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Article type : Primary Research Articles

Running Title: Microbial composition mediates soil C storage

Anthropogenic N deposition alters soil organic matter biochemistry and microbial communities on decaying fine roots

Submitted as a Primary Research Article to: *Global Change Biology*

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ABSTRACT

Fine root litter is a primary source of soil organic matter (SOM), which is a globally important pool of C that is responsive to climate change. We previously established that ~20 years of experimental nitrogen (N) deposition has slowed fine root decay and increased the storage of soil carbon (C; +18%) across a widespread northern hardwood forest ecosystem. However, the microbial mechanisms that have directly slowed fine root decay are unknown. Here, we show that experimental N deposition has decreased the relative abundance of Agaricales fungi (-31%) and increased that of partially ligninolytic Actinobacteria (+24%) on decaying fine roots. Moreover, experimental N deposition has increased the relative abundance of lignin-derived compounds residing in SOM (+53%), and this biochemical response is significantly related to shifts in both fungal and bacterial community composition. Specifically, the accumulation of lignin-derived compounds in SOM is negatively related to the relative abundance of ligninolytic *Mycena* and *Kuehneromyces* fungi, and positively related to Microbacteriaceae. Our findings suggest that by altering the composition of microbial communities on decaying fine roots such that their capacity for lignin degradation is reduced, experimental N deposition has slowed fine root litter decay, and increased the contribution of lignin-derived compounds from fine roots to SOM. The microbial responses we observed may explain widespread findings that anthropogenic N deposition increases soil C storage in terrestrial ecosystems. More broadly, our findings directly link composition to function in soil microbial communities, and implicate compositional shifts in mediating biogeochemical processes of global significance.

Key Words: *Soil carbon, root decay, microbial decomposition, fungal community, bacterial community, lignin, biogeochemical feedback*

INTRODUCTION

The microbial decay of fine root litter is a major component of the terrestrial carbon (C) cycle (Schlesinger & Bernhardt, 2013), but our understanding of the soil microorganisms mediating this biogeochemically important process is limited (Silver & Miya, 2001). Globally, the production of fine root litter accounts for ~22% of terrestrial net primary production (NPP; McCormack et al., 2015) and ~50% of plant litter entering soil (Freschet et al., 2013). Moreover, mounting evidence indicates fine root litter is the primary source of soil organic matter (SOM; Jackson et al., 2017; Rasse, Rumpel, & Dignac, 2005; Thomas, Zak, & Filley, 2012), which is

the largest pool of terrestrial C (Batjes, 1996). However, it is presently unclear which ecological factors control the decay of fine roots (Hobbie, Oleksyn, Eissenstat, & Reich, 2010; Schimel & Schaeffer, 2012; Silver & Miya, 2001; Sun et al., 2018), as well as how the microbial metabolism of fine roots into SOM will be impacted by anthropogenic environmental change.

We have established that *ca.* 20 years of experimental nitrogen (N) deposition, which simulates a pervasive driver of global change (Galloway et al., 2004, 2008), has slowed fine root decay and increased soil C (+18%) across the geographic extent of a northern hardwood forest ecosystem in the Upper Great Lakes region (Xia, Talhelm, & Pregitzer, 2017, 2018; Zak, Holmes, Burton, Pregitzer, & Talhelm, 2008). Although experimental N deposition has not altered the production of leaf (Pregitzer, Burton, Zak, & Talhelm, 2008) or fine root litter (Burton, Pregitzer, Crawford, Zogg, & Zak, 2004), it has slowed the decay of both (Xia et al., 2017, 2018; Zak et al., 2008). Previously, we established that fine root litter accounts for 70% of lignified plant material entering soil in our experiment (Xia, Talhelm, & Pregitzer, 2015), as well as the majority of lignin-derived monomers in SOM (Thomas et al., 2012). Thus, it appears C derived from fine roots, not leaf litter, has increased soil C storage under experimental N deposition. However, we presently do not understand how experimental N deposition has altered the community of microorganisms metabolizing fine root litter into SOM.

We previously obtained evidence that experimental N deposition has slowed lignin decay in fine root litter to a greater extent than leaf litter, a response that has occurred despite no effect of experimental N deposition on the biochemistry of fine root litter (Xia et al., 2017, 2018). This difference plausibly arises from the high lignin content of fine roots (45%) relative to leaf litter (14%; Xia et al., 2015), and because lignin content controls the long-term rate of plant litter decay (Barnes, Zak, Denton, & Spurr, 1998; Berg, 2014). Although lignified material was previously quantified as acid insoluble fraction (AIF) in our long-term experiment, which can include other recalcitrant compounds (Xia et al., 2015, 2017), AIF was highly predictive of lignin content in fine roots (Xia et al., 2017). Importantly, the physiological capacity to metabolize lignin varies among and within fungi and bacteria. For example, some fungal species in the class, Agaricomycetes, deploy class II peroxidase enzymes to completely oxidize lignin to CO_2 (Floudas et al., 2012; Kirk & Farrell, 1987), whereas some species in the phylum, Actinobacteria, and other bacterial lineages, incompletely degrade lignin into soluble phenolic compounds (Ahmad et al., 2010; Bugg, Ahmad, Hardiman, & Singh, 2011; Kirk & Farrell,

1987). In our long-term study, experimental N deposition has slowed leaf litter decay by reducing peroxidase gene expression (-73%; Zak et al., 2019) and increasing the potential for incomplete lignin decay by bacteria (Eisenlord et al., 2013; Freedman & Zak, 2014), but it has not altered the abundance of ligninolytic fungi on this substrate (Entwistle, Zak, & Argiroff, 2018; Freedman, Upchurch, Zak, & Cline, 2016; Hassett, Zak, Blackwood, & Pregitzer, 2009). However, the concentration of lignin in fine root litter is three times greater than in leaf litter (Xia et al., 2015), and we previously found that experimental N deposition decreases the abundance of ligninolytic fungi on lignin-rich artificial substrates decaying in the field (Entwistle et al., 2018). If experimental N deposition has also decreased the abundance of ligninolytic fungi on fine root litter, this response could explain why fine root decay has slowed to a greater extent than leaf litter. If this expectation is correct, then reduced fine root decay under experimental N deposition should be the primary source of C accumulating in soil due to experimental N deposition, which should alter SOM biochemistry by increasing the contribution of lignin-derived compounds to SOM formation.

Here, our objective was to determine if anthropogenic N deposition has altered the composition of soil microorganisms decaying fine root litter. To accomplish this, we compared the composition of fungal and bacterial communities colonizing decaying fine root litter exposed to ambient N and experimental N deposition. We also investigated the biochemical composition of SOM under ambient and experimental N deposition to determine if, by slowing the decay of fine roots, experimental N deposition has increased the concentration of lignin-derived compounds in SOM.

MATERIALS AND METHODS

Description of study sites

We tested the effects of experimental N deposition on the composition of microbial communities decomposing fine root litter and the biochemical composition of both fine root litter and SOM in four replicate northern hardwood forest stands in upper and lower Michigan, USA (Fig. S1). Each stand contains six 30-m x 30-m plots; half receive ambient N deposition (n = 3) and half have received experimental N deposition since 1994 (n = 3; ambient N + 30 kg N ha^{-1} yr^{-1} as $NaNO_3$ pellets in 6 equal applications during the growing season). To reduce edge effects, each plot is surrounded by a 10-m wide buffer zone that receives the same treatment as its respective plot. The forest stands are dominated by sugar maple (*Acer saccharum* Marsh., >80% basal area)

on sandy spodosols that are Typic Haplorthods of the Kalkaska series (>85% sand). The forest floor consists of a thick Oe/Oa horizon that contains a mat of fine roots at its boundary with the A horizon. The forest stands are matched in both vegetation and soil characteristics (Burton, Ramm, Pregitzer, & Reed, 1991) and encompass the full latitudinal range of the northern hardwood ecosystem in the Upper Great Lakes region; this ~500 km distance spans gradients of ambient N deposition, mean annual temperature, and precipitation (Table S1). Thus, our experimental design allows us to generalize our findings across this important and widespread ecosystem.

Field-based decomposition experiment

To obtain fine roots for our field decomposition experiment, we collected 60 soil cores (5-cm diameter) to a depth of 10 cm in each plot, which included both Oe/Oa and A horizons (*sensu* Xia et al., 2018). Although these soil cores contain fine root material from both the O and A horizons, the vast majority are derived from the dense mat of fine roots that sits at the O/A horizon boundary (Xia et al., 2018; Zak, Freedman, Upchurch, Steffens, & Kögel-Knabner, 2017). We transported the cores on ice to the University of Michigan and stored them at -20 °C. Sample collection was carried out in September and October 2013. We thawed the soil cores, passed them through a 2-mm sieve, retrieved first through third order fine roots (Pregitzer et al., 2002; Xia et al., 2015), and pooled the roots by plot. We rinsed soil from the roots and dried them at 60 °C for 24 hrs. We collected the three distal root orders because, as the ephemeral absorptive modules of the root network, they are morphologically similar and exhibit the highest turnover (Guo et al., 2008; McCormack et al., 2015; Xia, Guo, & Pregitzer, 2010), thus comprising the largest input of fine root C to soil.

We placed three mesh litter bags of fine roots (~2 g dry mass in each bag) at three separate positions in the same plot from which the roots originated, in their original location in the soil profile at the boundary of the Oe/Oa and A horizons (3 litter bags x 24 plots = 72 litter bags total). While it could be argued that fine roots may have decayed differently had they been incubated at the surface of the O horizon or deeper in the mineral soil, one of the few studies to test the effects of vertical location in the soil profile on fine root decay found that fine roots located in the O and A horizons of a red pine (*Pinus resinosa*) plantation did not decay at different rates (Li, Fahey, Pawlowska, Fisk, & Burtis, 2015). Moreover, the vast majority of fine roots in these northern hardwood forest stands are located at the boundary of the O and A

horizons (Xia et al., 2018; Zak et al., 2017). Thus, we are confident the abiotic and biotic conditions experienced by the fine roots we deployed reflected those experienced by the majority of fine root litter in these forests. We constructed each 15-cm x 15-cm litter bag with 300 µm polyester mesh on top and 20 µm polyester mesh on the bottom, which allowed microfauna and fungal hyphae to enter the bags, respectively (Hobbie, 2005; Xia et al., 2018). Litter bags were placed in the field in June 2014, collected after 12 months of decomposition, and immediately stored on ice. Each bag was weighed, and its contents were homogenized by hand. A subsample was removed for physical and chemical analyses, dried at 60 °C for 24 hrs, and the remaining material was stored at -80 °C prior to microbial community analyses.

