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UNIVERSITY OF CALIFORNIA
RIVERSIDE

Responses of Arbuscular Mycorrhizal Fungi to Multiple Global Change Drivers in
Coastal Sage Scrub

A Thesis submitted in partial satisfaction
of the requirements for the degree of

Master of Science

in

Plant Biology

by

Sören Eliot Weber

June 2017

Thesis Committee:

Dr. Jeffrey Diez, co- Chairperson

Dr. Michael Allen, co- Chairperson

Dr. Emma Aronson

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The Thesis of Sören Eliot Weber is approved:

Committee co-Chairperson

Committee co-Chairperson

University of California, Riverside

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ABSTRACT OF THE THESIS

Responses of Arbuscular Mycorrhizal Fungi to Multiple Global Change Drivers in Coastal Sage Scrub

by

Sören Eliot Weber

Master of Science, Graduate Program in Plant Biology

University of California, Riverside, June 2017

Dr. Jeffrey Diez, co-Chairperson

Dr. Michael Allen, co-Chairperson

While the importance of animal and plant responses to global change is generally appreciated, comparatively little is known about fungal community responses to shifting environmental conditions. My study evaluated the role of aridity, atmospheric nitrogen (N) deposition and annual grass invasion in driving responses of the fungal community in roots, focusing on the arbuscular mycorrhizal fungi (AMF). Previous work has found that AMF with high root colonization (rhizophilic AMF) reduce root pathogen infection and respond positively to N deposition and annual grass invasion. Other work has found that AMF with high soil colonization (edaphophilic AMF) are more important for nutrient uptake and generally respond negatively to additional N, drought and association with grasses. I ask: do guilds of AMF respond differently to multiple drivers of global change and does this impact community biomass allocation and interactions between fungi?

I sampled roots and soils from native shrubs and invasive grasses in coastal sage scrub within a long-term experiment manipulating N and precipitation. I extracted

and counted spore and hyphal densities from soils, percent root length colonized by AM and non-AM fungi, and measurements of soil chemistry (Total N, C, P, NH₄, NO₃ and pH). Additionally, I estimated the composition of fungi in plant roots using two rRNA loci: SSU with AMF specific primers and ITS2 with universal fungal primers. I evaluated these responses of fungal composition and biomass with generalized linear models.

I found that drought reduces the relative abundance of edaphophilic AMF and overall AMF biomass. Nitrogen addition reduces the relative abundance of edaphophilic AMF, and increases AMF allocation to root colonization and spore production while reducing the extent of nutrient foraging soil hyphae. Both drought and N deposition increased the extent of root colonization by saprotrophic and pathogenic fungi, suggesting that plants become more susceptible to infection by non-mutualistic fungi as water becomes more limiting. Invasive annual grasses hosted less edaphophilic AMF than did native shrubs, while one grass species also hosted a higher abundance of ancestral AMF. Overall, this suggests that with increasing drought, N deposition and invasion of shrub communities by annual grasses, the abundance of edaphophilic AMF in coastal sage scrub will decline.

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INTRODUCTION

Plant and animal responses to changing environmental conditions have been extensively studied, but little is known about the sensitivity or direction of fungal responses to these shifts. In the US southwest, precipitation frequency is expected to decline over the next century (Seager and Vecchi 2010), leading to an increased regional aridity. In this same region, anthropogenic atmospheric nitrogen (N) deposition has altered N cycling, leading to changes in the composition of arbuscular mycorrhizal fungi (AMF; Egerton-Warburton and Allen 2000) and the broader fungal community in general (Amend et al. 2016). Arbuscular mycorrhizal fungi are important mutualists of plants, associating with plant roots and providing a variety of functions in exchange for photosynthetically derived sugars, including uptaking nutrients (primarily P: Smith et al. 2011; but also N, see Hodge and Storer 2014), altering plant drought response (Auge 2001; Worchel, Giaque, and Kivlin 2013), and reducing root pathogen infection (Sikes, Cottenie, and Klironomos 2009; Sikes, Powell, and Rillig 2010). Our current understanding of these AMF community responses is limited to coarse patterns estimated from spore composition and other fungal morphological data. However, recent developments in molecular sequencing technologies offer great potential for understanding how fungal communities respond to changing environmental conditions. New challenges arise with the use of these molecular data, specifically in interpreting the ecological significance of fungal responses. To better interpret responses in composition estimated from high-throughput sequencing datasets, there is a pressing need to classify AMF into functional guilds.

Arbuscular mycorrhizal fungi can be broadly classified into guilds by their patterns of biomass allocation to extraradical hyphae, intraradical hyphae, spores, and

their primary dispersal mode (Tab. 1; Maherali and Klironomos 2007). Based on published descriptions of these patterns at the family level, I will refer to these functional groups as ‘edaphophilic’ (preference for soil colonization), ‘rhizophilic’ (preference for root colonization) and ‘ancestral’ (lack preference, ancestral condition for AMF, *sensu* Powell et al. 2009). These AMF guilds have important differences in how they interact with and affect plant hosts. Rhizophilic AMF (e.g. Glomeraceae) reduce root pathogen infection by heavily colonizing roots, primarily benefiting plants with fine-roots prone to pathogen infection (Sikes, Powell, and Rillig 2010). Edaphophilic AMF (e.g. Gigasporaceae) increase plant foliar P via their extensive extraradical mycelium, primarily benefiting plants with coarse-roots with poor nutrient uptake capacity (Sikes, Powell, and Rillig 2010). While the effect of ancestral AMF on plant performance remains unclear, Maherali and Klironomos 2007 showed that plant performance improved with the inoculation of this guild, suggesting functional complementarity between ancestral and other AMF. Because these guilds are defined by functional characters that likely influence the ecology of AMF, it may be a useful framework for understanding the functional implications of shifts in community composition.

Table 1. Description of AMF guilds.

Guild	Intraradical hyphae	Extraradical hyphae	Spore size	Dispersal mode	Families
Rhizophilic	High	Low	Low	Colonized roots	Glomeraceae * ◊ ⊙ † ‡ Claroideo- ◊ glomeraceae Paraglomeraceae
Edaphophilic	Low	High	Mid-High	Spores and extraradical mycelium	Gigasporaceae * ◊ † Diversisporaceae * ◊ ‡
Ancestral	Low	Low	Low-High	Variable: roots, spores and extra-radical mycelium	Archaeosporaceae Ambisporaceae Acaulosporaceae * ◊ Pacisporaceae ‡

Hart and Reader 2002*, Powell et al. 2009◊, Varela-Cervero et al. 2015⊙, 2016a†, b‡.
Family assignments without citations were based upon prior family affiliation.

These guilds of AMF also have different affinities for soil N and moisture that may be useful in predicting their responses to environmental change. For example, in arid environments edaphophilic AMF exhibit lower abundance and diversity compared to rhizophilic AMF (Stutz et al. 2000; Stutz and Morton 1996; Chaudhary et al. 2014). Hawkes et al. 2011 also found variation among functional groups in their responses to a precipitation gradient in a mediterranean climate. Although fungal diversity declined overall with increasing rainfall, root colonization by aseptate fungi (presumably AMF) and septate fungi (other symbionts as well as pathogens & saprotrophs) did not respond, suggesting that responses of AMF composition to precipitation may not result in shifts in biomass allocation.

In addition to changes in precipitation, changes in nutrient dynamics affect AMF functional groups. Additional N largely increases the abundance of rhizophilic AMF and decreases the abundance of edaphophilic AMF (Egerton-Warburton and Allen 2000). This decline in edaphophilic AMF is potentially due to a decreased dependence of host plants on the uptake of nutrients primarily by edaphophilic AMF (Johnson 1993). However, this pattern appears to be dependent upon initial soil N:P (i.e. when the initial N:P ratio of soil is high, additional N results in a higher abundance of edaphophilic AMF; Egerton-Warburton, Johnson, and Allen 2007, Treseder and Allen 2002). Given that soils in southern California are relatively P rich, additional N in the form of atmospheric N deposition may result in an increased abundance of rhizophilic AMF, as was found along N deposition gradients in coastal sage scrub (Egerton-Warburton and Allen 2000). Previous research has shown that leaf litter fungi with strong responses to N addition also responded to drought (Amend et al. 2016; Martiny et al. 2017). Moreover,

ectomycorrhizal fungi may respond similarly to N as do rhizophilic and edaphophilic AMF (Lilleskov et al. 2002).

I ask: *Do edaphophilic and rhizophilic AMF and pathogenic and saprotrophic fungi differ in their responses to host plant identity, N deposition and precipitation? Furthermore, do these responses in relative abundances by different functional groups determine fungal biomass allocation to intra- and extraradical hyphae and spores?*

I hypothesized that edaphophilic AMF abundance and richness: (1) negatively respond to N deposition and (2) positively respond to soil moisture, (3) positively respond to association with (coarse-rooted) shrubs, (4) and that edaphophilic abundance drives AMF hyphal density in soil and (5) spore biovolume (Fig. 1). I expect that rhizophilic AMF abundance and richness: (6) respond positively to N deposition (7) respond positively to grasses and (8) drive AMF root colonization (Fig. 1). I also hypothesize that (fine-rooted) grasses will host a higher abundance and richness of (9) pathogens and saprotrophs, (10) that saprotroph and pathogen abundance drives non-AMF colonization that (11 & 12) rhizophilic AMF abundance and AMF colonization negatively affect non-AMF colonization and that (13) rhizophilic AMF abundance reduces the abundance of saprotrophic and pathogenic fungi (Fig. 1).

In addition to these hypotheses regarding edaphophilic and rhizophilic AMF, I also ask: *What are the main drivers of ancestral AMF abundance and richness?*

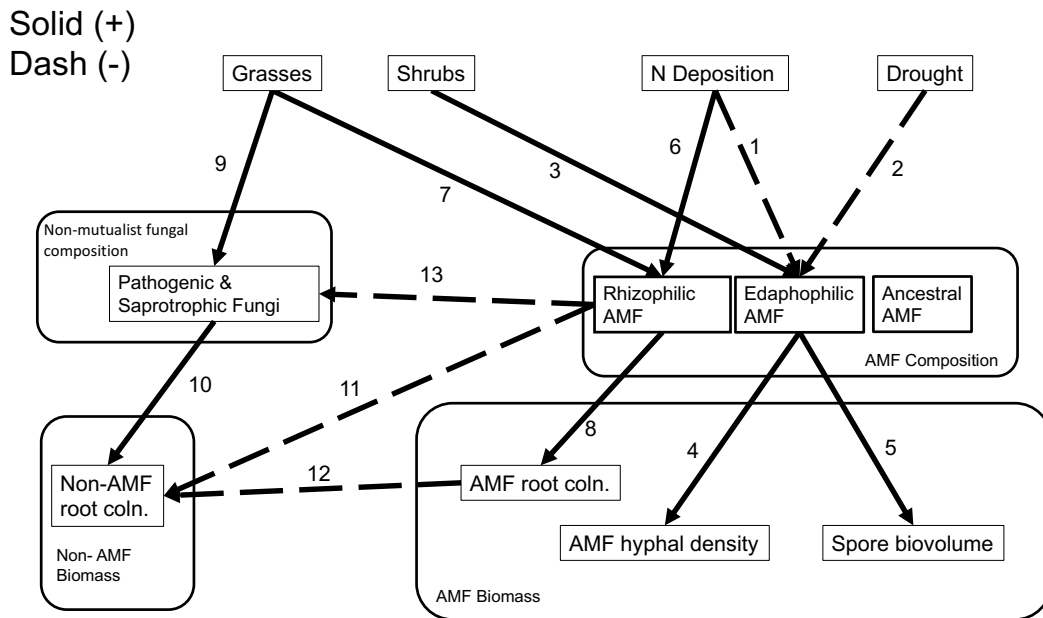


Figure 1. Conceptual diagram of hypotheses. Hypothesized positive interactions are solid, negative are dashed.

METHODS

Study system

The study site is coastal sage scrub, located in the foothills of the Santa Ana Mountains at Loma Ridge, near Irvine, CA (117.7048° W, 33.7428° N). This plant community is comprised of native crown-sprouting shrubs (e.g. *Salvia mellifera*, *Artemisia californica*, and *Eriogonum fasciculatum*) with interspaces predominantly composed of invasive grasses (e.g. *Bromus rubens*, *Schismus barbatus* and *Avena sp.*), though some native forbs and sub-shrubs are present (e.g. *Acemison glaber*, *Deinandra fasciculata*). The climate is mediterranean, with the wet, winter season lasting from November to April and a dry summer from May through October. Soils are of the Myford Sandy Loam type (Kimball et al. 2014), and a characterization of their soil chemistry

from my samples is provided in Table 2. This site has burned in 1914, 1948, 1967, 1998 and 2007. While this study site was developed to understand the role of changing precipitation and N deposition on coastal sage scrub succession following fire, within a year of experimentally burning half of the plots (Feb. 2007), the remaining plots burned in the Santiago wildfire (Kimball et al. 2014). Despite the difference in burn seasons, community responses following fire did not differ between these two sets of plots (Kimball et al. 2014). Application of precipitation and N treatments began after this last burn in 2007. Precipitation was experimentally reduced with the use of ‘rain-out’ shelters, this water was in turn captured and used to create water addition plots, resulting in three levels, 40% added, 40% reduced and an ambient precipitation treatment. Nitrogen was added to treatment plots as 2 gm⁻² of quick-release CaNO₃ prior to the first storms in winter, and 4 gm⁻² as slow-release CaNO₃ a month into the winter growing season, resulting in two N levels: added (6 gm⁻²yr⁻¹) and ambient (1.5 gm⁻² yr⁻¹). Precipitation and N treatments were crossed in a full factorial design.

Table 2. Characterization of soil chemistry across nitrogen & precipitation treatments.

Nitrogen Treatment	Precip. Treatment	P (ppm)	N (ppm)	C (ppm)	NO ₃ N (ppm)	NH ₄ N (ppm)	pH
Added	Added	20.8 ± 8.4	1082 ± 234	12496 ± 3060	8.8 ± 7.8	18.5 ± 14.3	6.39 ± 0.37
	Ambient	19.3 ± 11	1280 ± 348	14772 ± 3443	26.7 ± 82.2	15.6 ± 13.2	6.41 ± 0.3
	Reduced	17.2 ± 8.5	1109 ± 199	12900 ± 2903	45.9 ± 48.8	19.5 ± 13.8	6.43 ± 0.26
Ambient	Added	20.9 ± 8.6	1088 ± 225	12367 ± 2447	13.4 ± 37.7	16.9 ± 12.9	6.42 ± 0.33
	Ambient	18.1 ± 6.5	1229 ± 133	14257 ± 1525	6.6 ± 5.6	20 ± 16.9	6.26 ± 0.38
	Reduced	17.9 ± 6.5	1157 ± 228	13055 ± 2286	11.8 ± 18.5	16.9 ± 13.8	6.36 ± 0.34

Sampling and Storage

From seven plant species (Tab. 3), I sampled roots and soils across N and precipitation treatments in September 30, 2015 (dry season) and February 25, 2016 (wet season) to capture precipitation variability (Fig. 2). My target was to sample three

individual plants from each species per precipitation treatment per N treatment, however as Table 3 shows, my sampling effort was highest for *Artemisia californica*, *Salvia mellifera* and *Bromus rubens*. I selected randomly selected individual plants at a minimum of 1 m apart to reduce the potential for spatial autocorrelation (Hart et al. 2015). I collected approximately 0.5 L of bulk roots and soils from the base of each plant, and transported these samples to the University of California, Riverside.

