99. Melting curve analyses provided no evidence for primer dimers. Three analytical replicates of each sample were run through the preceding qPCR process, data were averaged per sample, and values were expressed as ITS1 gene copies per gram dry peat.

To further characterize fungal communities in each sample, community metabarcode sequencing was conducted at the U.S. Department of Energy Joint Genome Institute (JGI, Walnut Creek, California). Sample prep followed Caporaso *et al.* (2012), and utilized a PerkinElmer Sciclone NGS G3 Liquid Handling Workstation (Waltham, Massachusetts, USA) and 5 PRIME's HotMasterMix amplification kit. The fungal ITS2 region was targeted with the forward primer sequence fITS9 (Ihrmark *et al*. 2012) and the reverse primer ITS4 (White *et al*. 1990). The full-length primer contained an Illumina adapter sequence, an 11bp index (on the reverse primer only) which was unique to each sample, a primer pad, a 0-3 bp spacer pad and the ITS2 primer sequence. Prepared amplicon libraries were normalized, pooled, and quantified using KAPA Biosystem's (Wilmington, Maryland, USA) next-generation sequencing library qPCR kit using a Roche LightCycler 480 real-time PCR instrument. The quantified amplicon pool was sequenced with an Illumina MiSeq (San Diego, California, USA) using 2 x 250 bp paired-end chemistry. Data are available through the JGI genome portal (project ID 1021300, folder iTAGs_2014Jan10_ITS_M2943; http://genome.jgi.doe.gov/).

Bioinformatics

The Itagger pipeline, version 1.1 (https://bitbucket.org/berkeleylab/jgi_itagger), was used for initial data processing. Duk (http://duk.sourceforge.net/) was used to filter PhiX 174, human,

and Illumina adapter sequences from demultiplexed reads. Primers were removed with Cutadapt (Martin 2011). Reads were quality trimmed based on the expected error rate over a 5 base window at their 3' ends and merged with Pandaseq (minimum overlap = 15 bp, quality threshold = 0.25; Masella *et al.* 2012) if their combined length was ± 3 standard deviations of the mean ITS2 length. The 5' and 3' ends of merged reads were trimmed by 94 and 35 bases, respectively, to remove the conserved 5.8S and 28S rRNA gene flanking regions. Reads were then discarded when their expected number of errors (calculated as the product of error probabilities from Phred scores) exceeded three. Sequences were dereplicated at 100% identity and operational taxonomic units (OTUs) were clustered iteratively at 99, 98, 97, 96 and 95% identity with USEARCH (Edgar 2010). Reference-based chimera detection was run with UCHIME (Edgar, Haas and Clemente 2011) using UNITE (2011-07-22 release; https://unite.ut.ee). Clusters formed at 95% sequence similarity were used in subsequent analyses. Using 95% sequence similarity is slightly more conservative than the frequently used 97% cutoff, however there is no single % similarity cut-off that is perfect for delineating species in sequence datasets. We felt that it was most important to guard against superfluous OTU propagation, which may be common in environmental sequence datasets, and a recent mock community study using the ITS2 region suggested that similarity cut-offs lower than the typically used 97% may yield a more accurate number of OTU clusters (Taylor *et al.* 2016).

Comment [LL3]: How does this sound?

Further processing, using OTUs generated from the Itagger pipeline, proceeded as follows. Taxonomy was assigned using the Ribosomal Database Project (RDP) Classifier with confidence set at 0.5 (Porras-Alfaro *et al*. 2014), implemented in Qiime 1.9 (Caporaso *et al*. 2010). The RDP Classifier was trained with the UNITE 7 species hypothesis dynamic clustering dataset (released 02 March 2015; https://unite.ut.ee/repository.php; Kõljalg, Nilsson and Abarenkov 2013),

supplemented with additional ITS sequences from non-fungal eukaryotic lineages obtained from the NCBI nucleotide database (Accession numbers: JF444765.1, JN853795.1, KF977223.1, AY398500.1, AY455777.1, GU097876.1, AY070244.1, HQ156450.1, JF742525.1, KC594036.1, AF317109.1, AY368576.1, AF401150.1, AY346506.1, AY570231.1, AY836783.1, FJ572393.1, AY396437.1, JF801558.1, KPU48597.1; http://ncbi.nlm.nih.gov). OTUs from non-fungal lineages and those that the RDP Classifier could not assign to a lineage were then filtered from the dataset. OTUs whose taxonomy was resolved only to fungal class, or higher, were subjected to BLASTn searches in the NCBI nucleotide database. These OTUs were retained only if BLASTn hits were of clear fungal origin and had an E-value $\leq 1x10^{-20}$. OTUs represented by less than 10 sequences were removed to limit sources of sequencing error. OTUs were tentatively assigned to functional groups using FUNGuild (Nguyen *et al.* 2015), complemented with our own literature searches. Functional assignments are based on the best available knowledge, however we stress that these are putative. The final OTU matrix was rarefied to 20 000 sequences per sample.

Chemical and physical characteristics of pore water and peat

We measured a suite of abiotic characteristics to investigate potential correlations with fungal community structure. Pore water was collected on 22 September 2011 from piezometers covered on their ends with 37 µm nylon mesh and installed at 20 cm and 40 cm depths. Samples were filtered (0.45 µm) and acidified with hydrochloric acid. Dissolved organic carbon (DOC) and total dissolved nitrogen (TDN) concentrations were measured using a Shimadzu TOC-V Combustion Analyzer (Shimadzu Scientific Instruments, Columbia, MD, USA). Three optical properties indicative of DOC composition were also quantified. First, specific ultraviolet

247 absorbance ($SUVA_{254}$) was calculated by dividing UV absorbance at λ = 254 nm by total DOC
248 concentration. The $SUVA_{254}$ index should increase linearly with DOC aromaticity (Weishaar *et*
249 *al*. 2003). The second property, E2:E3 (UV absorbance ratio of λ = 254 nm to λ = 365 nm)
250 decreases as molecular size of dissolved organic matter (DOM) increases (De Haan and De Boer
251 1987). The third optical property, E4:E6 (UV absorbance ratio at λ = 465 nm to λ = 665 nm)
252 increases with DOC aromaticity and is inversely related to DOC humification (lower values =
253 more decomposed; Zhang and He 2015). Total phenolics were quantified using Hach (Loveland,
254 CO, USA) reagents scaled to a microplate (Sinsabaugh, Reynolds and Long 2000), at 700 nm
255 absorbance on a SpectraMax M2 plate reader (Molecular Devices, Sunnyvale, California).
256 Ammonium was determined spectrophotometrically using Hach salicylate and cyanurate
257 reagents, also scaled to a microplate. Temperature was continuously recorded in each mesocosm
258 (see Potvin *et al.* 2015). We used the average temperature over one month (August 15 to
259 September 15), from probes at 20 and 40 cm depths. pH was measured (all but three samples) on
260 fresh peat collected during microbial coring using a peat slurry (1 g peat: 30 mL deionized
261 water), with a Denver Instrument Model 220 pH meter (Bohemia, New York). The von Post
262 score, an ordinal index of peat decomposition (see Rydin and Jeglum 2013), was measured on
263 peat from both sampling depths collected in May 2011 (prior to initiation of experimental
264 treatments).
265
266 *Statistical Analyses*
267 A suite of analyses were used to address hypotheses 1 to 3, focused on understanding how
268 depth in the peat profile, PFG and WT influence fungi. First, linear mixed models were run with
269 the following response variables: ITS1 gene abundance, OTU richness (S), Pielou's OTU

evenness (J'), and the relative abundance and richness of the three most abundant functional groups (saprotrophs, ErMF, root endophytes). Additionally, we examined the relative abundance of the three most common putative ErMF lineages: *Rhizoscyphus ericae* (= *Pezoloma ericae*), Sebacinales group B (= Serindipitaceae spp.) and *Oidiodendron maius*. Relative abundances were calculated as the proportion of sequences representing a specific taxa or functional group divided by the total number of sequences in a sample (20 000). Linear mixed models included PFG (Sedge, Ericaceae, Unmanipulated), WT (High, Low), sampling depth (10-20 cm, 30-40 cm), all two and three-way interactions, and block as fixed factors. Individual mesocosm bin was included as a random effect. Variables were log or square root transformed when necessary. Models were fit in R 3.0.2 (R Core Team, 2013) with the package *lme4* (Bates *et al*. 2014), fixed effects were tested with the *lmerTest* package using the Kenward-Roger approximation, and post hoc tests, when appropriate, were run with the *lsmeans* and *multcompView* packages (Graves *et al.* 2012; Lenth and Hervé 2015).

To test responses of fungal composition, matrices of fungal OTUs and orders were analyzed using distance-based permutation MANOVA (PERMANOVA) and non-metric multidimensional scaling (NMDS), with Bray-Cutis dissimilarity. PERMANOVA models included the same factors as described above for linear mixed models, including individual mesocosm bin as a random effect. Type III sums of squares were used for PERMANOVA, with null distributions created by permuting residuals from partial models lacking the factor being tested (Anderson, Gorley and Clarke 2008). Prior to PERMANOVA and NMDS, matrices were 4^{th} root transformed to down-weight the influence of the most abundant taxa (Clarke and Gorley 2006). The variance in community composition explained by each NMDS axis was estimated by calculating the coefficient of determination (R^2) between the original Bray-Curtis matrix and the

distances between communities on an ordination axis (McCune and Grace 2002). Indicator species analysis was run to understand which OTUs were driving the strongest patterns in the dataset, and a chi-squared test was used to test whether the functional groups of indicator species shifted between sampling depths. PERMANOVA was also conducted on the OTU matrix after transformation to presence-absence, and the square root of the variance component for the depth effect was used to estimate the average percentage change in OTU membership between communities from one sampling depth to the other (i.e., OTU turnover between depths; Anderson, Gorley and Clarke 2008). PERMANOVA was conducted in Primer 6.1.15 with PERMANOVA+ 1.0.5 (PRIMER-E, Plymouth, UK). NMDS and indicator species analysis were run in R 3.0.2 with the packages *vegan* (Oksanen *et al.* 2013) and *indicspecies* (De Caceres and Jansen 2009), respectively.

To further understand the effects of PFG, WT and depth in the peat profile, we examined whether shifts in relative abundances were mirrored by similar shifts in qPCR-adjusted abundances for the dominant functional groups (ErMF, root endophytes, saprotrophs). This adjustment was accomplished by multiplying a functional group's relative abundance (the proportion of sequences out of 20 000) by a sample's total fungal ITS1 gene abundance (ITS1 gene copies per gram dry peat). This conversion generated a qPCR-adjusted abundance that should semi-quantitatively reflect variation in a functional group's total abundance among samples. We recognize that artifacts may arise from biases associated with sequencing, and the use of ITS2 sequence data in conjunction with qPCR data generated using ITS1; however, we believe this metric is informative because it adjusts for the huge decline in fungal abundance with depth. qPCR-adjusted data were tested with the linear mixed model approach described above.

316 The final set of analyses tested hypothesis 4, that fungal communities covary with pore
317 water and peat characteristics. To understand the sources of variation in abiotic variables, their
318 responses to sampling depth, PFG and WT were examined using the linear mixed model
319 approach as described above for fungal community variables. However, the effect of depth on
320 von Post humification was tested with a paired *t*-test (paired within mesocosm), with *P*-values
321 obtained through permutation using the *broman* package (Broman 2014) in R. Vectors for each
322 abiotic variable were then fit to NMDS ordinations using the 'envfit' function in the R package
323 *vegan*. Because pore water variables primarily responded only to peat depth (see Results), we
324 focused these analyses on understanding covariation between abiotic variables and the fungal
325 community across the peat depth gradient.
326
327 **Results**
328 *The fungal community*
329 A diverse community was recovered through sequencing. The data set contained a total of 5
330 205 263 sequences (22 697-190 244 per sample) and 1489 OTUs, after clustering and chimera
331 filtering but prior to further OTU filtering. The RDP classifier categorized the majority of these
332 remaining OTUs as fungal, however upon manual checking some OTUs were unclassifiable or
333 matched non-fungal lineages. Furthermore, the RDP classifier identified some OTUs as fungal,
334 but did not provide taxonomy below the kingdom or phylum; nearly all of these OTUs were
335 unclassifiable through BLASTn or strongly matched non-fungal lineages. After removing OTUs
336 with uncertain identities and those represented by less than 10 sequences, the dataset included 4
337 977 065 fungal sequences (20 970-182 143 sequences per sample; Fig. S2, Supporting
338 Information). The final dataset contained 630 OTUs (56-325 OTUs per sample; Fig. S2,

339 Supporting Information), with OTU reference sequences being 160 bp on average (range = 100-
340 214 bp). Rarefaction to 20 000 sequences per sample reduced the number of OTUs to 623 (50-
341 226 OTUs per sample). The OTUs represented three phyla, at least 30 orders from 12 classes,
342 and were dominated by the Ascomycota order Helotiales (Table S1, Supplementary Information;
343 Fig. 1).
344
345 *The fungal community and depth in the peat profile*
346 In support of hypothesis 1, there was a large shift in the fungal community with increasing
347 depth in the peat profile. Fungal ITS1 gene abundance was four-fold greater at the 10-20 cm than
348 the 30-40 cm depth, and OTU evenness increased slightly with depth (Table 1; Fig. 2a and c).
349 However, there was no evidence of an OTU richness response to depth (Table 1; Fig. 2b).
350 Composition changed with sampling depth, at both the ordinal and OTU-level (Table 1; Fig.
351 3). Furthermore, the identity of OTUs occurring in the community changed by an average of
352 ~21% between sampling depths (i.e., there was a turnover in approximately 21% of the
353 communitie's OTUs from one depth to the other; square root of the variance component for the
354 depth effect from the presence-absence matrix = 21.15). Indicator species analysis identified a
355 suite of indicators for each peat depth (Table S2, Supplementary Information), and the functional
356 group to which indicator OTUs tended to belong differed between depths ($X^2 = 31.21$, $P <$
357 0.001). Indicator OTUs of the 10-20 cm depth were typically ErMF, whereas indicators of the
358 30-40 cm depth were primarily saprotrophs and root endophytes (Table S2, Supplementary
359 Information; Fig. 3a). At the order-level, the Rhytismatales, Archaeorhizomycetales, Sebacinales
360 and Xylariales were identified as indicators of the 10-20 cm depth, while the Polyporales was an
361 indicator of the 30-40 cm depth (Table S2; Fig. 3b).