DNA isolation

To determine if experimental N deposition altered the composition of fungal and bacterial communities, we characterized these communities using ribosomal DNA (rDNA) sequence abundances. We isolated total genomic DNA from three replicate subsamples taken from each root litter bag (0.05 g fine root material per subsample) using the DNeasy Plant Mini Kit (Qiagen, Valencia, CA, USA) following a modified manufacturer's protocol. Specifically, following chemical lysis as specified, we performed physical lysis by bead beating with four 2.38-mm stainless steel beads at 1,200 rpm for 45 s using the PowerLyzer 24 Bench Top Bead-Based Homogenizer (MoBio Laboratories, Carlsbad, CA, USA). Debris was pelleted by centrifugation at 16,000 x *g* for 5 min. After DNA extractions were completed, we verified the quality of extracted DNA with a NanoDrop 8000 Spectrophotometer (Thermo Scientific, Waltham, MA, USA) and gel electrophoresis. We pooled replicate extractions from each litter bag and stored DNA at -80 °C prior to PCR amplification.

PCR amplification, amplicon sequencing, and sequence quality control

We performed PCR amplification of fungal rDNA using the primers LROR and LR3 (Vilgalys & Hester, 1990) that target the D1-D2 region of the 28S rRNA gene, which is suitable for both taxonomic and phylogenetic analyses (Liu, Porras-Alfaro, Kuske, Eichorst, & Xie, 2012; Porter & Golding, 2012). The V1-V3 regions of the bacterial 16S rRNA gene were targeted using the primers 27f and 519r (Lane, 1991). For each gene, we performed triplicate PCR reactions for each sample using the Expand High Fidelity PCR System (Roche, Indianapolis, IN, USA) and a Mastercycler ProS thermocycler (Eppendorf, Hauppauge, NY, USA). PCR reaction conditions

are described in Table S2. Primers contained an additional 16 bp barcode for sample multiplexing for sequencing (described below; for barcode sequences, see Table S3).

We pooled triplicate reactions and purified PCR products using the MinElute PCR Purification Kit (Qiagen). The quality of purified PCR products was assessed as described above, and we quantified DNA mass with the Quant-iT PicoGreen dsDNA Assay Kit (LifeTechnologies, Carlsbad, CA, USA) and a BioTek SynergyHT Multi-Detection Microplate Reader (BioTek Instruments, Winooski, VT, USA). Sequencing was performed at the University of Michigan DNA Sequencing Core on 16 SMRT chips with a PacBio RS II system (Pacific Biosciences, Menlo Park, CA, USA) utilizing circular consensus sequencing, which achieves error rates comparable to other high-throughput sequencing platforms (Fichot & Norman, 2013; Travers, Chin, Rank, Eid, & Turner, 2010). PCR products were pooled in equal masses per sample per SMRT chip prior to sequencing. Mean amplicon lengths were 688 bp and 525 bp for fungal 28S and bacterial 16S, respectively. Only sequences with at least five-fold circular consensus coverage were retained.

We processed sequences using mothur v1.40.5 (Schloss et al., 2009). We removed sequences containing homopolymers >8 nucleotides in length, with average quality scores <30 using a 50-nt sliding window, an ambiguous base call, or >1 mismatch in either the barcode or primer sequence. Fungal sequences were aligned against a 28S reference alignment from the RDP LSU training set (Mueller, Balasch, & Kuske, 2014) and bacterial 16S sequences were aligned against the SILVA v132 reference alignment (Quast et al., 2013). Chimeric sequences were identified using UCHIME (Edgar, Haas, Clemente, Quince, & Knight, 2011) and removed. We clustered fungal sequences and bacterial sequences into operational taxonomic units (OTUs) at 99% and 97% sequence similarity, respectively. The most abundant sequence for each OTU was used as the representative for that OTU, and taxonomic assignments were made using the RDP classifier with the LSU training set v11 for fungi (Cole et al., 2014) and the SILVA v132 reference alignment with the naive Bayesian classifier (Q. Wang, Garrity, Tiedje, & Cole, 2007) in mothur for bacteria. Raw sequences are available in fastq format in GenBank under the accession numbers SRR8591550 (16S) and SRR8591551 (28S).

Microbial community composition

Some fungi in the class Agaricomycetes, and some bacteria in the phylum Actinobacteria, can metabolize lignin (Floudas et al., 2012; Kirk & Farrell, 1987); thus, we tested if experimental

N deposition altered the relative abundances of these two groups. We further summed sequence abundances in fungal orders and bacterial families, and compared relative abundances between the ambient and experimental N deposition treatments for orders and families that accounted for at least 1% of fungal and bacterial sequences, respectively, and exhibited a change in relative abundance of at least 20%. Further, species of Agaricomycete fungi and Actinobacteria span a diverse range of autecologies (Hibbett et al., 2014; Kirk & Farrell, 1987), and it is difficult to directly interpret the functional consequences of changes in the relative abundance of these broad groups. Thus, we assessed the effect of experimental N deposition on fungal and bacterial community composition (*i.e.*, β-diversity), using multivariate analyses at the genus and family levels, respectively. First, abundances were Hellinger-transformed to avoid subsampling biases (McMurdie & Holmes, 2013, 2014). We then performed distance-based redundancy analysis (db-RDA) on Bray-Curtis dissimilarity calculated from these abundances to visualize differences in community composition due to site and experimental N deposition. We plotted the scores for abundant (≥1%) classified fungal genera and bacterial families to determine which taxa drove differences in community composition in response to experimental N deposition.

Biochemical analyses and relationships with microbial community composition

We characterized the biochemical composition of undecomposed fine roots, decayed fine roots, and SOM using pyrolysis gas chromatography-mass spectrometry (py-GC/MS). Mineral soil (0-10 cm) was obtained from each plot receiving ambient N and experimental N for biochemical analysis of SOM. We elected to characterize the biochemistry of SOM in mineral soil for four reasons. First, organic matter has rapidly accumulated (+18%) in the mineral soil of our experiment (Zak et al., 2008). Second, the lignin-derived compounds remaining in mineral soil appear to be derived primarily from fine root litter (Thomas et al., 2012), emphasizing the importance of relating microbial composition on fine root litter to the biochemistry of SOM in mineral soil. Third, we recently obtained evidence that experimental N deposition has caused an accumulation of occluded particulate organic matter in our experiment, which was hypothesized to be an accumulation of fine-root derived C (Zak et al., 2017). Finally, previous biochemical characterizations of mineral soil SOM have not detected the expected accumulation of lignin-derived compounds in response to experimental N deposition (Thomas et al., 2012; Zak et al., 2017); thus, we employed a high-resolution method (*i.e.*, py-GC/MS) to definitively test this alternative. Dried fine root and soil samples (~1 g per sample type per plot) were ground for 6

minutes using a ball mill. Samples were then pyrolyzed at 600 °C in quartz tubes for 20 s using a DS Pyroprobe 5150 pyrolyzer, and analyzed using a ThermoTrace GC Ultra gas chromatograph (Thermo Fisher Scientific, Austin, TX, USA) and ITQ 900 mass spectrometer (Thermo Fisher Scientific; *sensu* Pold, Grandy, Melillo, & DeAngelis, 2017). Mass spectrometry peaks were assigned to compounds using AMDIS software and a previously-compiled compound library, and relative abundances for each compound were determined by dividing by the largest peak present in that sample (Grandy, Neff, & Weintraub, 2007; Grandy, Strickland, Lauber, Bradford, & Fierer, 2009; Wickings, Grandy, Reed, & Cleveland, 2011). Individual compounds were summed by their origins to determine the relative abundances of broad compound classes (*i.e.*, aromatic, lignin, lipids, N-bearing, phenols, polysaccharides, proteins, and compounds of unknown origin). To evaluate if SOM biochemistry was related to microbial community composition on decaying fine roots, we fit vectors of compound abundances in SOM to db-RDA ordinations and overlaid vectors with a significant fit (see *Statistical analyses*).

Although compounds other than lignin, such as suberin, are also important biochemical constituents of fine roots (McCormack et al., 2015), we elected to focus our study on lignin for four reasons. First, lignin dominated fine root litter biochemistry (35-45%) in our long-term experiment based on previous findings (Xia et al., 2015, 2017) and the results we have obtained in our present study (see Fig. 1). Second, the biochemical composition of lignin-derived monomers in SOM in our experiment was biochemically more similar to fine root-derived lignin than to leaf litter-derived lignin (Thomas et al., 2012), a finding that specifically implicates fine root-derived lignin as an important source of SOM. Third, the decay of AIF in fine roots (which is dominated by lignin in our long-term experiment) was reduced under experimental N deposition (Xia et al., 2017, 2018), leading us to address the mechanism by which this reduction of decay has occurred in the present study. Finally, suberin is relatively more abundant in higher order (e.g., 4th and 5th order) transport fine roots, as opposed to the ephemeral absorptive fine root modules (orders 1-3; McCormack et al., 2015) that are the focus of our present study due to their dominance of fine root turnover (Xia et al., 2010, 2015). Taken together, these lines of evidence support our focus on the microbial degradation of fine root lignin in response to experimental N deposition.

Statistical analyses

We used two-way ANOVA to test the effect of experimental N deposition, site, and their interaction on Hellinger-transformed taxon abundances (*e.g.*, Agaricales) and $\log_2$-transformed compound abundances. Among-group means were compared using protected Fisher's least significant difference (LSD) test in the agricolae package (de Mendiburu, 2017) in R. We tested the effects of experimental N deposition, site, and their interaction on community composition using two-way permutational multivariate analysis of variance (PERMANOVA; Anderson, 2001) and Bray-Curtis dissimilarity matrices calculated from Hellinger-transformed fungal genus and bacterial family abundances. PERMANOVA was implemented in the vegan package v2.5-3 (Oksanen et al., 2018) in R. PERMANOVA cannot distinguish differences in composition from heterogeneous variance; thus, we tested the homogeneity of multivariate dispersion using PERMDISP (Anderson, 2004) in vegan ('betadisper' function). A non-significant PERMDISP result confirms that a significant PERMANOVA test has detected a true difference in composition. Vectors for compound abundances were fit to db-RDA ordinations using the 'envfit' function in vegan. Due to the broad geographic expanse of our experiment and inherent heterogeneity of the soil environment, we accepted statistical significance at $\alpha = 0.1$. Data processing and visualization were performed using the collection of packages comprising the tidyverse v1.2.1 (Wickham, 2017) in R. Statistical analyses were performed in R v3.5.1 (R Core Team, 2018) and RStudio v1.1.453 (RStudio Team, 2018), and code for sequence processing and statistical analyses is available at https://github.com/ZakLab-Soils/N-deposition_roots.

RESULTS

Fine root and SOM biochemistry

Experimental N deposition did not affect the relative abundance of any compound class in undecayed or decaying fine root litter (ANOVA, $P > 0.1$; Fig. 1). However, we found that experimental N deposition increased the relative abundance of lignin-derived compounds in SOM by 53% (5.2% under ambient N to 7.9% under experimental N; $P = 0.092$; Fig. 1). Although this response was not highly statistically significant, it was ecologically-significant due to its magnitude (>50% change), its uniformity across a large geographic expanse (site by treatment interaction, $P > 0.1$), and the rapidity with which it occurred (~20 years).