Table 3. Description of host plant species and sampling coverage.

Species	Growth Form	Origin	Sample Number (Molecular Coverage)
<i>Salvia mellifera</i>	Shrub	California native	54 (17)
<i>Artemisia californica</i>	Shrub	California native	54 (16)
<i>Eriogonum fasciculatum</i>	Shrub	California native	2 (2)
<i>Bromus rubens</i>	Grass	Europe	53 (17)
<i>Schismus barbatus</i>	Grass	Europe/North Africa	8 (4)
<i>Avena sp.</i>	Grass	Europe/North Africa	3 (3)
<i>Erodium moschatum</i>	Forb	Europe/North Africa	1 (1)

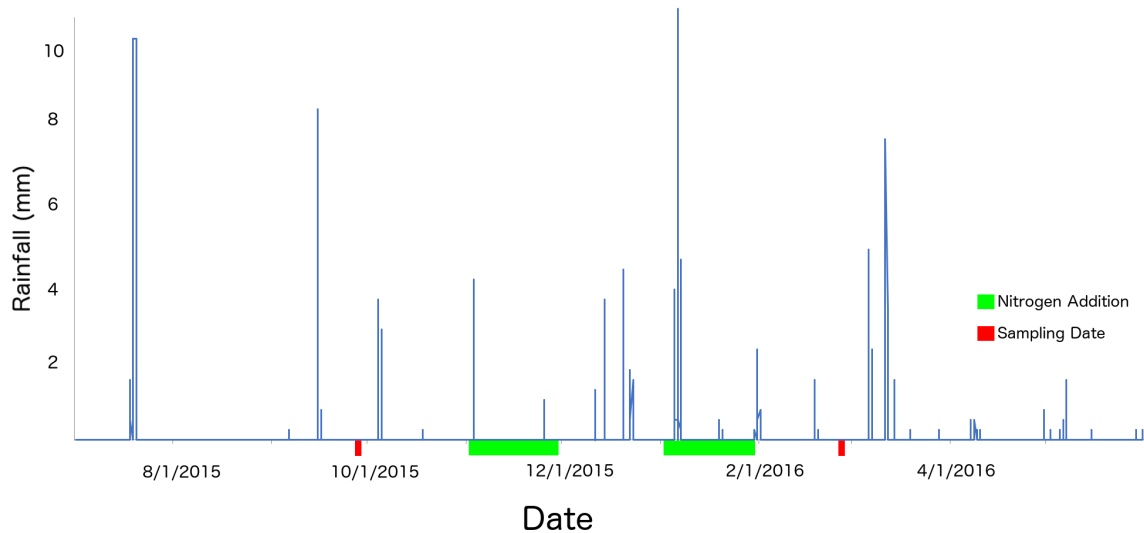


Figure 2. Timing of rainfall, nitrogen addition and sample collections for this study.

Samples collected during the summer (dry soils) originated from two treatment blocks for a total of 108 samples, and were stored in paper bags and left at ambient temperatures while samples collected during the winter (wet soils) were collected from one treatment block for a total of 58 samples and were initially stored in Ziplock bags on ice and then stored in a -20°C freezer upon return to UC Riverside. Samples from both dates were sieved with a 500 µm mesh bleach-sterilized between samples, roots were picked out with sterile forceps and stored in a separate container (coin envelopes, summer; sterile Whirlpak bags, winter). Due to the different conditions for sample preservation, only samples collected in February were used for molecular analyses, while both sets of samples were used to examine fungal community morphological responses.

Environmental covariates

From soil samples I measured soil pH, available N (NH_4 & NO_3), Total C, N and P. Available N was estimated from pooling N as NO_3 and NH_4 from KCl extractable fractions, after calculating ppm NO_3 and NH_4 as N (Hofer 2003; Keeney and Nelson 1982). A pH meter was used to measure pH from a soil paste (U.S. Salinity Laboratory 1954). Phosphorus was extracted with bicarbonate and quantified using molybdenumb-blue chemistry and 880 nm absorbance on a spectrophotometer (Olsen 1954). Total C and N were measured from Dumas combustion on an Leco Truspec CN Analyzer. For all samples, total C, N and P were measured at the USDA-ARS Soils Lab in Reno, NV. For summer samples, KCL extractable N and pH were also measured at USDA-ARS, while for winter samples these were measured at the University of California Davis Analytical laboratory. Protocols used at both labs were the same.

Molecular Analyses

Frozen root samples were first homogenized, and then DNA was extracted using a Qiagen Plant Minikit (Qiagen, Hilden, DE). Extracted DNA was kept frozen in -80 °C and transported on dry ice to the Environmental Genetics and Genomics Laboratory (EnGGen) at Northern Arizona University. Samples were cleaned as needed with a modified magnetic bead cleanup method of (Rohland and Reich 2012). DNA concentrations were checked with PicoGreen dsDNA Quantitation (Molecular Probes Inc., Eugene OR, USA) and then standardized to ~10 ng/μL.

I examined AMF composition with the small subunit of the rRNA gene (SSU), using the Glomeromycota specific AML2, and the universal eukaryote WANDA, primer set (Lee, Lee, and Young 2008; Dumbrell et al. 2011). For the broader fungal community, I used the internal transcribed spacer region 2 (ITS2) to estimate composition responses, with the 5.8S_Fun and ITS4_Fun primer set (Taylor et al. 2016). Library construction involved two rounds of polymerase-chain-reactions (PCR), for amplification and indexing per locus. For my first round of PCR I used fusion primers with universal 5' tail sequences (Appendix A). The first round of PCR involved a 10 μL reaction in triplicate with three separate dilutions (1/10, 1/100, 1/1000) in 384 well plates, with 5μL *Taq* polymerase DNTPs mix, 0.3 μL MgCl₂, 0.4 μL of 200 nM primers, 3.3 μL Milli-Q H₂O and 1 μL DNA template. Reaction conditions were as follows: initial denature 95 °C-2min, denature 95°C-30s, anneal 55°C-30s extend 60°C-4min for 34 cycles and then refrigerate at 10°C. I checked for reaction success on 3% gel agarose, pooled successful amplifications by sample, and purified products with bead-prep prior to the second round of PCR. I added flowcell and index sequences in the second round of PCR using primers with sequences matching the universal tails at the 3' end (Appendix

A). I kept reactions the same as the first round of PCR but used only 100 nM of each primer, 1 μ L template and ran PCR for 15 cycles. I checked for successful amplification on 3% agarose gel, purified with bead-prep, quantified concentrations with PicoGreen dsDNA Quantitation (Molecular Probes Inc., Eugene OR, USA), diluted to equimolar concentrations (1.8pM SSU, 4.5pM ITS2) using a Packard MultiProbe II Plus HT EX automated liquid handling system. I further quantified this resulting pool using qPCR and a Bioanalyzer 2100 (Agilent Technologies, Santa Clara, CA) prior to sequencing on a MiSeq Desktop Sequencer (Illumina, Inc., San Diego, CA) in 2x300 mode paired end mode.

All sequences were processed in QIIME 1.9.1 (Caporaso et al. 2010). For both SSU and ITS2, sequences were filtered for locus-specific primer sequences and contamination by PhiX, the viral genome used as a control sequence on Illumina Platforms using Cut-Adapt (Martin 2011). I then merged paired-end reads with ea-utils (Aronesty 2011), checked merged-sequence quality with FastQC (Andrews S. 2010. FastQC: a quality control tool for high throughput sequence data. Available online at: <http://www.bioinformatics.babraham.ac.uk/projects/fastqc>) and trimmed sequences to retain quality above q20. I demultiplexed these reads in QIIME (Caporaso et al. 2010) with a phred score of 15 (q=14), sequence truncation after 1bp below 15 (r=0) and retention of reads only if they retain 95% of initial sequence length (p = 0.95). I screened demultiplexed reads for chimeras with VSEARCH (Rognes et al. 2016) in *denovo* mode for SSU and usearch_ref mode against the UNITE-based fungal chimera dataset for ITS (Nilsson et al. 2015). Fungal ITS2 data were checked for ITS2 sequences with ITSx (Bengtsson-Palme et al. 2013). For both loci, data were dereplicated for the first 100 bp with prefix_suffix OTU picker in QIIME. OTUs were clustered *denovo* with a resolution of

d4 in Swarm (Mahé et al. 2014). I assigned taxonomy with BLAST at 90% sequence similarity (Altschul et al. 1990) in reference to respective databases (ITS2 - UNITE database, Koljalg et al. 2014; SSU - MaarJAM database, Öpik et al. 2010) after manually adding '*Glomus tenue*' reference sequences (Orchard et al. 2017) to the MaarJAM database. I normalized my read data through cumulative sum scaling (CSS normalization) in the metagenomeSeq package of Bioconductor (Paulson et al. 2013) in the R language environment (R Core Team 2016) prior to downstream analyses. I chose to normalize rather than rarefy my read data because of the demonstrated improvement in statistical power that normalization provides over rarefaction (McMurdie and Holmes 2014).

Guild Assignment

I assigned families of Glomeromycota to AMF functional groups based upon studies detailing functionally relevant morphological differences between families (Sikes, Powell, and Rillig 2010; Powell et al. 2009; Maherali and Klironomos 2007; Hart and Reader 2002; Varela-Cervero et al. 2015, 2016 [a,b]; Sikes, Cottenie, and Klironomos 2009). Because of recent changes in the taxonomy of Glomeromycota, not all currently described families have been studied for their patterns of biomass allocation. Families that did not contain taxa specifically under study for their extent of root versus soil hyphal colonization were assigned to the functional groups of related families, assuming phylogenetic trait conservatism, supported in part by Powell et al. 2009. I kept sequences identified as *Geosiphon pyriformis* (90% sequence similarity) as ancestral AMF under the assumption that these were close relatives of this fungus and would behave similarly to other ancestral AMF. To examine responses of the pathogenic and

saprotrophic fungal community, I assigned OTUs from my ITS2 workflow to functional groups based on taxonomic assignment through the online FUNGuild application ("<http://www.stbates.org/guilds/app.php>", Nguyen et al. 2015). I further curated these assignments for simplicity by considering 'pathotrophs', 'pathotroph-saprotrophs' and 'pathotroph-symbiotrophs' as 'pathogens'; 'saprotrophs' and 'saprotroph-pathotroph' as 'saprotrophs' and removed Glomeromycota (AMF) from Symbiotrophs. These criteria reduced the number of OTUs from my ITS2 dataset from 23925 to 10615.

AMF Soil Hyphae

Soil hyphal lengths were estimated using a modified version of the membrane filter protocol described in Looby et al. 2016. Approximately 10 g of soil were added to 500 ml 0.4% w/v sodium hexametaphosphate:DI H₂O (aka detergent solution) and stirred on a stir plate for 5 minutes. 200 ml of this soil solution were then transferred into 180 ml of the detergent solution and stirred for another two minutes. 5 ml of this solution was then pipetted onto gridded 25 mm diameter, 0.2 µm membrane filters and vacuum filtered through Millipore Fritted Glass (Thermo Fisher Scientific). Hyphae on the filters were then stained with an acid fuchsin solution. This last step was repeated once, resulting in two filters per sample. Filters were then placed onto microscope slides and let dry. Once dry, filters were mounted with poly-vinyl alcohol lactic-acid glycerol (PVLG) and dried overnight at 60 C. Hyphal density (length per gram soil) was estimated from these slides under a Zeiss Axioskop 2 compound microscope at 200x using the gridline length estimate method of Marsh 1971.

Root colonization

I estimated percent root length colonized (PRLC) from AM and non-AM fungi from a subset of my fine roots. Prior to staining AMF structures, I first cleared root tissues by boiling roots in 10% KOH for 3-5 minutes until blonde, rinsed these roots with DI H₂O, acidified and then stained AMF structures in boiling 5% India Ink:Acetic Acid for 3 minutes and destained root tissue in mildly acidified DI H₂O until roots were unstained and fungal structures were discernible, generally overnight. I then mounted roots on microscope slides with PVLG. I measured PRLC under a Zeiss Axioskop 2 compound microscope at 200x using a modified version of the random intersect method of Giovannetti and Mosse 1980.

AMF Spore Production

I extracted spores from 2.5 - 5 g soil using a sucrose-detergent centrifugation method as in Allen et al. 1979, and then counted according to diameters (25-50, 50-100, 100-200, and 200-300 μm ; no spores larger than 300 μm were observed in my samples) under an Olympus SZ40 dissecting scope at 4x magnification. I did not identify AMF spores to any taxonomic level, and this spore diameter classification only roughly estimates responses of spore production by AMF guilds. Spore diameters from 25-100 μm generally correspond to rhizophilic AMF, while 100-300 μm to ancestral and edaphophilic AMF, though spore size varies both within, and between, taxa in these guilds. Spore counts were converted into volume of spores per gram soil prior to analysis.

Generalized linear modeling

I built generalized linear models (GLMs) to test my hypotheses regarding fungal guild responses to the experimental treatments, interactions between AMF and saprotrophic and pathogenic fungi, and the correlation between relative abundances of guilds and fungal biomass allocation. Because I estimated composition from molecular markers for samples in winter alone, all generalized linear models are based exclusively on these samples. Environmental covariates were standardized prior to inclusion in models. I used Gaussian distributions (with identity link function) when responses were normally distributed, Gamma distributions (inverse link) for continuous data with distributions close to zero, and fitted zero-inflated models to count data with high zeroes, (negative binomial when variance \neq mean, Poisson when \approx mean; Table 4; zero-inflated models were fitted with 'zeroinfl' of the 'pscl' package in R; Jackman et al. 2015; Zeileis, Kleiber, and Jackman 2008). Full models for each response were fitted, nonsignificant interactions were removed and models were selected with stepwise AIC model selection ('stepAIC' from MASS package in R, Venables and Ripley 2002). Table 4 gives a complete list of variables used in the full and final models, and full model output of final models can be found in Appendix B. We did not use measured available N as a covariate in any of our models as this did not reflect N treatments. Additionally, other research at this site has found that applied available N is rapidly taken up by microbes and plants from the soil in the presence of moisture (Emma Aronson, personal communication).

Table 4. Descriptions of generalized linear models. Variables in bold are significant at $p < 0.05$, italicized are significant at $p < 0.10$. Variables in parentheses were evaluated, but not retained in final models after model selection. Negative binomial and Poisson models (log link), Gaussian models (identity link) and Gamma models (inverse link).

