SENSITIVITY IN GROWTH RESPONSES OF TREE SEEDLINGS TO VARIATION IN IDENTITY AND ABUNDANCE OF ECTOMYCORRHIZAL FUNGI

by

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Abstract

Interdependent organisms such as trees and ectomycorrhizal fungi are described as coevolved. Partner species in coevolved interactions are expected to be sensitive to intraspecific variation of each partner due to the intimate and interdependent nature of their interactions. In this thesis, I considered specific aspects of variation in each of the ectomycorrhizal partners and how this variation influenced the other partner. In particular, I used experimental and meta-analytical approaches to evaluate 1. how colonization levels, regardless of ectomycorrhizal fungal taxon, correlated to host growth; 2. how ectomycorrhizal fungi differentially influenced growth of different genera of plant hosts, and 3. how variation in growth of a single host species was correlated to the composition of ectomycorrhizal fungal communities in various soil environments. Because controlling for and manipulating ectomycorrhizal fungi on host plants is integral to these questions, I also tested the efficacy of two methods to control colonization by ectomycorrhizal fungi on host plants and found that fungicides and mesh can be effective barriers to colonization. Results from the meta-analysis and experiments indicated that colonization levels did not consistently scale with host growth response, however, suggesting that colonization levels may not be an ecologically useful factor to gauge the growth responses of host plants to ectomycorrhizal fungi. In addition, there was little sensitivity in growth responses of host plants to variation in the identity of ectomycorrhizal fungi. Seedlings across multiple host genera increased in biomass and shoot height when inoculated with ectomycorrhizal fungi regardless of the identity of the fungal associate. When ectomycorrhizas were considered in a multi-specific context (i.e. one host species associated with a community of ectomycorrhizal fungi), variation in host shoot properties was not correlated with species composition of the community of ectomycorrhizal fungi on their roots but rather appeared to be coupled to edaphic conditions. These results indicate that the variation in ectomycorrhizal fungi perceived and selected for by the host plant may be of a discrete (presence/absence of ectomycorrhizal fungi) rather than continuous nature (variation in identity or abundance of ectomycorrhizal fungi).

Table of Contents

'n

Abstract	. ii
Table of Contents	.iii
List of Tables	vii
List of Figures	iix
Acknowledgements	xii
Co-authorship Statement	xiii
1 Introduction	. 1
Context	. 1
Literature Review	4
Causes of specialization versus generalization	4
Specialization versus generalization in ectomycorrhizal associations	5
Ecological material for specialization: what variation is present among	
ectomycorrhizal fungi to which plant hosts could respond?	6
Overview of Thesis	6
References	8
2 The mutualism-parasitism continuum in ectomycorrhizas: A quantitative	
assessment using meta-analysis	13
Introduction	13
Methods	15
Data collection	15
Data analysis	16
Results	17
Seedling response to ectomycorrhizal inoculation	17
Seedling response to ectomycorrhizal inoculation and phosphorus addition	19
Discussion	20

iv
Seedling response to ectomycorrhizal inoculation20
The spectrum is reduced: Publication bias inflates measures of effect sizes20
The spectrum is distorted: Factors that covary with time may cause spurious
effects21
The spectrum is distorted: Effects of crossing hosts and ectomycorrhizal fungi not
known to co-occur remain poorly understood22
The role of variation in fungal properties in host response to ectomycorrhizal
inoculation23
Conclusions and future directions26
References
3 Methods to control ectomycorrhizal colonization: Effectiveness of chemical and
physical barriers
Introduction
Materials and methods50
Field soil collection
Plant material51
Fungicide experiment51
Experimental design and treatments51
Seedling measurements52
Mesh barrier experiment53
Experimental design and treatments53
Seedling measurements
Molecular confirmation of ectomycorrhizal fungal species identification54
Statistical analysis55
Results
Fungicide treatments
Mesh barrier treatments57
Discussion
Fungicide effects on ectomycorrhizal colonization58
Mesh barrier effects on hyphal penetration61

Conclusions	62			
References	78			
4 Ectomycorrhizal colonization and intraspecific variation in growth response				
lodgepole pine	83			
Introduction	83			
Methods	84			
Greenhouse experimental set-up	84			
Assessment of ectomycorrhizal fungal colonization	85			
Molecular analyses	86			
Statistical analyses	86			
Results	87			
Discussion	88			
Seed family effects on the relationship between colonization level and host g	rowth			
· · · · · · · · · · · · · · · · · · ·	88			
Ectomycorrhizal colonization and host phenotypic variation	89			
The prevalence of contamination on seedlings	91			
Conclusions	91			
References	97			
5 Interactions among soil characteristics, host intraspecific variation and				
ectomycorrhizal fungal communities	100			
Introduction	100			
Materials and methods	101			
Overview	101			
Origin of soils	102			
Soil collection	102			
Plant material	103			
Maintenance of soil moisture	103			
Final harvest	104			
Statistical analyses	105			

-

v

			vi
	Resul	lts	105
	Refer	rences	119
6	Concl	lusions	123
	The re	relationship between colonization level and host growth response is nsistent	124
	There identi	e is little sensitivity in growth responses of host plants to variation in the ity of ectomycorrhizal fungi) 124
	Public	cation bias exists in the ectomycorrhizal literature	125
	Futur	re research directions	125
	Final	conclusion	127
	Refer	rences	128
Appe	ndices	3	130
F	A. for se meta =ull cita manipu	Identity of host plant and fungal species pairings and effect sizes (Ln eedling biomass, shoot height and shoot:root ratio for each study used a-analysis ation of each study used in meta-analysis (excluding studies involving ulations of nutrients)	R) in 130 152
1	B. sizes Full cita phosph	Identity of host plant and fungal species pairings with associated effe s (Ln R) for seedling biomass ation of each study used in the meta-analysis examining the effects of norus addition on the outcome of ectomycorrhizal associations	ect 160 169

, , ,

List of Tables

Table 2.1:Means and standard errors (SE) for the influence of location of experiment on
the magnitude of contamination28
Table 3.1: Analysis of variance for effect of fungicide type (F), concentration (C), and
application frequency (A) on square root percent ectomycorrhizal colonization (%)
and size of Douglas-fir (Pseudotsuga menziesii var. glauca) seedlings after five
months64
Table 3.2: Description of morphological characteristics of ectomycorrhizas observed on
Douglas-fir (Pseudotsuga menziesii var. glauca) seedlings grown in the fungicide
(F) and mesh (M) study65
Table 3.3: Effect of sterilization on growth and ectomycorrhizal (EM) colonization of
Douglas-fir (Pseudotsuga menziesii var. glauca) seedlings. A series of t-tests were
used to determine differences among source (S) and recipient (R) seedlings grown
for each mesh barrier treatment68
Table 3.4: Effect of mesh treatment on growth and ectomycorrhizal (EM) colonization of
Douglas-fir (<i>Pseudotsuga menziesii</i> var. glauca) seedlings. Response differences
between source and recipient seedlings were calculated for each pot. This single
number was used in the ANOVA for each response variable. Statistically significant
mesh treatment effects detected by a Bonferroni multiple comparison test are
designated by different letters (p < 0.05)70
Table 4.1: Analysis of covariance for effects of seed family, percent ectomycorrhizal
fungal colonization of root tips (% colonization) and their interaction on growth
responses of Pinus contorta Dougl. ex Loud. var. latifolia Engelm. seedlings93
Table 4.2: Mean shoot height of full sib families of Pinus contorta Dougl. ex Loud. var.
latifolia Engelm. Seedlings grown for 36 weeks (n=8). British Columbia Ministry of
Forests seed family identification follows in brackets seed family designation94
Table 5.1: Site coordinates and elevation of soil sampling locations
Table 5.2: Fertility characteristics of soils collected from six sites from the Thompson-
Okanagan region of British Columbia. Values are from a composite of 6 samples
per site
Table 5.3: Types of statistical analyses (canonical correspondence analysis [CCA] or

redundancy analysis [RA]) used and significance of explanatory variables tested to

List of Figures

- Figure 2.3: Mean effect size for shoot:root ratio by fungal genus. Means with 95% bootstrapped confidence intervals are shown. Means followed by the same letter are not statistically different (95% bootstrapped confidence intervals overlap).
 Positive values indicate allocation of biomass to shoots was higher than that allocated to roots.

- Figure 3.1: Effect of a) fungicide type and b) application frequency on percent ectomycorrhizal colonization (determined by clearing and staining root tips) of

Figure 3.4: Abundance of morphotypes (*Thelephora terrestris* (T); *Mycelium radicis atrovirens*-type (MRA); *Wilcoxina rehmii* (W); *Cenococcum geophilum* (Cg); *Rhizopogon/Suillus*-type (R/S); and Undifferentiated (Undif), as a percentage of all root tips examined on recipient (R) and source (S) soil seedlings separated by a mesh barrier.

xi

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Co-authorship Statement

Chapter 2 was co-authored with Drs. Laurie Marczak, Melanie Jones and Roy Turkington. I identified, designed and conducted the research, including data collection, analysis and manuscript preparation. Laurie Marczak assisted with data collection, analysis and manuscript preparation and revision. Melanie Jones and Roy Turkington assisted with manuscript revision.

Chapter 3 was co-authored with François Teste, Drs. Melanie Jones, Suzanne Simard and Dan Durall. François Teste and I are equal contributors, with authorship ranking determined by a coin toss. He and I identified, designed and conducted the research, including data collection, analysis and manuscript preparation. Melanie Jones, Suzanne Simard and Dan Durall assisted with manuscript revision. Suzanne Simard also assisted with data analysis and Dan Durall was responsible for the molecular analysis of fungal samples.

Chapter 4 was co-authored by Drs. Melanie Jones and Roy Turkington. I identified, designed and conducted the research, including data collection, analysis and manuscript preparation. Melanie Jones and Roy Turkington assisted with manuscript revision.

Chapter 5 was co-authored by Drs. Melanie Jones and Roy Turkington. I identified, designed and conducted the research, including data collection, analysis and manuscript preparation. Melanie Jones and Roy Turkington assisted with experimental design and manuscript revision.

xiii

1 Introduction

Context

Interdependent species that adapt to changes in each other are described as coevolved. Each partner in the relationship exerts selective pressures on the other, thereby affecting each others' evolution. Coevolution is the process resulting from a close association between the individuals of two, or more, different species (Thompson 1994). Plants and mycorrhizal fungi appear to have had such an interdependent relationship since plants invaded land. The association between plants and mycorrhizal fungi can also be considered symbiotic, defined by de Bary (1878 as cited in Sapp 1994) as "the living together of unlike named organisms".