Sequence processing, OTU clustering, and taxonomic distribution

Our sequencing effort yielded 126,159 high-quality (*i.e.*, passed filtering steps described in *Materials and Methods*) fungal sequences (5,257 ± 1,656 per sample; mean ± SD) and 154,135 high-quality bacterial sequences (6,422 ± 1,058 per sample). We obtained 2,071 non-singleton fungal OTUs and 5,957 non-singleton bacterial OTUs across all samples. Basidiomycota (63%) and Ascomycota (35%) represented the majority of fungal sequences. The fungal classes Agaricomycetes (57%), Sordariomycetes (11%), unclassified Ascomycota (8%), Leotiomycetes (6%), Tremellomycetes (5%), and Eurotiomycetes (5%) were most abundant. Dominant bacterial phyla included Proteobacteria (55%), Bacteroidetes (15%), Acidobacteria (10%), and Actinobacteria (7%).

Effects of experimental N deposition on microbial community composition

The abundance of Agaricomycetes declined (-22%, from 62.3 ± 4.8% to 48.8 ± 7.5%, mean ± SE) in response to experimental N deposition (ANOVA, $P = 0.085$; Fig. S2). Similarly, experimental N deposition reduced the abundance of Agaricales (-31%; $P = 0.059$; Fig. 2), the most abundant order of Agaricomycetes colonizing fine root litter. Fungal orders that responded positively to experimental N deposition did not belong to the class, Agaricomycetes. For example, experimental N deposition increased the abundance of fungal orders Chaetothyriales (+566%; $P = 0.011$), Hypocreales (+37%; $P = 0.033$), and Tremellales (+291%; $P = 0.009$; Fig. 2). The responses of Hypocreales (site by treatment; $P = 0.017$) and Tremellales ($P = 0.042$) varied in magnitude, but not direction by site (Fig. S3). Additionally, the relative abundance of Actinobacteria increased (+24%, from 6.5 ± 0.5% to 8.1 ± 0.7%) in response to experimental N deposition (ANOVA; treatment; $P = 0.025$), driven primarily by sites B and C (site by treatment interaction; $P = 0.024$; Fig. S2). Among bacterial families, Microbacteriaceae were favored by experimental N deposition (+81%; $P = 0.005$); this response varied in magnitude by site, but not in direction (site by treatment; $P = 0.053$; Fig. S3).

Experimental N deposition significantly altered the genus-level composition of fungal communities on decaying fine roots (PERMANOVA; $P = 0.001$; Fig. 3a), without altering dispersion (PERMDISP; $P = 0.17$). The shift in community composition due to experimental N deposition (denoted by the "*Exp. N*" vector in Fig. 3b) was associated with a lower abundance of the ligninolytic fungal genera *Mycena* and *Kuehneromyces* (Fig. 3b). Specifically, the points labeled "*Myc"* and "*Kue"* in Fig. 3b represent the loadings for these genera in the site by treatment ordination in Fig. 3a; if an arrow were drawn from the origin in the ordination to a

genus loading, it would represent the direction in which the abundance of that genus increases. Thus, the relative abundance of *Mycena* and *Kuehneromyces* increase in the opposite direction of the vectors representing the shift in fungal community composition due to experimental N deposition ("*Exp. N")*. In other words, the experimental N deposition treatment is associated with a lower abundance of these two genera. This pattern indicates that a decline in the abundance of these genera drove the significant change in fungal community composition on decaying fine roots in response to experimental N deposition.

Similarly, experimental N deposition significantly altered bacterial community composition on decaying fine roots (PERMANOVA; $P = 0.014$; PERMDISP; $P = 0.39$; Fig. 3c). The Actinobacterial family, Microbacteriaceae, was among the bacterial families positively associated with the change in community composition due to experimental N deposition (Fig. 3d). This family contains ligninolytic species (Taylor et al., 2012), which incompletely metabolize lignocellulose into soluble phenolic compounds. The effects of experimental N deposition on other bacterial families putatively involved in lignin degradation (Wilhelm, Singh, Eltis, & Mohn, 2018) were idiosyncratic. The community composition of fungal and bacterial communities differed among sites (PERMANOVA, site; $P < 0.001$). The effect of experimental N deposition was not uniform across sites for fungi or bacteria (site by treatment; $P < 0.05$). However, the significant site by treatment interaction was apparent in db-RDA ordinations (Fig. 3a,c), in which clear separation occurred between communities under ambient and experimental N deposition at all sites, except site D.

Relationships between SOM biochemistry and microbial community composition

To directly link changes in SOM biochemistry with changes in bacterial and fungal community composition elicited by experimental N deposition, we fit a vector for the relative abundance of each compound class in SOM to fungal and bacterial db-RDA ordinations. We found that the shift in fungal community composition driven by experimental N deposition was significantly associated with greater relative abundances of lignin-derived compounds ($r^2 = 0.39$; $P = 0.011$) and N-bearing compounds ($r^2 = 0.33$; $P = 0.022$) in SOM (Fig. 3b). Similarly, the change in bacterial community composition elicited by experimental N deposition was significantly related to a greater relative abundance of lignin-derived compounds ($r^2 = 0.29$; $P = 0.032$; Fig. 3d), although the relationship was less direct than that with fungal community composition (Fig. 3b).

In contrast, a lower abundance of lipids was associated with changes in bacterial community composition under experimental N deposition ($r^2 = 0.21$; $P = 0.072$; Fig. 3d).

DISCUSSION

Anthropogenic N deposition has slowed the accumulation of CO_2 in the atmosphere by increasing C storage in northern forests (Keenan et al., 2017; Pan et al., 2011). Nitrogen deposition fosters this terrestrial C sink by slowing microbial litter decay and increasing SOM (Chen et al., 2018; Frey et al., 2014; Janssens et al., 2010; Pregitzer et al., 2008; Zak et al., 2008). Here, we provide evidence that anthropogenic N deposition has altered the composition of fungal and bacterial communities on decaying fine root litter by suppressing the relative abundance of ligninolytic fungi and favoring bacteria with weaker ligninolytic capacity, which plausibly explains why the decay of fine root litter has declined and soil C storage has increased in our long-term N deposition experiment (Xia et al., 2017, 2018; Zak et al., 2008). Moreover, we demonstrate that shifts in microbial community composition are significantly related to an increase in the relative abundance of lignin-derived compounds in SOM, which suggests that changes in the microbial decay of fine root litter have caused the end products of this process to accumulate as SOM to a greater extent under experimental N deposition. A recent modeling study estimated that up to 51% of C accumulating in surface soil (O and A horizons to a depth of 10 cm) in this experiment could be explained by reduced decay of fine root litter (Xia et al., 2018), and our findings shed light onto the compositional changes in microbial communities eliciting this response. Furthermore, mounting evidence suggests that anthropogenic N deposition slows fine root decay in other ecosystems (Kou et al., 2018; Sun, Dong, Wang, Lü, & Mao, 2016), and that fine root C is a primary source of SOM in general (Jackson et al., 2017; Rasse et al., 2005; Thomas et al., 2012). Thus, the microbial responses we observed here may underlie widespread findings that anthropogenic N deposition increases soil C storage in terrestrial ecosystems, including those contributing to the increasing C sink in the Northern Hemisphere that has slowed the rate at which anthropogenic CO_2 has accumulated in the atmosphere (Frey et al., 2014; Janssens et al., 2010; Keenan et al., 2017; Maaroufi et al., 2015; Pan et al., 2011).

Our findings suggest that declines in the relative abundance of ligninolytic fungi have reduced fine root decay in our experiment, as well as the others detailed above. Specifically,

399 experimental N deposition decreased the relative abundance of Agaricomycetes (-22%) and its
400 most abundant order, Agaricales (-31%; Fig. 2). Agaricomycetes contains the "white-rot" fungi,
401 which decay lignin using class II peroxidases (Baldrian, 2008; Floudas et al., 2012; Kirk &
402 Farrell, 1987). However, there is considerable functional diversity within the Agaricomycetes
403 (Hibbett et al., 2014); thus, the lower relative abundance of the genera *Mycena* and
404 *Kuehneromyces* associated with experimental N deposition (Fig. 3b) is a particularly important
405 piece of evidence we obtained. Specifically, *Kuehneromyces* and *Mycena* are genera of white-rot
406 fungi that decay lignin using class II peroxidases (Ghosh, Frankland, Thurston, & Robinson,
407 2003; Hofrichter, 2002; Kellner et al., 2014; Miyamoto, 2000). *Mycena* were the most abundant
408 fungi on decaying fine roots (~22% of fungal sequences overall) in our study, and were also
409 dominant saprotrophs on decaying fine roots in other forest ecosystems (Kohout et al., 2018;
410 Philpott, Barker, Prescott, & Grayston, 2018); thus, this genus may be important for how fine
411 root decay responds to anthropogenic N deposition more generally. Taken together, our results
412 clearly demonstrate that experimental N deposition is associated with a lower relative abundance
413 of ligninolytic fungi on decaying fine roots.
414 In contrast, experimental N deposition favored ligninolytic bacteria and non-ligninolytic
415 fungi. The relative abundance of Actinobacteria increased under experimental N deposition
416 (+24%), including the family, Microbacteriaceae (+81%; Fig. 2 and 3d). Experimental N
417 deposition also increased the abundance of Saccharibacteria (+46%) and the fungal orders
418 Chaetothyriales (+566%), Hypocreales (+37%), and Tremellales (+291%; Fig. 2). These
419 responses are likely ecologically important because ligninolytic Actinobacteria, including some
420 Microbacteriaceae, degrade lignin to soluble phenolic compounds rather than oxidizing the
421 polymer to CO_2 (Ahmad et al., 2010; Bugg et al., 2011; Taylor et al., 2012); this is consistent
422 with greater phenolic dissolved organic C production in our experiment (Pregitzer, Zak, Burton,
423 Ashby, & Macdonald, 2004). Some Saccharibacteria can modify aromatic compounds, but there
424 is no evidence to indicate they degrade lignin (Luo, Xie, Sun, Li, & Cupples, 2009). Other
425 bacterial lineages have been implicated in lignin decay, including some that have responded to
426 experimental N deposition (Fig. 3d; Janusz et al., 2017); however, the cumulative effect of these
427 changes in composition on bacterial lignin degradation remains to be tested. Some Hypocreales
428 and Chaetothyriales also possess oxidases that could modify lignin (Assavanig,
429 Amornikitticharoen, Ekpaisal, Meevootisom, & Flegel, 1992; Hölker, Dohse, & Höfer, 2002;

Martinez et al., 2008; Teixeira et al., 2017), and yeasts in Tremellales dominate the late, lignin-rich stages of oak leaf litter decomposition (Voriskova & Baldrian, 2013). However, these fungal lineages lack peroxidases capable of complete lignin oxidation (Floudas et al., 2012). Together, these responses suggest that experimental N deposition has favored a microbial community with a lower capacity to degrade lignin in fine root litter.