Response	Probability Distribution	Predictors
Edaphophilic AMF Abundance	Zero-inflated negative binomial	Host Plant , Precipitation treatment , N treatment , Total P , Total N, Total C, C:N (pH, N:P, Precipitation treatment x N Treatment, Host Plant x Precipitation treatment, Host Plant x N Treatment)
Edaphophilic AMF OTU Richness	Zero-inflated Poisson	<i>Precipitation treatment</i> (Host Plant, N treatment, Total N, Total P, Total C, pH, C:N, N:P, Precipitation treatment x N Treatment, Host Plant x Precipitation treatment, Host Plant x N Treatment)
Rhizophylic AMF Read Abundance	Gaussian	Precipitation treatment, N treatment, Total N, Total P, Total C, C:N (pH, Host Plant, N:P, Precipitation treatment x N Treatment, Host Plant x Precipitation treatment, Host Plant x N Treatment)
Rhizophylic AMF OTU Richness	Gaussian	Total N , Total C , C:N (Host Plant, Precipitation treatment, N treatment, Total P, pH, N:P, Precipitation treatment x N Treatment, Host Plant x Precipitation treatment, Host Plant x N Treatment)
Ancestral AMF Abundance	Gaussian	Host Plant , Total C, Total N (Precipitation treatment, N treatment, C:N, Total P, pH, N:P, Precipitation treatment x N Treatment, Host Plant x Precipitation treatment, Host Plant x N Treatment)
Ancestral AMF OTU Richness	Gaussian	Total N , Total C , C:N (Host Plant, Precipitation treatment, Total P, N treatment, pH, N:P, Precipitation treatment x N Treatment, Host Plant x Precipitation treatment, Host Plant x N Treatment)
Saprotrophic Fungi Read Abundance	Gaussian	Rhizophylic AMF Abundance , Host Plant , Total N , Total C , C:N , N:P , <i>Total P</i> (Edaphophilic AMF Abundance, Ancestral AMF Abundance, Precipitation treatment, N treatment, pH, Precipitation treatment x N Treatment, Host Plant x Precipitation treatment, Host Plant x N Treatment)
Saprotrophic Fungi OTU Richness	Gaussian	Host Plant , Total N , Total C , C:N , N:P , <i>Total P</i> , pH, Rhizophylic AMF OTU Richness, Edaphophilic AMF Abundance, Ancestral AMF Abundance (Precipitation treatment, N treatment, Precipitation treatment x N Treatment, Host Plant x Precipitation treatment, Host Plant x N Treatment)
Pathogenic Fungi Read Abundance	Gaussian	Host Plant , pH , <i>Rhizophylic Abundance</i> , C:N (Total N, Total P, Total C, N:P, Ancestral AMF Abundance, Edaphophilic AMF Abundance, Precipitation treatment, N treatment, Precipitation treatment x N Treatment, Host Plant x Precipitation treatment, Host Plant x N Treatment)
Pathogenic Fungi OTU Richness	Gaussian	Rhizophylic AMF OTU Richness , Host Plant , Total N , Total C , C:N , N:P , Precipitation treatment, Total P (Edaphophilic AMF Abundance, Ancestral AMF Abundance, N treatment, pH, Precipitation treatment x N Treatment, Host Plant x Precipitation treatment, Host Plant x N Treatment)
AMF Root Colonization	Gaussian	Precipitation treatment , Host Plant , Rhizophylic AMF Abundance, N treatment, Total N, Total P, Total C, C:N (Ancestral AMF Abundance, Edaphophilic AMF Abundance, pH, N:P, Precipitation treatment x N Treatment, Host Plant x Precipitation treatment, Host Plant x N Treatment)
Non-AMF Root Colonization	Gaussian	Host Plant , Pathogenic Fungi Abundance, Precipitation treatment, N treatment, Total N, Total P, Total C, C:N (Saprotrophic Fungi Abundance, Pathogenic Fungi Abundance, AMF Colonization, Rhizophylic AMF Abundance, N:P, pH, Precipitation treatment x N Treatment, Host Plant x Precipitation treatment, Host Plant x N Treatment)
AMF Hyphal Length	Zero-inflated negative binomial	N treatment (Rhizophylic AMF Abundance, Ancestral AMF Abundance, Edaphophilic AMF Abundance, Host Plant, Precipitation treatment, Total N, Total P, Total C, pH, C:N, N:P, Precipitation treatment x N Treatment, Host Plant x Precipitation treatment, Host Plant x N Treatment)
Spore Biovolume	Gamma	Rhizophylic AMF Abundance , Host Plant , Total P , C:N , N:P (Precipitation treatment, N treatment, Total C, Edaphophilic AMF Abundance, Ancestral AMF Abundance, Total N, pH, Precipitation treatment x N Treatment, Host Plant x Precipitation treatment, Host Plant x N Treatment)
Average Spore Diameter	Gaussian	Rhizophylic AMF abundance , Edaphophilic AMF abundance , Total P , Total C , N:P , C:N , pH (Precipitation treatment, N treatment, Total N, Ancestral AMF abundance, Precipitation treatment x N Treatment, Host Plant x Precipitation treatment, Host Plant x N Treatment)

RESULTS

SSU

I observed an average of 612 ± 162 (SD) reads and 122 ± 43.9 OTU's per sample. These reads and OTUs belonged to Glomeromycota, with a small fraction belonging to the fine endophyte '*Glomus tenue*', which may be more closely aligned with the Mucoromycotina (Orchard et al. 2017). These OTU's belonged to 6 orders, 10 families and 10 genera. I placed these OTUs into three functional groups based on my earlier descriptions (Tab. 1), rhizophilic AMF: 100 ± 38 OTUs & 499 ± 156 reads per sample, ancestral AMF: 16 ± 6 OTUs & 84 ± 29 reads per sample, edaphophilic AMF: 3 ± 2 OTUs & 18 ± 11 reads per sample, and Fine Endophyte: 1 ± 4 OTUs & 4 ± 16 reads per sample (Fig 2.).

ITS

I found an average. of 628 ± 169 (SD) reads and 110 ± 36 OTUs per sample belonging to 5 phyla, 14 classes, 43 orders, 73 families and 119 genera. My most abundant phylum was Ascomycota, with an average of 568 ± 149 reads and 98 ± 32 OTUs per sample, followed by Basidiomycota with 42 ± 24 reads and 8 ± 4 OTUs per sample. Of these groups, the most abundant families were the Dothideomycetes (41.5% reads per sample), Sordariomycetes (26.2% reads per sample) and a currently unidentified family of Ascomycota (11.1% reads per sample). After using FUNGuild, these reads and OTUs were assigned to trophic based functional groups, Saprotrophs: 28 ± 10 OTUs & 163 ± 48 reads per sample, Pathogens: 21 ± 6 OTUs & 121 ± 31 reads per sample, non-Glomeromycotan Symbionts: 0.33 ± 0.64 OTUs & 2 ± 4 reads per sample.

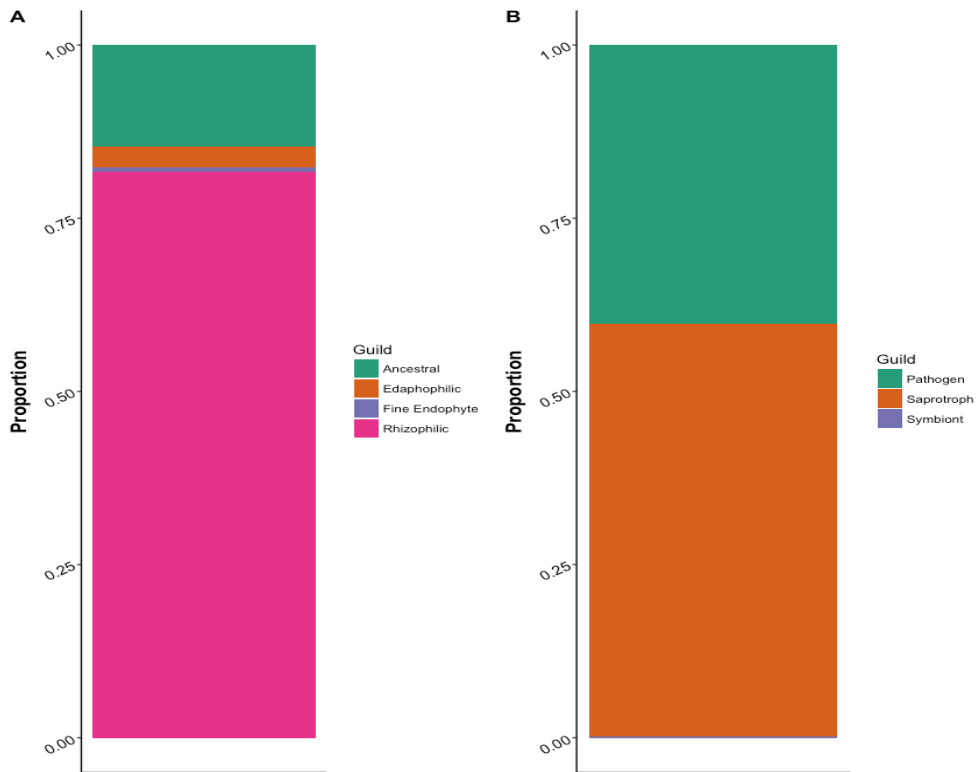


Figure 3. Proportions of fungal functional groups across samples. AMF from SSU data are presented in panel A, broader fungal community from ITS data are presented in panel B.

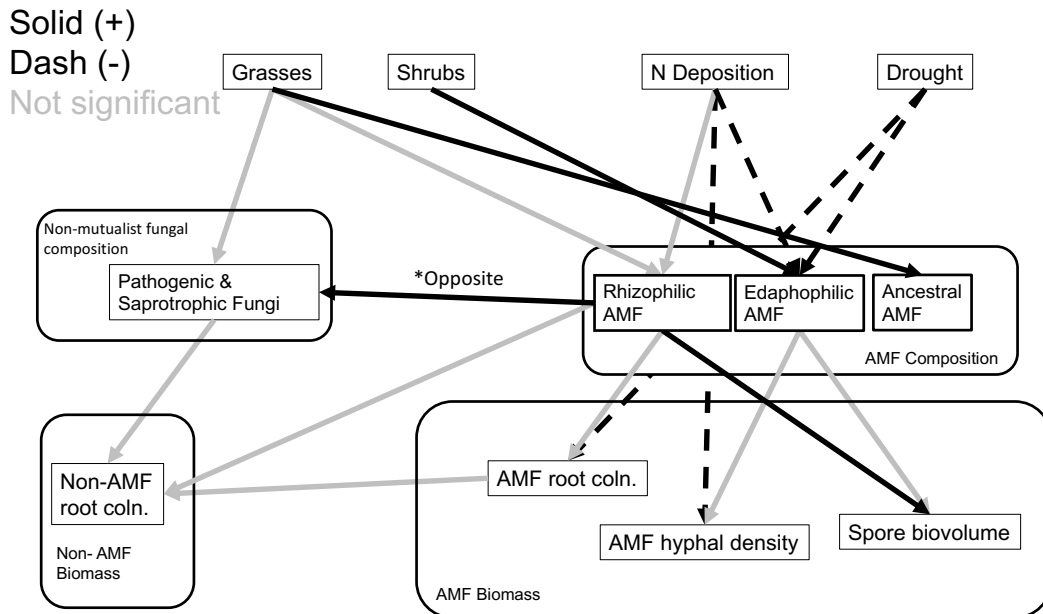


Figure 4. Summary diagram of major results from generalized linear models. Significant and positive drivers are shown with solid lines, while significant and negative drivers with dashed lines, and nonsignificant drivers with gray lines. *Opposite direction than hypothesized.

Precipitation

Edaphophilic AMF taxa richness and abundance were both negatively associated with the reduced precipitation treatment than other precipitation treatments ($p = 0.098$ & $p = 0.004$, respectively, Fig. 4, Suppl. Tab. 1 & 2). Neither rhizophilic or ancestral AMF taxa richness nor read abundance responded to precipitation treatments (Suppl. Tab. 3-6). Both saprotrophic and pathogenic fungi taxa richness and abundance did not respond to precipitation treatments (Suppl. Tab. 7-10).

AMF root colonization was negatively associated with the reduced precipitation treatment ($p = 0.014$, Suppl. Tab. 11) while non-AMF root colonization did not respond to precipitation treatment (Suppl. Tab. 12). Neither AMF hyphal length nor spore biovolume responded to precipitation (Suppl. Tab. 13 & 14).

N deposition

Additional N was negatively associated with the abundance, but not richness, of edaphophilic AMF ($p = 0.049$, Suppl. Tab. 1 & 2). Nitrogen treatments did not affect either the read abundance nor OTU richness of either rhizophilic or ancestral AMF (Suppl. Tab. 3-6). While rhizophilic and ancestral AMF did not respond to N deposition, taxonomic richness's of these fungi were negatively associated with increasing total N ($p = 0.067$, $p = 0.016$, Suppl. Tab. 4 & 6). In addition to associating negatively with total N, ancestral AMF taxa richness associated negatively with C:N ($p = 0.046$) but positively with total C ($p = 0.017$, Suppl. Tab. 6). Neither pathogenic fungal taxa richness or abundance responded to N treatments, though pathogenic fungi taxonomic richness positively associated with total N ($p = 0.006$, Suppl. Tab. 8). Neither saprotrophic fungi taxa richness or abundance responded to N treatment, though both were positively associated with increases in total N ($p = 0.035$, $p = 0.016$, Suppl. Tab. 9 & 10).

Neither AM or non-AM fungal root colonization responded to N treatment or to total N (Suppl. Tab. 11 & 12). The additional N treatment was negatively associated with AMF hyphal length ($p=0.003$, Suppl. Tab. 13). Spore biovolume was not affected by N treatment (Suppl. Tab. 14).

Host Plant

Edaphophilic AMF abundance, but not richness, correlated negatively with the invasive grasses *Schismus barbatus*, *Bromus rubens* and *Avena sp.* ($p=0.019$, $p=0.081$, $p=0.071$, Suppl. Tab. 1 & 2). Richness and abundance of rhizophilic AMF was not correlated with any host plant (Suppl. Tab. 3 & 4). Ancestral AMF positively associated with the grass *B. rubens* and in the shrub *Eriogonum fasciculatum* ($p=0.005$, $p=0.056$), though ancestral AMF taxonomic richness was not correlated with any host plant (Suppl. Tab. 5 & 6). Pathogenic fungi taxonomic richness was positively associated with the shrub *Salvia mellifera*, and the abundance of these fungi were positively correlated with *S. mellifera* and the grass *S. barbatus* ($p=0.003$, $p=0.052$, Suppl. Tab. 7 & 8). Saprotrophic fungi taxonomic richness and abundance were positively associated with *S. barbatus*, *S. mellifera* and *E. fasciculatum*, while *B. rubens* was positively correlated with saprotrophic fungi abundance (Suppl. Tab. 9 & 10).

The extent of AMF root colonization was positively associated with *Salvia mellifera* ($p=0.010$, Suppl. Tab. 11), and increased non-AMF root colonization was associated with *S. mellifera* and *Bromus rubens* ($p=0.076$, $p=0.007$, Suppl. Tab. 12). AMF hyphal length did not differ among host plants (Suppl. Tab. 13). AMF spore biovolume was negatively associated with the shrubs *E. fasciculatum* and *S. mellifera* ($p=0.064$, $p=0.039$, Suppl. Tab. 14).