362 The dominant fungal functional groups were also influenced by depth in the peat profile.
363 ErMF relative abundance decreased more than one-third, and OTU richness decreased by
364 approximately one-fourth, from the 10-20 cm to 30-40 cm depths (Table1; Fig. 4a and c). In
365 contrast, saprotroph relative abundance was more than five-fold greater at the 30-40 cm than 10-
366 20 cm depth, and OTU richness increased by one-third from the upper to lower depth (Table1;
367 Fig. 4d and f). The relative abundance of root endophytes increased six-fold and OTU richness
368 nearly doubled, from the 10-20 cm to 30-40 cm depth (Table 1; Fig. 4g and i). However, root
369 endophyte relative abundance exhibited a complex three-way interaction with other factors (see
370 details below).
371 qPCR-adjusted abundances provided a different view of functional group responses to depth
372 in the peat profile. After qPCR-adjustment, ErMF still decreased with increasing depth, and at
373 the 30-40 cm depth were only one-sixth of their value at the 10-20 cm depth (Table 1; Fig. 4b).
374 However, the depth effect on root endophytes lost statistical significance after qPCR adjustment
375 (Table 1; Fig. 4e). Although depth remained a marginally significant effect on saprotrophs after
376 qPCR adjustment, its effect was largely obscured by its interaction with WT (Table 1; Fig. 4h).
377 Each of the three putative ErMF lineages examined individually (*Rhizoscyphus ericae*,
378 *Oidiodendron maius*, Sebacinales Group B) decreased sharply with increasing depth (Table 1;
379 Fig. 5). This decrease was observed in relative and qPCR-adjusted abundances (Fig. 5).
380
381 *Fungal community responses to plant functional group and water table*
382 Although PFG and WT effects were less pronounced than those of sampling depth, there
383 was modest support for hypotheses 2 and 3. OTU evenness showed a marginal response to WT,
384 being slightly greater in the Low WT treatment within most PFG by depth factor-levels (Table 1;

385 Fig. 2c). However, neither ITS1 gene abundance nor OTU richness showed clear evidence of a
386 response to PFG or WT (Table 1; Fig. 2a and b).

387 Fungal composition responded to PFG at the order-level but not at the OTU-level, and
388 showed no evidence of a response to WT (Table 1; Fig. 3). At the 10-20 cm depth, ordination
389 (Fig. 3b) coupled with post-hoc PERMANOVA suggested that the composition of orders in
390 mesocosms containing ericaceous shrubs was distinct from the Sedge treatment (Unmanipulated
391 vs. Ericaceae: $P = 0.298$; Unmanipulated vs. Sedge: $P = 0.033$; Ericaceae vs. Sedge: $P = 0.071$).
392 This PFG effect was not evident at 30-40 cm depth (Sedge vs. Ericaceae: $P = 0.544$; Sedge vs.
393 Umanipulated: $P = 0.885$; Ericaceae vs. Unmanipulated: $P = 0.383$). Ordination also revealed
394 that the Sedge treatment at the 10-20 cm depth was more similar to all treatment groups at the
395 30-40 cm depth than were the 10-20 cm Unmanipulated and Ericaceae treatments (Fig. 3b).

396 In some cases, responses to PFG and WT were exhibited by fungal functional groups. Root
397 endophyte relative abundance exhibited a WT x depth interaction, although post-hoc analyses
398 revealed a complicated WT x depth response that was specific to each PFG treatment (Table 1
399 and S3, Supplementary Material; Fig. 4d). Root endophyte OTU richness responded to PFG,
400 where it was lowest in the Ericaceae relative to other treatments at both depths (Table 1 and S3,
401 Supplementary Material; Fig. 4f). qPCR-adjusted saprotroph abundance responded significantly
402 to WT (Table 1; Fig. 4h), being greater in the Low compared to the High WT treatment at the
403 10-20 cm depth (Table S3, Supplementary Material). There were also several cases with
404 marginally significant *P*-values that suggest incipient WT and PFG effects (e.g. 3-way
405 interactions for ErMF and root endophyte relative abundance; Table 1).

406 Some individual ErMF lineages also responded to PFG. While *Rhizoscyphus ericae* did not
407 respond significantly to experimental manipulations, abundance of Sebacinales Group B

responded marginally to PFG (Table 1; Fig. 5a and c), and qPCR-adjusted abundances of both *Oidiodendron maius* and Sebacinales Group B were affected by PFG. Specifically, the Untreated and Ericaceae PFG treatments were generally higher than Sedge in these taxa, driven primarily by a PFG effect in the 10-20 cm depth only (Table 1 and S3, Supplementary Material; Fig. 5d and f).

Fungal community relationships with abiotic variables of peat and pore water

Consistent with hypothesis 4, some abiotic peat and pore water variables covaried with the fungal community (Table S4, Supplementary Material; Fig. 3). However, the abiotic variables were primarily influenced by depth in the peat profile; inconsistent with hypothesis 4, only one variable (pore water pH) exhibited responses to WT and PFG manipulation and these were very small in magnitude (Table 2 and S4, Supplementary Material). Compared to the 10-20 cm depth, the 30-40 cm depth had higher DOC, TDN, E4:E6 and Von Post values, but had lower temperature, E2:E3, and $SUVA_{254}$. The vectors with the strongest relationships in OTU- and order-level ordinations were von Post humification, temperature, and the E2:E3 and E4:E6 organic matter features (Table S5, Supplementary Material; Fig. 3). Von Post humification increased as composition shifted along NMDS axis 1 from the shallow to deeper depth, and this axis explained the majority of variation in the original Bray-Curtis distance matrices for both ordinations (Table S5, Supplementary Material; Fig. 3). In contrast, temperature and E2:E3 vectors increased from the deeper to shallower depth, although these variables' were less colinear with NMDS axis 1 in the OTU-level ordination than was von Post humification. Many of the other pore water variables also exhibited significant relationships with fungal OTU composition, and there was a clear gradient in the community along which TDN, phenolics,

431 $NH4^+$ and DOC decreased, and $SUVA_{254}$ and E2:E3 increased.

432

433 **Discussion**

434 *Fungal community stratification with depth in the peat profile*

435 In support of hypothesis 1, depth in the peat profile had the strongest effect on fungi. Depth
436 stratification of fungal communities has been documented by a number of studies in upland and
437 peat soils (e.g. Artz *et al.* 2007; Taylor *et al.* 2014). For example, in agreement with our findings,
438 sharp decreases in total fungal abundance within the upper 40 cm of peat were recently observed
439 in a bog and poor fen (Lin *et al*. 2014). Such drops in fungal abundance likely reflect the
440 intolerance of many fungi to anoxic conditions below the WT (Kavanagh 2011), combined with
441 declining root subsidy to symbiotic fungi with depth.

442 As predicted, the fungal community shifted from ErMF to saprotroph dominance with
443 increasing depth in the peat profile. This result was supported by relative abundance and OTU
444 richness of functional groups, as well as indicator species analysis. Most indicators of the upper
445 depth were putative ErMF OTUs while those of the lower depth included many saprotrophs, as
446 well as endophytes of unclear function. In fact, the only putative ErMF indicators of the deeper
447 depth were classified as *Rhizoscyphus* sp. These OTUs are likely related to the confirmed ErMF
448 *Rhizoscyphus ericae* as well as potentially non-ErMF fungi in the greater *R. ericae* aggregate;
449 because their function has not been directly characterized, it is possible that they may not be
450 ErMF. Roots at 30-40 cm depth are below the growing season typical WT minimum, the limit to
451 active ericaceous roots (Wallèn 1987; Moore *et al.* 2002). This suggests that the shift from ErMF
452 to saprotroph dominance with increasing depth was also driven by aging and senescence of
453 submerged ericaceous roots buried by accumulating peat. Importantly, ErMF (a whole and the

three lineages examined individually) still decreased with depth after qPCR-adjustment while the depth effect on saprotrophs and endophytes diminished. This highlights the primary role of ErMF in driving the shift with depth, and indicates that saprotrophs and endophytes do not necessarily prefer the deeper depth.

Vertical stratification of communities may also be driven by mycorrhizal fungi actively excluding saprotrophs (Gadgil and Gadgil 1971; Lindahl *et al.* 2007; Fernandez and Kennedy 2016). Extensive extracellular enzymatic capabilities and access to host-derived carbon likely make ErMF formidable competitors with saprotrophs for nutrients in recalcitrant organic matter. Most filamentous saprotrophic fungi likely prefer oxic conditions and should therefore have the greatest abundances in surface peat. A lack of saprotroph preference for the upper depth may indicate that, despite favorable redox and litter quality, saprotrophs were inhibited by ErMF in the upper peat. In upland forests, it is hypothesized that mycorrhizal inhibition of saprotrophs creates depth stratification, where saprotrophs colonize litter at the soil surface and mycorrhizal fungi colonize more humified organic matter in subsurface horizons (Lindahl *et al.* 2007; Fernandez and Kennedy 2016). The vertical distribution of functional group dominance in our peat system was the inverse of this pattern, which likely reflects fundamental differences between the systems: deeper peat is water saturated and the entire soil profile is composed of organic matter. We did not sample the upper 0-10 cm of peat because most of it is represented by living moss, and so the 10-20 cm depth includes what may be considered new litter inputs; this is reflected by low von Post scores.

Consistent with the hypothesis of suppression of saprotrophs in surface peat, our results indicate that taxa capable of decomposing recalcitrant plant material are relatively more important deeper in the peat. As an order and as individual OTUs, Polyporales were indicators of

477 the deeper depth. Polyporales largely specialize in wood decomposition, and the Polyporales
478 OTUs found as indicators are placed in genera (*Phanerochaete*, *Hypochnicium*) that have white
479 rot capabilities (i.e. the enzymatic potential for complete mineralization of lignocellulose; Aust
480 1995). Certain other non-polypore white rot fungi were also indicators of deeper peat, including
481 *Hypholoma*, *Gymnopilus* and *Pleurotus*. In contrast, only one white rot fungus (*Ganoderma*) was
482 an indicator of the shallower depth. Of the four orders that were indicators of surface peat, none
483 is a white rot lineage: one contains fungi that are ErMF in our system (Sebacinales), one contains
484 members with unknown functions (although some may be root-associated;
485 Archaeorhizomycetales) and two contain pathogens, endophytes and non-white rot saprotrophs
486 (Xylariales and Rhytismatales). In fact, the 10-20 cm indicator OTUs found in these two orders
487 are related to plant pathogens: *Physalospora vaccinii* (Xylariales) attacks cranberry fruit
488 (Polashock et al. 2009) and *Colpoma* (Rhytismatales) can infect Ericaceae wood (Johnston
489 1991).
490 Differential patterns of dormancy or preservation of DNA from dead fungal tissues may
491 also influence vertical stratification, although the results suggest that vertical stratification in the
492 fungal community is due to environmental preferences, life histories and interactions among
493 OTUs of active fungi. For example, extracellular relic DNA in soil can affect the picture of
494 community structure revealed through environmental sequencing (Carini *et al.* 2016). However,
495 the sharp decrease in fungal abundance with depth revealed through qPCR suggests that much of
496 the fungal DNA of fungi active in upper peat degrades as it becomes part of the deeper, more
497 humified peat. Furthermore, results indicate that depth stratification in peat is strongly shaped by
498 the presence of ErMF in the active rooting zone of host plants dependent on the these fungi,
499 lending additional support for the role of active fungi driving the patterns of depth stratification.

The future application of RNA sequencing (e.g., Lin *et al.* 2014) will shed further light on the active fungal lineages driving depth stratification in fungal community structure.

Comment [LL4]: I added this paragraph in, to respond to one of the reviewer's comments. Howe does it sound?