1

Ectomycorrhizas are characteristic of tree species within the families Pinaceae, Cupressaceae, Fagaceae, Myrtaceae, Betulaceae, and Salicaceae and coevolution between phyto- and mycobionts from several orders including Agaricales, Gautieriales, Hymenogastrales, Phallales, Lycoperdales, Melanogastrales, Sclerodermatales, Aphyllophorales, Pezizales and Elaphomycetales has been occurring for about 200 million years (Kendrick 2000). An ectomycorrhiza is the physical association of roots and ectomycorrhizal fungi, with the fungus forming a compact layer of hyphae around the roots (mantle) connected to a network of hyphae growing in between root cells (Hartig net). Nutrient transfer (carbon to the mycobiont supplied by the host plant and mineral nutrients via the fungus to roots of the phytobiont), occurs at the interface between the Hartig net and root cells (Smith and Read 1997). Historically, ectomycorrhizas have been categorized as mutualistic because each symbiont was deemed to benefit from the exchange of resources (Sapp 1994).

Ectomycorrhizal symbionts vary in taxonomic identity, morphology, function and abundance, and symbionts may evolve to these characteristics in response to each other. In spite of their intimate interactions with their symbiotic partner, plants and fungi also respond to abiotic and biotic factors external to the symbiosis. Fungi forming ectomycorrhizal associations with roots of a host plant will interact with the biotic (e.g. bacteria, microfauna) and abiotic (e.g. soil solution chemistry, water potential) environment of the soil matrix. For example, soil fauna can consume up to 50% of ectomycorrhizal hyphae (Setala 1995) and up to 55 isolates of bacteria are reported to

occur on ectomycorrhizas formed between a single host-fungus combination (Bending et al. 2002). The ecological amplitude of host plants (measured by height and biomass performance) is clearly dependent on soil properties such as nutrient and moisture availability (Burns and Honkala 1990). Thus, ectomycorrhizas exist in a complex biotic and abiotic milieu, and heterogeneity in either the biotic or abiotic portions of that milieu will be ecologically significant to the association.

Within a forest stand the number of ectomycorrhizal fungal species is an order of magnitude higher than that of host species (Bruns 1995). Dickie (2007) recently showed that total ectomycorrhizal fungal richness is a linear function of the number of ectomycorrhizal plant species; one hundred fungal species are predicted to associate with just 2 host plant species. Within a forest stand, both edaphic conditions (Farley and Fitter 1999, James et al. 2003) and the distribution of ectomycorrhizal fungi are spatially heterogeneous (Jonsson et al. 2000, Lilleskov et al. 2004, Izzo et al. 2005). Root systems of individual trees normally experience temporal and spatial variation both in soil properties and in the taxonomic identity and abundance of ectomycorrhizal fungi present in the soil. As a result, individual trees form mycorrhizas with a diverse community of ectomycorrhizal fungi.

In this thesis I consider specific aspects of variation in each of the ectomycorrhizal partners and how this variation may influence the other partner. Hosts can vary in taxonomic identity, and within a species, hosts vary genetically and phenotypically. Similarly, ectomycorrhizal fungal communities vary in species composition, individual fungi vary in anatomy and physiology, and populations of different fungal species vary in their abundance on root systems and in the soil as inoculum.

We do not yet have a clear understanding of how finely-tuned phyto- and mycobionts are to each other. Statistically expressed, this means that we do not have a sense of the proportion of the total variation in a particular aspect of one partner that is explained by variation in the other. In this thesis, I use experimental and meta-analysis approaches to evaluate:

- i. how colonization levels, regardless of ectomycorrhizal fungal taxon, correlate to host growth
- ii. how ectomycorrhizal fungi differentially influence growth of different genera of plant hosts, and

iii. how variation in growth of a single host species correlates to the composition of ectomycorrhizal fungal communities in various soil environments.
 Integral to these questions, and an issue that is central to my thesis, is how to control

for and manipulate ectomycorrhizal fungi on host plants.

In my experiments, I used growth of seedlings as a measure of host response. I did this for two reasons. First, experimenting with adult trees is intractable. Second, while the seedling phase is relatively short in comparison to the entire lifespan of the tree, selection pressures are high at this stage (Harper 1977). It has also been shown that tree species are more strongly adapted to their regeneration niche than to the adult niche (Poorter 2007), thus the conditions influencing seedlings are important for predicting the distribution of adult trees. Because seedlings cannot reproduce, I use growth as my primary measure of performance as is typically done in ectomycorrhizal studies (see those in Chapter 2).

Consideration of variation in both partners of the ectomycorrhizal symbiosis to the growth response of either partner has been investigated over the past few decades of mycorrhizal research. The novelty of this thesis is the evaluation of this variation from multi-specific and coevolutionary perspectives. I use the term multi-specific to denote the situation where a host plant interacts with many species of ectomycorrhizal fungi. Most research has focused on evaluation of host plants inoculated by a single, target fungal species (but see Baxter and Dighton 2001, Kranabetter 2004), yet in nature seedlings are almost always colonized by several ectomycorrhizal fungi concurrently. I consider responses both to different individual fungi and to different communities of fungi. I use the term coevolution in the broad sense meaning "trait-matching" (Bronstein et al. 2006), in contrast to the more restrictive definition meaning reciprocal evolutionary change in interacting species (Thompson 1994). No formal definition of trait-matching exists; however, Gomulkiewicz et al. (2007) illustrate the concept with the example of plant flowering time synchronized to time of pollinator emergence.

Implicit in my thesis is the understanding that host plants and ectomycorrhizal fungi are coevolved. Understanding precisely how variation in either partner of the ectomycorrhizal symbiosis is matched by the other partner allows us to make conclusions about the sensitivity of the growth responses between symbionts. Host plants showing the same growth response to variation in mycobionts, regardless of fungal taxon or extent of colonization, suggests a response of low sensitivity.

Synchronized responses between variation in host plant growth and that present in mycobionts is suggestive of a more sensitive response. Additionally, because each symbiont can also respond independently to its abiotic environment, variation in the abiotic component may alter the association or even supercede the importance of changes in fungi or host plants involved in the symbiosis.

Literature Review

The level of sensitivity between symbiont responses can be viewed as a measure of the generalization or specialization that has occurred as a result of coevolution. For example, if growth responses of a host plant species are independent of variation in taxonomic identity of its ectomycorrhizal fungi, and in nature host plants were found to associate with a very large number different species of ectomycorrhizal fungi, these findings would indicate this particular host plant is a generalist. Conversely, if it were shown that host growth responses were highly sensitive to the identity of the ectomycorrhizal fungus, and that in nature the host plant was found to associate with a narrower range of fungi, this would suggest that host plants are specialized.

Causes of specialization versus generalization

Specialization is a somewhat arbitrary and relative term used to represent the range of resources a species uses. In the context of coevolution of mycorrhizas, this could refer to the number of species with which a particular species interacts. Generalization and specialization are not static categories (Holmes 1977) and evidence has rejected the hypothesis that specialization is a "dead-end". It is clear that switches between each mode over evolutionary time have been frequent (Thompson 1994, Janz et al. 2001, Nosil and Mooers 2005). Additionally, accumulating research suggests that coevolved partners are highly asymmetric in their degree of specialization (Bronstein et al. 2006). For example, in plant-pollinator systems pollinators tend to specialize on a plant species, but a given plant species may be visited by many different species of pollinators (Vázquez and Aizen 2004). Most theories on the causes of specialization invoke the role of variation in the environment or in some attribute of the organisms involved. For example, within trophic groups, specialization is thought to be a response to environmental constancy and the presence of interspecific interactions, most notably competition (Futuyma and Moreno 1988). The degree of specialization across trophic

groups, such as that observed between coevolved organisms is hypothesized to be a result of variation in availability of partners. For example, Stebbins (1970) posited that generalization in plant-pollinator systems is favored when the availability of the most effective pollinator is unpredictable and conversely, specialization is favored when pollinator availability is reliable. Within symbiotic systems, Douglas (1998) reviewed causes of generalization between hosts and symbionts. She suggested that when effectiveness of symbionts varies differentially with environmental conditions, and these conditions are unpredictable relative to host generation time, host specialization should not be favoured. Specialization is also disadvantageous when the abundance of symbionts in free-living condition is low or their spatial distribution is unpredictable.

Specialization versus generalization in ectomycorrhizal associations

The degree of specialization within ectomycorrhizal associations is typically asymmetric between myco- and phytobionts. Host plant species tend to associate with a higher number of fungal species compared to the number of host species with which an ectomycorrhizal fungal species forms associations (Malloch et al. 1980; Borowicz and Juliano 1991). Generally, most ectomycorrhizal fungi form associations with multiple host species (Horton and Bruns 1998, Simard et al. 1997, Massicotte et al. 1999, Kennedy et al. 2003, Nara 2006), with some exceptions: the genera *Rhizopogon* and *Suillus* associate primarily only with *Pseudotsuga menziesii* and *Pinus* spp. There are also several fungal species that are found only in association with *Alnus* spp. (Molina et al. 1992). Hosts appear broadly receptive to different species of ectomycorrhizal fungi, with *Alnus* having a somewhat restricted receptivity. One exception to this pattern is the high specificity observed between plants in the Monotropoideae and their ectomycorrhizal fungi (Bruns et al. 2002, Bidartondo and Bruns 2005).

When considered in a multi-specific context, plant host attributes often structure the composition of ectomycorrhizal fungal communities. For example, the composition of ectomycorrhizal fungal communities varies among clones of *Picea abies* differing in relative growth rate but grown in the same soil (Korkama et al. 2006). In addition, there is a negative relationship between similarity among ectomycorrhizal fungal communities and taxonomic distance among hosts – similarity among ectomycorrhizal fungal communities is higher on hosts of the same genus or family (Ishida et al. 2007). Thus, variation in host characteristics may be an ecologically important gradient which is partitioned by ectomycorrhizal fungal species.

Ecological material for specialization: what variation is present among ectomycorrhizal fungi to which plant hosts could respond?