Interactions between AMF and pathogenic and saprotrophic fungi

Both pathogenic and saprotrophic fungi abundances positively covaried with rhizophilic AMF abundances ($p=0.051$ and $p=0.012$, Suppl. Tab. 7 & 9) as did pathogenic taxa richness ($p=0.007$, Suppl. Tab. 8). Neither rhizophilic abundance nor AMF root colonization were correlated with non-AMF root colonization (Suppl. Tab. 12).

Morphological responses to fungal composition

Rhizophilic AMF abundance was not correlated with AMF colonization, nor was the abundance of edaphophilic or ancestral AMF (Suppl. Tab. 11). While the abundance of pathogenic fungi was retained in the final model, this was not associated with non-AMF root colonization (Suppl. Tab. 12). Rhizophilic, but not edaphophilic or ancestral, AMF abundance, was positively associated with total spore biovolume ($p=0.043$, Suppl. Tab. 14), though average spore diameter was negatively associated with rhizophilic AMF abundance and positively correlated with edaphophilic AMF abundance ($p=0.017$, $p=0.034$; Suppl. Table 15).

DISCUSSION

Overall, reduced precipitation was associated with lower AMF abundance in roots, and edaphophilic AMF were more sensitive to drought than either ancestral or rhizophilic AMF (Fig. 3). Nitrogen addition was negatively correlated with both edaphophilic abundance and overall allocation to AMF soil colonizing hyphae. I found that while grasses did not host more rhizophilic AMF than shrubs, they hosted less edaphophilic AMF. I also found that *Bromus rubens* and *Eriogonum fasciculatum* hosted a higher abundance of ancestral AMF. Rather than a negative correlation between

rhizophilic AMF and pathogenic and saprotrophic fungi, I found these fungi to positively covary. I found that the relative abundance in roots of edaphophilic and rhizophilic AMF partially explains responses of the biovolume and average diameter of AMF spores.

Precipitation

I found support for my hypothesis that both edaphophilic AMF abundance and richness would positively respond to soil moisture, as I found less edaphophilic AMF in the reduced precipitation treatment. Rhizophilic AMF did not respond to precipitation treatments (neither read abundance nor OTU richness), concurring with my hypothesis that this AMF guild is relatively insensitive to changes in soil moisture. The reduction of edaphophilic taxa richness and abundance in response to the reduced water treatment, while neither ancestral nor rhizophilic AMF were affected, is potentially due to the differences between these groups in their allocation of biomass. The higher amount of biomass that edaphophilic AMF allocate to soil colonizing hyphae leads to increased contact with the surrounding soil, potentially making this group more sensitive to changes in soil moisture because of changing climate. Reducing precipitation negatively affects AMF root colonization, though not hyphal length, spore production, or the root colonization by non-AM fungi. It is important to note that while I observed a decrease in the extent of AMF root colonization to reduced precipitation, this study occurred during a record breaking drought, potentially swamping the responses of the other fungal biomass variables to precipitation treatments. Overall, this suggests that drought reduces the total abundance of AMF in roots and that edaphophilic AMF respond more negatively to drought than either ancestral and rhizophilic AMF.

N deposition

I found support for my hypothesis that increasing N availability would reduce edaphophilic AMF abundance, but not for my hypothesis that this would also reduce edaphophilic richness. This negative response of edaphophilic AMF abundance concurs with previous work in coastal sage scrub that has found a decline in the abundance of edaphophilic AMF spores with increasing levels of N deposition, both across a gradient and within a N addition treatment (Egerton-Warburton and Allen 2000). In addition to finding that the additional N treatment reduces the abundance of edaphophilic AMF more than other guilds of AMF, I found this treatment to also reduce the extent of soil hyphal density. This reduction in allocation to nutrient foraging soil hyphae is potentially because of increased nitrate availability, which reduces the dependence of plants on AMF derived nutrients. This suggests that additional N deposition will lead to a lower abundance of both edaphophilic AMF taxa (Sikes, Powell, and Rillig 2010) and AMF structures that contribute most to nutrient uptake.

Host Plant

I found support for my expectation that fine-rooted grasses would host a lower abundance of edaphophilic AMF than shrubs, as all three grass species had less edaphophilic AMF than other host plants. However, I would like to note that *Erodium moschatum*, an invasive forb, did not differ from shrubs in the abundance of edaphophilic AMF that it hosted. This suggests in part that edaphophilic AMF are hosted at higher rates by shrub species at my site, potentially because of the role that these AMF play in the uptake of nutrients for plants. Contrary to my hypothesis I did not find that rhizophilic AMF were more taxonomically rich or abundant in grasses than in

shrubs. I did however find that *Bromus rubens* and *Eriogonum fasciculatum* host a higher abundance of ancestral AMF (however fungal composition of *E. fasciculatum* is only characterized from 2 samples vs. 17 for *B. rubens*, and may possibly not be a reliable estimate, Tab. 3). Neither the relative abundance of pathogenic and saprotrophic fungi nor root colonization by non-AMF were higher in grasses overall, countering my hypothesis that shrubs are less susceptible to infection by pathogenic and saprotrophic fungi than grasses because of their coarser root architecture (Suppl. Tables 7 & 9).

The importance of ancestral AMF being preferentially hosted by *Bromus rubens* and by *E. fasciculatum* is unclear as we know little about how ancestral AMF affect their host plants. Studies have proposed that *B. rubens* invasion of coastal sage scrub may be aided in part by a changing AMF community under N deposition (Kimball et al. 2014; Egerton-Warburton and Allen 2000). It is possible that this AMF guild is contributing to *B. rubens* success in invading coastal sage scrub, however I do not know the mechanism by which these fungi may aid *B. rubens* invasion, again because we know little about the biology of this AMF group. These results suggest that continued invasion of coastal sage scrub by these annual grasses will reduce the relative abundance of edaphophilic AMF while invasion by *B. rubens* specifically may result in a higher abundance of ancestral AMF.

Interactions between AMF and pathogenic and saprotrophic fungi

Counter to my hypotheses, both pathogenic and saprotrophic fungi abundance positively covaried with rhizophilic AMF, and neither rhizophilic AMF abundance nor AMF colonization were negatively correlated with non-AMF colonization. While it is possible that these saprotrophs and pathogens are not directly infecting the same root

spaces as rhizophilic AMF, I did not identify non-AMF hyphae microscopically, and AM and non-AM fungi frequently co-occurred in my roots (17 +/- 12% co-colonization per sample). It is also possible that these non-AMF are mutualists, and are not inhibited by AMF root colonization. While the read abundance of non-Glomeromycotan fungi known to be plant mutualists in my samples was low, in general pathogenic and saprotrophic fungi are better described than mutualists. I cannot rule out that many of the taxa assigned to coarse taxonomies (e.g. 'Ascomycota sp. '; Appendix D) may in fact be mutualists, complicating interactions within the root space. I therefore did not find support for my hypothesis that grasses in my system preferentially associate with rhizophilic AMF to reduce the abundance of pathogenic and saprotrophic fungal root colonization. Our understanding of these fungal interactions in field settings would likely benefit from combining more powerful models (e.g. structural equation models, joint-species distribution models) with greenhouse experiments.

Morphological responses to fungal composition

Counter to my hypothesis, the abundance of edaphophilic AMF did not positively correlate with soil hyphal length. This is potentially because hyphal growth and dieback is a dynamic process (Hernandez and Allen 2013), and my estimates of soil hyphal length were gathered from two time points, both during extreme drought. This is in part supported by the lack of response in hyphal length between summer (dry) and winter (wet). It is also possible that I did not pick up on responses of this group from root based read abundance data because edaphophilic AMF have more biomass as extraradical hyphae than intraradical hyphae (Maherali and Klironomos 2007).

Spore biovolume did not respond to edaphophilic AMF abundance but responded positively to rhizophilic AMF abundance. I could examine responses of the spore community to AMF composition only from samples taken in winter. However, total spore biovolume was higher in summer (Suppl. Fig. 1), which is the dormant season in this system (Egerton-Warburton and Allen 2000). While total spore biovolume was lower in winter, average spore diameter was higher in winter (Suppl. Fig. 2), and rhizophilic AMF negatively, and edaphophilic AMF positively affected, this average spore diameter, respectively (Suppl. Tab. 15). This suggests that while the spores that rhizophilic AMF produce are smaller than those of edaphophilic AMF, rhizophilic AMF produced more spores than did edaphophilic AMF, and edaphophilic AMF spores germinated at lower rates at the onset of the growing season than did rhizophilic AMF. The low production and germination of possible edaphophilic AMF spores relative to rhizophilic AMF spores during this study may be because this study occurred during an intense drought. This would explain the positive association between rhizophilic AMF abundance and spore biovolume and the lack of a positive correlation between edaphophilic AMF and spore biovolume.

I did not find that overall AMF root colonization was driven by the relative abundance of rhizophilic AMF in roots. Across all my samples, rhizophilic AMF were the most rich and abundant AMF group, and so while their absolute abundances in plant roots may have varied, their relative abundances were invariant. This lack of variance in the relative abundance of rhizophilic AMF could be a confounding factor between absolute rhizophilic AMF abundance and root colonization. Also, it is possible that some taxa delineated as ancestral AMF may not show the low root colonization that other relatives have shown in past studies. This is corroborated in part by the high abundance

of ancestral AMF in the roots of *Bromus rubens*, a plant with similar levels of AMF root colonization to other plants, other than *Salvia mellifera* (Suppl. Tab. 11).

In conclusion, increasing aridity and continued atmospheric N deposition and invasion of coastal sage scrub by annual grasses will reduce the abundance of edaphophilic AMF, potentially impacting feedbacks between host plants and soil biota in this community. Specifically, my results suggest that increasing aridity over the next century will reduce the overall abundance of arbuscular mycorrhizal fungi, particularly reducing the abundance of edaphophilic AMF. My findings also suggest that atmospheric N deposition will reduce the abundance of edaphophilic AMF and reduce the extent of nutrient foraging hyphae. Continued invasion of coastal sage scrub by invasive annual grasses may increase the abundance of ancestral AMF at the expense of the edaphophilic AMF. Using my broad guild level approach, I found saprotrophic and pathogenic fungi to positively covary with rhizophilic AMF abundance, while more delicate examination of interactions at the 'species-level' may resolve the relevance of these interactions. The broader ecological implications of these responses within the fungal community to multiple, coinciding global change drivers is still unclear. Moving the community ecology of AMF past descriptions of communities and into predicting community responses to an increasingly changing world requires an increased effort to tie molecular information to basic biological information within a unified framework.

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APPENDIX A: Description of Primers

Initial Round of PCR

Universal 5' tails - Locus specific primers

WANDA 5' CCTATGTGGAGAGCCAGTAAGCGATGCTATGGT-CAGCCGCGGTAATTCCAGCT 3'
AML2 5' GTCAACGCTCACTACTGCGATTACCCAAGTCAG-GAACCCAAACACTTTGGTTTCC 3'
ITS4_Fun 5' GTCAACGCTCACTACTGCGATTACCCAAGTCAG-AGCCTCCGCTTATTGATATGCTTAART 3'
5.8S_Fun 5' CCTATGTGGAGAGCCAGTAAGCGATGCTATGGT-AACTTTYRCAAYGGATCWCT 3'

Second round of PCR

5' Flowcell sequences - Indexes - Universal 3' tails

5' AATGATACGGCGACCACCGAGATCTACAC-NNNNNNNN-CCTATGTGGAGAGCCAGTAA 3'
5' CAAGCAGAAGACGGCATAACGAGAT-NNNNNNNN-GTCAACGCTCACTACTGCGA 3'

APPENDIX B: Supplemental Tables

For all supplemental tables, bold values are significant at $p < 0.05$ and *Italicized values are significant at $p < 0.10$.*

Table 1: Edaphophilic AMF Read Abundance, zero-inflated negative binomial GLM Negative Binomial (log link)

	Estimate	Std. Error	Z value	Pr(>—z—)
(Intercept)	2.822	0.172	16.44	0
<i>Avena sp.</i>	<i>-0.853</i>	<i>0.473</i>	<i>-1.803</i>	<i>0.071</i>
<i>Bromus rubens</i>	<i>-0.291</i>	<i>0.167</i>	<i>-1.743</i>	<i>0.081</i>
<i>Eriogonum fasciculatum</i>	-18.29	2019.787	-0.009	0.993
<i>Erodium moschatum</i>	-17.764	1888.747	-0.009	0.992
Schismus barbatus	-0.821	0.35	-2.348	0.019
<i>Salvia mellifera</i>	0.103	0.156	0.66	0.51
Ambient Precipitation treatment	-0.232	0.167	-1.395	0.163
Reduced Precipitation treatment	-0.444	0.153	-2.898	0.004
Ambient nitrogen treatment	0.268	0.136	1.972	0.049
Total N	-1.365	1.191	-1.146	0.252
Total P	-0.297	0.127	-2.332	0.02
Total C	1.359	1.252	1.086	0.278
C:N	-0.734	0.534	-1.374	0.169
Log(theta)	2.446	0.356	6.862	0

Binomial (logit link)

	Estimate	Std. Error	Z value	Pr(>—z—)
(Intercept)	-3.071	0.725	-4.233	0

Table 2: Edaphophilic AMF OTU richness zero-inflated Poisson GLM Poisson (log link)

	Estimate	Std. Error	Z value	Pr(>—z—)
(Intercept)	1.280	0.174	7.336	0.000
Ambient Precipitation treatment	0.011	0.214	0.050	0.960
<i>Reduced Precipitation treatment</i>	<i>-0.352</i>	<i>0.213</i>	<i>-1.656</i>	<i>0.098</i>
Total N	-1.616	1.269	-1.274	0.203
Total C	1.656	1.339	1.237	0.216
C:N	-0.826	0.564	-1.464	0.143

Binomial (logit link)

	Estimate	Std. Error	Z value	Pr(>—z—)
(Intercept)	-2.779	0.763	-3.644	0.000

Table 3: Rhizophilic AMF Read Abundance, Gaussian GLM

	Estimate	Std. Error	t value	Pr(> t)
(Intercept)	503.563	54.789	9.191	0.000
Ambient Precipitation treatment	-8.721	59.668	-0.146	0.885
Reduced Precipitation treatment	-34.929	56.233	-0.621	0.538
Ambient nitrogen treatment	45.425	44.620	1.018	0.315
Total N	-438.804	293.103	-1.497	0.142
Total P	-37.012	37.367	-0.991	0.328
Total C	467.222	311.038	1.502	0.141
C:N	-156.113	125.930	-1.240	0.223

Table 4: Rhizophilic OTU Richness, Gaussian GLM

	Estimate	Std. Error	t value	Pr(> t)
(Intercept)	107.940	7.883	13.694	0.000
Total N	-128.974	68.507	-1.883	0.067
Total C	138.483	73.002	1.897	0.065
C:N	-47.907	29.277	-1.636	0.109