Rapid responses to plant functional group and water table manipulation

PFG and WT manipulation should provide evidence for the mechanisms causing depth stratification of fungal communities. If sedges homogenize the community, as we hypothesize, their presence should drive both depths of treatments in which they are present (Unmanipulated and Sedge) to be similar to each other and intermediate between the 10-20 cm and 30-40 cm depths in the treatment from which they were removed (Ericaceae). However, results (for *Oidiodendron maius*, Sebacinales group B and order-level composition) show that PFG primarily influenced the upper depth, and communities in Sedge mesocosms at the 10-20 cm depth were intermediate between mesocosms with ericaceous shrubs at 10-20 cm depth (Ericaceae and Unmanipulated) and all communities at the 30-40 cm depth. This indicates that ericaceous roots and ErMF, which dominate the 10-20 cm depth, are stronger structuring agents for fungal communities than sedge roots present at both depths. This should facilitate depth stratification of fungal communities.

WT manipulation had the least effect on fungi, which is not surprising given the small depth difference of the initial WT treatment. Contrary to our hypotheses, the responses of ErMF and total fungal abundance to WT were too variable to be statistically significant. Instead, saprotrophs and root endophytes both responded to WT, where WT level tended to modulate the effects of PFG or depth in the peat profile. Concerning root endophytes, their co-dominance in the deeper depth suggests they may not be dependent on active host roots, perhaps acting saprotrophically on senescent roots and moss (Day and Currah 2011; Mandyam and Jumpponen

2015). Perhaps consistent with this interpretation, root endophyte relative abundance was primarily affected by WT at the 10-20 cm depth, where endophytes decreased with lower WT in treatments containing ericaceous shrubs (Ericaceae and Unmanipulated) and increased in the Sedge treatment. This could arise if reduced flooding stress on ericaceous roots favors ErMF over root endophytes. In Sedge mesocosms, lowered WTs might have favored endophyte colonization of living roots and/or saprotrophic utilization of dying shrub roots.

Many of the detectable rapid fungal responses to experimental manipulations were modest. Community inertia may slow the response of fungi to PFG manipulation due to survival of hyphae, dormant propagules and/or DNA in the absence of hosts, perhaps explaining why the Sedge treatment supported many ErMF OTUs. Facultative saprotrophy, as has been reported for some ErMF (e.g. *Oidiodendron maius*; Rice and Currah, 2006), may also mute the effects of PFG manipulation. Finally, misassignment of taxa to functional guilds, as discussed earlier for *Rhizoscyphus* sp., could blur the signal of community responses to PFG manipulation. The possibility of misassignment points to the tentative nature of functional group designation in amplicon sequencing datasets, highlighting the importance of efforts to characterize the natural history of a greater range of fungal species (Peay 2014).

Relationship of fungi with abiotic peat and pore water variables

Fungal community composition covaried with several properties of peat and pore water. This could have arisen from a causal link, with fungi affecting peat characteristics or vice versa, or correlation with another variable (e.g. presence of host roots or redox conditions associated with depth). Fungi associated with the 10-20 cm depth (e.g. ErMF) were living in less decomposed peat (lower von Post), with less degraded DOC that was of relatively lower

molecular size (lower E4:E6, higher E2:E3), and had lower overall DOC and TDN concentrations, relative to fungi associated with the 30-40 cm depth (e.g. Polyporales). While the higher $SUVA_{254}$ observed in the shallower depth is at odds with the observed E2:E3 data, it is consistent with less-processed inputs from the breakdown of litter (lignin-like), which is supported by lower E4:E6 (Zhang and He 2015). Many of the differences between depths can be attributed to the 30-40 cm depth being older. However, WT and PFG should have direct and indirect (via microbial community alteration) influences on the vertical stratification of peat and pore water variables; over time, experimental PFG and WT manipulation should outline how these factors promote such vertical stratification.

Conclusions

This study highlights the strong depth stratification of peatland fungal communities. The precipitous drop in total fungal abundance with increasing depth indicate that fungi thrive best in the oxic conditions near the surface. However, the shift in fungal composition with depth in the peat profile was driven by a strong decrease in ErMF that dominate the shallow oxic peat in the sphere of active host roots. The preference of ErMF for the upper peat may constrain saprotrophs and root endophytes to dominating communities in deeper peat, in low oxygen conditions that they may not prefer. Such patterns support the hypothesis that ErMF competitively suppress other fungi in surface peat. Furthermore, the rapid responses to PFG and WT manipulation highlight the importance of these factors in stratifying fungi by depth. Given the abundance of ErMF in surface peat, the likelihood that ErMF effectively compete with saprotrophs, and the potential for a lowered WT to increase ericaceous shrub abundance over time, ErMF are likely to become increasingly important players in peatland carbon cycling as the climate warms.

Comment [LL5]: I had to significantly modify the ending here because a reviewer criticized what we wrote originally. I agree with their criticism, so let me know if the revision sounds OK.

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Table 1. Mixed model results for the effect of plant functional group (PFG), depth to water table (WT) and depth in the peat profile (Depth) on fungal community variables.[abcd]

Response variable[b]	PFG ($F_{2,15}$ P)		WT ($F_{1,15}$ P)		Depth ($F_{1,18}$ P)		PFG x WT ($F_{2,15}$ P)		PFG x Depth ($F_{2,18}$ P)		WT x Depth ($F_{1,18}$ P)		PFG x WT x Depth ($F_{2,18}$ P)	
ITS1 gene abundance	2.13	0.154	0.74	0.404	41.14	***<0.001***	0.21	0.815	0.93	0.413	2.54	0.129	0.79	0.468
Rarefied OTU richness	2.44	0.121	1.48	0.243	0.03	0.855	0.28	0.760	0.43	0.658	0.05	0.823	0.23	0.797
Pielou's OTU evenness	1.21	0.325	3.34	**0.087**	14.3	***0.001***	0.46	0.641	0.33	0.724	0.00	0.901	0.78	0.475
OTU composition	0.96	0.554	0.79	0.782	13.25	***<0.001***	0.86	0.731	0.76	0.811	0.89	0.552	0.91	0.585
OTU composition (presence/absence)	1.01	0.452	0.79	0.744	11.33	***<0.001***	0.89	0.686	0.85	0.689	0.95	0.502	0.92	0.570
Order composition	1.74	***0.039***	0.86	0.568	10.10	***<0.001***	0.63	0.879	0.71	0.753	1.13	0.339	0.75	0.715
Ericoid mycorrhizal fungi														
Relative abundance	1.80	0.199	0.03	0.867	14.11	***0.001***	0.00	0.998	1.09	0.356	0.04	0.843	2.68	**0.096**
qPCR-adjusted abundance	2.09	0.158	0.43	0.524	40.22	***<0.001***	0.03	0.969	1.46	0.258	0.70	0.413	1.23	0.316
OTU richness	0.26	0.773	0.47	0.502	9.05	***0.008***	0.22	0.803	0.73	0.494	0.58	0.456	0.75	0.485
Root endophytes														
Relative abundance	1.42	0.271	0.30	0.594	102.6	***<0.001***	0.53	0.598	1.49	0.251	4.72	***0.043***	2.90	**0.081**
qPCR-adjusted abundance	0.48	0.625	0.01	0.917	2.94	0.104	2.05	0.163	0.14	0.871	0.03	0.861	0.23	0.796
OTU richness	4.22	***0.035***	1.34	0.265	39.11	***<0.001***	0.137	0.873	1.00	0.387	0.01	0.906	2.29	0.130
Total saprotrophs														
Relative abundance	1.08	0.366	1.21	0.289	35.1	***<0.001***	0.75	0.488	0.12	0.901	0.34	0.565	0.80	0.465
qPCR-adjusted abundance	0.01	0.986	4.71	***0.046***	3.77	**0.068**	2.00	0.170	0.48	0.629	3.79	**0.067**	2.52	0.109
OTU richness	2.94	**0.083**	2.40	0.142	15.37	***0.001***	2.12	0.154	0.31	0.739	0.05	0.820	0.22	0.808

Rhizoscyphus ericae														
Relative abundance	0.22	0.804	0.00	0.959	40.77	***<0.001***	0.51	0.608	1.32	0.291	0.50	0.487	1.49	0.251
qPCR-adjusted abundance	1.01	0.389	0.11	0.749	65.96	***<0.001***	0.15	0.862	1.73	0.205	0.06	0.815	1.46	0.259
Sebacinales Group B														
Relative abundance	3.10	**0.075**	0.01	0.926	4.50	***0.050***	0.24	0.788	0.23	0.789	0.242	0.630	036	0.702
qPCR-adjusted abundance	3.85	***0.045***	0.10	0.753	20.95	***<0.001***	0.13	0.881	0.69	0.515	1.22	0.284	0.21	0.816
Oidiodendron maius														
Relative abundance	1.72	0.212	0.69	0.419	14.75	***0.001***	0.19	0.825	1.50	0.249	2.68	0.119	0.70	0.510
qPCR-adjusted abundance	4.33	***0.033***	0.06	0.805	23.91	***<0.001***	0.83	0.453	1.64	0.222	2.14	0.161	0.26	0.771

[a] Models included individual *mesocosm* (random effect) and *block* (fixed effect); no hypothesis test was applied to these factors.

[b] *F* for univariate variables are *F*-ratios for mixed linear models, and *F* for composition are pseudo-*F*-ratios from PERMANOVA.

[c] OTU = operational taxonomic unit.

[d] Bold indicate $0.1>P>0.05$, and bold italics indicate $P \leq 0.05$. Greater than 16% of the tests are significant at $P \leq 0.05$, which is much more than are expected by chance. Additionally, we emphasize that interpretation of $0.1>P>0.05$ should be treated with caution.

Table 2. Pore water and other peat variables (mean ± 1SD).

Response variable[a]	Depth (cm)	Ericaceae High WT	Ericaceae Low WT	Sedge High WT	Sedge Low WT	Unmanipulated High WT	Unmanipulated Low WT	Overall mean	Statistically significant factors[b]
DOC (mgL^{-1})	20	118.2 ± 29.4	112.0 ± 25.1	86.4 ± 11.8	98.7 ± 25.9	112.7 ± 28.3	110.6 ± 16.3	106.4 ± 23.7	***D***
	40	123.3 ± 24.9	119.8 ± 25.7	91.4 ± 11.5	107.9 ± 27.4	119.9 ± 31.3	115.2 ± 14.2	112.9 ± 23.6	
Total phenolics (mgL^{-1})	20	18.22 ± 2.77	20.39 ± 4.57	18.11 ± 2.69	19.44 ± 4.25	20.68 ± 3.45	19.74 ± 3.18	19.43 ± 3.30	
	40	19.32 ± 2.10	21.47 ± 3.59	17.72 ± 3.01	20.78 ± 5.15	21.06 ± 3.51	19.40 ± 1.21	19.96 ± 3.23	
E2:E3	20	6.82 ± 0.68	6.47 ± 0.92	7.11 ± 0.57	6.91 ± 0.95	6.59 ± 0.88	6.33 ± 0.81	6.71 ± 0.77	***D***
	40	6.08 ± 0.75	5.75 ± 0.86	6.58 ± 0.42	6.20 ± 0.85	5.92 ± 0.93	5.89 ± 0.52	6.07 ± 0.71	
E4:E6	20	4.34 ± 0.50	4.05 ± 0.93	4.55 ± 0.43	4.54 ± 0.94	4.37 ± 0.94	4.20 ± 0.95	4.34 ± 0.74	***D***
	40	4.86 ± 0.66	5.57 ± 0.51	5.08 ± 0.69	5.40 ± 0.87	5.17 ± 0.78	5.16 ± 0.69	5.21 ± 0.67	
$SUVA_{254}$	20	3.69 ± 0.87	4.27 ± 0.30	4.57 ± 0.47	4.62 ± 0.81	4.17 ± 0.70	4.18 ± 0.58	4.25 ± 0.66	***D***
	40	3.64 ± 0.71	3.95 ± 0.42	4.37 ± 0.29	4.20 ± 0.79	3.99 ± 0.66	3.97 ± 0.22	4.02 ± 0.54	
TDN (mgL^{-1})	20	3.37 ± 0.94	2.79 ± 0.68	2.57 ± 0.57	3.15 ± 1.28	2.67 ± 0.69	3.05 ± 0.57	2.93 ± 0.79	***D***
	40	3.53 ± 0.84	3.04 ± 0.78	2.58 ± 0.61	3.26 ± 1.19	3.01 ± 0.94	3.19 ± 0.62	3.10 ± 0.81	
NH_4^+ (mgL^{-1})	20	0.47 ± 0.35	0.25 ± 0.09	0.24 ± 0.18	0.41 ± 0.30	0.26 ± 0.19	0.40 ± 0.22	0.34 ± 0.23	
	40	0.53 ± 0.42	0.36 ± 0.16	0.20 ± 0.22	0.46 ± 0.43	0.25 ± 0.26	0.37 ± 0.17	0.36 ± 0.29	
pH	20	3.99 ± 0.09	3.79 ± 0.07	3.99 ± 0.16	3.99 ± 0.21	3.74 ± 0.09	3.89 ± 0.26	3.88 ± 0.17	***D, PFGxD,*** **PFGxWTxD**
	40	3.81 ± 0.04	3.74 ± 0.11	3.87 ± 0.10	3.85 ± 0.13	3.81 ± 0.10	3.84 ± 0.17	3.82 ± 0.11	
Temperature °C	20	18.33 ± 2.25	17.86 ± 0.51	18.19 ± 1.06	18.13 ± 0.16	18.64 ± 0.66	17.96 ± 0.43	18.19 ± 0.99	***D***
	40	17.41 ± 1.46	17.41 ± 0.45	17.32 ± 0.34	17.35 ± 0.26	17.85 ± 0.82	17.40 ± 0.4	17.45 ± 0.69	
Von Post[c]	10-20							2.88 ± 0.95	***D***
	30-40							5.04 ± 1.00	

[a] DOC = dissolved organic carbon, E2:E3 = ratio of absorption spectra at λ = 254 nm to λ = 365 nm, E4:E6 = ratio of absorption spectra at λ = 465 nm to λ = 665 nm, $SUVA_{254}$ = specific ultraviolet absorbance calculated as absorption spectra at λ = 254 nm divided by the DOC, TDN = total dissolved nitrogen.