In combination with a higher relative abundance of lignin-derived compounds in SOM, our observations specifically link changes in microbial community composition on fine root litter to the accumulation of SOM (Table S1; Pregitzer et al., 2008; Zak et al., 2008). Foremost, experimental N deposition significantly altered fungal community composition by decreasing the relative abundance of ligninolytic *Mycena* and *Kuehneromcyes*, and these shifts in composition were significantly associated with a greater relative abundance of lignin-derived compounds in SOM (Fig. 3a,b). Similarly, the relative abundance of lignin-derived compounds in SOM was positively related to the shift in bacterial community composition elicited by experimental N deposition (Fig. 3c,d). The substantial declines in the relative abundance of ligninolytic fungi and increases in the relative abundance of bacteria with weaker ligninolytic capacity we observed (Fig. 2 and 3) likely account for the reduction in fine root lignin decay (Xia et al., 2017) and mass loss (Xia et al., 2018) previously reported from our experiment, wherein fine root litter was allowed to decay in the field in an identical manner as our current study. Moreover, our findings suggest that by substantially altering the composition of microbial communities on fine roots, experimental N deposition has slowed the decay of lignin-rich fine root litter, thereby increasing the contribution of lignin-derived compounds from fine roots to SOM formation.

It is unclear why experimental N deposition decreased the abundance of ligninolytic fungi on fine root litter, whereas this response has not occurred on leaf litter in the same long-term experiment or others (*e.g.*, Morrison et al., 2016; Morrison, Pringle, van Diepen, & Frey, 2018; Whalen, Smith, Grandy, & Frey, 2018). A reduction in the competitive ability of ligninolytic fungi on lignin-rich substrates has been proposed to explain the negative effects of experimental N deposition on ligninolytic enzyme activity and litter decay (*e.g.*, DeForest, Zak, Pregitzer, & Burton, 2004; Entwistle et al., 2018; Janssens et al., 2010; Morrison et al., 2018; Talbot & Treseder, 2012; Waldrop, Zak, Sinsabaugh, Gallo, & Lauber, 2004), but the mechanisms underlying putative changes in competitive ability on lignin-rich substrates are not understood. Our observation that the relative abundance of ligninolytic fungi was reduced to a

greater extent on fine root litter than leaf litter could be consistent with this hypothesis, although the role of competition and its specific mechanisms are unknown. A trade-off between stress tolerance and competitive ability has recently been proposed to explain the effects of experimental N deposition on ligninolytic fungi (Morrison et al., 2018), and numerous other mechanisms involving niche differentiation and an increased efficiency of non-ligninolytic fungi have also been suggested (*e.g.*, Talbot & Treseder, 2012). Our findings, including the relationships between microbial composition and other components of SOM (*e.g.*, N-bearing compounds and lipids; Fig. 3), emphasize the need to understand whether biotic interactions influence how experimental N deposition alters microbial community composition. For example, the distinction between these putative competition-mediated changes in composition and physiological responses (*i.e.*, down-regulated peroxidase transcription) would be represented differently in mechanistic ecosystem models (Allison, 2012; Hawkes & Keitt, 2015; Treseder et al., 2012). At present, these competitive processes are speculative and their mechanisms are not understood; a mechanistic understanding of these interactions will facilitate their extension to the effects of anthropogenic N deposition on fine root decay and soil C storage in other ecosystems.

The fact that experimental N deposition did not alter the biochemical composition of fine roots after one year of decay (Fig. 2 and 3), and that it did increase the lignin content of SOM (Fig. 1 and 3), indicates that the changes in microbial community composition we documented have functional implications during the later stages of fine root decay (*i.e.,* beyond one year). Several pieces of evidence from our long-term experiment are consistent with this expectation. For example, based on the decay of identical fine root litter in identical litter bags, there was no effect of experimental N deposition on the mass loss (Xia et al., 2018) or biochemistry (Xia et al., 2017) of fine root litter after one year of decay. However, experimental N deposition significantly increased the mass of fine root litter remaining after three years of decay (Xia et al., 2018) due to a reduction in the decay of lignin (Xia et al., 2017). These reductions in the later stages of fine root decay align with the accumulation of lignin-derived compounds in SOM revealed in our current study (Fig. 1 and 3). An important assumption is that the changes in microbial community composition we observed after one year persist to later stages of decay, thereby decreasing the loss of lignin and overall mass loss of fine root litter. Although this assumption remains to be tested, our findings clearly suggest that changes in microbial community composition (Fig. 2 and 3) have slowed the decay of lignin in fine root litter (Xia et

al., 2017, 2018), thereby increasing the amount of lignin-derived compounds from fine root litter in SOM (Fig. 1 and 3).

The biochemical changes in SOM we observed may explain how experimental N deposition has increased the physical protection of SOM by mineral occlusion, as we have previously reported (Zak et al., 2017). Although relatively unmodified lignin is not thought to remain in long-term pools of SOM (Grandy et al., 2007), it can be stabilized through the adsorption of dissolved organic matter to mineral surfaces, or the physical occlusion of particulate litter by clay and silt particles in microaggregates (Cotrufo et al., 2015; Lehmann & Kleber, 2015). In our experiment, experimental N deposition has not altered the amount of C in the highest density soil fraction (>1.8 g cm^{-1}) that represents mineral-adsorbed SOM; however, it has increased mineral-occluded particulate SOM, which indicates greater physical protection of litter fragments in microaggregates (Zak et al., 2017). Previous analyses have revealed no effect of experimental N deposition on SOM biochemistry or other factors involved in aggregate formation (Thomas et al., 2012; Zak et al., 2017). However, it is plausible that a reduction in the microbial decay of fine root litter has increased the amount of time a given mass of fine root fragments remain in contact with soil particles, thereby fostering their occlusion (Cotrufo et al., 2015). Although this mechanism remains to be directly tested, our results suggest that reduced microbial decay of fine root litter may increase the physical stabilization of fine root material in microaggregates, which could influence the longevity of the terrestrial C sink.

A reduction in soil pH has recently been proposed as the primary mechanism by which experimental N deposition decreases the microbial decay of plant litter and increases soil C storage (Averill & Waring, 2018, and references therein); however, our findings provide a distinct and novel mechanism that is independent of soil pH. For example, experimental N deposition induced Mn-limitation in soils receiving experimental N deposition in an oak-dominated forest in New England, likely due to enhanced leaching of Mn from soils at low pH (Whalen et al., 2018). Since the late stages of litter decay (dominated by lignin degradation) occur more rapidly when Mn concentrations are high (Berg, 2014), likely due to the role of Mn as a diffusible redox mediator for ligninolytic manganese peroxidase enzymes (Hofrichter, 2002), pH-induced Mn-limitation was thought to explain reduced rates of litter decay (Whalen et al., 2018). Additionally, experimental N deposition could reduce microbial activity due to the direct negative effects of low pH on microbial physiology (Averill & Waring, 2018). However,

soil pH does not differ among sites in our long-term experiment (Table S1), nor has experimental N deposition decreased soil pH (4.5 $\pm$ 0.25 under ambient N conditions and 4.7 $\pm$ 0.32 under experimental N conditions; Eisenlord & Zak, 2010). Thus, neither Mn-limitation nor the direct negative effects of low soil pH on microbial activity explain reductions in fine root decay in our experiment. Instead, our findings suggest a pH-independent mechanism, in which the decreased abundance of highly ligninolytic fungi and increased role for less complete bacterial lignin degradation has slowed the decay of fine root litter.

In summary, we demonstrated that over 20 years of experimental N deposition has reduced the relative abundance of ligninolytic fungi and increased that of ligninolytic bacteria on decaying fine roots, which plausibly explains how fine root decay has slowed and SOM has accumulated in our study (Xia et al., 2017, 2018; Zak et al., 2008). Furthermore, we found that an accumulation of lignin-derived compounds in SOM was significantly related to changes in microbial community composition on decaying fine root litter, particularly a decline in the relative abundance of ligninolytic fungi. Together, this evidence suggests that by altering microbial community composition on fine root litter, which is the dominant source of lignified plant material to soil, experimental N deposition has caused an accumulation of root-derived C as SOM. It is important to point out that fine root litter may account for a smaller proportion of lignin-derived compounds that enter soil in forest ecosystems dominated by species with higher leaf litter lignin concentrations (*e.g.*, *Quercus*, *Pinus*) than sugar maple. Nonetheless, our findings unite a growing body of evidence that experimental N deposition enriches SOM in compounds that are abundant in fine roots (*e.g.*, lignin and suberin; Frey et al., 2014; Grandy, Sinsabaugh, Neff, Stursova, & Zak, 2008; vandenEnden et al., 2018; J.-J. Wang et al., 2019) with the changes in microbial composition that are responsible for their accumulation. To better understand how experimental N will modify terrestrial C storage and mediate climate under future rates of anthropogenic N deposition (Galloway et al., 2004, 2008), we must explicitly test ecological mechanisms (*e.g.*, putative competitive interactions) that may alter microbial community composition and slow fine root decay, as well as better understand how the altered products of fine root decomposition are stabilized into SOM. Taken together, our findings link the composition and function of microbial communities, as well as highlight the role of compositional shifts in mediating biogeochemical processes of global significance.

ACKNOWLEDGEMENTS

We sincerely thank Kimberly Martin, Remy Long, Kathryn Kelley, Allison Sharrar, Kerri Metz, and Sisimac Duchicela for their assistance with fine root processing and litter bag construction. We thank Zachary Freedman and Karl Romanowicz for their assistance with soil collection. We also thank Peter Pellitier, Deborah Goldberg, Timothy James, the James lab, and the plant ecology discussion group at the University of Michigan for their insightful comments on previous versions of this manuscript. This work was supported by funding from the United States Department of Energy Biological and Environmental Research program. Maintenance of our long-term N deposition project is supported by the National Science Foundation Long-term Research in Environmental Biology program.

AUTHOR CONTRIBUTIONS

DRZ designed the study. RAU, SOS, and WAA optimized and performed laboratory analyses. ASG performed biochemical analyses. WAA analyzed the data and wrote the first draft of the manuscript. DRZ, RAU, SOS, and ASG provided significant feedback on later versions.

CONFLICT OF INTEREST

The authors declare that they have no conflict of interest.

REFERENCES

Ahmad, M., Taylor, C. R., Pink, D., Burton, K., Eastwood, D., Bending, G. D., & Bugg, T. D. H. (2010). Development of novel assays for lignin degradation: Comparative analysis of bacterial and fungal lignin degraders. *Molecular BioSystems*, *6*(5), 815–821. https://doi.org/10.1039/b908966g

Allison, S. D. (2012). A trait-based approach for modelling microbial litter decomposition. *Ecology Letters*, *15*(9), 1058–1070. https://doi.org/10.1111/j.1461-0248.2012.01807.x

Anderson, M. J. (2001). A new method for non-parametric multivariate analysis of variance. *Austral Ecology*, *26*, 32–46.