Table 5: Ancestral AMF Read Abundance, Gaussian GLM

	Estimate	Std. Error	t value	Pr(> t)
(Intercept)	78.187	8.168	9.573	0.000
<i>Avena sp.</i>	-10.372	19.226	-0.539	0.593
<i>Bromus rubens</i>	29.666	10.091	2.940	0.006
<i>Eriogonum fasciculatum</i>	52.152	26.492	1.969	0.056
<i>Erodium moschatum</i>	31.860	26.950	1.182	0.244
<i>Schismus barbatus</i>	27.961	19.318	1.447	0.156
<i>Salvia mellifera</i>	10.292	9.485	1.085	0.285
Total N	-21.015	12.652	-1.661	0.105
Total C	22.511	14.541	1.548	0.130

Table 6: Ancestral AMF OTU Richness, Gaussian GLM

	Estimate	Std. Error	t value	Pr(> t)
(Intercept)	17.636	1.300	13.568	0.000
Total N	-28.196	11.297	-2.496	0.016
Total C	29.895	12.038	2.483	0.017
C:N	-9.937	4.828	-2.058	0.046

Table 7: Pathogenic Fungi Read Abundance, Gaussian GLM

	Estimate	Std. Error	t value	Pr(> t)
(Intercept)	102.950	7.909	13.017	0.000
<i>Rhizophylic AMF abundance</i>	8.393	4.145	2.025	0.051
<i>Avena sp.</i>	-21.358	26.495	-0.806	0.426
<i>Bromus rubens</i>	15.188	9.546	1.591	0.121
<i>Eriogonum fasciculatum</i>	1.340	25.064	0.053	0.958
<i>Erodium moschatum</i>	13.424	26.987	0.497	0.622
<i>Schismus barbatus</i>	41.152	20.410	2.016	0.052
<i>Salvia mellifera</i>	30.259	9.561	3.165	0.003
pH	-13.082	5.647	-2.317	0.027
C:N	2.607	5.815	0.448	0.657

Table 8: Pathogenic Fungi OTU Richness, Gaussian GLM

	Estimate	Std. Error	t value	Pr(> t)
(Intercept)	16.270	1.976	8.234	0.000
Rhizophylic AMF OTU richness	2.570	0.884	2.907	0.007
<i>Avena sp.</i>	-16.660	7.197	-2.315	0.028
<i>Bromus rubens</i>	2.629	2.012	1.306	0.201
<i>Eriogonum fasciculatum</i>	6.884	5.323	1.293	0.206
<i>Erodium moschatum</i>	3.820	6.352	0.601	0.552
<i>Schismus barbatus</i>	4.381	3.867	1.133	0.266
<i>Salvia mellifera</i>	7.093	1.930	3.675	0.001
Ambient Precipitation treatment	-0.597	2.217	-0.269	0.790
Reduced Precipitation treatment	-2.171	1.951	-1.113	0.275
Total N	46.368	15.698	2.954	0.006
Total P	4.515	2.985	1.513	0.141
Total C	-51.357	17.131	-2.998	0.005
C:N	20.846	6.797	3.067	0.005
N:P	6.948	2.953	2.353	0.025

Table 9: Saprotrophic Fungi Read Abundance, Gaussian GLM

	Estimate	Std. Error	t value	Pr(> t)
(Intercept)	150.019	16.778	8.942	0.000
Rhizophylic AMF abundance	22.370	8.350	2.679	0.012
<i>Avena sp.</i>	-45.934	63.076	-0.728	0.472
<i>Bromus rubens</i>	37.429	18.443	2.029	0.051
<i>Eriogonum fasciculatum</i>	124.925	48.876	2.556	0.016
<i>Erodium moschatum</i>	31.444	56.172	0.560	0.580
<i>Schismus barbatus</i>	94.122	35.699	2.637	0.013
<i>Salvia mellifera</i>	51.192	18.028	2.840	0.008
Total N	355.396	140.244	2.534	0.016
Total P	50.945	26.416	1.929	0.063
Total C	-391.922	152.737	-2.566	0.015
C:N	170.842	61.278	2.788	0.009
N:P	58.410	27.107	2.155	0.039

Table 10: Saprotrophic Fungi OTU Richness, Gaussian GLM

	Estimate	Std. Error	t value	Pr(> t)
(Intercept)	26.363	3.603	7.317	0.000
Rhizophylic AMF OTU richness	2.967	2.774	1.070	0.294
Ancestral AMF OTU richness	2.453	2.229	1.101	0.280
Edaphophilic AMF OTU richness	1.537	2.143	0.717	0.479
<i>Avena sp.</i>	-6.456	14.063	-0.459	0.650
<i>Bromus rubens</i>	4.357	4.222	1.032	0.311
<i>Eriogonum fasciculatum</i>	23.485	10.881	2.158	0.039
<i>Erodium moschatum</i>	4.944	12.889	0.384	0.704
<i>Schismus barbatus</i>	18.768	8.300	2.261	0.031
<i>Salvia mellifera</i>	9.514	3.953	2.407	0.023
Total N	70.881	31.998	2.215	0.035
Total P	11.058	5.791	1.910	0.066
Total C	-77.876	34.826	-2.236	0.033
pH	-0.108	2.572	-0.042	0.967
C:N	33.569	13.963	2.404	0.023
N:P	13.021	5.941	2.192	0.037

Table 11: AMF Root Colonization, Gaussian GLM

	Estimate	Std. Error	t value	Pr(> t)
(Intercept)	0.528	0.073	7.210	0.000
Rhizophylic AMF abundance	0.044	0.030	1.487	0.148
<i>Avena sp.</i>	-0.034	0.157	-0.219	0.828
<i>Bromus rubens</i>	-0.017	0.071	-0.235	0.816
<i>Eriogonum fasciculatum</i>	0.028	0.182	0.153	0.879
<i>Schismus barbatus</i>	-0.149	0.131	-1.135	0.266
<i>Salvia mellifera</i>	0.190	0.069	2.766	0.010
Ambient Precipitation treatment	-0.142	0.072	-1.984	0.057
Reduced Precipitation treatment	-0.177	0.068	-2.612	0.014
Ambient Nitrogen treatment	-0.074	0.055	-1.355	0.186
Total N	0.694	0.459	1.512	0.141
Total P	-0.081	0.053	-1.537	0.135
Total C	-0.768	0.485	-1.584	0.124
C:N	0.292	0.200	1.463	0.154

Table 12: Non-AMF Root Colonization, Gaussian GLM

	Estimate	Std. Error	t value	Pr(> t)
(Intercept)	0.164	0.070	2.333	0.027
Pathogenic fungi abundance	-0.019	0.031	-0.600	0.553
<i>Avena sp.</i>	-0.053	0.240	-0.219	0.828
<i>Bromus rubens</i>	0.220	0.076	2.912	0.007
<i>Eriogonum fasciculatum</i>	0.134	0.182	0.734	0.469
<i>Schismus barbatus</i>	0.113	0.134	0.843	0.407
<i>Salvia mellifera</i>	0.157	0.085	1.841	0.076
Ambient Precipitation treatment	-0.077	0.076	-1.007	0.323
Reduced Precipitation treatment	-0.107	0.069	-1.550	0.132
Ambient nitrogen treatment	0.071	0.063	1.127	0.269
Total N	0.796	0.523	1.523	0.139
Total P	-0.132	0.109	-1.217	0.234
Total C	-0.856	0.574	-1.492	0.147
pH	-0.021	0.049	-0.428	0.672
N:P	0.019	0.112	0.168	0.868
C:N	0.340	0.224	1.518	0.140

Table 13: AMF hyphal density, zero-inflated negative binomial GLM
Negative Binomial (log link)

	Estimate	Std. Error	Z value	Pr(>—z—)
(Intercept)	4.815	0.101	47.792	0
Ambient nitrogen treatment	0.385	0.129	2.992	0.003
Total N	1.344	0.888	1.513	0.13
Total C	-1.337	0.945	-1.414	0.157
C:N	0.529	0.364	1.456	0.145
Log(theta)	1.802	0.217	8.319	0

Binomial (logit link)

	Estimate	Std. Error	Z value	Pr(>—z—)
(Intercept)	-2.708	0.596	-4.542	0

Table 14: Total spore biovolume, gamma GLM

	Estimate	Std. Error	t value	Pr(>—t—)
(Intercept)	147797.643	34589.700	4.273	0.000
Rhizophilic AMF abundance	26324.047	12408.046	2.122	0.043
Edaphophilic AMF abundance	-19896.448	17082.934	-1.165	0.254
<i>Avena sp.</i>	127742.077	84272.946	1.516	0.140
<i>Bromus rubens</i>	13033.643	35402.530	0.368	0.715
<i>Eriogonum fasciculatum</i>	-123857.768	57270.736	-2.163	0.039
<i>Erodium moschatum</i>	237616.977	218255.808	1.089	0.285
<i>Schismus barbatus</i>	40377.361	99042.407	0.408	0.687
<i>Salvia mellifera</i>	-50564.152	26248.988	-1.926	0.064
Ambient Precipitation treatment	-70763.884	45756.431	-1.547	0.133
Reduced Precipitation treatment	-57320.219	44214.394	-1.296	0.205
Ambient nitrogen treatment	-20129.963	32968.392	-0.611	0.546
Total P	-98164.451	36504.024	-2.689	0.012
Total C	27293.160	21171.740	1.289	0.208
N:P	-92455.760	40258.969	-2.297	0.029
C:N	-62115.488	18878.054	-3.290	0.003

Table 15: Average spore diameter (μm), Gaussian GLM

	Estimate	Std. Error	t value	Pr(> t)
(Intercept)	89.473	2.870	31.174	0.000
Rhizophilic AMF abundance	-5.318	2.077	-2.560	0.017
Edaphophilic AMF abundance	4.675	2.083	2.244	0.034
Total P	13.681	5.016	2.727	0.012
Total C	-6.751	2.396	-2.818	0.010
pH	3.435	2.330	1.474	0.153
N:P	18.932	5.351	3.538	0.002
C:N	7.447	2.810	2.650	0.014

APPENDIX C: Supplemental Figures

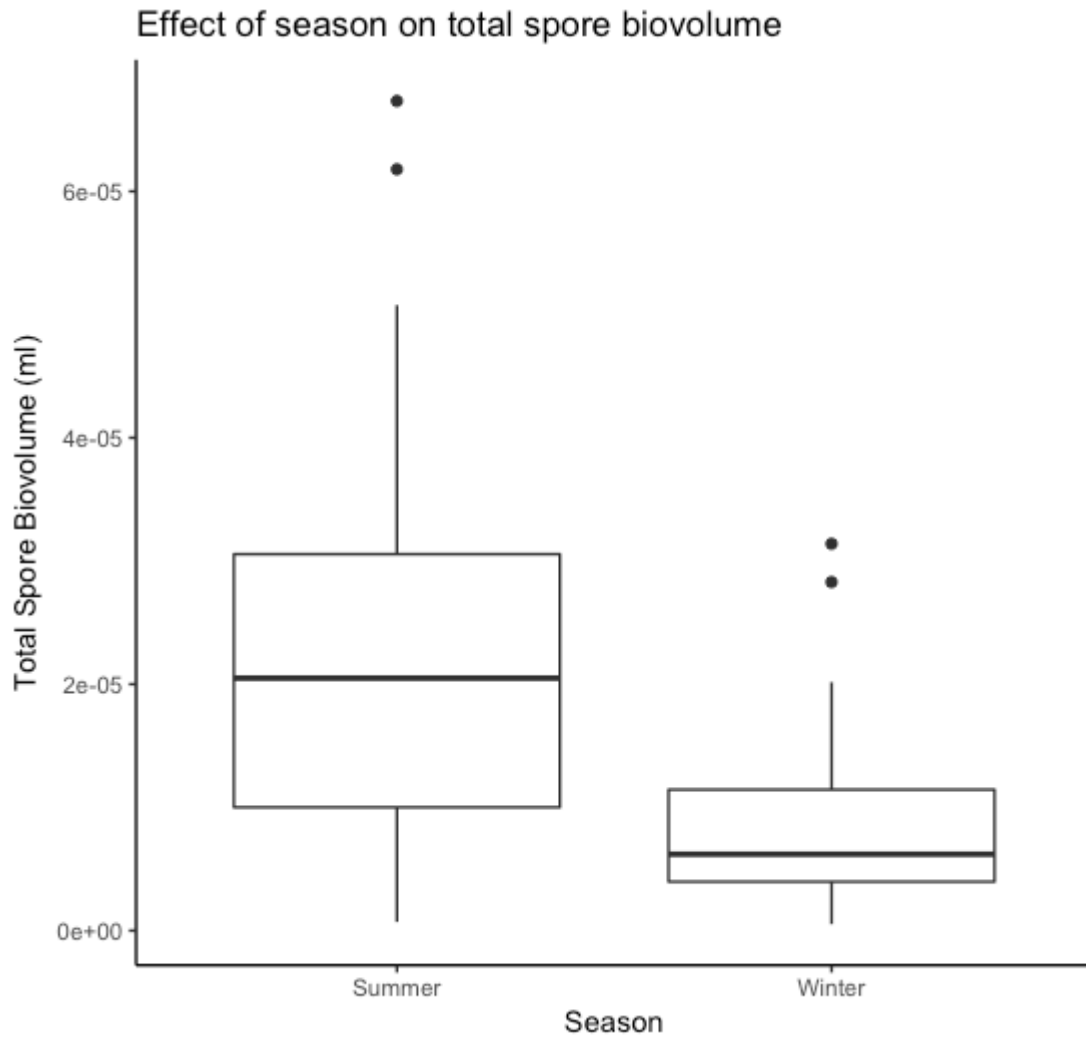


Figure 1. Total AMF spore biovolume across seasons.