[b] Results of mixed model analyses or a permutation-based paired *t*-test (Von Post only), see Table S2. Bold indicate $0.1>P>0.05$, and bold italics indicate $P \leq 0.05$. D = depth in peat profile, PFG = plant functional group, WT = water table manipulation. An "x" indicates interactions between factors.

[c] The Von Post humification index was quantified on samples taken prior to experimental manipulation, so its values are averages by depth only.

Figure Legends

Figure 1. Composition by relative abundance and number of OTUs (operational taxonomic units), of the rarefied sequence matrix. OTUs are grouped by class, unless otherwise noted. Graphs are ordered from bottom to top by decreasing number of total sequences per class.

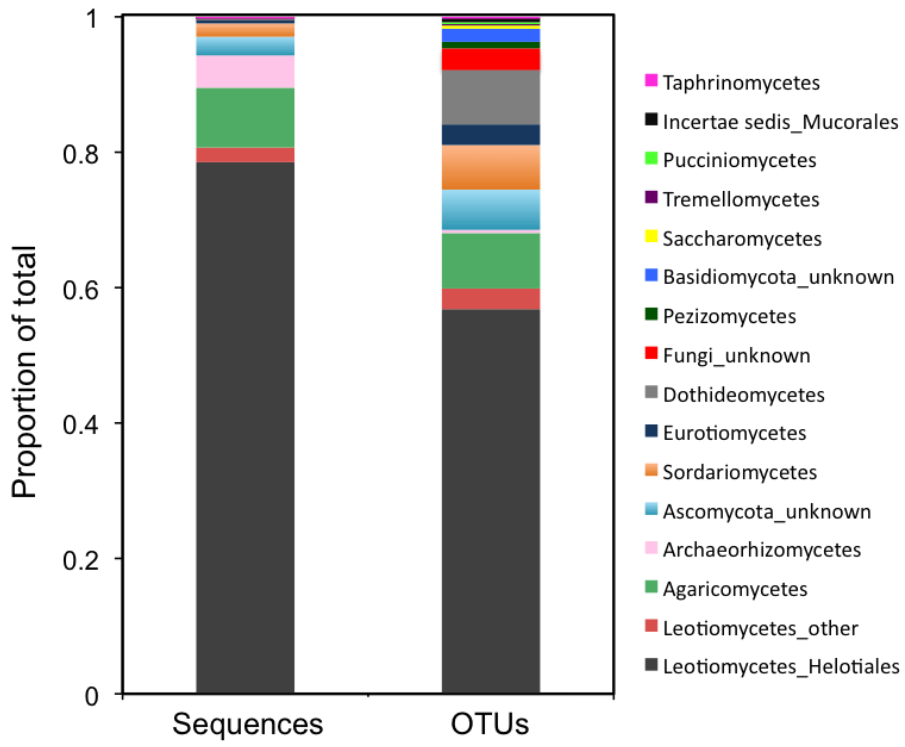
Figure 2. Total ITS1 gene abundance from qPCR (a), as well as OTU richness (b) and evenness (c), for each factor-level combination and averaged by depth. Bars are means ± 1 standard error of the raw data. * indicates a significant (alpha ≤ 0.05) main effect of sampling depth.

Figure 3. Non-metric multidimensional scaling (NMDS) ordinations of fungal OTU (a) and order (b) composition. Arrows represent vectors of variables with their lengths scaled to their relative magnitude (TDN = total dissolved nitrogen, DOC = dissolved organic carbon, Temp. = temperature, VP = von Post score). The locations of individual taxa with the highest indicator values for each depth are plotted by their OTU code numbers or the first four letters of their order (red = 10-20 cm indicators, blue = 30-40 cm indicators; Arch = Archaeorhizomycetales , Seba = Sebacinales, Rhyt = Rhytismatales, Xyla = Xylariales, Polyporales = Poly.). See Tables S1 and S2, Supplementary Material, for OTU taxonomy and indicator species analysis results. WT was not a significant factor and is omitted for clarity of presentation.

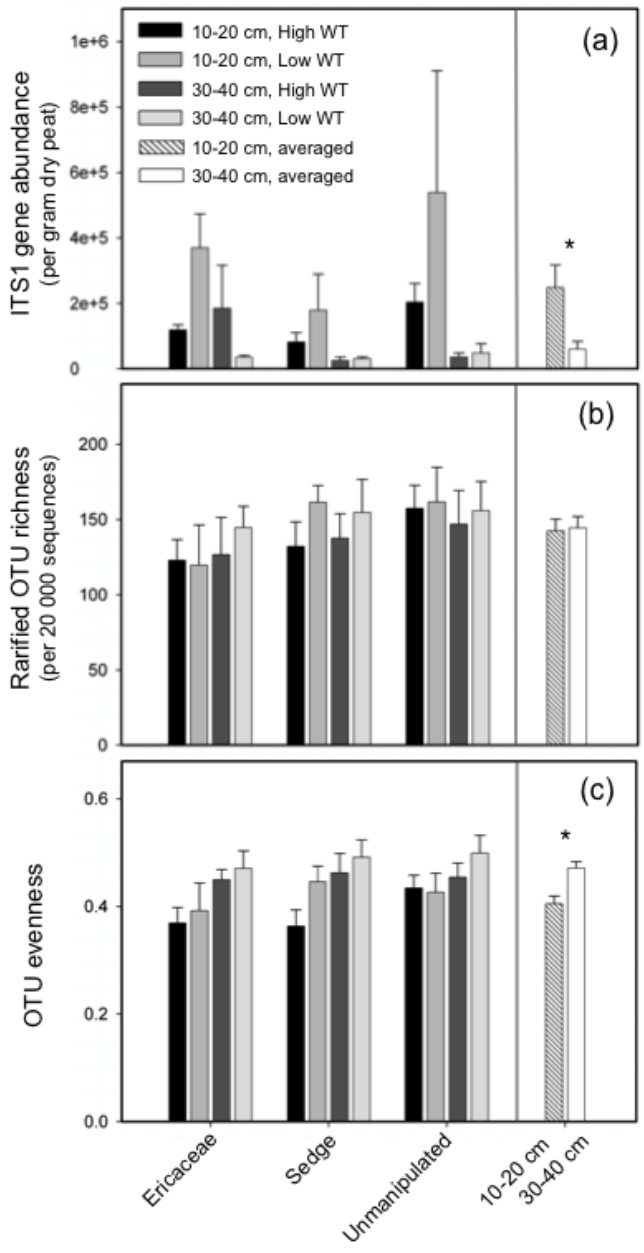
Figure 4. Relative abundance, qPCR-adjusted abundance, and richness of ericoid mycorrhizal fungi (ErMF; a,b,c), root endophytes (d,e,f) and saprotrophic fungi (f,g,h) for each factor-level combination and averaged by depth. Note the variation in y-axis scales. Bars are means ± 1 standard error. * indicates a significant (alpha ≤ 0.05) main effect of sampling depth; see Table S3, Supplementary Material, for pair-wise post hoc tests between specific factor-level combinations.

Figure 5. Relative and qPCR-adjusted abundances of the most common ericoid mycorrhizal fungal lineages in our study: *Rhizocyphus ericae* (a), Sebacinales group B (b), *Oidiodendron maius* (c), for each factor-level combination and pooled by depth. Note the variation in y-axis scales. Bars are means ± 1 standard error. * indicates a significant (alpha ≤ 0.05) main effect of sampling depth; see Table S3, Supplementary Material, for pair-wise post hoc tests between specific factor-level combinations.

Figure 1.

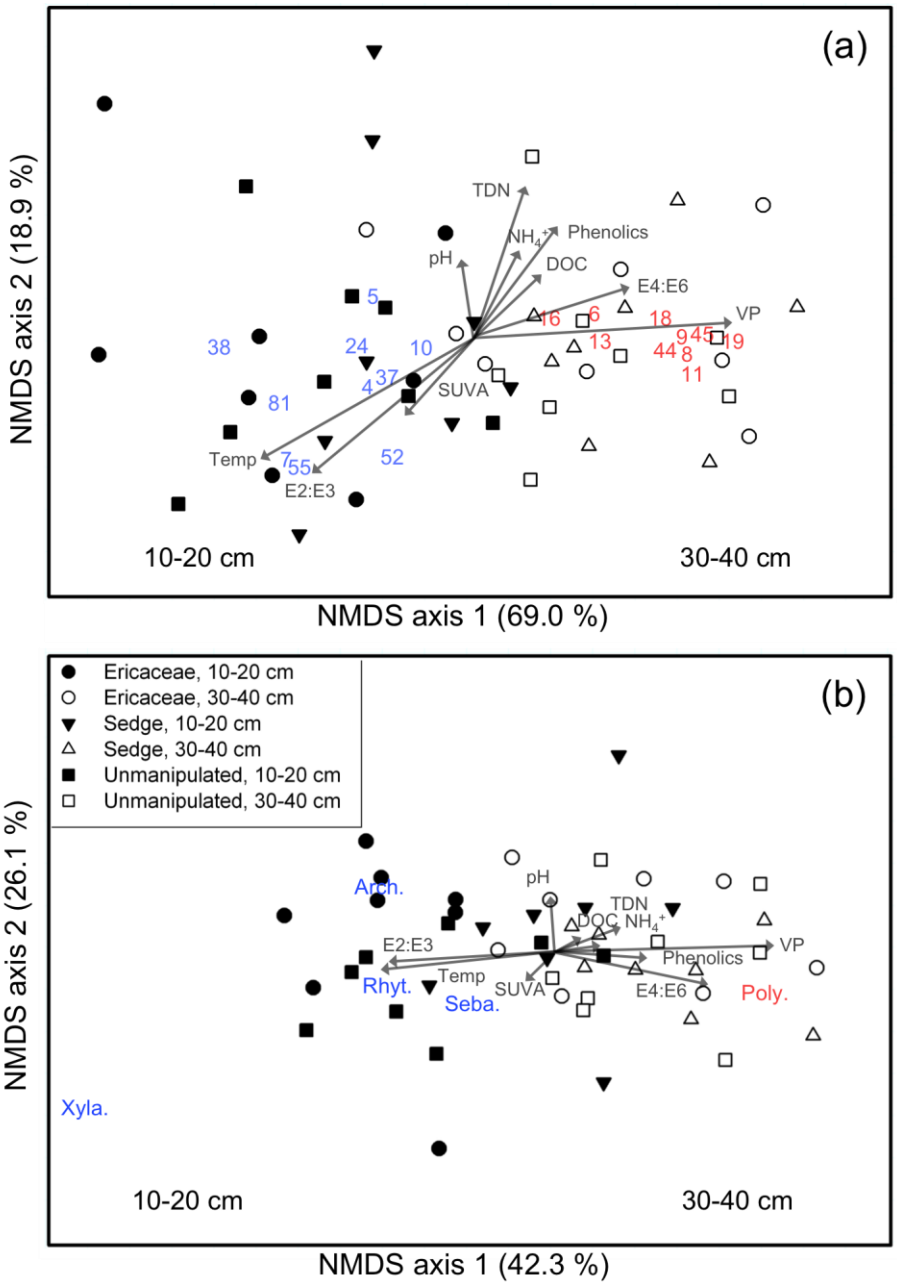

Proportion of total
1
0.8
0.6
0.4
0.2
0
Sequences
OTUs
Taphrinomycetes
Incertae sedis_Mucorales
Pucciniomycetes
Tremellomycetes
Saccharomycetes
Basidiomycota_unknown
Pezizomycetes
Fungi_unknown
Dothideomycetes
Eurotiomycetes
Sordariomycetes
Ascomycota_unknown
Archaeorhizomycetes
Agaricomycetes
Leotiomycetes_other
Leotiomycetes_Helotiales

1 Figure 2


10-20 cm, High WT
10-20 cm, Low WT
30-40 cm, High WT
30-40 cm, Low WT
10-20 cm, averaged
30-40 cm, averaged
(a)
ITS1 gene abundance
(per gram dry peat)
1e+6
8e+5
6e+5
4e+5
2e+5
0
*
(b)
Rarified OTU richness
(per 20 000 sequences)
200
150
100
50
0
(c)
OTU evenness
0.6
0.4
0.2
0.0
*
Ericaceae
Sedge
Unmanipulated
10-20 cm
30-40 cm