Ectomycorrhizal fungi vary in their abundance and spatial and temporal distribution within the soil (Jonsson et al. 2000, Lilleskov et al. 2004, Izzo et al. 2005, Koide et al. 2007). Hence, as roots of an individual host forage through soil, they will encounter different species and genotypes of ectomycorrhizal fungi. Fungal portions of the mycorrhiza, such as mantle and extramatrical hyphae, vary morphologically depending on the fungal species involved (Agerer 1987-1998, Goodman et al. 1996). Functional variation among species of ectomycorrhizal fungi has been reported for carbon demand (Bidartondo et al. 2001), nutrient uptake (Read and Perez-Moreno 2003), and pH (Wallander 2002, Yamanaka 2003, Dunabeitia et al. 2004) and drought tolerance (Parke et al. 1983, Boyle and Hellenbrand 1991, Dixon and Hiol-Hiol 1992). Variation among fungal isolates of the same species has also been reported for nutrient uptake (Cairney 1999, Sawyer et al. 2003, Guidot et al. 2005). Overall colonization levels and hyphal biomass of ectomycorrhizal fungal usually decreases in soils having high nitrogen or phosphorus levels (Treseder 2004), but different species of ectomycorrhizal fungi differ in their sensitivity to changes in nitrogen and phosphorus (Jones et al. 1990, Brandrud and Timmermann 1998, Wallenda and Kottke 1998, Nilsson and Wallander 2003, but see Clemmensen et al. 2006).

Overview of Thesis

In Chapter 2 using meta-analysis, I quantitatively assess which causes more variation in host growth responses to ectomycorrhizas: changes in host or fungal taxonomic identity? In addition, I examine whether colonization levels, regardless of fungal identity, correlate to plant host response. In the meta-analysis, the effect of ectomycorrhizas is based on comparisons of non-inoculated to inoculated seedlings. I highlight limitations to this approach in Chapter 2, but I also review and test the major techniques currently available to create ectomycorrhizal controls in Chapter 3, where the results of implementing physical and chemical barriers to ectomycorrhizal controls of seedling growth of

6

variation in ectomycorrhizal colonization levels, relative to genetic variation, in a host species, lodgepole pine (*Pinus contorta* var. *latifolia*). Finally in Chapter 5, 1 experimentally examine the response of Douglas-fir (*Pseudotsuga menziesii* var. *glauca*) to variation in ectomycorrhizal community composition and in soil fertility and moisture characteristics. The relative importance of variation in the abiotic versus symbiotic environment for both host growth and ectomycorrhizal community is separated statistically using a multivariate approach. Both species used in experiments are common, widely distributed trees in British Columbia. I end the thesis with general conclusions and suggested future research in Chapter 6.

7

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2 The mutualism-parasitism continuum in ectomycorrhizas: A quantitative assessment using meta-analysis¹

Introduction

Host plants do not always respond positively to mycorrhizas; thus, defining mycorrhizas as mutualists has been challenged (Francis and Read 1995, Johnson et al. 1997, Brundrett 2004, Jones and Smith 2004). Mycorrhizal fungi benefit from these associations because fungal reproduction is dependent on symbiosis with a plant host (Jones and Smith 2004). Data from large, single studies of arbuscular mycorrhizal associations indicate that host plants have a continuum of positive to negative responses to mycorrhizas (e.g. Klironomos 2003), but data for ectomycorrhizal associations are scattered among many small studies. Hence we have much less understanding of the range of host responses to ectomycorrhizal associations.

The validity of altering the definition of mycorrhizas to remove the requirement for mutualistic responses can be quantitatively evaluated by measuring the mean and variation of host response over many pairwise combinations of host and fungus. The mean indicates whether hosts have a positive, neutral or negative response to mycorrhizas, and variation around the mean indicates whether there is a range of host responses and outcomes are dependent on the context of the association. Variation in host response from positive to negative outcomes would support the continuum concept. The absence of variation around the mean indicates that regardless of the biotic or abiotic environment of the association, host responses are consistent.

Ectomycorrhizal plants, which include many tree species in the northern hemisphere, experience two main kinds of variation in ectomycorrhizal associations: the identity and abundance of fungal species. The manner by which a host responds to variation in mycobiont identity has important evolutionary consequences. If there has been selection for specialization among mycobionts, we predict that growth responses of hosts will depend upon the taxonomic identity of the fungus. Functional variation among taxa of ectomycorrhizal fungi is well documented for characteristics including nutrient uptake (e.g. Abuzinadah and Read 1989, Dighton et al. 1990, Jongbloed et al. 1991, Lilleskov et al. 2002), and drought (Parke et al. 1983, Boyle and Hellenbrand

¹A version of this chapter has been submitted to Ecology as: Karst J, Marczak L, Jones MD, Turkington R. The mutualism-parasitism continuum in ectomycorrhizas: A quantitative assessment using metaanalysis. 1991, Dixon and Hiol-Hiol 1992) and pH tolerance (Wallander 2002, Yamanaka 2003, Dunabeitia et al. 2004).

Each ectomycorrhizal root tip represents a conduit for resource exchange. As such, the extent to which a root system is colonized could also influence response of the phytobiont to mycorrhization. If ectomycorrhizs are mutualisms, we would predict that higher levels of colonization are positively correlated to growth of the host; however, this relationship is not consistent (e.g. Jones et al. 1990, Thompson et al. 1994). As well, Treseder and Allen (2002) predict a unimodal relationship between increasing nutrients in the soil and mycorrhizal biomass, although how this relationship affects host growth is uncertain. Nutrient status of the soil is hypothesized to be a key factor in determining host position on the mutualism-parasitism continuum (Johnson et al. 1997).

The past few decades have generated sufficient individual studies on plant host responses to ectomycorrhizal associations that some generalizations can now be made about the nature of the association (mutualistic to parasitic) across different host-fungus pairings. But, to date there has been no quantitative synthesis that allows us to determine the general direction or magnitude of this phenomenon, or the variation in these responses. Meta-analysis is an increasingly common analytical tool used by ecologists to quantitatively summarize the results of multiple independent studies (e.g. Gurevitch et al. 2000, Treseder 2004, Cardinale et al. 2006, Lortie and Callaway 2006), and is particularly useful when published studies have conflicting results. Meta-analyses have also been used to highlight gaps in the data and to identify common methodological problems or constraints. More importantly, by treating separate empirical studies as independent data points weighted by their replication and precision. meta-analysis allows us to discern general patterns already existing in the data that might not be otherwise evident. We used meta-analysis to determine: 1) how hosts respond to different ectomycorrhizal fungi; 2) if the response is host or fungal specific; 3) if levels of colonization modify the response; 4) if soil nutrient conditions modify host growth responses, and 5) if the perception of mycorrhizas as mutualisms has biased publication of results. We posed two additional questions about the role of experimental conditions in modifying host response: 6) does contamination of controls modify detectable host response to ectomycorrhizas? and 7) does host response change with the length of association between host and fungus (i.e. experiment length)?

Methods

Data collection

We searched ISI Web of Science (1965 – present) using the keyword 'ectomycorrhiza'. Of the 3591 hits, we selected papers written in English reporting either total biomass (g), shoot height (cm) or shoot:root ratio of tree seedlings inoculated with ectomycorrhizal fungi paired with non-inoculated control seedlings. We also checked the "literature cited" section of these papers for additional references. Total biomass is a measure of productivity. Shoot height may be indicative of competitive ability in the seedling establishment phase, where tree seedlings have to compete with rapidly growing herbs. Changes in shoot:root ratio may identify factors that increase seedling survival in nutrient limited environments or that control the potential carbon supply to ectomycorrhizal fungi, the currency mediating the association.

For each study, we recorded the mean, standard deviation and sample size for both inoculated and control seedlings. When necessary, we digitized graphs to obtain this information. When experimental treatments involved several combinations of host species with ectomycorrhizal fungal species or fungal isolates, we treated each combination as a separate study, although not all studies were completely independent. Inclusion of several studies from one paper tends to reduce the overall heterogeneity in effect sizes, but excluding multiple results from a paper could underestimate effect sizes (Gurevitch and Hedges 1999). When results from papers involved inoculation trials in combination with explicit manipulations of the environment, other than nutrient levels (e.g. pH, pathogen abundance, nematode density, salinity, soil moisture, CO₂), we used data from "ambient treatments". For example, we recorded data for inoculated and control seedlings from ambient CO₂ levels while excluding data from treatments featuring elevated CO₂ levels. Among those papers that manipulated fertilizer types and amounts, only the manipulation of inorganic phosphorus levels was reported in a sufficient number of studies to merit further analysis. We converted phosphorus additions to a common unit, mg P kg⁻¹ substrate, and treated it as a continuous predictor with values ranging from 0 to 136 mg kg⁻¹ substrate. We did not include studies where inoculation resulted in no colonization, or where there were no control data (non-inoculated treatments). When repeated measures were taken in a study, we used data from the last sampling period to capture the maximal length of association between host and fungus.

Host and fungal identity were treated as categorical explanatory variables in the meta-analytic model. We recorded the species of host and, when given, ectomycorrhizal fungus (in some cases the fungus was an unknown isolate, or the species epithet was not provided). We then grouped species into genera for both host and fungus, and when testing for differences among genera, we included only those that were represented by at least 10 studies. Duration of association and colonization level (percent of root tips colonized or percent root length colonized) of inoculated seedlings were investigated as possible continuous explanatory variables in the model. When colonization level was given as a range, we used the median value.

Contamination of non-inoculated seedlings reduces differences in colonization levels between control seedlings and inoculated seedlings. Consequently, the perceived response of hosts to ectomycorrhizal inoculation may be reduced as a result of contamination. We determined the magnitude of contamination by calculating the level of colonization on control seedlings relative to that measured on inoculated seedlings according to the proportion:

 $C_C / (C_C + C_{TR})$

where C_{TR} is the percent colonization of target fungi on inoculated seedlings, and C_C is the percent colonization of contaminant fungi on control seedlings.

We quantified the duration of the association by recording the number of weeks each experiment ran. This measure was the only consistent proxy to evaluate the influence of experimental duration on host outcome to ectomycorrhizal associations; however, we recognize that extreme differences in growth rates among host species would render absolute length of time irrelevant. We also examined the relationship between time and the variation among effect sizes. To do so, residuals were calculated using the absolute difference of effect sizes from the cumulative mean and weighted by their sample sizes. Residuals were then regressed against duration of association. We performed identical calculations to examine residuals for effects sizes across phosphorus levels.

Data analysis

The effect size of ectomycorrhizal inoculation for total biomass, shoot height and shoot:root ratio was calculated as the natural log of the response ratio of inoculated to control seedlings. The response ratio (R) is the ratio of the mean outcome in the

experimental (inoculated) group to that of the control (non-inoculated) group (Rosenberg et al. 2000). Only 12% of the studies in our analysis reported measures of variation around means. Consequently we weighted values by their sample size instead (Shurin et al. 2002, Lajeunesse and Forbes 2003, Marczak et al. 2006), and while this increases the probability of Type II errors, it avoids underestimating effect sizes (Gurevitch and Hedges 1999). Effect sizes were considered significantly different than zero when 95% confidence intervals did not overlap zero; explanatory variables were considered significant at $\alpha = 0.05$.