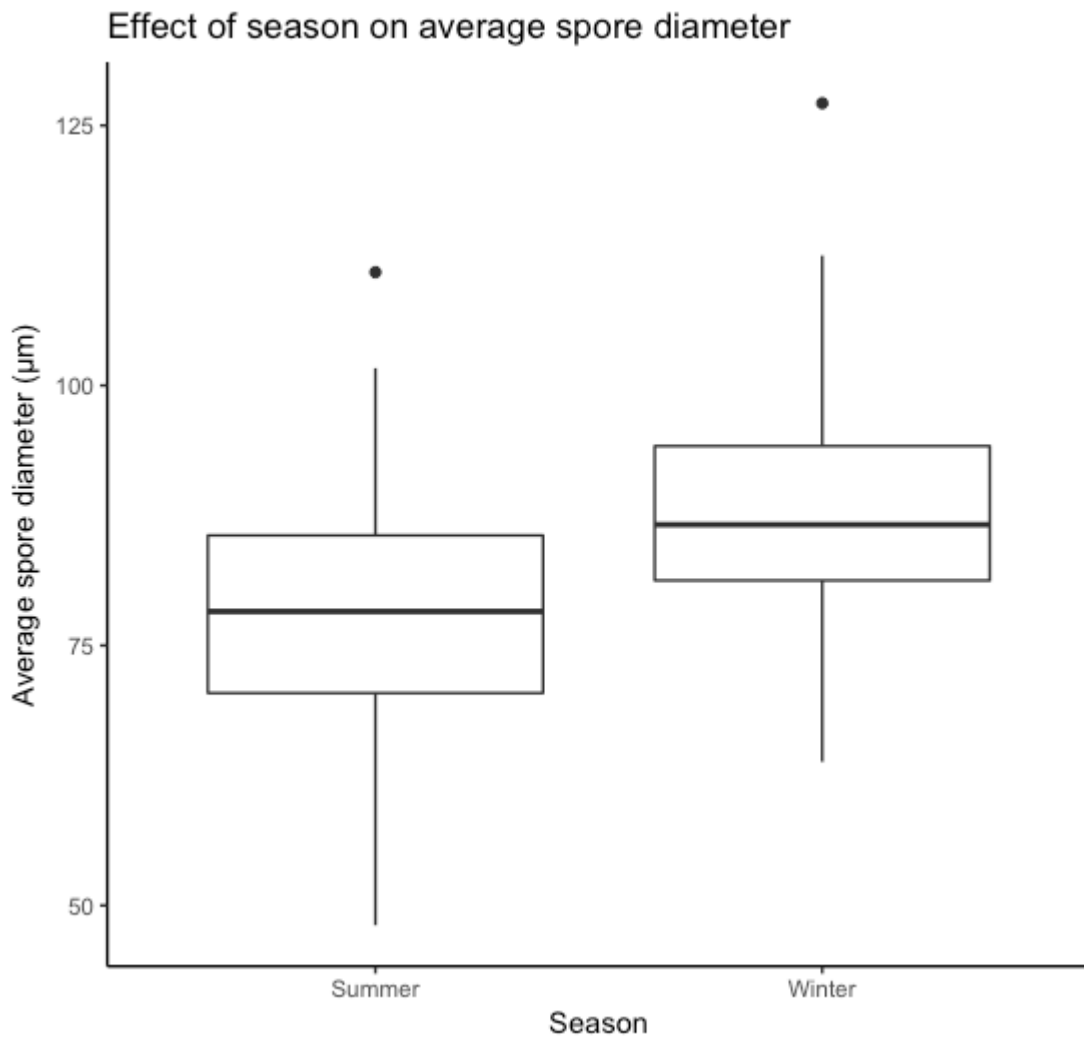


Figure 2. Average AMF spore diameter across seasons.

APPENDIX D: List of Fungal Taxa

Fungal taxa arranged by Phylum-p, Class-c, Order-o, Family-f, Genus-g, Species-s.

p__Ascomycota; c__Dothideomycetes; o__Botryosphaerales; f__Botryosphaeriaceae;
g__Macrophoma; s__Macrophoma sp 242_275

p__Ascomycota; c__Dothideomycetes; o__Botryosphaerales; f__Botryosphaeriaceae;
g__Microdiplodia; s__Microdiplodia sp

p__Ascomycota; c__Dothideomycetes; o__Botryosphaerales; f__Botryosphaeriaceae;
g__Thyrostroma; s__Thyrostroma carpophilum

p__Ascomycota; c__Dothideomycetes; o__Botryosphaerales; f__Incertae sedis;
g__Camarosporium; s__Camarosporium psoraleae

p__Ascomycota; c__Dothideomycetes; o__Botryosphaerales; f__unidentified;
g__unidentified; s__Botryosphaerales sp

p__Ascomycota; c__Dothideomycetes; o__Capnodiales; f__Davidiellaceae; g__Davidiella;
s__Davidiella tassiana

p__Ascomycota; c__Dothideomycetes; o__Capnodiales; f__Davidiellaceae; g__unidentified;
s__Davidiellaceae sp

p__Ascomycota; c__Dothideomycetes; o__Capnodiales; f__Incertae sedis;
g__Capnobotryella; s__Capnobotryella sp

p__Ascomycota; c__Dothideomycetes; o__Capnodiales; f__Mycosphaerellaceae;
g__Caryophylloseptoria; s__Caryophylloseptoria pseudolychnidis

p__Ascomycota; c__Dothideomycetes; o__Capnodiales; f__Teratosphaeriaceae;
g__Catenulostroma; s__Catenulostroma hermanusense

p__Ascomycota; c__Dothideomycetes; o__Capnodiales; f__Teratosphaeriaceae;
g__Devriesia; s__Devriesia fraseriae

p__Ascomycota; c__Dothideomycetes; o__Capnodiales; f__Teratosphaeriaceae;
g__Devriesia; s__Devriesia sp

p__Ascomycota; c__Dothideomycetes; o__Capnodiales; f__Teratosphaeriaceae;
g__Teratosphaeria; s__Teratosphaeria knoxdavesii

p__Ascomycota; c__Dothideomycetes; o__Capnodiales; f__Teratosphaeriaceae;
g__unidentified; s__Teratosphaeriaceae sp

p__Ascomycota; c__Dothideomycetes; o__Capnodiales; f__unidentified; g__unidentified;
s__Capnodiales sp

p__Ascomycota; c__Dothideomycetes; o__Dothideales; f__Dothioraceae;
g__Aureobasidium; s__Aureobasidium pullulans

p__Ascomycota; c__Dothideomycetes; o__Dothideales; f__Dothioraceae; g__Hormonema;
s__Hormonema sp

p__Ascomycota; c__Dothideomycetes; o__Dothideales; f__Dothioraceae; g__Selenophoma;
s__Selenophoma mahoniae

p__Ascomycota; c__Dothideomycetes; o__Incertae sedis; f__Pseudeurotiaceae;
g__Pseudogymnoascus; s__Pseudogymnoascus roseus

p__Ascomycota; c__Dothideomycetes; o__Pleosporales; f__Corynesporascaceae;
g__Corynespora; s__Corynespora citricola

p__Ascomycota; c__Dothideomycetes; o__Pleosporales; f__Corynesporascaceae;
g__Corynespora; s__Corynespora sp

p__Ascomycota; c__Dothideomycetes; o__Pleosporales; f__Dothidotthiaceae;
g__Spencermartinsia; s__Spencermartinsia viticola

p__Ascomycota; c__Dothideomycetes; o__Pleosporales; f__Incertae sedis; g__Ascochyta;
s__Ascochyta maackiae

p__Ascomycota; c__Dothideomycetes; o__Pleosporales; f__Incertae sedis; g__Boeremia;
s__Boeremia exigua var. populi

p__Ascomycota; c__Dothideomycetes; o__Pleosporales; f__Incertae sedis; g__Didymella;
s__Didymella sp

p__Ascomycota; c__Dothideomycetes; o__Pleosporales; f__Incertae sedis;
g__Massariosphaeria; s__Massariosphaeria sp FAEII23a

p__Ascomycota; c__Dothideomycetes; o__Pleosporales; f__Incertae sedis; g__Paraphoma;
s__Paraphoma sp

p__Ascomycota; c__Dothideomycetes; o__Pleosporales; f__Incertae sedis; g__Periconia;
s__Periconia sp BP9

p__Ascomycota; c__Dothideomycetes; o__Pleosporales; f__Incertae sedis; g__Periconia;
s__Periconia sp LVPEIH4157_10

p__Ascomycota; c__Dothideomycetes; o__Pleosporales; f__Incertae sedis; g__Peyronellaea;
s__Peyronellaea sancta

p__Ascomycota; c__Dothideomycetes; o__Pleosporales; f__Incertae sedis; g__Phoma;
s__Phoma multirostrata

p__Ascomycota; c__Dothideomycetes; o__Pleosporales; f__Incertae sedis; g__Phoma;
s__Phoma sp

p__Ascomycota; c__Dothideomycetes; o__Pleosporales; f__Incertae sedis;
g__Stagonosporopsis; s__Stagonosporopsis loticola

p__Ascomycota; c__Dothideomycetes; o__Pleosporales; f__Incertae sedis;
g__Xenobotryosphaeria; s__Xenobotryosphaeria calamagrostidis

p__Ascomycota; c__Dothideomycetes; o__Pleosporales; f__Leptosphaeriaceae;
g__Leptosphaeria; s__Leptosphaeria proteicola

p__Ascomycota; c__Dothideomycetes; o__Pleosporales; f__Leptosphaeriaceae;
g__Leptosphaeria; s__Leptosphaeria sp

p__Ascomycota; c__Dothideomycetes; o__Pleosporales; f__Lophiostomataceae;
g__Lophiostoma; s__Lophiostoma sp

p__Ascomycota; c__Dothideomycetes; o__Pleosporales; f__Montagnulaceae;
g__unidentified; s__Montagnulaceae sp

p__Ascomycota; c__Dothideomycetes; o__Pleosporales; f__Phaeosphaeriaceae;
g__Neostagonospora; s__Neostagonospora caricis

p__Ascomycota; c__Dothideomycetes; o__Pleosporales; f__Phaeosphaeriaceae;
g__Phaeosphaeria; s__Phaeosphaeria juncicola

p__Ascomycota; c__Dothideomycetes; o__Pleosporales; f__Phaeosphaeriaceae;
g__Phaeosphaeria; s__Phaeosphaeria sp TMS_2011

p__Ascomycota; c__Dothideomycetes; o__Pleosporales; f__Phaeosphaeriaceae;
g__Phaeosphaeria; s__Phaeosphaeria triglochicola

p__Ascomycota; c__Dothideomycetes; o__Pleosporales; f__Phaeosphaeriaceae;
g__Stagonospora; s__Stagonospora pseudovitensis

p__Ascomycota; c__Dothideomycetes; o__Pleosporales; f__Phaeosphaeriaceae;
g__unidentified; s__Phaeosphaeriaceae sp

p__Ascomycota; c__Dothideomycetes; o__Pleosporales; f__Pleomassariaceae;
g__unidentified; s__Pleomassariaceae sp

p__Ascomycota; c__Dothideomycetes; o__Pleosporales; f__Pleosporaceae; g__Alternaria;
s__Alternaria eichhorniae

p__Ascomycota; c__Dothideomycetes; o__Pleosporales; f__Pleosporaceae; g__Drechslera;
s__Drechslera sp BAFC 3419

p__Ascomycota; c__Dothideomycetes; o__Pleosporales; f__Pleosporaceae; g__Embellisia;
s__Embellisia planifunda

p__Ascomycota; c__Dothideomycetes; o__Pleosporales; f__Pleosporaceae; g__Pyrenophora;
s__Pyrenophora lolii

p__Ascomycota; c__Dothideomycetes; o__Pleosporales; f__Pleosporaceae; g__unidentified;
s__Pleosporaceae sp

p__Ascomycota; c__Dothideomycetes; o__Pleosporales; f__Sporormiaceae; g__Preussia;
s__Preussia sp

p__Ascomycota; c__Dothideomycetes; o__Pleosporales; f__Sporormiaceae; g__Sporormiella;
s__Sporormiella sp

p__Ascomycota; c__Dothideomycetes; o__Pleosporales; f__Sporormiaceae; g__unidentified;
s__Sporormiaceae sp

p__Ascomycota; c__Dothideomycetes; o__Pleosporales; f__Tubeufiaceae; g__unidentified;
s__Tubeufiaceae sp

p__Ascomycota; c__Dothideomycetes; o__Pleosporales; f__unidentified; g__unidentified;
s__Pleosporales sp

p__Ascomycota; c__Dothideomycetes; o__unidentified; f__unidentified; g__unidentified;
s__Dothideomycetes sp

p__Ascomycota; c__Dothideomycetes; o__Venturiales; f__Venturiaceae; g__unidentified;
s__Venturiaceae sp

p__Ascomycota; c__Eurotiomycetes; o__Chaetothyriales; f__Herpotrichiellaceae;
g__Capronia; s__Capronia sp

p__Ascomycota; c__Eurotiomycetes; o__Chaetothyriales; f__Herpotrichiellaceae;
g__Capronia; s__Capronia sp 94006a

p__Ascomycota; c__Eurotiomycetes; o__Chaetothyriales; f__Herpotrichiellaceae;
g__Cladophialophora; s__Cladophialophora sp

p__Ascomycota; c__Eurotiomycetes; o__Chaetothyriales; f__Herpotrichiellaceae;
g__Phaeococcomyces; s__Phaeococcomyces sp

p__Ascomycota; c__Eurotiomycetes; o__Chaetothyriales; f__Herpotrichiellaceae;
g__unidentified; s__Herpotrichiellaceae sp

p__Ascomycota; c__Eurotiomycetes; o__Chaetothyriales; f__unidentified; g__unidentified;
s__Chaetothyriales sp

p__Ascomycota; c__Eurotiomycetes; o__Eurotiales; f__Trichocomaceae; g__Aspergillus;
s__Aspergillus fumisynnematus

p__Ascomycota; c__Eurotiomycetes; o__Eurotiales; f__Trichocomaceae; g__Penicillium;
s__Penicillium cf parviverrucosum CMV_2013

p__Ascomycota; c__Eurotiomycetes; o__Eurotiales; f__Trichocomaceae; g__Penicillium;
s__Penicillium corylophilum

p__Ascomycota; c__Eurotiomycetes; o__Eurotiales; f__Trichocomaceae; g__Penicillium;
s__Penicillium meridianum

p__Ascomycota; c__Eurotiomycetes; o__Eurotiales; f__Trichocomaceae; g__Penicillium;
s__Penicillium nodositatum

p__Ascomycota; c__Eurotiomycetes; o__Eurotiales; f__Trichocomaceae; g__Penicillium;
s__Penicillium novae-zeelandiae

p__Ascomycota; c__Eurotiomycetes; o__Eurotiales; f__Trichocomaceae; g__Penicillium;
s__Penicillium roseopurpureum

p__Ascomycota; c__Eurotiomycetes; o__Eurotiales; f__Trichocomaceae; g__Penicillium;
s__Penicillium sp SW_2014f

p__Ascomycota; c__Eurotiomycetes; o__Eurotiales; f__Trichocomaceae; g__Penicillium;
s__Penicillium thomii

p__Ascomycota; c__Eurotiomycetes; o__Eurotiales; f__Trichocomaceae; g__Rasamsonia;
s__Rasamsonia cylindrospora

p__Ascomycota; c__Eurotiomycetes; o__Eurotiales; f__Trichocomaceae; g__unidentified;
s__Trichocomaceae sp

p__Ascomycota; c__Eurotiomycetes; o__Mycocaliciales; f__Mycocaliciaceae;
g__Mycocalicium; s__Mycocalicium albonigrum

p__Ascomycota; c__Eurotiomycetes; o__Onygenales; f__Arthrodermataceae;
g__Arthroderma; s__Arthroderma cookiellum

p__Ascomycota; c__Eurotiomycetes; o__Onygenales; f__Gymnoascaceae; g__Gymnoascus;
s__Gymnoascus sp 02NH07

p__Ascomycota; c__Eurotiomycetes; o__Onygenales; f__unidentified; g__unidentified;
s__Onygenales sp

p__Ascomycota; c__Incertae sedis; o__Incertae sedis; f__Incertae sedis; g__Ochroconis;
s__Ochroconis sp

p__Ascomycota; c__Incertae sedis; o__Incertae sedis; f__Incertae sedis; g__Triscelophorus;
s__Triscelophorus cf acuminatus UMB_55810

p__Ascomycota; c__Incertae sedis; o__Incertae sedis; f__Incertae sedis; g__Tumularia;
s__Tumularia sp