585 Anderson, M. J. (2004). PERMDISP: a FORTRAN computer program for permutational analysis
586 of multivariate dispersions (for any two-factor ANOVA design) using permutation tests.
587 Assavanig, A., Amornikitticharoen, B., Ekpaisal, N., Meevootisom, V., & Flegel, T. W. (1992).
588 Isolation, characterization and function of laccase from Trichoderma. *Applied Microbiology*
589 *and Biotechnology*, *38*(2), 198–202. https://doi.org/10.1007/BF00174468
590 Averill, C., & Waring, B. (2018). Nitrogen limitation of decomposition and decay: How can it
591 occur? *Global Change Biology*, *24*(4), 1417–1427. https://doi.org/10.1111/gcb.13980
592 Baldrian, P. (2008). Enzymes of Saprotrophic Basidiomycetes. In *Ecology of Saprotrophic*
593 *Basidiomycetes. British Mycological Symposia Series* (Vol. 28, pp. 19–41).
594 https://doi.org/10.1016/S0275-0287(08)80004-5
595 Barnes, B. V., Zak, D. R., Denton, S. R., & Spurr, S. H. (1998). Nutrient Cycling. In E. Schatz,
596 S. Russell, & E. Starr (Eds.), *Forest Ecology* (4th ed., pp. 524–576). New York: John Wiley
597 & Sons, Inc.
598 Batjes, N. H. (1996). Total carbon and nitrogen in the soils of the world. *European Journal of*
599 *Soil Science*, *47*(2), 151–163. https://doi.org/10.1111/ejss.12114_2
600 Berg, B. (2014). Decomposition patterns for foliar litter - A theory for influencing factors. *Soil*
601 *Biology and Biochemistry*, *78*, 222–232. https://doi.org/10.1016/j.soilbio.2014.08.005
602 Bugg, T. D. H., Ahmad, M., Hardiman, E. M., & Singh, R. (2011). The emerging role for
603 bacteria in lignin degradation and bio-product formation. *Current Opinion in*
604 *Biotechnology*, *22*(3), 394–400. https://doi.org/10.1016/j.copbio.2010.10.009
605 Burton, A. J., Pregitzer, K. S., Crawford, J. N., Zogg, G. P., & Zak, D. R. (2004). Simulated
606 chronic NO-3deposition reduces soil respiration in northern hardwood forests. *Global*
607 *Change Biology*, *10*(7), 1080–1091. https://doi.org/10.1111/j.1365-2486.2004.00737.x
608 Burton, A. J., Ramm, C. W., Pregitzer, K. S., & Reed, D. D. (1991). Use of Multivariate
609 Methods in Forest Research Site Selection. *Canadian Journal of Forest Research*, *21*,
610 1573–1580.
611 Chen, J., Luo, Y., Jan van Groenigen, K., Hungate, B. A., Cao, J., Zhou, X., & Wang, R. (2018).
612 A keystone microbial enzyme for nitrogen control of soil carbon storage. *Science Advances*,
613 *4*(8), 2–8. https://doi.org/10.1126/sciadv.aaq1689
614 Cole, J. R., Wang, Q., Fish, J. A., Chai, B., McGarrell, D. M., Sun, Y., … Tiedje, J. M. (2014).
615 Ribosomal Database Project: Data and tools for high throughput rRNA analysis. *Nucleic*

Acids Research, *42*(D1), 633–642. https://doi.org/10.1093/nar/gkt1244

Cotrufo, M. F., Soong, J. L., Horton, A. J., Campbell, E. E., Haddix, M. L., Wall, D. H., & Parton, W. J. (2015). Formation of soil organic matter via biochemical and physical pathways of litter mass loss. *Nature Geoscience*, *8*(10), 776–779. https://doi.org/10.1038/ngeo2520

de Mendiburu, F. (2017). agricolae: Statistical Procedures for Agricultural Research.

DeForest, J. L., Zak, D. R., Pregitzer, K. S., & Burton, A. J. (2004). Atmospheric Nitrate Deposition, Microbial Community Composition, and Enzyme Activity in Northern Hardwood Forests. *Soil Science Society of America Journal*, *68*(1), 132. https://doi.org/10.2136/sssaj2004.1320

Edgar, R. C., Haas, B. J., Clemente, J. C., Quince, C., & Knight, R. (2011). UCHIME improves sensitivity and speed of chimera detection. *Bioinformatics*, *27*(16), 2194–2200. https://doi.org/10.1093/bioinformatics/btr381

Eisenlord, S. D., Freedman, Z., Zak, D. R., Xue, K., He, Z., & Zhou, J. (2013). Microbial mechanisms mediating increased soil C storage under elevated atmospheric N deposition. *Applied and Environmental Microbiology*, *79*(4), 1191–1199. https://doi.org/10.1128/AEM.03156-12

Eisenlord, S. D., & Zak, D. R. (2010). Simulated Atmospheric Nitrogen Deposition Alters Actinobacterial Community Composition in Forest Soils. *Soil Science Society of America Journal*, *74*(4), 1157. https://doi.org/10.2136/sssaj2009.0240

Entwistle, E. M., Zak, D. R., & Argiroff, W. A. (2018). Anthropogenic N deposition increases soil C storage by reducing the relative abundance of lignolytic fungi. *Ecological Monographs*, *0*(0), 1–20. https://doi.org/10.1002/ecm.1288

Fichot, E. B., & Norman, R. S. (2013). Microbial phylogenetic profiling with the Pacific Biosciences sequencing platform. *Microbiome*, *1*(1), 2–6. https://doi.org/10.1186/2049-2618-1-10

Floudas, D., Binder, M., Riley, R., Barry, K., Blanchette, R. A., Henrissat, B., … Hibbett, D. S. (2012). The paleozoic origin of enzymatic lignin decomposition reconstructed from 31 fungal genomes. *Science*, *336*(6089), 1715–1719. https://doi.org/10.1126/science.1221748

Freedman, Z. B., Upchurch, R. A., Zak, D. R., & Cline, L. C. (2016). Anthropogenic N deposition slows decay by favoring bacterial metabolism: Insights from metagenomic

analyses. *Frontiers in Microbiology*, *7*(MAR), 1–11. https://doi.org/10.3389/fmicb.2016.00259

Freedman, Z. B., & Zak, D. R. (2014). Atmospheric N deposition increases bacterial laccase-like multicopper oxidases: Implications for organic matter decay. *Applied and Environmental Microbiology*, *80*(14), 4460–4468. https://doi.org/10.1128/AEM.01224-14

Freschet, G. T., Cornwell, W. K., Wardle, D. A., Elumeeva, T. G., Liu, W., Jackson, B. G., … Cornelissen, J. H. C. (2013). Linking litter decomposition of above- and below-ground organs to plant-soil feedbacks worldwide. *Journal of Ecology*, *101*(4), 943–952. https://doi.org/10.1111/1365-2745.12092

Frey, S. D., Ollinger, S., Nadelhoffer, K., Bowden, R., Brzostek, E., Burton, A., … Wickings, K. (2014). Chronic nitrogen additions suppress decomposition and sequester soil carbon in temperate forests. *Biogeochemistry*, *121*(2), 305–316. https://doi.org/10.1007/s10533-014-0004-0

Galloway, J. N., Dentener, F. J., Capone, D. G., Boyer, E. W., Howarth, R. W., Seitzinger, S. P., … Vörösmarty, C. J. (2004). *Nitrogen cycles: Past, present, and future*. *Biogeochemistry* (Vol. 70). https://doi.org/10.1007/s10533-004-0370-0

Galloway, J. N., Townsend, A. R., Erisman, J. W., Bekunda, M., Cai, Z., Freney, J. R., … Sutton, M. A. (2008). Transformation of the Nitrogen Cycle: Recent Trends, Questions, and Potential Solutions. *Science*, *320*(5878), 889–892. https://doi.org/10.1126/science.1136674

Ghosh, A., Frankland, J. C., Thurston, C. F., & Robinson, C. H. (2003). Enzyme production by Mycena galopus mycelium in artificial media and in Picea sitchensis F1horizon needle litter. *Mycological Research*, *107*(8), 996–1008. https://doi.org/10.1017/S0953756203008177

Grandy, A. S., Neff, J. C., & Weintraub, M. N. (2007). Carbon structure and enzyme activities in alpine and forest ecosystems. *Soil Biology and Biochemistry*, *39*(11), 2701–2711. https://doi.org/10.1016/j.soilbio.2007.05.009

Grandy, A. S., Sinsabaugh, R. L., Neff, J. C., Stursova, M., & Zak, D. R. (2008). Nitrogen deposition effects on soil organic matter chemistry are linked to variation in enzymes, ecosystems and size fractions. *Biogeochemistry*, *91*(1), 37–49. https://doi.org/10.1007/s10533-008-9257-9

Grandy, A. S., Strickland, M. S., Lauber, C. L., Bradford, M. A., & Fierer, N. (2009). The

influence of microbial communities, management, and soil texture on soil organic matter chemistry. *Geoderma*, *150*(3–4), 278–286. https://doi.org/10.1016/j.geoderma.2009.02.007

Guo, D., Xia, M., Wei, X., Chang, W., Liu, Y., & Wang, Z. (2008). Anatomical traits associated with absorption and mycorrhizal colonization are linked to root branch order in twenty-three Chinese temperate tree species. *New Phytologist*, *180*(3), 673–683. https://doi.org/10.1111/j.1469-8137.2008.02573.x

Hassett, J. E., Zak, D. R., Blackwood, C. B., & Pregitzer, K. S. (2009). Are basidiomycete laccase gene abundance and composition related to reduced lignolytic activity under elevated atmospheric NO3- Deposition in a northern hardwood forest? *Microbial Ecology*, *57*(4), 728–739. https://doi.org/10.1007/s00248-008-9440-5

Hawkes, C. V., & Keitt, T. H. (2015). Resilience vs. historical contingency in microbial responses to environmental change. *Ecology Letters*, *18*(7), 612–625. https://doi.org/10.1111/ele.12451

Hibbett, D. S., Bauer, R., Binder, M., Giachini, A. J., Hosaka, K., Justo, A., … Thorn, R. G. (2014). Agaricomycetes. In D. J. McLaughlin & J. W. Spatafora (Eds.), *The Mycota vol. 7A: Systematics and Evolution* (2nd ed., pp. 373–429).