Tests for homogeneity of effect sizes were based on the statistic Q_T , with larger values indicating greater heterogeneity in effect sizes among comparisons (Rosenberg et al. 2000). We assessed the importance of publication bias using a non-parametric rank correlation test (Spearman's rho). A significant correlation between effect size and sample size across studies would indicate bias in the publication of extreme effect sizes. Effect sizes for all analyses were not normally distributed, so we relied on randomization tests (4999 iterations) to assess significance levels.

We first tested the null hypothesis that all effect sizes were equal, and if rejected, we examined the categorical (fungal and host genus identity) and continuous (colonization levels, magnitude of contamination, and duration of association) explanatory variables described above. When categorical predictors were significant, we assessed differences among groups based on 95% bootstrapped confidence intervals. We then regressed effect size against all continuous predictor variables. For any significant explanatory variable, we only report those explaining > 5% of the variation in effect sizes as estimated by Q_M/Q_T , where Q_M is the variation in effect sizes that is explained by a particular model (Rosenberg et al. 2000). All data analyses were performed in MetaWin software version 2.1.4 (Rosenberg et al. 2000).

Results

Seedling response to ectomycorrhizal inoculation

Overall we extracted 459 studies of inoculation response of total biomass from 36 papers, 329 studies of shoot height from 24 papers, and 235 studies of shoot:root ratio from 20 papers (Appendix A). Across all growth traits, we assessed the outcome of 21 host genera inoculated with 31 fungal genera; however, these inoculations were not represented in all possible combinations. The mean age of seedlings at the end of experiments was 23 weeks (range = 10 to 104 weeks).

On average, seedlings increased in total biomass and shoot height, but did not change in shoot:root biomass allocation when inoculated with ectomycorrhizal fungi (mean cumulative effect sizes = 0.208, 0.113, -0.0174, respectively; Fig. 2.1). However, there was significant heterogeneity in the data ($Q_T = 10152$, df = 458; $Q_T = 95389$, df = 328; $Q_T = 705$, df = 234, respectively; all p < 0.001) to indicate that further structure existed.

The identity of the host genus was significant in explaining variation in effect sizes for both total biomass (p = 0.028, df = 4, 409, $Q_M/Q_T = 0.18$) and shoot:root ratio (p < 0.001, df = 3, 191, $Q_M/Q_T = 0.22$). In particular, inoculated seedlings of the genera *Quercus, Pseudotsuga* and *Eucalyptus* increased in total biomass more than those of *Pinus* and *Picea* (Fig. 2.2a), while *Picea* seedlings allocated more biomass to shoots than seedlings of *Quercus, Pseudotsuga* and *Pinus* and *Pinus* when inoculated (Fig. 2.2b). Although there was a positive relationship between total biomass and shoot height (p < 0.001, df = 1, 567, $r^2 = 0.37$), neither categorical nor continuous predictors explained variation in effect sizes of shoot height. Fungal genus influenced allocation of biomass to shoots versus roots (p < 0.001, df = 5, 199, $Q_M/Q_T = 0.26$), but did not explain variation in effect sizes for total biomass or shoot height. Seedlings inoculated with fungi from the genus *Scleroderma* allocated more biomass to roots than that observed for other genera (Fig. 2.3).

Level of colonization of inoculated seedlings, ranging from 0.5 to 98%, was not important in explaining variation in effect sizes for total biomass (p = 0.043 df = 1, 349, $Q_M/Q_T = 0.03$), shoot height (p = 0.30, df = 1, 220) or shoot:root ratio (p = 0.03, df = 1, 211, $Q_M/Q_T = 0.03$) (note that although level of colonization was significant, $Q_M/Q_T <$ 0.05 for both total biomass and shoot:root ratio [see Methods])(Fig. 2.4). Heterogeneity in effect sizes was unrelated to the magnitude of contamination for total biomass (p =0.20, df = 1, 324), shoot height (p = 0.48, df = 1, 211) and shoot:root ratio (p = 0.063, df = 1, 197)(Fig. 2.5). Contamination levels were highest in those experiments performed in nurseries and in the field, and lowest in those in growth chambers (p < 0.001, $F_{3,416} =$ 76.9) (Table 2.1).

The average length of experiments was 21 weeks (range = 8 to 104 weeks), slightly less than the average age of seedlings used in experiments. Duration of

association between host plant and fungus did not explain variation in effect sizes for total biomass (p = 0.86, df = 1, 457) or shoot height (p = 0.97, df = 1, 327) (Fig.2.6a, b). On average, seedlings allocated more biomass to roots than shoots, with increasing duration of association (p < 0.001, df = 1, 233, $Q_M/Q_T = 0.06$) (Fig.2.6c). The magnitude of contamination was positively related to duration of experiment (p < 0.001, df = 1, 418, $r^2 = 0.14$) (Fig. 2.7). Variability among effect sizes decreased with duration of association for both total biomass (p < 0.001, df = 1, 457, $r^2 = 0.12$) and shoot height (p < 0.001, df = 1, 327, $r^2 = 0.25$), but was unrelated to duration for shoot:root ratio (p = 0.033, df = 1, 233 (Fig. 2.8). That is, longer running experiments had effect sizes more similar to the cumulative mean. In particular, for measures of total biomass and shoot height, variation among effect sizes declined to nearly zero (effect sizes converged on the cumulative mean) at approximately 30 weeks (Fig. 2.8). The level of contamination for control seedlings was predicted to increase by 84% for this time period (Fig. 2.7).

There was evidence for significant publication bias in data for total biomass; Spearman's rho for the correlation between effect size and sample size was -0.28 (p < 0.001), indicating that there was an over-representation of studies with positive effect sizes at low replication. There was no evidence of publication bias in data for shoot height (Rs = 0.054, p = 0.33) or shoot:root ratio (Rs = -0.105, p = 0.109).

Seedling response to ectomycorrhizal inoculation and phosphorus addition

We analyzed 234 studies (6 host and 15 fungal genera) from 10 papers for changes in total biomass of seedlings inoculated with ectomycorrhizal fungi under phosphorus (P) additions ranging from 0 to 136 mg P kg⁻¹ (Appendix B). The cumulative effect size was positive (0.0769), but the 95% confidence intervals overlapped zero, indicating there was no average change in total biomass of seedlings inoculated with ectomycorrhizal fungi subjected to manipulated phosphorus levels when all levels of substrate P, including no additions, were included. There was underlying structure in the data (p < 0.001, df = 232, Q_T = 1236); however, of the explanatory variables, only host genus explained a significant amount of variation in effect size (p < 0.001, df = 3, 24, Q_M/Q_T = 0.31). Specifically, seedlings of the genera *Eucalyptus, Pinus* and *Larix* had relatively less biomass than those of *Picea* when inoculated, regardless of phosphorus level. There was a negative relationship between the residuals of effect size and amount of phosphorus added, indicating that variation among effect sizes decreased

with levels of phosphorous (Fig. 2.9). Publication bias was also evident in these data (Rs = 0.31, p < 0.001), i.e. there were a lack of studies with positive effect sizes at low sample sizes.

Discussion

Seedling response to ectomycorrhizal inoculation

Across the studies included in our analysis, it appears that on average, hosts respond positively to ectomycorrhizal inoculation; both total biomass and shoot height are greater in inoculated seedlings. However, when all available studies are considered and weighted by their sample sizes, the evidence in support of positive growth outcomes through ectomycorrhizal inoculation is considerably weaker than many single studies suggest. Additionally, factors unrelated to inoculation *per se* have influenced interpretation of host responses to ectomycorrhizal inoculation, namely publication bias towards large positive effects, the duration of experiments and artificial pairing of host and fungal symbionts. The presence of these factors effectively reduces and distorts the spectrum on which host responses to ectomycorrhizal inoculation are evaluated.

The spectrum is reduced: Publication bias inflates measures of effect sizes

Under a model of no publication bias, estimated effects should be distributed around the unknown true effect, with the spread of the effects representing their variances. As sample sizes increase, the spread of the distribution should decrease resulting in a funnel shaped distribution of effect sizes. Publication bias against studies with negative results will produce a negative correlation between sample size and the magnitude of effect (Begg and Mazumdar 1994) and this inflates the magnitude of overall effect sizes calculated in a meta-analysis. We detected publication bias for measures of total biomass but not for shoot:root ratio or shoot height responses to inoculation. Shoot height increases with ectomycorrhizal inoculation, but it is independent of the identity of host and fungal genus, colonization levels and duration of association. Because the lower limit of the cumulative effect on total biomass is well above zero, there may indeed be a change in seedling biomass upon inoculation.

Among the papers used in this meta-analysis, Dixon et al. (1984) and Hung and Molina (1986) explicitly reported that data had been omitted due to non-significant differences between control and inoculated seedlings. It is unlikely that these particular omissions alone caused publication bias in our dataset, but they may be symptomatic of bias in the selection of data reported in published papers. At the other extreme, although they did not affect the results of the meta-analysis, host-fungus pairings extracted from Burgess et al. ([1994]; identified as outliers in Fig. 2.4a and b) were irregularities in our dataset, reporting highly positive responses to ectomycorrhizal inoculation by various strains of *Pisolithus*. Due to the tradition of categorizing mycorrhizal fungi as mutualists, such extreme positive results are unlikely to go unpublished. Negative results in mycorrhizal research may be more likely to go unpublished compared to other fields in which no *a priori* expectation exists of the magnitude or direction of the outcome of species interactions.

From a silvicultural perspective, interest primarily in positive growth responses to ectomycorrhizal inoculation may be warranted, but it has hindered our ability to evaluate the full spectrum of responses. Moreover, negative responses are not aberrant outcomes when we consider that hosts are evolutionarily compatible with both mutualistic and parasitic modes of symbioses. For example, the pathways and physiological machinery involved in arbuscular mycorrhizal development are conserved among symbiosis types, including those that are parasitic (Mathesius 2003, Paszkowski 2006). As arbuscular mycorrhizas are considered to be ancestral to all other mycorrhizal types (Wang and Qiu 2006), there is no biological basis to presume that responses to ectomycorrhizal inoculation should be solely positive. Changing our definition of ectomycorrhizas (Johnson et al. 1997, Brundrett 2004, Jones and Smith 2004) will become necessary as evidence accumulates on their evolutionary origins (Hibbett et al. 2000) and on variation in the outcomes of ectomycorrhizal associations (Sachs and Simms 2006). This will also broaden the view of their ecological role.