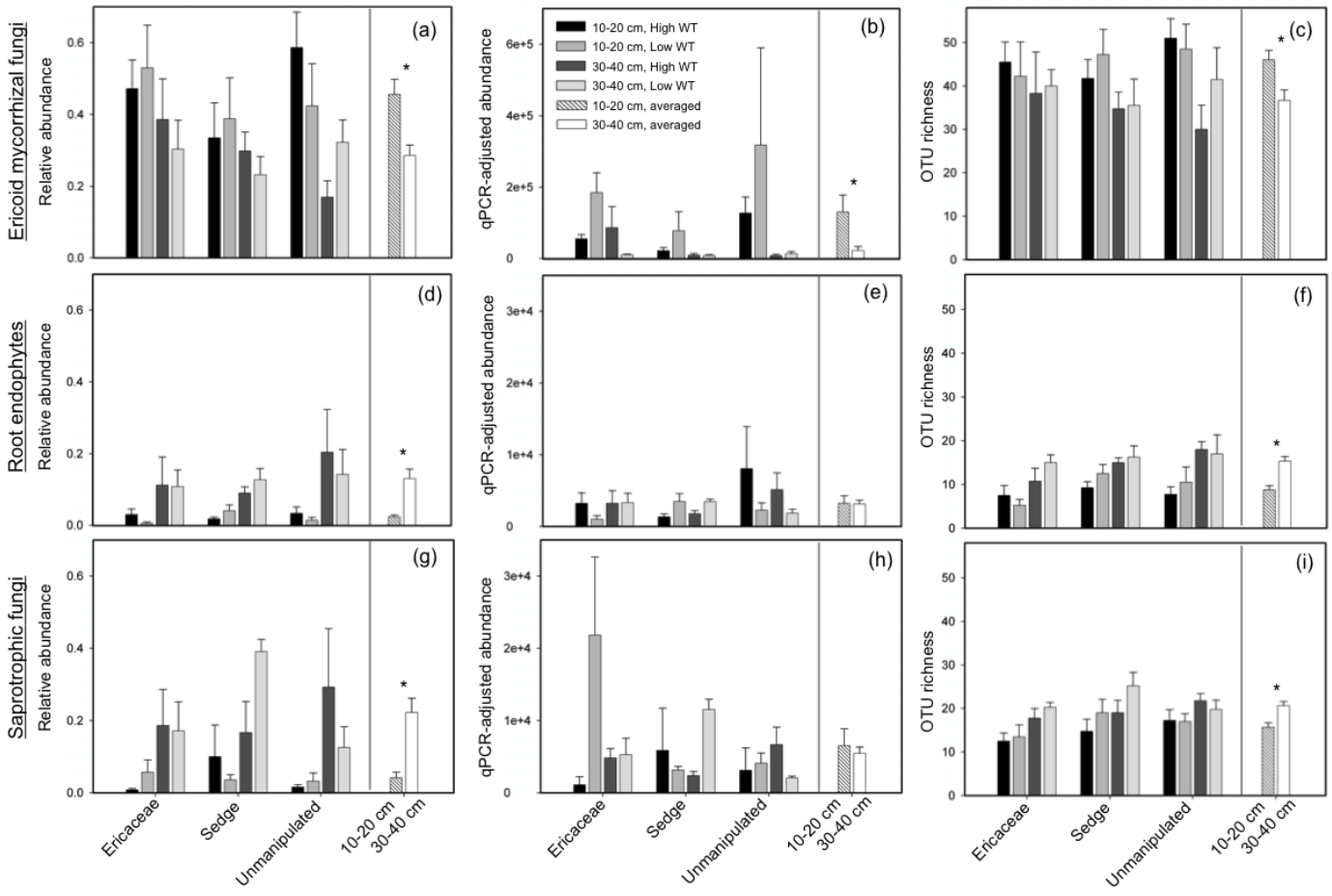
2

1 Figure 3

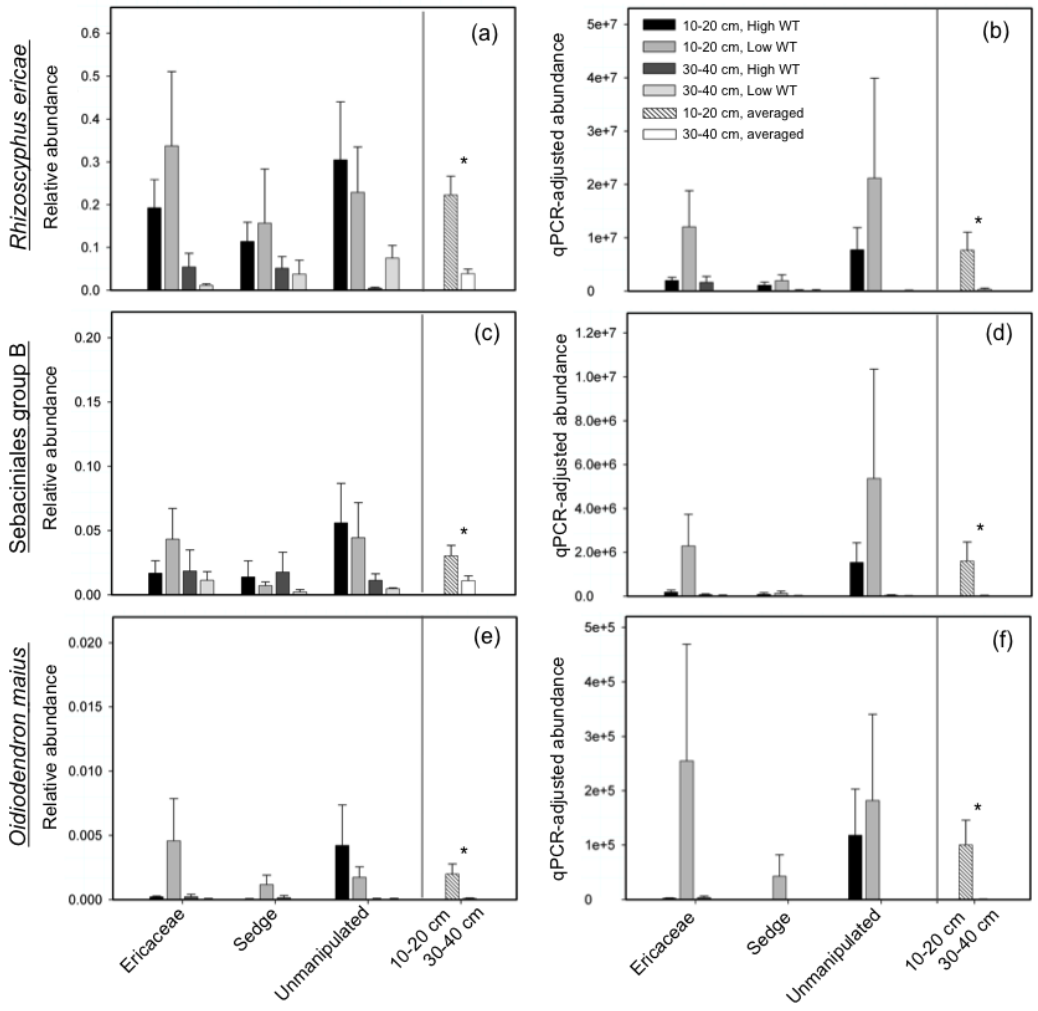

(a)
NMDS axis 2 (18.9 %)
TDN
NH4+
Phenolics
pH
DOC
E4:E6
VP
SUVA
Temp
E2:E3
10-20 cm
30-40 cm
NMDS axis 1 (69.0 %)
(b)
Ericaceae, 10-20 cm
Ericaceae, 30-40 cm
Sedge, 10-20 cm
Sedge, 30-40 cm
Unmanipulated, 10-20 cm
Unmanipulated, 30-40 cm
NMDS axis 2 (26.1 %)
Arch.
Rhyt.
Seba.
Xyla.
Poly.
10-20 cm
30-40 cm
NMDS axis 1 (42.3 %)

2

Figure 4


Ericoid mycorrhizal fungi
Root endophytes
Saprotrophic fungi
Relative abundance
qPCR-adjusted abundance
OTU richness
(a)
(b)
(c)
(d)
(e)
(f)
(g)
(h)
(i)
10-20 cm, High WT
10-20 cm, Low WT
30-40 cm, High WT
30-40 cm, Low WT
10-20 cm, averaged
30-40 cm, averaged
Ericaceae
Sedge
Unmanipulated
10-20 cm
30-40 cm

1 Figure 5


Rhizoscyphus ericae
Relative abundance
qPCR-adjusted abundance
Sebaciniales group B
Relative abundance
qPCR-adjusted abundance
Oidiodendron maius
Relative abundance
qPCR-adjusted abundance
(a)
(b)
(c)
(d)
(e)
(f)
10-20 cm, High WT
10-20 cm, Low WT
30-40 cm, High WT
30-40 cm, Low WT
10-20 cm, averaged
30-40 cm, averaged
Ericaceae
Sedge
Unmanipulated
10-20 cm
30-40 cm

1

1

2

Table S2. Peat depth indicator species analysis results for operational taxonomic units (OTUs) and orders, listed from highest to lowest indicator value within each peat depth.

OTU code #	Indicator specificity	Indicator fidelity	Indicator value	*P*-value	Indicator peat depth (cm)	Taxonomy[a]	Functional group[b]
38	0.981	0.958	0.969	0.0001	10-20	k__Fungi; p__Basidiomycota; c__Agaricomycetes; o__Sebacinales; f__Sebacinales Group B; g__unidentified; s__Sebacinales Group B sp	ErMF
5	0.865	1.000	0.930	0.0071	10-20	k__Fungi; p__Ascomycota; c__Leotiomycetes; o__Helotiales; f__Helotiaceae; g__Rhizoscyphus; s__Rhizoscyphus ericae	ErMF
24	0.895	0.958	0.926	0.0023	10-20	k__Fungi; p__Basidiomycota; c__Agaricomycetes; o__Sebacinales; f__Sebacinales Group B; g__unidentified; s__Sebacinales Group B sp	ErMF
4	0.855	1.000	0.924	0.0004	10-20	k__Fungi; p__Ascomycota; c__Archaeorhizomycetes; o__Archaeorhizomycetales; f__Archaeorhizomycetaceae; g__Archaeorhizomyces; s__Archaeorhizomyces sp	Unknown
37	0.852	1.000	0.923	0.0002	10-20	k__Fungi; p__Ascomycota; c__Leotiomycetes; o__Helotiales; f__Helotiaceae; g__Rhizoscyphus; s__Rhizoscyphus sp	ErMF
102	0.949	0.875	0.911	0.0001	10-20	k__Fungi	Unknown
81	0.952	0.833	0.891	0.0004	10-20	k__Fungi; p__Ascomycota; c__Dothideomycetes; o__Incertae sedis; f__Myxotrichaceae; g__Oidiodendron; s__Oidiodendron maius	ErMF
7	0.905	0.875	0.890	0.0239	10-20	k__Fungi; p__Ascomycota; c__Leotiomycetes; o__Helotiales; f__Helotiaceae; g__Rhizoscyphus; s__Rhizoscyphus ericae	ErMF
55	0.920	0.792	0.853	0.0052	10-20	k__Fungi; p__Ascomycota; c__Leotiomycetes; o__Helotiales	Unknown
197	0.912	0.792	0.849	0.0002	10-20	k__Fungi; p__Ascomycota; c__Leotiomycetes; o__Helotiales; f__Helotiaceae; g__Rhizoscyphus; s__Rhizoscyphus ericae	ErMF
10	0.711	1.000	0.843	0.0012	10-20	k__Fungi; p__Ascomycota; c__Leotiomycetes; o__Helotiales; f__Helotiaceae; g__Rhizoscyphus; s__Rhizoscyphus sp	ErMF
52	0.808	0.833	0.821	0.0209	10-20	k__Fungi; p__Ascomycota; c__Leotiomycetes; o__Helotiales	Unknown
172	0.952	0.708	0.821	0.0001	10-20	k__Fungi; p__Ascomycota; c__Leotiomycetes; o__Helotiales; f__Helotiaceae; g__Rhizoscyphus; s__Rhizoscyphus ericae	ErMF
94	0.832	0.792	0.812	0.006	10-20	k__Fungi; p__Ascomycota; c__Leotiomycetes; o__Rhytismatales; f__Rhytismataceae; g__Colpoma; s__Colpoma sp	Plant pathogen