p__Ascomycota; c__Incertae sedis; o__Incertae sedis; f__Incertae sedis; g__Wojnowicia;
s__Wojnowicia viburni

p__Ascomycota; c__Lecanoromycetes; o__Candelariales; f__Candelariaceae; g__Candelaria;
s__Candelaria concolor

p__Ascomycota; c__Lecanoromycetes; o__Ostropales; f__unidentified; g__unidentified;
s__Ostropales sp

p__Ascomycota; c__Lecanoromycetes; o__Peltigerales; f__Lobariaceae;
g__Pseudocyphellaria; s__Pseudocyphellaria aurata

p__Ascomycota; c__Lecanoromycetes; o__Teloschistales; f__Teloschistaceae;
g__unidentified; s__Teloschistaceae sp

p__Ascomycota; c__Lecanoromycetes; o__Umbilicariales; f__Umbilicariaceae; g__Lasallia;
s__Lasallia rossica

p__Ascomycota; c__Lecanoromycetes; o__unidentified; f__unidentified; g__unidentified;
s__Lecanoromycetes sp

p__Ascomycota; c__Leotiomyces; o__Helotiales; f__Helotiaceae; g__Articulospora;
s__Articulospora sp

p__Ascomycota; c__Leotiomyces; o__Helotiales; f__Helotiaceae; g__Hymenoscyphus;
s__Hymenoscyphus sp SR_F14

p__Ascomycota; c__Leotiomyces; o__Helotiales; f__Incertae sedis; g__Glarea; s__Glarea
lozoyensis

p__Ascomycota; c__Leotiomyces; o__Helotiales; f__Incertae sedis; g__Phacidiella;
s__Phacidiella eucalypti

p__Ascomycota; c__Leotiomyces; o__Helotiales; f__Incertae sedis; g__Scytalidium;
s__Scytalidium circinatum

p__Ascomycota; c__Leotiomyces; o__Helotiales; f__Incertae sedis; g__Tetracladium;
s__Tetracladium maxilliforme

p__Ascomycota; c__Leotiomyces; o__Helotiales; f__Incertae sedis; g__Trimmatostroma;
s__Trimmatostroma salinum

p__Ascomycota; c__Leotiomyces; o__Helotiales; f__Rutstroemiaceae; g__unidentified;
s__Rutstroemiaceae sp

p__Ascomycota; c__Leotiomyces; o__Helotiales; f__unidentified; g__unidentified;
s__Helotiales sp

p__Ascomycota; c__Leotiomyces; o__Helotiales; f__Vibrisseaceae; g__Phialocephala;
s__Phialocephala sp CM16s1

p__Ascomycota; c__Leotiomyces; o__unidentified; f__unidentified; g__unidentified;
s__Leotiomyces sp

p__Ascomycota; c__Orbiliomyces; o__Orbiliales; f__Orbiliaceae; g__Dactylella;
s__Dactylella oviparasitica

p__Ascomycota; c__Orbiliomycetes; o__Orbiliiales; f__Orbiliaceae; g__Dactylella;
s__Dactylella sp

p__Ascomycota; c__Orbiliomycetes; o__unidentified; f__unidentified; g__unidentified;
s__Orbiliomycetes sp

p__Ascomycota; c__Pezizomycetes; o__Pezizales; f__Ascobolaceae; g__unidentified;
s__Ascobolaceae sp

p__Ascomycota; c__Pezizomycetes; o__Pezizales; f__Pyronemataceae; g__Scutellinia;
s__Scutellinia sp

p__Ascomycota; c__Pezizomycetes; o__Pezizales; f__Sarcosomataceae; g__unidentified;
s__Sarcosomataceae sp

p__Ascomycota; c__Pezizomycetes; o__Pezizales; f__unidentified; g__unidentified;
s__Pezizales sp

p__Ascomycota; c__Pezizomycetes; o__unidentified; f__unidentified; g__unidentified;
s__Pezizomycetes sp

p__Ascomycota; c__Sordariomycetes; o__Chaetosphaeriales; f__unidentified;
g__unidentified; s__Chaetosphaeriales sp

p__Ascomycota; c__Sordariomycetes; o__Coniochaetales; f__Coniochaetaceae;
g__Coniochaeta; s__Coniochaeta cateniformis

p__Ascomycota; c__Sordariomycetes; o__Coniochaetales; f__Coniochaetaceae;
g__Coniochaeta; s__Coniochaeta sp

p__Ascomycota; c__Sordariomycetes; o__Coniochaetales; f__Coniochaetaceae;
g__Lecythophora; s__Lecythophora hoffmannii

p__Ascomycota; c__Sordariomycetes; o__Diaporthales; f__Diaporthaceae; g__Diaporthe;
s__Diaporthe ambigua

p__Ascomycota; c__Sordariomycetes; o__Diaporthales; f__Diaporthaceae; g__Phomopsis;
s__Phomopsis sp C_1_BESC_294j

p__Ascomycota; c__Sordariomycetes; o__Diaporthales; f__Diaporthaceae; g__Phomopsis;
s__Phomopsis sp SS_1849

p__Ascomycota; c__Sordariomycetes; o__Hypocreales; f__Cordycipitaceae; g__Lecanicillium;
s__Lecanicillium dimorphum

p__Ascomycota; c__Sordariomycetes; o__Hypocreales; f__Incertae sedis; g__Acremonium;
s__Acremonium alternatum

p__Ascomycota; c__Sordariomycetes; o__Hypocreales; f__Incertae sedis; g__Acremonium;
s__Acremonium sp 274 OA_2013

p__Ascomycota; c__Sordariomycetes; o__Hypocreales; f__Incertae sedis; g__Ilyonectria;
s__Ilyonectria estremocensis

p__Ascomycota; c__Sordariomycetes; o__Hypocreales; f__Incertae sedis; g__Ilyonectria;
s__Ilyonectria macrodidyma

p__Ascomycota; c__Sordariomycetes; o__Hypocreales; f__Incertae sedis; g__Ilyonectria;
s__Ilyonectria mors-panacis

p__Ascomycota; c__Sordariomycetes; o__Hypocreales; f__Incertae sedis; g__Myrothecium;
s__Myrothecium inundatum

p__Ascomycota; c__Sordariomycetes; o__Hypocreales; f__Incertae sedis; g__Myrothecium;
s__Myrothecium sp

p__Ascomycota; c__Sordariomycetes; o__Hypocreales; f__Nectriaceae; g__Fusarium;
s__Fusarium concentricum

p__Ascomycota; c__Sordariomycetes; o__Hypocreales; f__Nectriaceae; g__Fusarium;
s__Fusarium sp

p__Ascomycota; c__Sordariomycetes; o__Hypocreales; f__Nectriaceae; g__Fusarium;
s__Fusarium tricinctum

p__Ascomycota; c__Sordariomycetes; o__Hypocreales; f__Nectriaceae; g__unidentified;
s__Nectriaceae sp

p__Ascomycota; c__Sordariomycetes; o__Hypocreales; f__Ophiocordycipitaceae;
g__Ophiocordyceps; s__Ophiocordyceps sinensis

p__Ascomycota; c__Sordariomycetes; o__Hypocreales; f__unidentified; g__unidentified;
s__Hypocreales sp

p__Ascomycota; c__Sordariomycetes; o__Incertae sedis; f__Annulatasceae; g__Conlarium;
s__Conlarium duplumascospora

p__Ascomycota; c__Sordariomycetes; o__Incertae sedis; f__Glomerellaceae;
g__Colletotrichum; s__Colletotrichum destructivum

p__Ascomycota; c__Sordariomycetes; o__Incertae sedis; f__Incertae sedis; g__Eucasphaeria;
s__Eucasphaeria capensis

p__Ascomycota; c__Sordariomycetes; o__Incertae sedis; f__Magnaporthaceae;
g__unidentified; s__Magnaporthaceae sp

p__Ascomycota; c__Sordariomycetes; o__Microascales; f__Halosphaeriaceae;
g__Clavatospora; s__Clavatospora longibrachiata

p__Ascomycota; c__Sordariomycetes; o__Microascales; f__Halosphaeriaceae;
g__unidentified; s__Halosphaeriaceae sp

p__Ascomycota; c__Sordariomycetes; o__Sordariales; f__Chaetomiaceae; g__Chaetomidium;
s__Chaetomidium galaicum

p__Ascomycota; c__Sordariomycetes; o__Sordariales; f__Chaetomiaceae; g__Chaetomium;
s__Chaetomium iraniamum

p__Ascomycota; c__Sordariomycetes; o__Sordariales; f__Chaetomiaceae; g__Chaetomium;
s__Chaetomium sp

p__Ascomycota; c__Sordariomycetes; o__Sordariales; f__Chaetomiaceae; g__Humicola;
s__Humicola fuscoatra var fuscoatra

p__Ascomycota; c__Sordariomycetes; o__Sordariales; f__Chaetomiaceae; g__unidentified;
s__Chaetomiaceae sp

p__Ascomycota; c__Sordariomycetes; o__Sordariales; f__Incertae sedis;
g__Ramophialophora; s__Ramophialophora sp FMR 9523

p__Ascomycota; c__Sordariomycetes; o__Sordariales; f__Lasiosphaeriaceae; g__Cercophora;
s__Cercophora sp

p__Ascomycota; c__Sordariomycetes; o__Sordariales; f__Lasiosphaeriaceae;
g__Cladorrhinum; s__Cladorrhinum sp

p__Ascomycota; c__Sordariomycetes; o__Sordariales; f__Lasiosphaeriaceae; g__Podospora;
s__Podospora decipiens

p__Ascomycota; c__Sordariomycetes; o__Sordariales; f__Lasiosphaeriaceae; g__Podospora;
s__Podospora intestinacea

p__Ascomycota; c__Sordariomycetes; o__Sordariales; f__Lasiosphaeriaceae; g__Podospora;
s__Podospora sp

p__Ascomycota; c__Sordariomycetes; o__Sordariales; f__Lasiosphaeriaceae;
g__Schizothecium; s__Schizothecium carpinicola

p__Ascomycota; c__Sordariomycetes; o__Sordariales; f__Lasiosphaeriaceae;
g__Schizothecium; s__Schizothecium curvisporum

p__Ascomycota; c__Sordariomycetes; o__Sordariales; f__Lasiosphaeriaceae;
g__unidentified; s__Lasiosphaeriaceae sp

p__Ascomycota; c__Sordariomycetes; o__Sordariales; f__Sordariaceae; g__unidentified;
s__Sordariaceae sp

p__Ascomycota; c__Sordariomycetes; o__Sordariales; f__unidentified; g__unidentified;
s__Sordariales sp

p__Ascomycota; c__Sordariomycetes; o__unidentified; f__unidentified; g__unidentified;
s__Sordariomycetes sp

p__Ascomycota; c__Sordariomycetes; o__Xylariales; f__Amphisphaeriaceae; g__unidentified;
s__Amphisphaeriaceae sp

p__Ascomycota; c__Sordariomycetes; o__Xylariales; f__Incertae sedis; g__Dinemasporium;
s__Dinemasporium pseudostrigosum

p__Ascomycota; c__Sordariomycetes; o__Xylariales; f__Incertae sedis; g__Microdochium;
s__Microdochium sp

p__Ascomycota; c__Sordariomycetes; o__Xylariales; f__Incertae sedis; g__Monographella;
s__Monographella nivalis

p__Ascomycota; c__Sordariomycetes; o__Xylariales; f__unidentified; g__unidentified;
s__Xylariales sp

p__Ascomycota; c__Sordariomycetes; o__Xylariales; f__Xylariaceae; g__Conioliariella;
s__Conioliariella hispanica

p__Ascomycota; c__Sordariomycetes; o__Xylariales; f__Xylariaceae; g__unidentified;
s__Xylariaceae sp

p__Ascomycota; c__Sordariomycetes; o__Xylariales; f__Xylariaceae; g__Xylaria; s__Xylaria
venosula

p__Ascomycota; c__unidentified; o__unidentified; f__unidentified; g__unidentified;
s__Ascomycota sp

p__Basidiomycota; c__Agaricomycetes; o__Agaricales; f__Agaricaceae; g__Leucoagaricus;
s__Leucoagaricus variicolor

p__Basidiomycota; c__Agaricomycetes; o__Agaricales; f__Agaricaceae; g__unidentified;
s__Agaricaceae sp

p__Basidiomycota; c__Agaricomycetes; o__Agaricales; f__Bolbitiaceae; g__Conocybe;
s__Conocybe aff ochrostriata NL_0830

p__Basidiomycota; c__Agaricomycetes; o__Agaricales; f__Clavariaceae; g__unidentified;
s__Clavariaceae sp

p__Basidiomycota; c__Agaricomycetes; o__Agaricales; f__Inocybaceae; g__Inocybe;
s__Inocybe sp AU52

p__Basidiomycota; c__Agaricomycetes; o__Agaricales; f__Inocybaceae; g__Tubaria;
s__Tubaria vinicolor

p__Basidiomycota; c__Agaricomycetes; o__Agaricales; f__Marasmiaceae; g__Calyptella;
s__Calyptella capula

p__Basidiomycota; c__Agaricomycetes; o__Agaricales; f__Marasmiaceae; g__Campanella;
s__Campanella aff olivaceonigra SMF2613

p__Basidiomycota; c__Agaricomycetes; o__Agaricales; f__Mycenaceae; g__Mycena;
s__Mycena rosella

p__Basidiomycota; c__Agaricomycetes; o__Agaricales; f__Mycenaceae; g__Mycena;
s__Mycena sp

p__Basidiomycota; c__Agaricomycetes; o__Agaricales; f__Mycenaceae; g__Mycena;
s__Mycena speirea

p__Basidiomycota; c__Agaricomycetes; o__Agaricales; f__Psathyrellaceae; g__Coprinospsis;
s__Coprinospsis sp SL 16

p__Basidiomycota; c__Agaricomycetes; o__Agaricales; f__Strophariaceae; g__Psilocybe;
s__Psilocybe sp

p__Basidiomycota; c__Agaricomycetes; o__Agaricales; f__Tricholomataceae;
g__Melanoleuca; s__Melanoleuca sp MSG_2013a

p__Basidiomycota; c__Agaricomycetes; o__Agaricales; f__unidentified; g__unidentified;
s__Agaricales sp

p__Basidiomycota; c__Agaricomycetes; o__Atheliales; f__Atheliaceae; g__Athelia; s__Athelia
sp

p__Basidiomycota; c__Agaricomycetes; o__Cantharellales; f__Ceratobasidiaceae;
g__Ceratobasidium; s__Ceratobasidium sp AG_I

p__Basidiomycota; c__Agaricomycetes; o__Cantharellales; f__Ceratobasidiaceae;
g__Thanatephorus; s__Thanatephorus cucumeris

p__Basidiomycota; c__Agaricomycetes; o__Cantharellales; f__Ceratobasidiaceae;
g__unidentified; s__Ceratobasidiaceae sp

p__Basidiomycota; c__Agaricomycetes; o__Cantharellales; f__Hydnaceae; g__Sistotrema;
s__Sistotrema sp