The spectrum is distorted: Factors that covary with time may cause spurious effects

Not surprisingly, levels of contamination were highest on seedlings grown in either the field or in nurseries, although most of the experiments from which the data were extracted were done in greenhouses. The magnitude of contamination was positively correlated to the duration of the experiment (Fig. 2.7). The problem of increased contamination could be alleviated if measurements were made earlier. This approach, however, is not recommended. Variation among effect sizes for both total biomass and shoot height significantly declined with the duration of the experiment. Factors such as maternal effects (Weiner et al. 1997), substrate differences, temperature and light conditions may all obfuscate the role of ectomycorrhizas in influencing seedling growth in shorter experiments. Seedlings also vary in the time it takes to develop ectomycorrhizal associations. On roots of *Eucalyptus globulus*, ectomycorrhizas formed by *Pisolithus tinctorius* and *Paxillus involutus* developed in 4 days when in direct contact (Horan et al. 1988). Conversely, colonization was not observed until 4 weeks on roots of *Eucalyptus coccifera* inoculated with *Thelephora terrestris* or *Laccaria bicolor* (Jones et al. 1990). Early measurements (prior to 30 weeks) may preclude detection of a mycorrhizal "signal" as the strength of this signal is likely to be weak compared to other factors influencing seedling growth.

The spectrum is distorted: Effects of crossing hosts and ectomycorrhizal fungi not known to co-occur remain poorly understood

Often inoculation trials are performed using artificial pairings of host and fungus (e.g. Chen et al. 2006) and rely on ectomycorrhizal fungi that are amenable to experimentation. Choosing fungi based upon characteristics that render them easy to work with in laboratory conditions may also have selected for uniformity in other traits. Until techniques become available to represent the diversity of ectomycorrhizal fungi observed in natural systems, interpretations of host response to ectomycorrhizal inoculation will be limited. Moreover, the geographic origin of fungi and hosts used in trials may affect inoculation responses in unpredictable ways. Similar to plants, some but not all species of ectomycorrhizal fungi are cosmopolitan in their distribution. One corollary to this pattern is that not all host and ectomycorrhizal fungal species will interact and that at any given location a host species will encounter a subset of the global pool of ectomycorrhizal fungi. This geographic variation in plant-mycorrhizal community structure has likely resulted in a mosaic of coevolution between plants and mycorrhizal fungi (Thompson 2005), but we still have very few data on the consequences of this mosaic on mycorrhizal inoculation responses (but see Hoeksema and Thompson 2007, Klironomos 2003, Monzon and Azcon 1996, Sylvia et al. 2003). This lack of knowledge of the range of host responses to exotic symbionts also carries over to conservation research; the ecological consequences of mycorrhizal fungal species' introductions are unpredictable (Schwartz et al. 2006).

In our meta-analysis, we could not categorize each host/fungus pairing as "local" or "foreign", as such information was either unavailable, or it was not clear at what scale we should consider a host and fungal species to co-occur (e.g. within a forest stand, region or country). Studies on arbuscular mycorrhizas have shown that crossing local plants and fungi produces a greater range in responses measured by plant biomass than for crosses involving foreign symbionts (Klironomos 2003). Conversely, variation in plant growth was independent of fungal isolates when different geographic populations of 3 host plant species were crossed with 4 populations of the ectomycorrhizal fungus *Rhizopogon occidentalis* (Hoeksema and Thompson 2007). Origin of fungal isolate was also not found to be important in modifying growth of *Eucalyptus globulus* (Thompson et al. 1994). These findings are consistent with our results that variation in fungal identity bears little consequence to variation in shoot height or seedling biomass.

The role of variation in fungal properties in host response to ectomycorrhizal inoculation

The magnitude of effect size for seedling biomass and shoot height for the most part did not covary with variables related to ectomycorrhizal fungi, namely colonization level and genus identity. Our results suggest that colonization levels are not an ecologically useful measure of host response to ectomycorrhizal inoculation (Fig. 2.4). Moreover, we suggest that focus on colonization levels has distracted investigation from other possible mechanisms that may be more critical determinants of host response to ectomycorrhizas.

Characteristics of fungi such as those associated with the development and differentiation of extramatrical mycelium may correlate better to the magnitude of host response as they represent a potential increase to the absorbing surface area of roots (Jones et al. 1990, Agerer 2001). This type of measurement relies on physical mechanisms underlying host benefits of being mycorrhizal. Our results suggest that these benefits may be equally expressed through colonization levels ranging from 0.5% to 98%. It is unlikely that similar resource transfers could occur at low (0.5%) and high (98%) levels of colonization that result in a comparable cumulative positive effect to inoculation among seedlings. Nevertheless, there are many examples of growth response to very low levels of colonization. It is possible that the presence of growth promoting hormones may be responsible for increases in seedling biomass and height

23
with inoculation. It is well established that plant-associated microorganisms are capable of synthesizing phytohormones that are used for communication between a host and its microflora (Tsavkelova et al. 2006). For example, small amounts of auxins increase shoot elongation and dry weight of wheat inoculated with rhizobacteria (Khalid et al. 2004). Auxins, which are involved in a wide variety of physiological responses that influence growth of woody plants (Kozlowski and Pallardy 1997), are also produced by ectomycorrhizal fungi (Barker and Tagu 2000). Though some research has been conducted on the effects of auxins on ectomycorrhizal development (e.g. Niemi et al. 2002, Rincon et al. 2003), its role at the level of the host has been neglected. Given that positive effects of fungal inoculation are often observed at low levels of colonization for both seedling biomass and shoot height, we suggest that chemical mechanisms may often underlie host responses to ectomycorrhizal inoculation.

We determined that on average, seedlings across multiple host species had more biomass when inoculated with any ectomycorrhizal fungus, regardless of the identity of the fungal associate. This supports findings from research on non-symbiotic interactions; for example, host plants are often generalists with response to different pollinators (Zamora 2000). This result conforms to theory predicting the outcome of multi-specific plant-pollinator systems, i.e. interactions involving many species tend to result in the evolution of generalists because reciprocal specialization is unlikely (Howe 1984). In forest stands, the number of species of ectomycorrhizal hosts is typically an order of magnitude less than that of its fungal symbionts (Bruns 1995). Reciprocal specialization is unlikely in this system due to the changing composition of ectomycorrhizal fungi both spatially (Izzo et al. 2005, Genney et al. 2006, Toljander et al. 2006) and temporally (Izzo et al. 2005, Koide et al. 2007). Thus, hosts may adapt to "landscapes" (*sensu* Howe 1984) of ectomycorrhizal fungi where fungal species diversity diffuses selection from one source.

Nonetheless, we cannot definitively conclude that the identity of the fungus has no role in modifying host response for two reasons. First, although it is evident that inoculation with most fungal genera results in increased biomass allocation to shoots, those fungi from the genus *Scleroderma* are an exception. Seedling allocation to roots increased by almost three times when inoculated by fungi from this particular genus. Diédhiou et al. (2004) concluded that *Scleroderma dictyosporum* has a higher requirement for glucose relative to thelephoroid species, perhaps related to construction costs of its network-like mycelium (Newton 1991). Plants growing in nutrient-depleted soils allocate more biomass to roots than shoots (Gedroc et al. 1996). If association with fungi from this taxon is perceived by the host as equivalent to growing in nutrient-depleted soils this would explain allocation patterns. Second, there appears to be a difference between those fungi that contaminate seedlings and those used to inoculate seedlings. Because there was no effect of magnitude of contaminant fungi are likely neutral in their effects. Species of contaminant fungi were for the most part unidentified but included those from the genera *Thelephora* and *Cenococcum*. These fungi are common, widespread, and widely dispersed via airborne spores; whether such characteristics of fungi and magnitude of host response covary should be further studied.

Although a positive growth response was expressed by the most common host genera in our analysis, hosts differed in the magnitude of response. In particular, Quercus seedling biomass and biomass allocation to roots ranked highest, and Picea lowest, with ectomycorrhizal inoculation. When phosphorus conditions were manipulated (i.e. the subset of studies that explicitly altered phosphorus levels), Picea ranked highest in increased seedling biomass with inoculation. We cannot say whether these outcomes are taxon or trait-specific, due to the relatively few genera included in the analysis. For example, mycorrhizal dependency has been hypothesized to relate to various root morphological traits such as root thickness, surface area and incidence of root hairs (Brundrett 2002). In addition, dependency on arbuscular mycorrhizas seems to be higher for hosts that have small seeds or have had seed reserves experimentally reduced (Janos 1980, Allsop and Stock 1995, Sigueira et al. 1998, Zangaro et al. 2003). Our results contrast with those observed for arbuscular hosts; seeds of Quercus are generally larger than those of *Picea*, yet are more responsive to ectomycorrhizal inoculation. Root morphology is sensitive to abiotic conditions of the soil, thus its role in determining mycorrhizal dependency is unclear. Going beyond taxonomic correlations with inoculation responses, and identifying those specific host traits that correlate to specific outcomes will enrich our understanding of ectomycorrhizal interactions. In particular, further research within a broad framework, such as that which has developed for leaf traits (Wright et al. 2004), would be especially fruitful to understand trade-offs among plant traits and mycorrhizal responsiveness.

Mycorrhizal associations are predicted to confer most benefit to the host plant in conditions of low nutrients. As such, we would expect a negative relationship between the magnitude of effect size and increasing phosphorus addition but our results do not support this prediction. The range of host responses appears to be environment specific; variation among effect sizes was high for studies with low phosphorus additions. Bougher et al. (1990) have indicated there is an interaction between the effects of fungal taxa and P additions. Specifically, at low P additions (2-12 mg P kg⁻¹ soil), differences among Desoclea maculate, Laccaria laccata and Pisolithus tinctorius in host dry mass production are apparent, but these differences are not apparent at greater than 16 mg P kg⁻¹ soil. A similar interaction was reported for seedlings colonized by Laccaria bicolor or Thelephora terrestris along a P gradient (Jones et al. 1990). Our meta-analysis could not detect such an interaction because not all host/fungi combinations were present across the range of P additions. Whether the response to ectomycorrhizal fungi is taxon- or environment-specific (or both) warrants further study as it has implications for the strategies plants may use to maintain ectomycorrhizal associations that confer benefits to the host (Hoeksema and Kummel 2003).