104	0.979	0.667	0.808	0.0031	10-20	k__Fungi; p__Ascomycota; c__Leotiomycetes; o__Helotiales; f__Helotiaceae; g__Rhizoscyphus; s__Rhizoscyphus ericae	ErMF
87	0.919	0.708	0.807	0.037	10-20	k__Fungi; p__Ascomycota; c__Leotiomycetes; o__Helotiales; f__Helotiaceae; g__Rhizoscyphus; s__Rhizoscyphus ericae	ErMF
219	0.812	0.792	0.802	0.0003	10-20	k__Fungi; p__Ascomycota; c__Leotiomycetes; o__Helotiales; f__Helotiaceae; g__Rhizoscyphus; s__Rhizoscyphus sp	ErMF
90	0.957	0.667	0.799	0.0097	10-20	k__Fungi; p__Ascomycota; c__Leotiomycetes; o__Helotiales; f__Dermateaceae; g__Phaeomollisia; s__Phaeomollisia piceae	Saprotroph
30	0.878	0.708	0.788	0.0494	10-20	k__Fungi; p__Ascomycota; c__Leotiomycetes; o__Helotiales	Unknown
150	0.920	0.667	0.783	0.0025	10-20	k__Fungi; p__Ascomycota; c__Leotiomycetes; o__Helotiales; f__Helotiaceae; g__Rhizoscyphus; s__Rhizoscyphus ericae	ErMF
106	0.816	0.750	0.782	0.0175	10-20	k__Fungi; p__Ascomycota; c__Leotiomycetes; o__Helotiales; f__unidentified; g__unidentified; s__Helotiales sp	Unknown
264	0.723	0.833	0.776	0.0011	10-20	k__Fungi; p__Ascomycota; c__Leotiomycetes; o__Helotiales; f__Helotiaceae; g__Rhizoscyphus	ErMF
123	0.683	0.875	0.773	0.0249	10-20	k__Fungi; p__Basidiomycota; c__Agaricomycetes; o__Polyporales; f__Ganodermataceae; g__Ganoderma; s__Ganoderma lucidum	Saprotroph, white rot
162	0.935	0.625	0.765	0.0008	10-20	k__Fungi; p__Ascomycota; c__Leotiomycetes; o__Helotiales; f__Incertae sedis; g__Cystodendron; s__Cystodendron sp EXP0561F	Pathotroph
151	0.853	0.667	0.754	0.0097	10-20	k__Fungi; p__Ascomycota; c__Leotiomycetes; o__Helotiales; f__Helotiaceae; g__Meliniomyces; s__Meliniomyces variabilis	ErMF
124	0.950	0.583	0.744	0.0065	10-20	k__Fungi; p__Ascomycota; c__Pezizomycetes; o__Pezizales; f__Sarcosomataceae; g__Pseudoplectania; s__Pseudoplectania episphagnum	Saprotroph
223	0.924	0.583	0.734	0.0017	10-20	k__Fungi; p__Ascomycota; c__Leotiomycetes; o__Helotiales; f__Helotiaceae; g__Rhizoscyphus; s__Rhizoscyphus ericae	ErMF
134	0.917	0.583	0.731	0.0065	10-20	k__Fungi; p__Ascomycota; c__Leotiomycetes; o__Helotiales; f__Helotiaceae; g__Rhizoscyphus; s__Rhizoscyphus ericae	ErMF
211	0.755	0.708	0.731	0.0074	10-20	k__Fungi; p__Ascomycota; c__Leotiomycetes; o__Helotiales	Unknown
182	0.795	0.667	0.728	0.0104	10-20	k__Fungi; p__Ascomycota	Unknown
142	0.977	0.542	0.727	0.0046	10-20	k__Fungi; p__Ascomycota; c__Leotiomycetes; o__Helotiales; f__Helotiaceae; g__Rhizoscyphus; s__Rhizoscyphus ericae	ErMF
240	0.904	0.583	0.726	0.0022	10-20	k__Fungi; p__Basidiomycota	Unknown
260	0.900	0.583	0.725	0.0017	10-20	k__Fungi; p__Ascomycota; c__Leotiomycetes; o__Helotiales; f__Helotiaceae; g__Rhizoscyphus;	ErMF

						s__Rhizoscyphus ericae	
146	0.892	0.583	0.721	0.0068	10-20	k__Fungi; p__Ascomycota; c__Leotiomycetes; o__Helotiales; f__Helotiaceae; g__Rhizoscyphus; s__Rhizoscyphus ericae	ErMF
227	0.823	0.625	0.717	0.0219	10-20	k__Fungi; p__Ascomycota; c__Leotiomycetes; o__Helotiales; f__Helotiaceae; g__Rhizoscyphus; s__Rhizoscyphus ericae	ErMF
117	0.747	0.667	0.706	0.0195	10-20	k__Fungi; p__Ascomycota; c__Leotiomycetes; o__Helotiales	Unknown
193	0.742	0.667	0.703	0.0137	10-20	k__Fungi; p__Ascomycota; c__Leotiomycetes; o__Helotiales; f__Helotiaceae	Unknown
371	0.889	0.542	0.694	0.0022	10-20	k__Fungi; p__Ascomycota; c__Leotiomycetes; o__Helotiales; f__Helotiaceae; g__Rhizoscyphus; s__Rhizoscyphus sp	ErMF
229	0.877	0.542	0.689	0.0028	10-20	k__Fungi; p__Ascomycota; c__Leotiomycetes; o__Helotiales; f__Incertae sedis; g__Catenulifera; s__Catenulifera sp	Saprotroph
252	0.922	0.500	0.679	0.0027	10-20	k__Fungi; p__Ascomycota; c__Leotiomycetes; o__Helotiales; f__Helotiaceae; g__Rhizoscyphus; s__Rhizoscyphus ericae	ErMF
161	0.844	0.542	0.676	0.0067	10-20	k__Fungi	Unknown
346	0.976	0.458	0.669	0.0015	10-20	k__Fungi; p__Ascomycota; c__Leotiomycetes; o__Helotiales; f__Helotiaceae; g__Rhizoscyphus	ErMF
160	0.807	0.542	0.661	0.032	10-20	k__Fungi; p__Ascomycota	Unknown
316	0.918	0.458	0.649	0.0203	10-20	k__Fungi; p__Ascomycota; c__Leotiomycetes; o__Helotiales; f__Helotiaceae; g__Rhizoscyphus; s__Rhizoscyphus ericae	ErMF
62	0.998	0.417	0.645	0.0078	10-20	k__Fungi; p__Ascomycota; c__Sordariomycetes; o__Xylariales; f__Hyponectriaceae; g__Physalospora; s__Physalospora vaccinii	Saprotroph
222	1.000	0.417	0.645	0.001	10-20	k__Fungi; p__Ascomycota; c__Leotiomycetes; o__Helotiales; f__Helotiaceae; g__unidentified; s__Helotiaceae sp	Unknown
347	1.000	0.417	0.645	0.0003	10-20	k__Fungi; p__Ascomycota; c__Leotiomycetes; o__Helotiales; f__Helotiaceae; g__Rhizoscyphus; s__Rhizoscyphus ericae	ErMF
364	0.829	0.500	0.644	0.0128	10-20	k__Fungi; p__Ascomycota; c__Leotiomycetes; o__Helotiales	Unknown
377	0.808	0.500	0.635	0.0112	10-20	k__Fungi; p__Ascomycota; c__Leotiomycetes; o__Helotiales	Unknown
248	0.942	0.417	0.627	0.0105	10-20	k__Fungi; p__Ascomycota; c__Leotiomycetes; o__Helotiales; f__Helotiaceae; g__Rhizoscyphus; s__Rhizoscyphus ericae	ErMF
308	0.927	0.417	0.621	0.0235	10-20	k__Fungi; p__Basidiomycota; c__Agaricomycetes	Unknown
401	1.000	0.375	0.612	0.0017	10-20	k__Fungi; p__Ascomycota; c__Leotiomycetes; o__Helotiales; f__Helotiaceae; g__Rhizoscyphus; s__Rhizoscyphus ericae	ErMF
629	1.000	0.375	0.612	0.0012	10-20	k__Fungi; p__Ascomycota; c__Leotiomycetes; o__Helotiales	Unknown

157	0.978	0.375	0.606	0.0153	10-20	k__Fungi; p__Ascomycota; c__Sordariomycetes; o__Chaetosphaeriales; f__unidentified; g__unidentified; s__Chaetosphaeriales sp	Unknown
331	0.800	0.458	0.606	0.0314	10-20	k__Fungi; p__Ascomycota; c__Leotiomycetes; o__Helotiales; f__Helotiaceae; g__Rhizoscyphus; s__Rhizoscyphus sp	ErMF
426	0.962	0.375	0.600	0.0059	10-20	k__Fungi; p__Ascomycota; c__Leotiomycetes; o__Helotiales; f__Helotiaceae; g__Rhizoscyphus; s__Rhizoscyphus ericae	ErMF
128	0.926	0.375	0.589	0.0392	10-20	k__Fungi; p__Basidiomycota; c__Agaricomycetes; o__Agaricales	Unknown
257	0.897	0.375	0.580	0.0246	10-20	k__Fungi; p__Ascomycota	Unknown
198	0.972	0.333	0.569	0.0374	10-20	k__Fungi; p__Ascomycota; c__Leotiomycetes; o__Helotiales; f__Helotiaceae; g__Rhizoscyphus; s__Rhizoscyphus ericae	ErMF
357	0.850	0.375	0.565	0.0416	10-20	k__Fungi; p__Ascomycota; c__Leotiomycetes; o__Helotiales	Unknown
224	0.944	0.333	0.561	0.0318	10-20	k__Fungi; p__Ascomycota; c__Archaeorhizomycetes; o__Archaeorhizomycetales; f__Archaeorhizomycetaceae; g__Archaeorhizomyces; s__Archaeorhizomyces sp	Unknown
187	0.906	0.333	0.550	0.0251	10-20	k__Fungi; p__Ascomycota; c__Leotiomycetes; o__Helotiales; f__Helotiaceae; g__Rhizoscyphus; s__Rhizoscyphus ericae	ErMF
515	1.000	0.292	0.540	0.0106	10-20	k__Fungi; p__Basidiomycota; c__Agaricomycetes; o__Agaricales; f__Clavariaceae; g__Clavaria; s__Clavaria acuta	Saprotroph
525	1.000	0.292	0.540	0.0102	10-20	k__Fungi; p__Ascomycota; c__Leotiomycetes; o__Helotiales; f__Helotiaceae; g__unidentified; s__Helotiaceae sp	Unknown
624	1.000	0.292	0.540	0.0096	10-20	k__Fungi; p__Ascomycota; c__Pezizomycetes; o__Pezizales; f__Sarcosomataceae; g__Urnula; s__Urnula craterium	Saprotroph
414	0.938	0.292	0.523	0.0285	10-20	k__Fungi; p__Ascomycota; c__Leotiomycetes; o__Helotiales; f__Vibrisseaceae; g__Phialocephala; s__Phialocephala hiberna	Root endophyte
362	1.000	0.250	0.500	0.0258	10-20	k__Fungi; p__Ascomycota; c__Leotiomycetes; o__Helotiales	Unknown
453	1.000	0.250	0.500	0.0241	10-20	k__Fungi; p__Ascomycota; c__Sordariomycetes; o__Hypocreales; f__Clavicipitaceae; g__Pochonia; s__Pochonia bulbillosa	Animal pathogen
467	1.000	0.250	0.500	0.0213	10-20	k__Fungi; p__Ascomycota; c__Dothideomycetes; o__Capnodiales	Unknown
544	1.000	0.250	0.500	0.0239	10-20	k__Fungi	Unknown
557	1.000	0.250	0.500	0.0227	10-20	k__Fungi; p__Ascomycota; c__Leotiomycetes; o__Helotiales; f__Helotiaceae; g__Rhizoscyphus; s__Rhizoscyphus sp	ErMF
567	1.000	0.250	0.500	0.0224	10-20	k__Fungi; p__Basidiomycota	Unknown
752	1.000	0.250	0.500	0.0216	10-20	k__Fungi	Unknown
354	0.970	0.250	0.492	0.0473	10-20	k__Fungi; p__Ascomycota; c__Leotiomycetes;	ErMF