p__Basidiomycota; c__Agaricomycetes; o__Corticiales; f__Corticaceae; g__Laetisaria;
s__Laetisaria arvalis

p__Basidiomycota; c__Agaricomycetes; o__Corticiales; f__Corticaceae; g__Laetisaria;
s__Laetisaria sp RhMY076Lzz7

p__Basidiomycota; c__Agaricomycetes; o__Corticiales; f__Corticaceae; g__unidentified;
s__Corticaceae sp

p__Basidiomycota; c__Agaricomycetes; o__Geastrales; f__Geastraceae; g__Sphaerobolus;
s__Sphaerobolus stellatus

p__Basidiomycota; c__Agaricomycetes; o__Gloeophyllales; f__Gloeophyllaceae;
g__Gloeophyllum; s__Gloeophyllum striatum

p__Basidiomycota; c__Agaricomycetes; o__Hymenochaetales; f__Schizoporaceae;
g__Hyphodontia; s__Hyphodontia alutaria

p__Basidiomycota; c__Agaricomycetes; o__Phallales; f__Phallaceae; g__Phallus; s__Phallus
sp

p__Basidiomycota; c__Agaricomycetes; o__Polyporales; f__Cystostereaceae;
g__Cystostereum; s__Cystostereum murrayi

p__Basidiomycota; c__Agaricomycetes; o__Sebacinales; f__Sebacinales Group B;
g__unidentified; s__Sebacinales Group B sp

p__Basidiomycota; c__Agaricomycetes; o__Thelephorales; f__Thelephoraceae;
g__Tomentellopsis; s__Tomentellopsis sp

p__Basidiomycota; c__Agaricomycetes; o__Trechisporales; f__Hydnodontaceae;
g__Trechispora; s__Trechispora sp

p__Basidiomycota; c__Agaricomycetes; o__unidentified; f__unidentified; g__unidentified;
s__Agaricomycetes sp

p__Basidiomycota; c__Agaricostilbomycetes; o__Agaricostilbales; f__Chionosphaeraceae;
g__Kurtzmanomyces; s__Kurtzmanomyces sp CBS 12707

p__Basidiomycota; c__Microbotryomycetes; o__Sporidiobolales; f__Incertae sedis;
g__Rhodotorula; s__Rhodotorula ferulica

p__Basidiomycota; c__Microbotryomycetes; o__Sporidiobolales; f__Incertae sedis;
g__Sporobolomyces; s__Sporobolomyces griseoflavus

p__Basidiomycota; c__Tremellomycetes; o__Filobasidiales; f__Filobasidiaceae;
g__Cryptococcus; s__Cryptococcus cerealis

p__Basidiomycota; c__Tremellomycetes; o__Filobasidiales; f__Filobasidiaceae;
g__Cryptococcus; s__Cryptococcus chernovii

p__Basidiomycota; c__Tremellomycetes; o__Filobasidiales; f__Filobasidiaceae;
g__Cryptococcus; s__Cryptococcus heimaeyensis

p__Basidiomycota; c__Tremellomycetes; o__Tremellales; f__Incertae sedis; g__Bullera;
s__Bullera miyagiana

p__Basidiomycota; c__Tremellomycetes; o__Tremellales; f__Incertae sedis;
g__Cryptococcus; s__Cryptococcus dimennae

p__Basidiomycota; c__Tremellomycetes; o__Tremellales; f__Incertae sedis;
 g__Cryptococcus; s__Cryptococcus magnus

p__Basidiomycota; c__Tremellomycetes; o__Tremellales; f__Incertae sedis;
 g__Cryptococcus; s__Cryptococcus podzolicus

p__Basidiomycota; c__Tremellomycetes; o__Tremellales; f__Incertae sedis;
 g__Cryptococcus; s__Cryptococcus sp

p__Basidiomycota; c__Tremellomycetes; o__Tremellales; f__Incertae sedis; g__Dioszegia;
 s__Dioszegia sp YM24626

p__Chytridiomycota; c__Chytridiomycetes; o__Rhizophlyctidales; f__Rhizophlyctidaceae;
 g__Rhizophlyctis; s__Rhizophlyctis rosea

p__Chytridiomycota; c__Chytridiomycetes; o__unidentified; f__unidentified;
 g__unidentified; s__Chytridiomycetes sp

p__Chytridiomycota; c__unidentified; o__unidentified; f__unidentified; g__unidentified;
 s__Chytridiomycota sp

p__Glomeromycota; c__Glomeromycetes; o__Glomerales; f__Glomeraceae; g__unidentified;
 s__Glomeraceae sp

p__unidentified; c__unidentified; o__unidentified; f__unidentified; g__unidentified; s__Fungi
 sp

p__unidentified; c__unidentified; o__unidentified; f__unidentified; g__unidentified;
 s__Slopeiomyces cylindrosporus

p__Zygomycota; c__Incertae sedis; o__Mortierellales; f__Mortierellaceae; g__Mortierella;
 s__Mortierella sp

p__Glomeromycota; c__Glomeromycetes; o__Archaeosporales; f__Ambisporaceae; g__Ambispora;
 s__leptoticha

p__Glomeromycota; c__Glomeromycetes; o__Archaeosporales; f__Archaeosporaceae;
 g__Archaeospora; s__Aca

p__Glomeromycota; c__Glomeromycetes; o__Archaeosporales; f__Archaeosporaceae;
 g__Archaeospora; s__MO_Ar1

p__Glomeromycota; c__Glomeromycetes; o__Archaeosporales; f__Archaeosporaceae;
 g__Archaeospora; s__Schechter08_Arch1

p__Glomeromycota; c__Glomeromycetes; o__Archaeosporales; f__Archaeosporaceae;
 g__Archaeospora; s__sp

p__Glomeromycota; c__Glomeromycetes; o__Archaeosporales; f__Geosiphonaceae;
 g__Geosiphon; s__pyriformis

p__Glomeromycota; c__Glomeromycetes; o__Diversisporales; f__Acaulosporaceae;
 g__Acaulospora; s__Acau16

p__Glomeromycota; c__Glomeromycetes; o__Diversisporales; f__Acaulosporaceae;
 g__Acaulospora; s__Acau2

p__Glomeromycota; c__Glomeromycetes; o__Diversisporales; f__Acaulosporaceae;
 g__Acaulospora; s__Acau4

p_Glomeromycota; c_Glomeromycetes; o_Diversisporales; f_Acaulosporaceae;
g_Acaulospora; s_Acau5

p_Glomeromycota; c_Glomeromycetes; o_Diversisporales; f_Acaulosporaceae;
g_Acaulospora; s_MO_A10

p_Glomeromycota; c_Glomeromycetes; o_Diversisporales; f_Diversisporaceae;
g_Diversispora; s_Div

p_Glomeromycota; c_Glomeromycetes; o_Diversisporales; f_Diversisporaceae;
g_Diversispora; s_MO_D2

p_Glomeromycota; c_Glomeromycetes; o_Diversisporales; f_Diversisporaceae;
g_Diversispora; s_sp

p_Glomeromycota; c_Glomeromycetes; o_Diversisporales; f_Diversisporaceae;
g_Diversispora; s_spurca

p_Glomeromycota; c_Glomeromycetes; o_Diversisporales; f_Gigasporaceae;
g_Scutellospora; s_LER04

p_Glomeromycota; c_Glomeromycetes; o_Diversisporales; f_Gigasporaceae;
g_Scutellospora; s_MO_S2

p_Glomeromycota; c_Glomeromycetes; o_Diversisporales; f_Gigasporaceae;
g_Scutellospora; s_pellucida

p_Glomeromycota; c_Glomeromycetes; o_Diversisporales; f_Gigasporaceae;
g_Scutellospora; s_spinosissima

p_Glomeromycota; c_Glomeromycetes; o_Glomerales; f_Claroideoglomeraceae;
g_Claroideoglomerus; s_Douhan9

p_Glomeromycota; c_Glomeromycetes; o_Glomerales; f_Claroideoglomeraceae;
g_Claroideoglomerus; s_Glo_G8

p_Glomeromycota; c_Glomeromycetes; o_Glomerales; f_Claroideoglomeraceae;
g_Claroideoglomerus; s_lamellosum

p_Glomeromycota; c_Glomeromycetes; o_Glomerales; f_Claroideoglomeraceae;
g_Claroideoglomerus; s_MO_GB1

p_Glomeromycota; c_Glomeromycetes; o_Glomerales; f_Claroideoglomeraceae;
g_Claroideoglomerus; s_sp

p_Glomeromycota; c_Glomeromycetes; o_Glomerales; f_Claroideoglomeraceae;
g_Claroideoglomerus; s_Torreillas12b_Glo_G5

p_Glomeromycota; c_Glomeromycetes; o_Glomerales; f_Glomeraceae; g_Glomerus;
s_acnaGlo2

p_Glomeromycota; c_Glomeromycetes; o_Glomerales; f_Glomeraceae; g_Glomerus;
s_Alguacil09b_Glo_G14

p_Glomeromycota; c_Glomeromycetes; o_Glomerales; f_Glomeraceae; g_Glomerus;
s_Alguacil09b_Glo_G16

p_Glomeromycota; c_Glomeromycetes; o_Glomerales; f_Glomeraceae; g_Glomerus;
s_Alguacil09b_Glo_G9

p_Glomeromycota; c_Glomeromycetes; o_Glomerales; f_Glomeraceae; g_Glomus;
s_Aguacil10_Glo1

p_Glomeromycota; c_Glomeromycetes; o_Glomerales; f_Glomeraceae; g_Glomus;
s_Aguacil10_Glo6

p_Glomeromycota; c_Glomeromycetes; o_Glomerales; f_Glomeraceae; g_Glomus;
s_caledonium

p_Glomeromycota; c_Glomeromycetes; o_Glomerales; f_Glomeraceae; g_Glomus; s_Glo_A

p_Glomeromycota; c_Glomeromycetes; o_Glomerales; f_Glomeraceae; g_Glomus; s_Glo_D

p_Glomeromycota; c_Glomeromycetes; o_Glomerales; f_Glomeraceae; g_Glomus; s_Glo16

p_Glomeromycota; c_Glomeromycetes; o_Glomerales; f_Glomeraceae; g_Glomus; s_Glo33

p_Glomeromycota; c_Glomeromycetes; o_Glomerales; f_Glomeraceae; g_Glomus; s_Glo72

p_Glomeromycota; c_Glomeromycetes; o_Glomerales; f_Glomeraceae; g_Glomus; s_LES15

p_Glomeromycota; c_Glomeromycetes; o_Glomerales; f_Glomeraceae; g_Glomus;
s_MO_G18

p_Glomeromycota; c_Glomeromycetes; o_Glomerales; f_Glomeraceae; g_Glomus;
s_MO_G20

p_Glomeromycota; c_Glomeromycetes; o_Glomerales; f_Glomeraceae; g_Glomus;
s_MO_G23

p_Glomeromycota; c_Glomeromycetes; o_Glomerales; f_Glomeraceae; g_Glomus;
s_MO_G27

p_Glomeromycota; c_Glomeromycetes; o_Glomerales; f_Glomeraceae; g_Glomus;
s_MO_G38

p_Glomeromycota; c_Glomeromycetes; o_Glomerales; f_Glomeraceae; g_Glomus;
s_MO_G42

p_Glomeromycota; c_Glomeromycetes; o_Glomerales; f_Glomeraceae; g_Glomus;
s_MO_G47

p_Glomeromycota; c_Glomeromycetes; o_Glomerales; f_Glomeraceae; g_Glomus;
s_MO_G48

p_Glomeromycota; c_Glomeromycetes; o_Glomerales; f_Glomeraceae; g_Glomus;
s_MO_G59

p_Glomeromycota; c_Glomeromycetes; o_Glomerales; f_Glomeraceae; g_Glomus; s_MO_G7

p_Glomeromycota; c_Glomeromycetes; o_Glomerales; f_Glomeraceae; g_Glomus; s_MO_G8

p_Glomeromycota; c_Glomeromycetes; o_Glomerales; f_Glomeraceae; g_Glomus;
s_mosseae

p_Glomeromycota; c_Glomeromycetes; o_Glomerales; f_Glomeraceae; g_Glomus;
s_MVK_06_IV

p_Glomeromycota; c_Glomeromycetes; o_Glomerales; f_Glomeraceae; g_Glomus; s_NES27

p_Glomeromycota; c_Glomeromycetes; o_Glomerales; f_Glomeraceae; g_Glomus; s_sp

p_Glomeromycota; c_Glomeromycetes; o_Glomerales; f_Glomeraceae; g_Glomus; s_sp_4

p_Glomeromycota; c_Glomeromycetes; o_Glomerales; f_Glomeraceae; g_Glomus;
s_VeGlo18

p_Glomeromycota; c_Glomeromycetes; o_Glomerales; f_Glomeraceae; g_Glomus;
s_Whitfield_type_18

p_Glomeromycota; c_Glomeromycetes; o_Glomerales; f_Glomeraceae; g_Glomus;
s_Whitfield_type_7

p_Glomeromycota; c_Glomeromycetes; o_Glomerales; f_Glomeraceae; g_Glomus;
s_Winther07_H

p_Glomeromycota; c_Glomeromycetes; o_Glomerales; f_Glomeraceae; g_Glomus;
s_Wirsel_OTU13

p_Glomeromycota; c_Glomeromycetes; o_Glomerales; f_Glomeraceae; g_Glomus;
s_Wirsel_OTU16

p_Glomeromycota; c_Glomeromycetes; o_Glomerales; f_Glomeraceae; g_Glomus;
s_Yamato08_C

p_Glomeromycota; c_Glomeromycetes; o_Glomerales; f_Glomeraceae; g_Glomus;
s_Yamato09_C1

p_Glomeromycota; c_Glomeromycetes; o_Paraglomerales; f_Paraglomeraceae;
g_Paraglomus; s_Alguacil12a_Para_1

p_Glomeromycota; c_Glomeromycetes; o_Paraglomerales; f_Paraglomeraceae;
g_Paraglomus; s_Alguacil12b_ACA1

p_Glomeromycota; c_Glomeromycetes; o_Paraglomerales; f_Paraglomeraceae;
g_Paraglomus; s_Alguacil12b_PARA1

p_Glomeromycota; c_Glomeromycetes; o_Paraglomerales; f_Paraglomeraceae;
g_Paraglomus; s_Glom_1B13

p_Glomeromycota; c_Glomeromycetes; o_Paraglomerales; f_Paraglomeraceae;
g_Paraglomus; s_laccatum

p_Glomeromycota; c_Glomeromycetes; o_Paraglomerales; f_Paraglomeraceae;
g_Paraglomus; s_MO_P1

p_Glomeromycota; c_Glomeromycetes; o_Paraglomerales; f_Paraglomeraceae;
g_Paraglomus; s_Pa_1

p_Glomeromycota; c_Glomeromycetes; o_Paraglomerales; f_Paraglomeraceae;
g_Paraglomus; s_sp

p_unknown; c_unknown; o_unknown; f_unknown; g_unknown; s_Fine Endophyte otu0

p_unknown; c_unknown; o_unknown; f_unknown; g_unknown; s_Fine Endophyte otu4