Conclusions and future directions

Publication bias clouds our ability to conclusively determine general principles of host response to ectomycorrhizal inoculation. With recognition that mycorrhizal associations could fall on a continuum of possible outcomes and that this range of responses is ecologically significant, the tendency not to report negative results must be reduced. Our criticism of methods employed to test host response to ectomycorrhizal inoculation is not one of mycorrhizal research in general, but instead reveals the limits of some of the methods used. In particular, there is tension between assessing the response too early when the mycorrhizal signal can be masked, and running the experiment too long and increasing the likelihood of contamination. We see no easy remedy to this problem. The use of mycorrhizal defective mutants, such as those used by Cavagnora et al. (2004) may offer a way to circumvent the issues highlighted with current methods. Even so, the reliance on comparisons between mycorrhizal and non-mycorrhizal phenotypes do not occur, except in very young seedlings. Finally, as recommended in non-symbiotic systems (e.g. Stanton 2003, Strauss and

Irwin 2004), a departure from focusing on pairwise species interactions and moving to consideration of host responses to variation in the composition of ectomycorrhizal fungal communities may encourage a broader perspective on the ecological and evolutionary consequences of ectomycorrhizal associations.

Table 2.1:Means and standard errors (SE) for the influence of location of experiment on the magnitude of contamination.

Source	n	Mean*	SE
Field	43	0.33 ^a	0.0251
Nursery	28	0.43 ^a	0.0311
Greenhouse	243	0.10 ^b	0.0105
Growth chamber	106	0.0026 ^c	0.0160

* Means followed by the same letter are not statistically different (Tukey-Kramer HSD, α = 0.05).

Figure 2.1: Cumulative mean effect sizes for total biomass, shoot height and shoot:root ratio. Error bars are 95% bootstrapped confidence intervals.



Figure 2.2: Mean effect size for a) total biomass and b) shoot:root ratio by host genus. Means with 95% bootstrapped confidence intervals are shown. Means followed by the same letter are not statistically different (95% bootstrapped confidence intervals overlap). For b), positive values indicate allocation of biomass to shoots was higher than allocation to roots.



Figure 2.3: Mean effect size for shoot:root ratio by fungal genus. Means with 95% bootstrapped confidence intervals are shown. Means followed by the same letter are not statistically different (95% bootstrapped confidence intervals overlap). Positive values indicate allocation of biomass to shoots was higher than that allocated to roots.



Figure 2.4: Relationship between mean effect sizes and level of ectomycorrhizal fungal colonization of inoculated seedlings for a) total biomass, b) shoot height and c) shoot:root ratio. Outliers (those data points falling above the 97th percentile of the distribution) are indicated as triangles; these were retained in the analysis.





c)



seedlings (%)

Figure 2.5: Relationship between mean effect sizes and magnitude of contamination for a) total biomass, b) shoot height and c) shoot:root ratio.

a)



Magnitude of contamination





Figure 2.6: Relationship between effect sizes and duration of association of ectomycorrhizal fungus and host for a) total biomass, b) shoot height and c) shoot:root ratio. Q_M/Q_T is the amount of total heterogeneity in the data due to variation in effect sizes explained by the model. Statistics are reported for significant models only.





Figure 2.7: Relationship between magnitude of contamination and duration of association of ectomycorrhizal fungus and host.



Figure 2.8: Relationship between effect size residuals and duration of association of ectomycorrhizal fungus and host for a) total biomass, b) shoot height and c) shoot:root ratio. Statistics are reported for significant models only.





Figure 2.9: Relationship between effect size residuals for total biomass and amount of phosphorus added.



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3 Methods to control ectomycorrhizal colonization: Effectiveness of chemical and physical barriers¹

Introduction

In mycorrhizal research, evaluation of mycorrhizal effects on plant performance often requires comparisons between mycorrhizal and non-mycorrhizal plants. Creating effective, yet feasible methods to control mycorrhizal colonization in the field has become of utmost importance as there has been a recent demand to increase the ecological relevance of mycorrhizal research (Read 2002). This requires moving away from laboratory based work to experiments conducted in natural environments.

Currently, most studies have obtained non-mycorrhizal plants by employing one of three methods: substrate sterilization (via autoclaving, steam sterilization or gamma irradiation), the creation of mutant plants unable to form mycorrhizas, or the use of fungicides applied to soil around plant roots. Sterilizing soil can result in substantial changes in its chemical and physical properties (Lenis et al. 1991, Chambers and Attiwill 1994, Sheremata et al. 1997, Shaw et al. 1999); moreover, its application in the field is futile because contamination is certain. The development of plants that lack the ability to form mycorrhizas has been limited to a few plant species associating with arbuscular mycorrhizal fungi (AMF) (Marsh and Schultze 2001). More research is also required to determine whether the functioning of mutants is otherwise identical to non-mutant plants (Kahiluoto et al. 2000). Of the fungicides, benomyl has been used effectively to reduce arbuscular mycorrhizal colonization of plants in the field by as much as 80% (Hartnett and Wilson 1999, Wilson et al. 2001, Callaway et al. 2004, Dhillion and Gardsjord 2004). Benomyl, no longer licensed for use in some countries and relatively ineffective against basidiomycetes, is however, not an option to control most ectomycorrhizal fungi. Fungicides have generally not been employed in ectomycorrhizal systems (but see Page-Dumroese et al. 1996, Manninen et al. 1998). Ectomycorrhizal fungal communities are more taxonomically diverse than arbuscular mycorrhizal fungal communities, thus requiring a broad spectrum fungicide to adequately decrease ectomycorrhizal colonization. Of the three methods currently employed to control mycorrhization, the use of fungicides appears the most feasible for field research in

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Two fungicides, Topas® and Senator®, have been suggested by greenhouse managers for control of ectomycorrhizal hyphal growth. Propiconazole, the active ingredient in Topas® (25% a.i.), interferes with ergosterol biosynthesis, which is critical to the formation of fungal cell membranes (Kendrick 2000). The lack of normal sterol production slows or stops the growth of the fungus, effectively preventing further infection and/or invasion of host tissues (Kendrick 2000). Propiconazole incorporated into agar media at 1 ppm or higher inhibited growth of many ectomycorrhizal fungal strains (Zambonelli and lotti 2001, Laatikainen and Heinonen-Tanski 2002). Colonization of *Pinus sylvestris* roots by ectomycorrhizal fungi decreased by approximately 20%, with some morphotypes affected more than others, when propiconazole was applied for two consecutive years in the field at a rate of 250g l⁻¹ every two weeks (Manninen et al. 1998). Thiophanate-methyl, the active ingredient in Senator® (70% a.i.), interferes with the functioning of microtubules, so that treated cells cannot divide. Thiophanate-methyl targets the cells of ascomycetes (Kendrick 2000), but to our knowledge has not been used to control ectomycorrhizal fungi.

Studies of common mycorrhizal networks (CMNs) in plant communities form a unique subset of studies on mycorrhizal effectiveness (Simard and Durall 2004). They require comparisons between plants that are linked with those that are not linked by a CMN (Simard et al. 1997, Booth 2004). In these studies, control plants may be mycorrhizal, but hyphal linkages between plants must be absent. While non-mycorrhizal or non-linked controls are easily established in the laboratory using substrate sterilization techniques, this is more problematic in the field where seedlings are grown in native soils. Mesh barriers constructed of either steel or nylon have been used to prevent formation of ectomycorrhizal connections between plants (e.g. Francis and Read 1984, Schüepp et al. 1992, Booth 2004, Kranabetter 2005), or provide root-free compartments where mycorrhizal hyphae can explore and grow. To restrict penetration of roots and hyphae, mesh with pores 1 µm or smaller has been used (Robinson and Fitter 1999, Johnson et al. 2001, Zabinski et al. 2002, Cardoso et al. 2004), however, given that hyphal width varies (from 1.5 to 9 µm), a mesh with pore sizes larger than 1 µm may restrict penetration of some mycorrhizal fungal species but not others. Consequently, the mesh pore size could alter the ectomycorrhizal fungal community composition. Ectomycorrhizal fungi vary in their ability to absorb and transport nutrients

and water (Simard and Durall 2004); therefore, any alteration of the community may affect transport within the CMN.

The objective of this study was to examine the effectiveness of chemical and physical methods at controlling formation of ectomycorrhizas on Douglas-fir seedlings. We tested the effectiveness of the fungicides, Topas® and Senator®, at various concentrations and application frequencies. We predicted that both fungicides would reduce ectomycorrhizal colonization, however, we expected that colonization of ascomycete fungi would be particularly reduced with the application of Senator®. Thus, the composition of the ectomycorrhizal fungal community would be altered compared to untreated controls. In addition, we tested the effectiveness of nylon mesh with various pore sizes at preventing hyphal penetration, and its effects on ectomycorrhizal community composition of neighboring seedlings. We predicted that percent colonization and similarity of ectomycorrhizal communities between seedlings on opposite sides of the mesh barrier would decrease with decreasing mesh pore size.

Materials and methods

Field soil collection

On August 27-28 of 2003, we collected 600 L of soil from the Black Pines variable retention cut (also known as a green-tree retention cut where some trees are not harvested) and adjacent forest approximately 50 km northwest of Kamloops, British Columbia (120°26'W, 50°42'N). The Black Pines variable retention cut occurs in the dry cool subzone of the Interior Douglas-fir (IDFdk) biogeoclimatic zone (Meidinger and Pojar 1991). It has an elevation of 1180 meters above sea level (masl) and loamy Gray Luvisolic soil (Krzic et al. 2004). The plant community is dominated by residual Douglas-fir *Pseudotsuga menziesii* var. *glauca* (Beissn.) Franco) and subalpine fir (*Abies lasiocarpa* (Hook.) Nutt.) trees and advanced regeneration (saplings), with shrub and herbaceous layers dominated by soopolallie (*Sherpherdia canadensis* (L.) Nutt.) and pinegrass (*Calamagrostis rubescens* Buckley), respectively.

We collected forest floor (30 cm x 30 cm) together with mineral soil (to 40 cm depth) from 15 random locations in 1 ha of the Black Pines forest. This soil was used for both experiments. The fifteen samples were combined and thoroughly mixed, then stored at room temperature until needed (see below).

Plant material

Interior Douglas-fir seedlings (seedlot #48520, British Columbia Ministry of Forest Tree Seed Center, Surrey, British Columbia, Canada) were grown at the University of British Columbia (Vancouver, Canada) greenhouse (temperature minimum 20°C, temperature maximum 24°C, average humidity 60%). Seeds were moist-stratified at 4°C for 21 days. Seeds were then sterilized in constantly mixed 3% H₂O₂ for two hours. Styroblock™ 512B travs (Beaver Plastics Ltd., Edmonton, Alberta, Canada) were cut in half horizontally and filled with autoclaved peat and sawdust (3:1, v:v). Three seeds were sown in each cavity and 4 weeks later were thinned to one seedling per cavity. The trays were placed under a mist tent for 12 days and then moved to a greenhouse bench for the remaining time. To improve seedling vigor and discourage mycorrhizal colonization, we applied 1.9 g L¹ water soluble Rose Plant Food (Miracle-Gro, Scotts) Canada Ltd., Mississauga, Ontario, Canada) (18:24:16 N:P:K) once per week for 4 weeks following germination. Afterwards, we fertilized with 4 ml L⁻¹ Peter's solution (Plant-Prod ®, Plant Products Co. Ltd., Brampton, Ontario, Canada) (20:20:20 N:P:K) once per week until the seedlings were transplanted into the treatment pots. For the duration of the two concurrent experiments (five months), natural daylight in the greenhouse was supplemented by 400 W high pressure sodium lamps to maintain an 18 hour photoperiod.