						o__Helotiales; f__Helotiaceae; g__Rhizoscyphus; s__Rhizoscyphus ericae	
575	1.000	0.208	0.456	0.0489	10-20	k__Fungi; p__Ascomycota; c__Leotiomycetes; o__Helotiales; f__Helotiaceae; g__Meliniomyces; s__Meliniomyces variabilis	ErMF
636	1.000	0.208	0.456	0.0483	10-20	k__Fungi; p__Ascomycota; c__Leotiomycetes; o__Helotiales; f__Helotiaceae; g__Rhizoscyphus; s__Rhizoscyphus sp	ErMF
18	0.989	1.000	0.995	0.0001	30-40	k__Fungi; p__Basidiomycota; c__Agaricomycetes; o__Polyporales; f__Phanerochaetaceae; g__Phanerochaete	Saprotroph, white rot
8	0.951	1.000	0.975	0.0001	30-40	k__Fungi; p__Ascomycota; c__Leotiomycetes; o__Helotiales; f__Helotiaceae; g__Hymenoscyphus; s__Hymenoscyphus sp aurim710	Saprotroph
9	0.978	0.958	0.968	0.0001	30-40	k__Fungi; p__Ascomycota; c__Leotiomycetes; o__Helotiales; f__Vibrisseaceae; g__Phialocephala; s__Phialocephala hiberna	Root endophyte
13	0.937	1.000	0.968	0.0001	30-40	k__Fungi; p__Ascomycota; c__Leotiomycetes; o__Helotiales; f__Helotiaceae; g__Rhizoscyphus; s__Rhizoscyphus sp	ErMF
19	0.976	0.958	0.967	0.0001	30-40	k__Fungi; p__Ascomycota; c__Leotiomycetes; o__Helotiales; f__Helotiaceae; g__Ascocoryne; s__Ascocoryne sp	Saprotroph
66	0.984	0.917	0.950	0.0001	30-40	k__Fungi; p__Basidiomycota; c__Agaricomycetes	Unknown
44	0.981	0.917	0.948	0.0001	30-40	k__Fungi; p__Ascomycota; c__Leotiomycetes; o__Helotiales; f__Incertae sedis; g__Leptodontidium; s__Leptodontidium sp	Root endophyte
125	0.981	0.917	0.948	0.0001	30-40	k__Fungi; p__Ascomycota; c__Leotiomycetes; o__Helotiales; f__Vibrisseaceae; g__Phialocephala	Root endophyte
69	0.899	0.958	0.928	0.0001	30-40	k__Fungi; p__Basidiomycota; c__Agaricomycetes; o__Agaricales; f__Strophariaceae; g__Hypholoma; s__Hypholoma udum	Saprotroph, white rot
75	0.984	0.875	0.928	0.0001	30-40	k__Fungi; p__Ascomycota; c__Sordariomycetes	Unknown
92	0.948	0.875	0.911	0.0001	30-40	k__Fungi; p__Ascomycota; c__Leotiomycetes; o__Helotiales; f__Vibrisseaceae; g__Phialocephala; s__Phialocephala hiberna	Root endophyte
45	0.960	0.833	0.894	0.0001	30-40	k__Fungi; p__Ascomycota; c__Leotiomycetes; o__Helotiales; f__Helotiaceae; g__Hymenoscyphus	Saprotroph
16	0.829	0.958	0.891	0.0037	30-40	k__Fungi; p__Ascomycota; c__Leotiomycetes; o__Helotiales; f__Vibrisseaceae; g__Phialocephala	Root endophyte
6	0.783	1.000	0.885	0.0308	30-40	k__Fungi; p__Basidiomycota; c__Agaricomycetes; o__Polyporales; f__Meruliaceae; g__Hypochnicium; s__Hypochnicium albostramineum	Saprotroph, white rot
11	0.989	0.792	0.885	0.0003	30-40	k__Fungi; p__Ascomycota; c__Leotiomycetes	Unknown
85	0.981	0.792	0.881	0.0001	30-40	k__Fungi; p__Ascomycota; c__Leotiomycetes; o__Helotiales	Unknown
41	0.911	0.792	0.849	0.0021	30-40	k__Fungi; p__Ascomycota	Unknown
100	0.926	0.708	0.810	0.0007	30-40	k__Fungi; p__Ascomycota; c__Eurotiomycetes; o__Eurotiales; f__Trichocomaceae; g__Penicillium;	Saprotroph

						s__Penicillium spinulosum	
40	0.982	0.667	0.809	0.0037	30-40	k__Fungi; p__Ascomycota; c__Leotiomycetes	Unknown
144	0.978	0.667	0.808	0.0001	30-40	k__Fungi; p__Ascomycota; c__Sordariomycetes; o__Coniochaetales; f__Coniochaetaceae; g__Lecythophora; s__Lecythophora sp	Root endophyte
153	0.733	0.875	0.801	0.0018	30-40	k__Fungi; p__Ascomycota; c__Leotiomycetes; o__Helotiales; f__Helotiaceae; g__unidentified; s__Helotiaceae sp	Unknown
111	0.895	0.708	0.796	0.0009	30-40	k__Fungi; p__Ascomycota; c__Leotiomycetes; o__Helotiales; f__Helotiaceae; g__Rhizoscyphus; s__Rhizoscyphus sp	ErMF
56	0.864	0.708	0.782	0.0112	30-40	k__Fungi; p__Ascomycota; c__Leotiomycetes; o__Helotiales; f__Vibrisseaceae; g__Phialocephala; s__Phialocephala hiberna	Root endophyte
267	0.891	0.667	0.771	0.0001	30-40	k__Fungi; p__Ascomycota; c__Leotiomycetes; o__Helotiales; f__Helotiaceae; g__Rhizoscyphus; s__Rhizoscyphus sp	ErMF
147	0.832	0.708	0.768	0.0004	30-40	k__Fungi; p__Ascomycota; c__Leotiomycetes; o__Helotiales; f__Helotiaceae; g__Rhizoscyphus; s__Rhizoscyphus sp	ErMF
170	1.000	0.583	0.764	0.0001	30-40	k__Fungi; p__Ascomycota	Unknown
195	0.766	0.750	0.758	0.0015	30-40	k__Fungi; p__Ascomycota; c__Leotiomycetes; o__Helotiales; f__Helotiaceae; g__unidentified; s__Helotiaceae sp	Unknown
164	0.842	0.667	0.749	0.0049	30-40	k__Fungi; p__Ascomycota; c__Leotiomycetes; o__Helotiales; f__Helotiaceae; g__Rhizoscyphus; s__Rhizoscyphus sp	ErMF
225	0.896	0.625	0.748	0.0007	30-40	k__Fungi; p__Ascomycota; c__Leotiomycetes; o__Helotiales; f__Vibrisseaceae; g__Phialocephala	Root endophyte
118	0.608	0.917	0.747	0.0277	30-40	k__Fungi; p__Ascomycota; c__Leotiomycetes; o__Helotiales; f__Helotiaceae; g__unidentified; s__Helotiaceae sp	Unknown
241	0.923	0.583	0.734	0.0002	30-40	k__Fungi; p__Ascomycota; c__Leotiomycetes; o__Helotiales; f__Helotiaceae	Unknown
234	0.959	0.542	0.721	0.0001	30-40	k__Fungi; p__Ascomycota; c__Leotiomycetes; o__Helotiales; f__Helotiaceae; g__Ascocoryne; s__Ascocoryne sp	Saprotroph
194	0.729	0.708	0.719	0.0154	30-40	k__Fungi; p__Ascomycota; c__Leotiomycetes; o__Helotiales; f__Helotiaceae; g__Rhizoscyphus; s__Rhizoscyphus sp	ErMF
206	0.880	0.583	0.716	0.0047	30-40	k__Fungi; p__Basidiomycota; c__Agaricomycetes; o__Agaricales; f__Pleurotaceae; g__Pleurotus; s__Pleurotus ostreatus	Saprotroph, white rot
338	0.929	0.542	0.709	0.0005	30-40	k__Fungi; p__Ascomycota; c__Leotiomycetes; o__Helotiales; f__Vibrisseaceae; g__Phialocephala	Root endophyte
312	1.000	0.500	0.707	0.0001	30-40	k__Fungi; p__Ascomycota; c__Leotiomycetes; o__Helotiales; f__Helotiaceae	Unknown

80	0.984	0.500	0.701	0.0035	30-40	k__Fungi; p__Ascomycota; c__Leotiomycetes; o__Helotiales; f__Incertae sedis; g__Leptodontidium; s__Leptodontidium sp	Root endophyte
418	0.900	0.542	0.698	0.0007	30-40	k__Fungi; p__Ascomycota; c__Leotiomycetes; o__Helotiales; f__Helotiaceae; g__unidentified; s__Helotiaceae sp	Unknown
221	0.772	0.625	0.695	0.0084	30-40	k__Fungi; p__Ascomycota; c__Leotiomycetes; o__Helotiales; f__Helotiaceae; g__unidentified; s__Helotiaceae sp	Unknown
349	0.958	0.500	0.692	0.0005	30-40	k__Fungi; p__Basidiomycota; c__Agaricomycetes; o__Agaricales; f__Strophariaceae; g__Gymnopilus	Saprotroph, white rot
22	0.996	0.458	0.676	0.0435	30-40	k__Fungi; p__Ascomycota; c__Leotiomycetes; o__Helotiales	Unknown
324	0.909	0.500	0.674	0.0007	30-40	k__Fungi; p__Ascomycota; c__Leotiomycetes; o__Helotiales; f__Helotiaceae; g__unidentified; s__Helotiaceae sp	Unknown
337	0.968	0.458	0.666	0.0009	30-40	k__Fungi; p__Basidiomycota; c__Agaricomycetes; o__Agaricales; f__Strophariaceae; g__Hypholoma; s__Hypholoma sp	Saprotroph, white rot
278	0.708	0.625	0.665	0.0438	30-40	k__Fungi; p__Ascomycota; c__Leotiomycetes; o__Helotiales	Unknown
199	0.851	0.500	0.652	0.005	30-40	k__Fungi; p__Ascomycota; c__Leotiomycetes; o__Helotiales; f__Helotiaceae; g__Hymenoscyphus; s__Hymenoscyphus sp aurim710	Saprotroph
470	1.000	0.417	0.645	0.0005	30-40	k__Fungi; p__Basidiomycota	Unknown
226	0.892	0.458	0.639	0.0059	30-40	k__Fungi; p__Ascomycota; c__Leotiomycetes; o__Helotiales; f__Vibrisseaceae; g__Phialocephala	Root endophyte
273	0.958	0.417	0.632	0.0023	30-40	k__Fungi; p__Basidiomycota; c__Agaricomycetes	Unknown
398	0.955	0.417	0.631	0.0028	30-40	k__Fungi; p__Ascomycota; c__Leotiomycetes; o__Helotiales; f__Helotiaceae; g__Rhizoscyphus; s__Rhizoscyphus sp	ErMF
381	0.857	0.458	0.627	0.0053	30-40	k__Fungi; p__Ascomycota; c__Leotiomycetes; o__Helotiales; f__Helotiaceae; g__Rhizoscyphus; s__Rhizoscyphus sp	ErMF
23	0.842	0.458	0.621	0.037	30-40	k__Fungi; p__Ascomycota; c__Leotiomycetes; o__Incertae sedis; f__Incertae sedis; g__Geniculospora; s__Geniculospora grandis	Saprotroph
289	0.909	0.417	0.615	0.0045	30-40	k__Fungi; p__Ascomycota; c__Pezizomycetes; o__Pezizales; f__Pyronemataceae; g__Scutellinia; s__Scutellinia sp	Saprotroph
145	1.000	0.375	0.612	0.0015	30-40	k__Fungi; p__Ascomycota	Unknown
286	1.000	0.375	0.612	0.0014	30-40	k__Fungi; p__Ascomycota; c__Leotiomycetes; o__Helotiales; f__Helotiaceae; g__Hymenoscyphus; s__Hymenoscyphus sp aurim710	Saprotroph
405	1.000	0.375	0.612	0.0017	30-40	k__Fungi; p__Ascomycota; c__Leotiomycetes; o__Helotiales; f__Helotiaceae; g__Rhizoscyphus; s__Rhizoscyphus sp	ErMF
237	0.742	0.500	0.609	0.0257	30-40	k__Fungi; p__Ascomycota; c__Leotiomycetes; o__Helotiales; f__Vibrisseaceae; g__Phialocephala	Root endophyte

61	0.986	0.375	0.608	0.0242	30-40	k__Fungi; p__Ascomycota; c__Leotiomycetes; o__Helotiales; f__Helotiaceae; g__Ascocoryne; s__Ascocoryne sp	Saprotroph
314	0.763	0.458	0.591	0.0362	30-40	k__Fungi; p__Ascomycota; c__Eurotiomycetes; o__Eurotiales; f__Trichocomaceae; g__Aspergillus; s__Aspergillus cibarius	Saprotroph
530	1.000	0.333	0.577	0.0037	30-40	k__Fungi; p__Basidiomycota; c__Agaricomycetes; o__Agaricales; f__Strophariaceae; g__Hypholoma; s__Hypholoma udum	Saprotroph, white rot
291	0.875	0.375	0.573	0.0243	30-40	k__Fungi; p__Ascomycota; c__Leotiomycetes; o__Helotiales	Unknown
313	0.938	0.333	0.559	0.0261	30-40	k__Fungi	Unknown
394	0.833	0.375	0.559	0.0215	30-40	k__Fungi; p__Ascomycota; c__Leotiomycetes; o__Helotiales; f__Vibrisseaceae	Unknown
442	0.929	0.333	0.556	0.014	30-40	k__Fungi; p__Ascomycota; c__Leotiomycetes; o__Helotiales; f__Helotiaceae; g__Rhizoscyphus; s__Rhizoscyphus sp	ErMF
380	0.885	0.333	0.543	0.0389	30-40	k__Fungi; p__Ascomycota; c__Leotiomycetes; o__Helotiales; f__Incertae sedis	Unknown
283	0.969	0.292	0.532	0.0154	30-40	k__Fungi; p__Ascomycota; c__Leotiomycetes	Unknown
396	0.960	0.292	0.529	0.0196	30-40	k__Fungi; p__Ascomycota; c__Pezizomycetes; o__Pezizales; f__Pyronemataceae; g__Scutellinia; s__Scutellinia sp	Saprotroph
606	1.000	0.250	0.500	0.0214	30-40	k__Fungi; p__Ascomycota; c__Leotiomycetes; o__Helotiales	Unknown
612	1.000	0.250	0.500	0.0218	30-40	k__Fungi; p__Ascomycota; c__Leotiomycetes; o__Helotiales; f__Helotiaceae	Unknown
667	1.000	0.250	0.500	0.0214	30-40	k__Fungi; p__Ascomycota; c__Eurotiomycetes; o__Eurotiales; f__Trichocomaceae; g__Penicillium; s__Penicillium melinii	Saprotroph
97	1.000	0.208	0.456	0.0499	30-40	k__Fungi; p__Ascomycota; c__Leotiomycetes; o__Helotiales; f__Vibrisseaceae; g__Acephala; s__Acephala sp 1	Root endophyte, Ectomycorrhizal
393	1.000	0.208	0.456	0.0487	30-40	k__Fungi; p__Ascomycota; c__Leotiomycetes; o__Helotiales	Unknown
792	1.000	0.208	0.456	0.0489	30-40	k__Fungi; p__Ascomycota; c__Leotiomycetes	Unknown
799	1.000	0.208	0.456	0.0464	30-40	k__Fungi	Unknown
Archaeorhizo-mycetales	0.8545	1	0.924	0.0003	10-20	k__Fungi; p__Ascomycota ;c__Archaeorhizomycetes; o__Archaeorhizomycetales	
Sebacinales	0.7335	1	0.856	0.0375	10-20	k__Fungi; p__Basidiomycota; c__Agaricomycetes; o__Sebacinales	
Rhytismatales	0.823	0.7917	0.807	0.0078	10-20	k__Fungi; p__Ascomycota; c__Leotiomycetes; o__Rhytismatales	
Xylariales	0.9979	0.4583	0.676	0.0033	10-20	k__Fungi; p__Ascomycota; c__Sordariomycetes; o__Xylariales	
Polyporales	0.8216	1	0.906	0.0059	30-40	k__Fungi; p__Basidiomycota; c__Agaricomycetes; o__Polyporales	

[a]Taxonomy is arranged in order by kingdom, phylum, class, order, family, genus and species, with the initial of the taxonomic ranking preceding each name. Taxonomy is based on RDP classifier assignments.