Hobbie, S. E. (2005). Contrasting effects of substrate and fertilizer nitrogen on the early stages of litter decomposition. *Ecosystems*, *8*(6), 644–656. https://doi.org/10.1007/s10021-003-0110-7

Hobbie, S. E., Oleksyn, J., Eissenstat, D. M., & Reich, P. B. (2010). Fine root decomposition rates do not mirror those of leaf litter among temperate tree species. *Oecologia*, *162*(2), 505–513. https://doi.org/10.1007/s00442-009-1479-6

Hofrichter, M. (2002). Review: Lignin conversion by manganese peroxidase (MnP). *Enzyme and Microbial Technology*, *30*(4), 454–466. https://doi.org/10.1016/S0141-0229(01)00528-2

Hölker, U., Dohse, J., & Höfer, M. (2002). Extracellular laccases in ascomycetes Trichoderma atroviride and Trichoderma harzianum. *Folia Microbiologica*, *47*(4), 423–427. https://doi.org/10.1007/BF02818702

Jackson, R. B., Lajtha, K., Crow, S. E., Hugelius, G., Kramer, M. G., & Piñeiro, G. (2017). The Ecology of Soil Carbon: Pools, Vulnerabilities, and Biotic and Abiotic Controls. *Annual Review of Ecology, Evolution, and Systematics*, *48*(1), annurev-ecolsys-112414-054234. https://doi.org/10.1146/annurev-ecolsys-112414-054234

709 Janssens, I. A., Dieleman, W., Luyssaert, S., Subke, J. A., Reichstein, M., Ceulemans, R., …
710 Law, B. E. (2010). Reduction of forest soil respiration in response to nitrogen deposition.
711 *Nature Geoscience*, *3*(5), 315–322. https://doi.org/10.1038/ngeo844
712 Janusz, G., Pawlik, A., Sulej, J., Świderska-Burek, U., Jarosz-Wilkołazka, A., & Paszczyński, A.
713 (2017). Lignin degradation: microorganisms, enzymes involved, genomes analysis and
714 evolution. *FEMS Microbiology Reviews*, (November), 1–22.
715 https://doi.org/10.1093/femsre/fux049
716 Keenan, T. F., Prentice, I. C., Canadell, J. G., Williams, C. A., Wang, H., Raupach, M. R., &
717 Collatz, G. J. (2017). Recent pause in the growth rate of atmospheric CO2 due to enhanced
718 terrestrial carbon uptake. *Nature Communications*, *7*(13428), 1.
719 https://doi.org/10.1038/ncomms13428
720 Kellner, H., Luis, P., Pecyna, M. J., Barbi, F., Kapturska, D., Krüger, D., … Hofrichter, M.
721 (2014). Widespread occurrence of expressed fungal secretory peroxidases in forest soils.
722 *PLoS ONE*, *9*(4). https://doi.org/10.1371/journal.pone.0095557
723 Kirk, T. K., & Farrell, R. L. (1987). Enzymatic "Combustion": the Microbial Degradation of
724 Lignin. *Annual Review of Microbiology*, *41*, 465–505.
725 https://doi.org/10.1146/annurev.mi.41.100187.002341
726 Kohout, P., Charvátová, M., Martina, Š., Ma, T., Tom, M., & Baldrian, P. (2018). Clearcutting
727 alters decomposition processes and initiates complex restructuring of fungal communities in
728 soil and tree roots. *ISME Journal*. https://doi.org/10.1038/s41396-017-0027-3
729 Kou, L., Jiang, L., Fu, X., Dai, X., Wang, H., & Li, S. (2018). Nitrogen deposition increases root
730 production and turnover but slows root decomposition in Pinus elliottii plantations. *New*
731 *Phytologist*. https://doi.org/10.1111/nph.15066
732 Lane, D. (1991). 16s/23s rRNA sequencing. In E. Stackebrandt & M. Goodfellow (Eds.), *Nucleic*
733 *acid techniques in bacterial systematics* (pp. 115–175). West Sussex, United Kingdom:
734 John Wiley & Sons, Inc.
735 Lehmann, J., & Kleber, M. (2015). The contentious nature of soil organic matter. *Nature*,
736 *528*(7580), 60–68. https://doi.org/10.1038/nature16069
737 Li, A., Fahey, T. J., Pawlowska, T. E., Fisk, M. C., & Burtis, J. (2015). Fine root decomposition,
738 nutrient mobilization and fungal communities in a pine forest ecosystem. *Soil Biology and*
739 *Biochemistry*, *83*, 76–83. https://doi.org/10.1016/j.soilbio.2015.01.019

740 Liu, K. L., Porras-Alfaro, A., Kuske, C. R., Eichorst, S. A., & Xie, G. (2012). Accurate, rapid
741 taxonomic classification of fungal large-subunit rRNA Genes. *Applied and Environmental*
742 *Microbiology*, *78*(5), 1523–1533. https://doi.org/10.1128/AEM.06826-11
743 Luo, C., Xie, S., Sun, W., Li, X., & Cupples, A. M. (2009). Identification of a novel toluene-
744 degrading bacterium from the candidate phylum TM7, as determined by DNA stable
745 isotope probing. *Applied and Environmental Microbiology*, *75*(13), 4644–4647.
746 https://doi.org/10.1128/AEM.00283-09
747 Maaroufi, N. I., Nordin, A., Hasselquist, N. J., Bach, L. H., Palmqvist, K., & Gundale, M. J.
748 (2015). Anthropogenic nitrogen deposition enhances carbon sequestration in boreal soils.
749 *Global Change Biology*, *21*(8), 3169–3180. https://doi.org/10.1111/gcb.12904
750 Martinez, D., Berka, R. M., Henrissat, B., Saloheimo, M., Arvas, M., Baker, S. E., … Brettin, T.
751 S. (2008). Genome sequencing and analysis of the biomass-degrading fungus Trichoderma
752 reesei (syn. Hypocrea jecorina). *Nature Biotechnology*, *26*(5), 553–560.
753 https://doi.org/10.1038/nbt1403
754 McCormack, M. L., Dickie, I. A., Eissenstat, D. M., Fahey, T. J., Fernandez, C. W., Guo, D., …
755 Zadworny, M. (2015). Redefining fine roots improves understanding of below-ground
756 contributions to terrestrial biosphere processes. *New Phytologist*, *207*(3), 505–518.
757 https://doi.org/10.1111/nph.13363
758 McMurdie, P. J., & Holmes, S. (2013). Phyloseq: An R Package for Reproducible Interactive
759 Analysis and Graphics of Microbiome Census Data. *PLoS ONE*, *8*(4).
760 https://doi.org/10.1371/journal.pone.0061217
761 McMurdie, P. J., & Holmes, S. (2014). Waste Not, Want Not: Why Rarefying Microbiome Data
762 Is Inadmissible. *PLoS Computational Biology*, *10*(4).
763 https://doi.org/10.1371/journal.pcbi.1003531
764 Miyamoto, T. (2000). Lignin-degrading ability of litter-decomposing basidiomycetes from Picea
765 forests of Hokkaido. *Mycoscience*, *41*(2), 105–110. https://doi.org/10.1007/BF02464317
766 Morrison, E. W., Frey, S. D., Sadowsky, J. J., van Diepen, L. T. A., Thomas, W. K., & Pringle,
767 A. (2016). Chronic nitrogen additions fundamentally restructure the soil fungal community
768 in a temperate forest. *Fungal Ecology*, *23*, 48–57.
769 https://doi.org/10.1016/j.funeco.2016.05.011
770 Morrison, E. W., Pringle, A., van Diepen, L. T. A., & Frey, S. D. (2018). Simulated nitrogen

771 deposition favors stress-tolerant fungi with low potential for decomposition. *Soil Biology*
772 *and Biochemistry*, *125*(June), 75–85. https://doi.org/10.1016/j.soilbio.2018.06.027
773 Mueller, R. C., Balasch, M. M., & Kuske, C. R. (2014). Contrasting soil fungal community
774 responses to experimental nitrogen addition using the large subunit rRNA taxonomic
775 marker and cellobiohydrolase i functional marker. *Molecular Ecology*, *23*(17), 4406–4417.
776 https://doi.org/10.1111/mec.12858
777 Oksanen, J., Blanchet, F. G., Friendly, M., Kindt, R., Legendre, P., McGlinn, D., … Wagner, H.
778 (2018). vegan: Community Ecology Package. Retrieved from https://cran.r-
779 project.org/package=vegan
780 Pan, Y., Birdsey, R. A., Fang, J., Houghton, R., Kauppi, P. E., Kurz, W. A., … Hayes, D. (2011).
781 A Large and Persistent Carbon Sink in the World's Forests. *Science*, *333*(6045), 988–993.
782 https://doi.org/10.1126/science.1201609
783 Philpott, T. J., Barker, J. S., Prescott, C. E., & Grayston, S. J. (2018). Limited effects of variable-
784 retention harvesting on fungal communities decomposing fine roots in coastal temperate
785 rainforests. *Applied and Environmental Microbiology*, *84*(3), 1–16.
786 https://doi.org/10.1128/AEM.02061-17
787 Pold, G., Grandy, A. S., Melillo, J. M., & DeAngelis, K. M. (2017). Changes in substrate
788 availability drive carbon cycle response to chronic warming. *Soil Biology and Biochemistry*,
789 *110*, 68–78. https://doi.org/10.1016/j.soilbio.2017.03.002
790 Porter, T. M., & Golding, G. B. (2012). Factors that affect large subunit ribosomal DNA
791 amplicon sequencing studies of fungal communities: Classification method, primer choice,
792 and error. *PLoS ONE*, *7*(4). https://doi.org/10.1371/journal.pone.0035749
793 Pregitzer, K. S., Burton, A. J., Zak, D. R., & Talhelm, A. F. (2008). Simulated chronic nitrogen
794 deposition increases carbon storage in Northern Temperate forests. *Global Change Biology*,
795 *14*(1), 142–153. https://doi.org/10.1111/j.1365-2486.2007.01465.x
796 Pregitzer, K. S., Deforest, J. L., Burton, A. J., Allen, M. F., Ruess, R. W., & L., H. R. (2002).
797 Fine root architecture of nine North American trees. *Ecological Mono*, *72*(2), 293–309.
798 Pregitzer, K. S., Zak, D. R., Burton, A. J., Ashby, J. A., & Macdonald, N. W. (2004). Chronic
799 nitrate additions dramatically increase the export of carbon and nitrogen from northern
800 hardwood ecosystems. *Biogeochemistry*, *68*(2), 179–197.
801 https://doi.org/10.1023/B:BIOG.0000025737.29546.fd