Fungicide experiment

Experimental design and treatments

On September 16, 2003, 14-week-old seedlings were transplanted into 3.2 L pots (175 mm x 180 mm) (Listo Products Ltd., Surrey, British Columbia, Canada) with drainage holes. The pots contained field soil mixed with perlite (3:1, v:v). A 3 x 3 x 3 factorial set of treatments with a separate control group was replicated 10 times in a completely randomized design, where the factors were fungicide type, rate of application, and frequency of application (270 seedlings + 10 controls = 280 total). The three fungicide types were Senator®, Topas®, and a combination of the two fungicides (both from Engage Agro Corporation, Guelph, Ontario, Canada). The three rates of application were: 0.5, 1 or 1.5 ml L⁻¹ of Senator®; and 0.5, 1 or 1.5 g L⁻¹ of Topas®. Recommended concentrations of Senator® and Topas® are 0.5 ml L⁻¹ and 0.5 g L⁻¹, respectively. To our knowledge this is the only study assessing the effect of these

fungicides on ectomycorrhizal fungi thus, we decided as a starting point to use the above rates. The fungicide was mixed with water and added at a constant volume of 600 mL pot⁻¹; therefore, seedlings that were treated with Senator® and Topas® in combination received 300 mL of each fungicide-water mixture. The three frequencies of application were: once at the beginning of the experiment, every two months (three applications total), or every month (five applications in total). For each fungicide application, we drenched the soil around the seedlings, avoiding contact with foliage. Additionally, ten control seedlings were grown in pots to which only water was applied. On September 30, 2003, initial height was recorded for all seedlings. The seedlings were watered as necessary and their locations re-randomized monthly.

Seedling measurements

On February 10, 2004, the height of all surviving seedlings was measured. Shoots were removed, dried at 65° C for 48 hours and weighed. The roots and intact soil of up to seven replicates were stored at 4°C for 45 days before processing. Each root system was soaked in tap water, rinsed clean of soil, and cut into 1 cm fragments. The sample was then divided approximately in half, and one half was dried and weighed. We used this measurement to estimate dry weight of the remaining roots, which were weighed wet, and then cleared and stained following the methodology of Phillips and Hayman (1970) to assess percent ectomycorrhizal colonization. For a given seedling, percent ectomycorrhizal colonization was calculated as:

Percent ectomycorrhizal colonization = (Active ectomycorrhizal root tips / Active ectomycorrhizal root tips + Active nonectomycorrhizal root tips) x 100

A root tip surrounded by a mantle was classified as mycorrhizal.

In addition to assessing percent colonization, we recorded the abundance and richness of ectomycorrhizal morphotypes in each of the treatments. Root systems of the remaining three replicates from each of the ten treatments were carefully washed under running tap water and then cut into approximately 1 cm pieces. All root fragments were placed in a baking dish containing water and thoroughly mixed. We randomly subsampled and counted up to 100 ectomycorrhizas, or 100 non-ectomycorrhizal root

tips, whichever came first. Generally, ectomycorrhizal tips were turgid and smooth, had emanating hyphae or rhizomorphs (Harvey et al. 1976), and had a Hartig net. A root tip that was dark and wrinkled, or was somewhat hollow and fragmented under minimal pressure was classified as 'dead'. Gross morphology of ectomycorrhizal roots and rhizomorphs were described using a stereomicroscope, while the mantle, cystidia, and emanating hyphae were described using a compound microscope under 400x or 1000x magnification. When possible, mantles were peeled by separating the fungal tissue from the root with forceps and micro-scalpels, and then described. Morphological descriptions were made with reference to Agerer (1985–1998), Ingleby et al. (1990), Goodman et al. (1996), and Hagerman et al. (2001). Morphotyped roots were then dried and weighed.

Mesh barrier experiment Experimental design and treatments

To test the effect of pore size on penetration by ectomycorrhizal fungi, we grew seedlings in 3.2 L pots divided vertically by nylon mesh barriers with different pore sizes. The pore sizes of the four meshes were: 0.2 µm (catalogue number 25007, polyamide type 250 membrane, Sartorius AG, Goettingen, Germany), 1 um (catalogue number 03-1/1 Nitex, Sefar America Inc., Depew, NY, USA), 20 µm (catalogue number 03-20/14 Nitex), and 500 µm (catalogue number 06-500/47 Nitex). Control pots were divided by an impermeable acetate sheet to test for ectomycorrhizal contamination through insufficient sterilization, or water and airborne ectomycorrhizal propagules. Each of the five barrier treatments was replicated 12 times in a completely randomized design. The pots were first sterilized in a 20% bleach solution for at least one hour, cut in half vertically, and then reassembled using non-toxic adhesive silicone sealant (catalogue number 3145-Grey-RTV; mil-A-46146, Dow Corning Midland, MI, USA) to attach the mesh and hold the two halves of the pot together. Each pot had two compartments. On August 30, 2003 one compartment was filled with field soil mixed with perlite (3:1, v:v), watered, and planted with14-week-old seedlings (see Plant Material for growth conditions). Three weeks after the seedlings were transplanted into the unsterilized soil, the second compartments were filled with sterilized field soil. Soil was sterilized by autoclaving at 15 p.s.i for 90 minutes, repeated 24 hours later. Uncolonized 17-week-old seedlings were then transplanted into the sterilized soil and

watered. The purpose of transplanting seedlings into the unsterilized field soil 3 weeks prior to the introduction of seedlings into the other half of the pot was to insure that the seedlings were already colonized by ectomycorrhizal fungi when the experiment was started. We refer to the initially transplanted seedlings as "source seedlings". If hyphae from the source seedlings were able to penetrate a mesh of a given pore size, we expected to see mycorrhizal root tips on "recipient" seedlings grown in sterilized field soil.

Once all source and recipient seedlings had been transplanted into the pots, the seedlings were watered as necessary. Just prior to transplanting, we destructively subsampled fifteen source seedlings to quantify ectomycorrhizal colonization following the methodology of Phillips and Hayman (1970). Afterwards, pot location on the greenhouse bench was re-randomized monthly. Initial shoot height was measured shortly after transplanting, on September 30, 2003.

Seedling measurements

At harvest, January 11, 2004, shoot height and biomass (dried at 65° C for 48 hours) were measured. During the harvest, we also inspected mesh barriers for signs of hyphal penetration using a stereomicroscope. We chose to randomly select ten replicates per mesh barrier treatment for morphotyping using similar methods outlined above (5 treatments x 2 seedlings per pot x 10 replicates = 100 seedlings). Three replicate sets of one root tip per morphotype from different seedlings were lyophilized prior to storage for subsequent molecular analysis. On average, 3% of the total roots tips per morphotype examined were sent for molecular analysis. The remainder of the morphotyped roots were dried and weighed with the remainder of the root sample.

Molecular confirmation of ectomycorrhizal fungal species identification

Total genomic DNA was extracted from single ectomycorrhizal tips by pulverizing them for 45 seconds at a speed of 5.0 units using a Bio101 Systems Fast Prep FP120 high frequency shaker (Q-biogene, Carlsbad, CA, USA). DNA was isolated using the procedure of Baldwin and Egger (1996). The final DNA pellet was dried using a speed vacuum concentrator and then re-suspended in 50 μ L EDTA-TE buffer.

Following DNA extraction and isolation, the internal transcribed spacer (ITS) region of the fungal nuclear rDNA was specifically amplified by the primers NSI1 and

NLC2 (Martin and Rygiewicz 2005). PCR reactions typically included 1 µL template DNA, 18.6 µL sterile purified water (Barnested Nanopure Diamond water purifier), 0.2 mM deoxyribonucleoties (dNTPs), 2.5 µl 10x PCR buffer, 1.5 mM MgCl₂, 0.48 mM each primer, 1.6 mg mL⁻¹ bovine serum albumin (BSA), and 0.25 U µL⁻¹ AmpliTag Gold™ (Applied Biosystems, Foster City, CA, USA). Samples were amplified using a PTC-200 thermal cycler (MJ Research Inc., Waltham, MA, USA). A 10 min hot start was followed by PCR cycling as follows: 45 seconds at 94°C followed by 34 cycles of denaturation at 94°C for 45 seconds, annealing at 54°C for 45 seconds, ramping 72°C for 1 minute with a 1 second extension after each cycle, and extension at 72°C for 10 minutes, and then the temperature was held at 4°C. The PCR products were visualized on 1.5% agarose gels using a Gel Logics 440 (Kodak Instruments, Rochester, NY, USA). The PCR product was cleaned using the QIAquick PCR Purification kit (Qiagen Inc., Valencia, CA, USA). Prior to sequencing, the large ITS fragment produced above, was reamplified in a nested PCR reaction using the primers ITS 1 and ITS 4 (White et al. 1990). PCR products were quantified and then sequenced using a 3730 DNA Capillary Sequencer (Applied Biosystems) at the University of British Columbia Nucleic Acid and Protein Services Unit. All unique morphotypes were sequenced and then aligned using Sequencher software (Gene Codes Corporation, Ann Arbor, MI, USA). Taxonomic matches were based on BLAST results with \geq 98% sequence similarity.

Statistical analysis

The fungicide experiment examined a 3 x 3 x 3 factorial set with a separate control group of treatments (i.e., separate from the factorial but combined in the layout) in a completely randomized design (Bergerud 1989). We used percent colonization data obtained from the cleared and stained roots and normalized the data with a square root transformation for analysis of variance (ANOVA). We analyzed ectomycorrhizal fungal community data (richness and diversity, relative abundance of morphotypes with >5% of ectomycorrhizal root tips), seedling growth, and square root of percent colonization, first by using the GLM procedure in SAS (SAS Institute Inc. 1999). We then ran a second GLM procedure with a contrast statement to compare the control treatment against all other treatment combinations. Analyses on data collected from cleared and stained roots and morphotyped root tips were done separately, and consequently graphed separately. ANOVA tables were constructed manually to obtain the proper experimental

error terms and degrees of freedom. When significant main treatment effects occurred, we separated means using the Bonferroni multiple comparison test.