[b]Functional assignments should be treated as putative. ErMF = ericoid mycorrhizal fungus.

Table S3. Least squares means for post hoc tests. Factor-level combinations that do not share a group number within a comparison are considered significantly different as a given alpha-level. The multivariate *t*-test method was used to correct for multiple comparisons, within a set of tests.

(a)

Root endophyte relative abundance

Among WT x Depth factor levels, within PFG

PFG	WT	Depth (cm)	LS mean	Lower 95% CL	Upper 95% CL	Group (P<0.1)	Group (P≤0.05)
Ericaceae	High	10-20	5.251	3.763	6.739	1,2	1,2
Ericaceae	Low	10-20	3.905	2.417	5.393	1	1
Ericaceae	High	30-40	6.272	4.784	7.760	3	1,2
Ericaceae	Low	30-40	7.105	5.617	8.593	2,3	2
PFG	WT	Depth (cm)	LS mean	Lower 95% CL	Upper 95% CL	Group (P<0.1)	Group (P≤0.05)
Sedge	High	10-20	5.799	4.311	7.287	1,2	1,2
Sedge	Low	10-20	6.246	4.758	7.734	1,3	1,3
Sedge	High	30-40	7.444	5.956	8.932	3,4	3,4
Sedge	Low	30-40	7.757	6.269	9.245	2,4	2,4
PFG	WT	Depth (cm)	LS mean	Lower 95% CL	Upper 95% CL	Group (P<0.1)	Group (P≤0.05)
Unmanipulated	High	10-20	5.724	4.236	7.212	1,2	1,2
Unmanipulated	Low	10-20	4.379	2.891	5.867	1	1
Unmanipulated	High	30-40	7.856	6.368	9.344	3	3
Unmanipulated	Low	30-40	7.086	5.598	8.574	2,3	2,3

(b)

Root endophyte OTU richness

Among PFG within Depths, WT pooled

PFG	Depth (cm)	LS mean	Lower 95% CL	Upper 95% CL	Group (P<0.1)	Group (P≤0.05)
ericaceae	10-20	6.375	3.643	9.107	1	1
sedge	10-20	10.875	8.143	13.607	2	1
unmanipulated	10-20	9.125	6.393	11.857	1,2	1
PFG	Depth (cm)	LS mean	Lower 95% CL	Upper 95% CL	Group (P<0.1)	Group (P≤0.05)
ericaceae	30-40	12.875	10.143	15.607	1	1
sedge	30-40	15.625	12.893	18.357	1,2	1
unmanipulated	30-40	17.500	14.768	20.232	2	1

(c)

Saprotroph qPCR-adjusted abundance (log transformed for analyses)

Between WT treatments within Depths, PFG pooled

WT	Depth (cm)	LS mean	Lower 95% CL	Upper 95% CL	Group (P<0.1)	Group (P≤0.05)
High	10-20	7.027	6.373	7.682	1	1
Low	10-20	8.380	7.726	9.035	2	2

WT	Depth (cm)	LS mean	Lower 95% CL	Upper 95% CL	Group (P<0.1)	Group (P≤0.05)
High	30-40	8.226	7.572	8.881	1	1
Low	30-40	8.378	7.724	9.033	1	1

(d)

Sebacinales group B qPCR-adjusted abundance (log transformed for analyses)

Among PFG within Depths, WT pooled

PFG	Depth (cm)	LS mean	Lower 95% CL	Upper 95% CL	Group (P<0.1)	Group (P≤0.05)
ericaceae	10-20	12.382	10.825	13.939	2	1,2
sedge	10-20	10.205	8.648	11.761	1	1
unmanipulated	10-20	13.129	11.572	14.686	2	2

PFG	Depth (cm)	LS mean	Lower 95% CL	Upper 95% CL	Group (P<0.1)	Group (P≤0.05)
ericaceae	30-40	9.904	8.348	11.461	1	1
sedge	30-40	8.244	6.688	9.801	1	1
unmanipulated	30-40	9.523	7.966	11.080	1	1

(e)

Oidiodendron maius qPCR-adjusted abundance (log transformed for analyses)

Among PFG within Depths, WT pooled

PFG	Depth (cm)	LS mean	Lower 95% CL	Upper 95% CL	Group (P<0.1)	Group (P≤0.05)
ericaceae	10-20	7.881	5.498	10.264	1,2	1,2
sedge	10-20	4.867	2.484	7.250	1	1
unmanipulated	10-20	9.873	7.491	12.256	2	2

PFG	Depth (cm)	LS mean	Lower 95% CL	Upper 95% CL	Group (P<0.1)	Group (P≤0.05)
ericaceae	30-40	1.391	-0.991	3.774	1	1
sedge	30-40	4.316	1.933	6.699	1	1
unmanipulated	30-40	2.608	0.225	4.991	1	1

Table S4. Mixed model results examining the effect of plant functional group (PFG), depth to water table (WT) and depth in the peat profile (Depth) on porewater and peat variables.[abcd]

Response variable	PFG (*F* df *P*)	WT (*F* df *P*)	Depth (*F* df *P*)	PFG x WT (*F* df *P*)	PFG x Depth (*F* df *P*)	WT x Depth (*F* df *P*)	PFG x WT x Depth (*F* df *P*)
DOC	1.92 2,15 0.181	0.04 1,15 0.839	34.16 1,18 ***<0.001***	0.39 2,15 0.683	0.10 2,18 0.906	0.416 1,18 0.527	0.89 2,18 0.429
Phenolics	0.26 2,15 0.777	0.53 1,15 0.480	1.92 1,18 0.183	0.67 2,15 0.523	0.66 2,18 0.527	0.19 1,18 0.671	0.92 2,18 0.417
E2:E3	1.04 2,15 0.376	0.70 1,15 0.416	165.9 1,18 ***<0.001***	0.04 2,15 0.963	1.16 2,18 0.336	0.07 1,18 0.799	1.44 2,18 0.263
E4:E6	0.27 2,15 0.771	0.16 1,15 0.699	10.74 1,18 ***<0.001***	0.16 2,15 0.851	0.25 2,18 0.783	1.68 1,18 0.211	0.47 2,18 0.631
$SUVA_{254}$	1.65 2,15 0.225	0.26 1,15 0.614	17.48 1,18 ***0.001***	0.40 2,15 0.676	0.52 2,18 0.602	2.55 1,18 0.128	0.43 2,18 0.659
TDN	0.23 2,15 0.799	0.13 1,15 0.727	11.92 1,18 ***0.003***	0.90 2,15 0.427	1.32 2,18 0.292	0.00 1,18 0.947	1.12 2,18 0.349
NH_4^+	0.20 2,15 0.819	0.19 1,15 0.666	0.81 1,18 0.381	1.22 2,15 0.322	1.20 2,18 0.325	0.46 1,18 0.507	0.29 2,18 0.752
pH	0.61 2,15.0 0.557	0.20 1,15.0 0.663	10.3 1,15.4 ***0.006***	0.1.3 2,15.0 0.290	3.73 2,15.4 ***0.048***	0.24 1,15.4 0.634	2.79 2,15.4 **0.092**
Temperature	0.16 2,15 0.855	0.73 1,15 0.406	38.71 1,18 ***<0.001***	0.27 2,15 0.765	0.131 2,18 0.878	0.314 1,18 1.07	0.24 2,18 0.792
			(*t*, *P*)				
Von Post			8.33 ***<0.001***				

[a] DOC = dissolved organic carbon, E2:E3 = ratio of absorption spectra at λ = 254 nm to λ = 365 nm, E4:E6 = ratio of absorption spectra at λ = 465 nm to λ = 665 nm, $SUVA_{254}$ = specific ultraviolet absorbance calculated as absorption spectra at λ = 254 nm divided by the DOC, TDN = total dissolved nitrogen.

[b] Models included individual *mesocosm* (random effect) and *block* (fixed effect); no hypothesis test was applied to these factors.

[c] *F* are *F*-ratios for linear mixed models. *t* is from a permutation-based paired *t*-test.

[d] Bold indicate $0.1 > P > 0.05$, and bold italics indicate $P \leq 0.05$.

Table S5. Results of ordination vector analysis with peat and pore water variables; bold italics indicate variables significant at $P \leq 0.05$.

	OTU			Order		
Variable	*r*	R^2	*P*	*r*	R^2	*P*
Tannins	0.353	0.125	***0.049***	0.233	0.054	0.285
DOC	0.222	0.049	0.326	0.054	0.003	0.935
TDN	0.380	0.144	***0.029***	0.190	0.036	0.435
TDN:DOC	0.465	0.216	***0.005***	0.293	0.086	0.132
Ammonium	0.252	0.064	0.225	0.093	0.009	0.821
E2:E3	0.496	0.246	***0.002***	0.386	0.149	***0.026***
E2:E4	0.389	0.151	***0.026***	0.401	0.161	***0.017***
SUVA254	0.232	0.054	0.293	0.112	0.013	0.754
Temperature	0.548	0.301	***<0.001***	0.394	0.155	***0.021***
pH	0.178	0.032	0.492	0.241	0.058	0.256
Von Post	0.631	0.398	***<0.001***	0.541	0.293	***<0.001***

Figure S1. Rainfall episodes and water table (WT) depths in mesocosm bins over the course of the 2011 growing season. Horizontal bars over rainfall events represent episodes where rain-out shelters were used to exclude precipitation from Low WT treatments. Lines for WT depths represent means and 95% confidence intervals for the 12 bins from each water table treatment. The two peat coring depths are placed across the time interval where cores were collected.

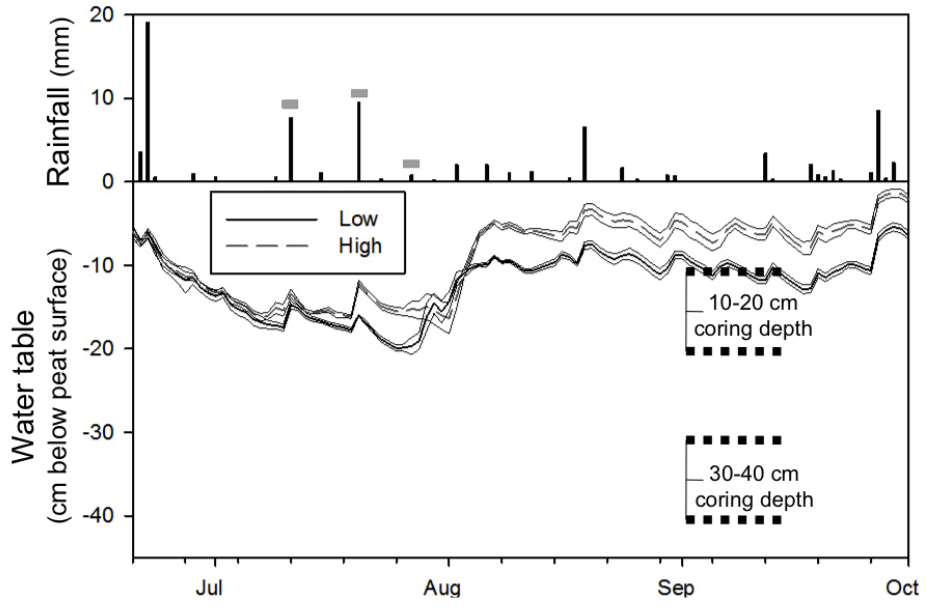


Figure S2. Individual rarefaction curves for each of the 48 samples. Final statistical analyses for this study were performed using a matrix rarefied to 20 000 operational taxonomic units (OTUs) per sample.