802 Quast, C., Pruesse, E., Yilmaz, P., Gerken, J., Schweer, T., Yarza, P., … Glöckner, F. O. (2013).
803 The SILVA ribosomal RNA gene database project: Improved data processing and web-
804 based tools. *Nucleic Acids Research*, *41*(D1), 590–596. https://doi.org/10.1093/nar/gks1219
805 R Core Team. (2018). R: A language and environment for statistical computing. Vienna, Austria:
806 R Foundation for Statistical Computing. Retrieved from https://www.r-project.org/
807 Rasse, D. P., Rumpel, C., & Dignac, M. F. (2005). Is soil carbon mostly root carbon?
808 Mechanisms for a specific stabilisation. *Plant and Soil*, *269*(1–2), 341–356.
809 https://doi.org/10.1007/s11104-004-0907-y
810 RStudio Team. (2018). RStudio: integrated development for R. Boston, MA, USA.
811 Schimel, J. P., & Schaeffer, S. M. (2012). Microbial control over carbon cycling in soil.
812 *Frontiers in Microbiology*, *3*(SEP), 1–11. https://doi.org/10.3389/fmicb.2012.00348
813 Schlesinger, W. H., & Bernhardt, E. S. (2013). The Carbon Cycle of Terrestrial Ecosystems. In
814 *Biogeochemistry: An Analysis of Global Change* (3rd ed., pp. 135–172). New York:
815 Academic Press.
816 Schloss, P. D., Westcott, S. L., Ryabin, T., Hall, J. R., Hartmann, M., Hollister, E. B., … Weber,
817 C. F. (2009). Introducing mothur: Open-source, platform-independent, community-
818 supported software for describing and comparing microbial communities. *Applied and*
819 *Environmental Microbiology*, *75*(23), 7537–7541. https://doi.org/10.1128/AEM.01541-09
820 Silver, W. L., & Miya, R. K. (2001). Global patterns in root decomposition: Comparisons of
821 climate and litter quality effects. *Oecologia*, *129*(3), 407–419.
822 https://doi.org/10.1007/s004420100740
823 Sun, T., Dong, L., Wang, Z., Lü, X., & Mao, Z. (2016). Effects of long-term nitrogen deposition
824 on fine root decomposition and its extracellular enzyme activities in temperate forests. *Soil*
825 *Biology and Biochemistry*, *93*, 50–59. https://doi.org/10.1016/j.soilbio.2015.10.023
826 Sun, T., Hobbie, S. E., Berg, B., Zhang, H., Wang, Q., Wang, Z., & Hättenschwiler, S. (2018).
827 Contrasting dynamics and trait controls in first-order root compared with leaf litter
828 decomposition. *Proceedings of the National Academy of Sciences*, 201716595.
829 https://doi.org/10.1073/pnas.1716595115
830 Talbot, J. M., & Treseder, K. K. (2012). Interactions between lignin, cellulose, and nitrogen
831 drive litter chemistry - decay relationships. *Ecology*, *93*(2), 345–354.
832 https://doi.org/10.1890/11-0843.1

833 Taylor, C. R., Hardiman, E. M., Ahmad, M., Sainsbury, P. D., Norris, P. R., & Bugg, T. D. H.
834 (2012). Isolation of bacterial strains able to metabolize lignin from screening of
835 environmental samples. *Journal of Applied Microbiology*, *113*(3), 521–530.
836 https://doi.org/10.1111/j.1365-2672.2012.05352.x
837 Teixeira, M. M., Moreno, L. F., Stielow, B. J., Muszewska, A., Hainaut, M., Gonzaga, L., … de
838 Hoog, G. S. (2017). Exploring the genomic diversity of black yeasts and relatives
839 (Chaetothyriales, Ascomycota). *Studies in Mycology*, *86*, 1–28.
840 https://doi.org/10.1016/j.simyco.2017.01.001
841 Thomas, D. C., Zak, D. R., & Filley, T. R. (2012). Chronic N deposition does not apparently
842 alter the biochemical composition of forest floor and soil organic matter. *Soil Biology and*
843 *Biochemistry*, *54*, 7–13. https://doi.org/10.1016/j.soilbio.2012.05.010
844 Travers, K. J., Chin, C. S., Rank, D. R., Eid, J. S., & Turner, S. W. (2010). A flexible and
845 efficient template format for circular consensus sequencing and SNP detection. *Nucleic*
846 *Acids Research*, *38*(15). https://doi.org/10.1093/nar/gkq543
847 Treseder, K. K., Balser, T. C., Bradford, M. A., Brodie, E. L., Dubinsky, E. A., Eviner, V. T., …
848 Waldrop, M. P. (2012). Integrating microbial ecology into ecosystem models: challenges
849 and priorities. *Biogeochemistry*, *109*(1–3), 7–18. https://doi.org/10.1007/s10533-011-9636-
850 5
851 vandenEnden, L., Frey, S. D., Nadelhoffer, K. J., LeMoine, J. M., Lajtha, K., & Simpson, M. J.
852 (2018). Molecular-level changes in soil organic matter composition after 10 years of litter,
853 root and nitrogen manipulation in a temperate forest. *Biogeochemistry*, *141*(2), 183–197.
854 https://doi.org/10.1007/s10533-018-0512-4
855 Vilgalys, R., & Hester, M. (1990). Rapid genetic identification and mapping of several
856 Cryptococcus species. *Journal of Bacteriology*, *172*(8), 4238–4246.
857 https://doi.org/10.1128/JB.172.8.4238-4246.1990
858 Voriskova, J., & Baldrian, P. (2013). Fungal community on decomposing leaf litter undergoes
859 rapid successional changes. *ISME Journal*, *7*(3), 477–486.
860 https://doi.org/10.1038/ismej.2012.116
861 Waldrop, M. P., Zak, D. R. Z., Sinsabaugh, R. L. S., Gallo, M. G. E., & Lauber, C. (2004).
862 Nitrogen Deposition Modifies Soil Carbon Storage Through Changes in Microbial
863 Enzymatic Activity. *Ecological Applications*, *14*(4), 1172–1177. https://doi.org/10.1890/03-

5120

Wang, J.-J., Bowden, R. D., Lajtha, K., Washko, S. E., Wurzbacher, S. J., & Simpson, M. J. (2019). Long-term nitrogen addition suppresses microbial degradation, enhances soil carbon storage, and alters the molecular composition of soil organic matter. *Biogeochemistry*, *4*. https://doi.org/10.1007/s10533-018-00535-4

Wang, Q., Garrity, G. M., Tiedje, J. M., & Cole, J. R. (2007). Naïve Bayesian classifier for rapid assignment of rRNA sequences into the new bacterial taxonomy. *Applied and Environmental Microbiology*, *73*(16), 5261–5267. https://doi.org/10.1128/AEM.00062-07

Whalen, E. D., Smith, R. G., Grandy, A. S., & Frey, S. D. (2018). Manganese limitation as a mechanism for reduced decomposition in soils under atmospheric nitrogen deposition. *Soil Biology and Biochemistry*, *127*, 252–263. https://doi.org/10.1016/J.SOILBIO.2018.09.025

Wickham, H. (2017). tidyverse: Easily Install and Load the "Tidyverse."

Wickings, K., Grandy, A. S., Reed, S., & Cleveland, C. (2011). Management intensity alters decomposition via biological pathways. *Biogeochemistry*, *104*(1–3), 365–379. https://doi.org/10.1007/s10533-010-9510-x

Wilhelm, R. C., Singh, R., Eltis, L. D., & Mohn, W. W. (2018). Bacterial contributions to delignification and lignocellulose degradation in forest soils with metagenomic and quantitative stable isotope probing. *ISME Journal*. https://doi.org/10.1038/s41396-018-0279-6

Xia, M., Guo, D., & Pregitzer, K. S. (2010). Ephemeral root modules in fraxinus mandshurica. *New Phytologist*, *188*(4), 1065–1074. https://doi.org/10.1111/j.1469-8137.2010.03423.x

Xia, M., Talhelm, A. F., & Pregitzer, K. S. (2015). Fine roots are the dominant source of recalcitrant plant litter in sugar maple-dominated northern hardwood forests. *New Phytologist*, *208*(3), 715–726. https://doi.org/10.1111/nph.13494

Xia, M., Talhelm, A. F., & Pregitzer, K. S. (2017). Chronic nitrogen deposition influences the chemical dynamics of leaf litter and fine roots during decomposition. *Soil Biology and Biochemistry*, *112*, 24–34. https://doi.org/10.1016/j.soilbio.2017.04.011

Xia, M., Talhelm, A. F., & Pregitzer, K. S. (2018). Long-Term Simulated Atmospheric Nitrogen Deposition Alters Leaf and Fine Root Decomposition. *Ecosystems*, *21*(1), 1–14. https://doi.org/10.1007/s10021-017-0130-3

Zak, D. R., Argiroff, W. A., Freedman, Z. B., Upchurch, R. A., Entwistle, E. M., &

Romanowicz, K. J. (2019). Anthropogenic N deposition, fungal gene expression, and an increasing soil carbon sink in the Northern Hemisphere. *Ecology*, e02804. https://doi.org/10.1002/ecy.2804

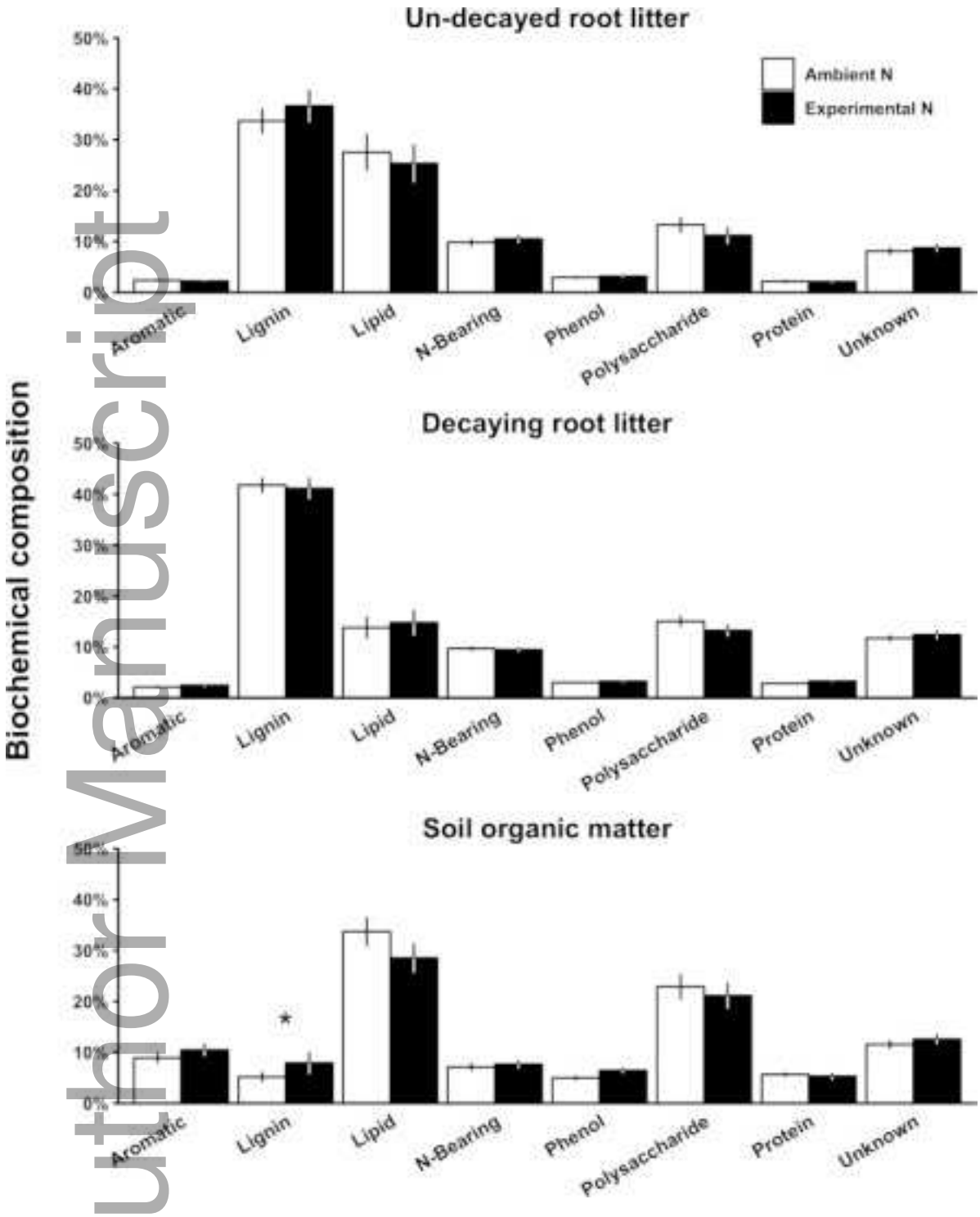
Zak, D. R., Freedman, Z. B., Upchurch, R. A., Steffens, M., & Kögel-Knabner, I. (2017). Anthropogenic N deposition increases soil organic matter accumulation without altering its biochemical composition. *Global Change Biology*, *23*(2), 933–944. https://doi.org/10.1111/gcb.13480

Zak, D. R., Holmes, W. E., Burton, A. J., Pregitzer, K. S., & Talhelm, A. F. (2008). Simulated atmospheric NO3− deposition increases organic matter by slowing decomposition. *Ecological Applications*, *18*(8), 2016–2027. https://doi.org/10.1890/07-1743.1

FIGURE CAPTIONS

926

927 **Figure 1** Biochemical composition of fine root litter and soil organic matter based on the relative
928 abundance (%) of compound classes. Bars represent mean relative abundances and error
929 bars are 1 standard error of the mean (n = 12). * $P < 0.1$ for effect of experimental N
930 deposition by two-way ANOVA.
931
932 **Figure 2** Relative abundance of fungal orders and bacterial families exhibiting significant
933 responses to experimental N deposition after 12 months. Bars represent mean relative
934 abundances and error bars are one standard error (n = 12). * $P < 0.1$, ** $P < 0.05$, for
935 effect of experimental N deposition by two-way ANOVA
936
937 **Figure 3** db-RDA ordinations determined from Bray-Curtis dissimilarity calculated using
938 Hellinger-transformed abundances of fungal genera (a, b) and bacterial families (c, d).
939 Ordinations were constrained to include variation due to experimental N deposition and
940 site, which together accounted for 37.7% of variation in Bray-Curtis dissimilarity for
941 fungi and 33.2% for bacteria. Panels (a) (fungi) and (c) (bacteria) display site by
942 treatment mean loadings (error bars are one standard error). Panels (b) (fungi) and (d)
943 (bacteria) include taxon loadings (which represent the direction from the origin in which
944 a genus increases in relative abundance) and compound class vectors from SOM.
945 Classified taxa that accounted for >1% of sequences were included. Involvement of non-
946 Actinobacterial families in lignin degradation was based on Wilhelm et al., (2018). * P <
947 0.1, ** P < 0.05 for vector fit. *Cha, Chaetomium*; *Chr*, *Christiansenia*; *Exo*, *Exophiala*;
948 *Hyp*, *Hypocrea*; *Hem*, *Hemimycena*; *Kue*, *Kuehneromyces*; *Myc*, *Mycena*; *Ram*,
949 *Ramariopsis*; *Umb*, *Umbelopsis*; Lig, lignin-derived compounds; N-Bear, N-bearing
950 compounds (b). Ace, Acetobacteraceae; Aci, Acidobacteriaceae Subgroup 1, Bur,
951 Burkholderiaceae; Cau, Caulobacteraceae, Chi, Chitinophagaceae; Gem,
952 Gemmatimonadaceae; Mib, Microbacteriaceae; Mip, Micromonosporaceae; Rho,
953 Rhodanobacteraceae; Sol, Solibacteraceae Subgroup 3; Spb, Sphingobacteriaceae; Spg,
954 Sphingomonadaceae; Xan, Xanthobacteraceae, Lig, lignin-derived compounds; Lip, lipid
955 (d).



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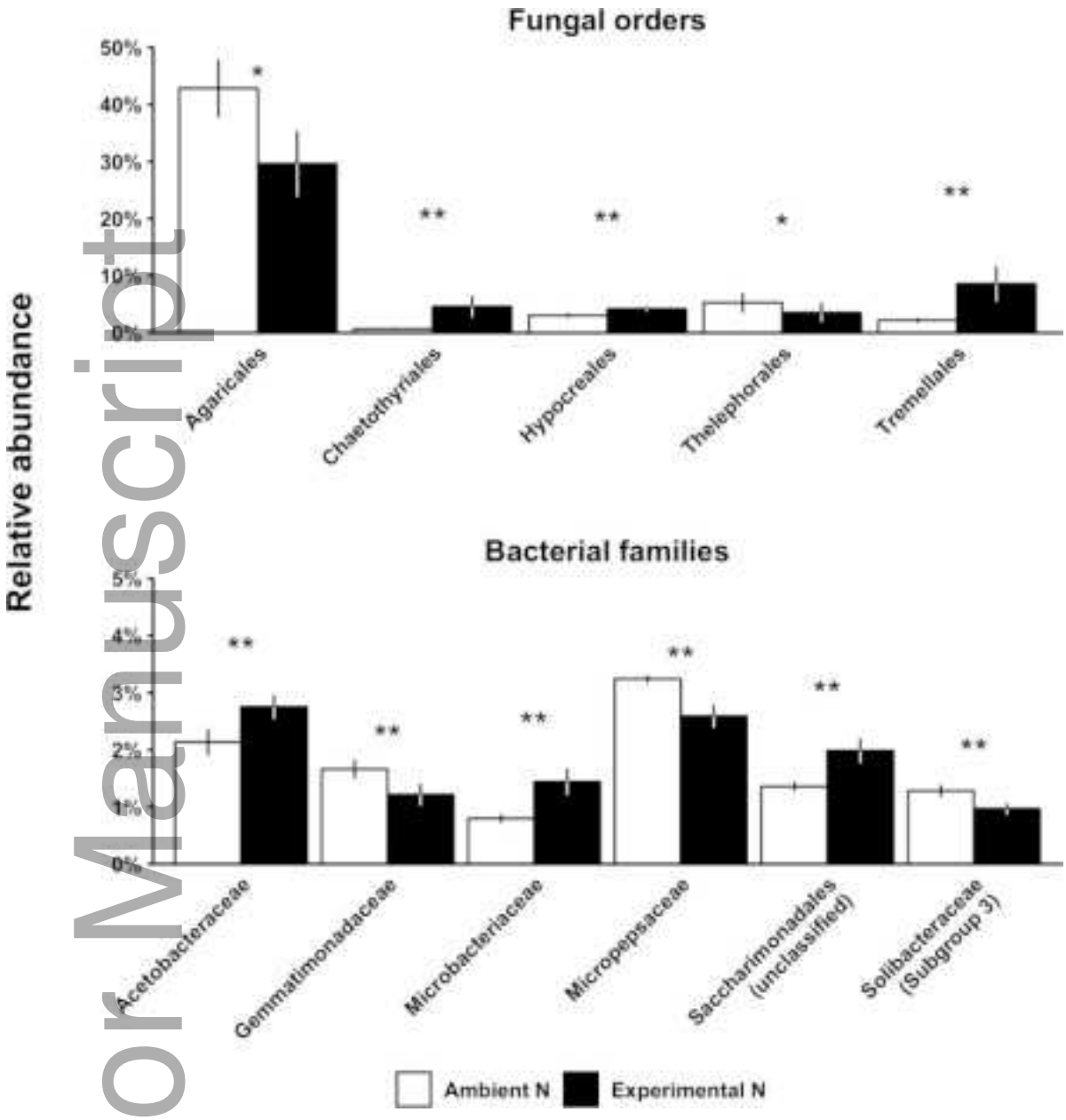

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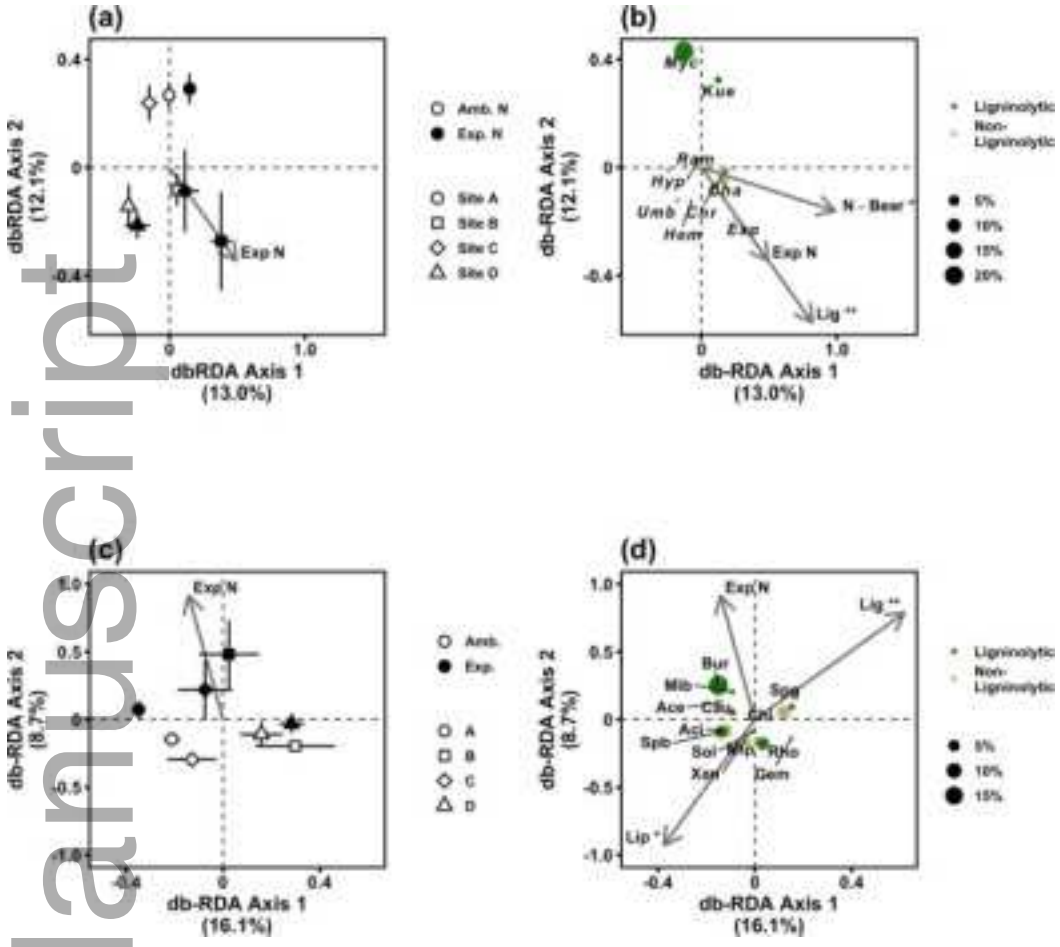

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