For the mesh barrier experiment, the percent colonization and ectomycorrhizal richness for both seedlings per pot were used to calculate the Steinhaus index of ectomycorrhizal community similarity (Legendre and Legendre 1998) and to calculate the difference in morphotype richness (the number of morphotypes on the donor root system minus the number on the receiver root system). The effects of mesh pore size on ectomycorrhizal fungal community data (richness difference and Steinhaus index of similarity), percent ectomycorrhizal colonization and seedling growth (shoot height, biomass and root biomass) were detected with a one-way ANOVA using the GLM procedure in SAS (SAS Institute Inc. 1999). For both percent ectomycorrhizal colonization and seedling growth, the difference in the response variable between source and recipient seedlings within a pot was calculated and used in the analysis. Differences were considered significant at $\alpha = 0.05$. Where significant mesh barrier treatment effects occurred, we separated means using the Bonferroni multiple comparison test. Effects of sterilization on seedling growth and total percent ectomycorrhizal colonization were analyzed using the TTEST procedure for each mesh size (SAS Institute Inc. 1999).

Results

Fungicide treatments

Approximately 30% of the roots of control seedlings (i.e., seedlings receiving only water) were colonized after 21 weeks in the treatment pots. Application of fungicide reduced ectomycorrhizal colonization by up to 50%, depending on fungicide type (p < 0.0001) but not application concentration (p = 0.9) (Table 3.1). The most effective treatment regime was Topas® applied alone or in combination with Senator® (Fig. 3.1a). Senator® alone was less effective at decreasing ectomycorrhizal colonization, with only a 36% reduction compared with 56% reduction using Topas®. There were no differences associated with different application frequencies (Fig. 3.1b) and there were no significant interactions among any combination of the three treatment factors (p > 0.05, Table 3.1). None of the fungicides applied at any concentration or application frequency, affected seedling height or shoot or root biomass (Table 3.1).

A total of eight morphotypes were identified and described (Table 3.2). Two had \geq 98% sequence matches of their ITS sequences to *Wilcoxina rehmi* and *Thelephora terrestris* accessions in Genbank. DNA from the other six morphotypes either did not amplify or had less than 98% sequence homology with genotypes in Genbank. One morphotype was not identifiable and was classified as undifferentiated. Only the *Rhizopogon/Suillus*-type formed rhizomorphs; the remainder had relatively smooth mantles (Table 3.2).

On average we observed more morphotypes on seedlings that were subject to fungicides than those that were not (Fig. 3.2). However, neither ectomycorrhizal community richness (p = 0.2) nor diversity (p = 0.3) was significantly affected by the fungicide types. The abundance of *Wilcoxina rehmii* mycorrhizas (the most common ectomycorrhiza) as a percentage of all root tips examined was reduced by Topas® applied alone or in combination with Senator®, when compared to Senator® alone or the control (Fig. 3.3). The abundance of *Cenococcum geophilum*, the other dominant ascomycetous mycorrhiza, was not affected by application of fungicides (p = 0.6, data not shown). Similarly, the abundances of *Rhizopogon/Suillus*- and *Tomentella*-type mycorrhizas, the most abundant basidiomycetes, were also not affected by fungicide treatment (p = 0.7, p = 0.8, respectively, data not shown).

Mesh barrier treatments

Source seedlings had greater shoot height, shoot biomass, root biomass, and ectomycorrhizal colonization than recipient seedlings across all mesh treatments except the 20 µm pore size (Table 3.3), and mesh size did not affect the magnitude of these differences (Table 3.4). Across all mesh sizes, on average, 50 and 21% of roots of source and recipient seedlings were colonized by ectomycorrhizal fungi, respectively. These colonization levels contrast measurements at planting where colonization of source seedlings was less than 1%.

We found six distinct morphotypes on source seedlings (Table 3.2). Most of the six morphotypes were represented in all mesh treatments (Fig. 3.4). *Wilcoxina rehmii* ectomycorrhizas comprised >85% of the community on source and recipient seedlings separated with mesh barriers of 1 μ m or larger (> 80%). By contrast, both the 0.2 μ m and 1 μ m pore-sized meshes blocked the formation of *Rhizopogon/Suillus*-type mycorrhizas on recipient seedlings (Fig. 3.4). This type formed approximately 5% of the

mycorrhizas on source seedlings. MRA-type morphotypes were found on all source seedlings, but were absent from recipient seedlings of all mesh treatments. *Thelephora terrestris* ectomycorrhizas formed an increasingly high proportion of the community on recipient seedlings as mesh size decreased, whereas they were not found on source seedlings. The abundance of *Cenococcum geophilum* mycorrhizas was too low to be useful in detecting mesh effects.

Ectomycorrhizal community similarity, which takes into account richness and relative abundance, between recipient seedlings versus source seedlings increased with mesh pore sizes greater than 0.2 μ m (p < 0.0001) (Fig. 3.5a). The ectomycorrhizal communities separated by the full barrier (control) or by mesh of pore size 0.2 μ m were significantly dissimilar from those separated by mesh with pore sizes 1 μ m and larger (Fig. 3.5a). The difference in morphotype richness between source and recipient seedlings was large in the full barrier treatment and generally decreased as mesh size increased (p = 0.09) (Fig. 3.5b). When examined under the microscope, we observed hyphae penetrating pore sizes of 1 μ m and larger, and roots penetrating only 500 μ m pores. Three of the mesh barriers were torn in pots of the 0.2 μ m mesh treatment; these replicates were omitted from the analyses.

Discussion

Fungicide effects on ectomycorrhizal colonization

This study shows that fungicides can be used to significantly reduce ectomycorrhizal colonization in controlled experiments. Topas® was more effective than Senator® at reducing ectomycorrhizal colonization levels. The manufacturer's recommended concentration was effective in reducing colonization, and there was no advantage to applying Topas® repeatedly during the course of the experiment. In our study, ectomycorrhizal colonization decreased by as much as 56% compared with the control. Douglas-fir control seedlings in this experiment had relatively low levels of colonization (approximately 30%) but these levels are typical for greenhouse-grown interior Douglas-fir (5-42%) (Hagerman and Durall 2004, Teste et al. 2004). Our results are consistent with another study using propiconazole. Manninen et al., (1998) found that 0.15 g of propiconazole applied to seedlings in the field (versus 9.6 g at the highest application frequency in our study) caused a decrease in ectomycorrhizal colonization of almost 33% (from 67 to 45% colonization) two years after 2 year-old nursery grown *Pinus sylvestris* seedlings were outplanted.

Although the fungicides did not eliminate ectomycorrhizal colonization altogether, we propose that Topas® reduces colonization to an extent to be useful for field studies. Similar decreases in arbuscular mycorrhizal colonization following benomyl application have resulted in substantial changes in structure of the plant community. For example, reductions in arbuscular mycorrhizal colonization of 60% have changed plant nitrogen and phosphorus concentrations and aboveground community productivity in Boreal grassland communities (Dhillion and Gardsjord 2004). Hartnett and Wilson (1999) found that a 75% decrease in arbuscular mycorrhizal colonization coincided with biomass decreases of dominant C₄ grasses. Callaway et al. (2004) reported that interactions between native grassland species and the invasive Centaurea maculosa were substantially altered when experimental plots were treated with benomyl; the fungicide decreased arbuscular mycorrhizal colonization by >80%, resulting in a C. maculosa biomass decrease when mixed with Koeleria cristata or Festuca idahoensia. Assuming reductions in arbuscular and ectomycorrhizal colonization result in similar functional responses in plant communities, we expect that Topas® applied at the recommended rate once every five months will reduce ectomycorrhizal colonization sufficiently to affect seedling performance in the field.

The specificity of the fungicides for ascomycetes and basidomycetes differed from that expected. Senator® is reported to be more effective against ascomycetes than basidiomycetes, and yet it appeared to have no effect on *Wilcoxina rehmii*, a dominant ascomycete in this study. Manninen et al. (1998) reported that propiconzaole was also more effective at inhibiting ascomycete than basidiomycete symbionts and this is confirmed by Laatikainen and Heinonen-Tanski (2002). The latter found that low concentrations of propiconazole (0.1 ppm) increased growth of *Suillus bovinus* and *S. variegatus* strains grown *in vitro*, and that these fungi were tolerant of concentrations up to 1 ppm. In our study, the effectiveness of propiconazole (Topas®) could not be predicted strictly by taxonomic status. For example, it caused a substantial reduction in colonization by *Wilcoxina rehmii*, but not by *Cenococcum geophilum*, another important ascomycete. Colonization by the basidiomycetes forming *Thelephora terrestris*, *Tomentella*-type, and *Rhizopogon/Suillus*-type mycorrhizas either increased or was not affected by either fungicide however. In our study, Topas® targeted the most abundant
ectomycorrhizal fungi, *Wilcoxina rehmii*, so that the additional application of Senator® provided no further advantage.

Other fungicides have had variable effects on ectomycorrhizal colonization. O'Neill and Mitchell (2000) applied benomyl to *Picea sitchensis* seedlings and found that colonization was reduced from 60% to 20%; however, only one morphotype, Wilcoxina mikolae, was observed on the nursery grown seedlings. In another study, the percent of roots colonized by Thelephora terrestris or Laccaria laccata decreased when 0.3% Dithane M-45 was applied to *Pinus patula* seedlings grown in pouches, and similar reductions in hyphal dry weight occurred when the fungicide was applied to in vitro cultures (Reddy and Natarajan 1995). A wide range of responses were exhibited by 64 strains of ectomycorrhizal fungi grown in vitro and exposed to relatively low concentrations (<10 ppm) of five fungicides (benomyl, chorothalonil, copper oxychloride, maneb and propiconazole) (Laatikainen and Heinonen-Tanski 2002). Conversely, in some other laboratory studies fungicides have increased ectomycorrhizal colonization (Pawuk et al. 1980, Marx and Rowan 1981, de la Bastide and Kendrick 1990). This effect is likely due to the selective inhibition of fungi that are competitive towards ectomycorrhizal fungi (Summerbell 1988). In our study, interactions among ectomycorrhizal fungi could have resulted in the increase of basidomyctes observed. Wilcoxina rehmii, a rapid colonizer of nursery seedlings (Mikola 1988) was suppressed by the application of Topas[®]. Removal of this rapid colonizer could have allowed other ectomycorrhizal fungi to colonize seedling root tips. Surveys of the entire fungal community on a large number of replicate seedlings is required to investigate this possibility.

Our results suggest that Topas® should be effective at reducing morphotypes commonly found in greenhouse bioassays of field soils, but there are two caveats. First, we could not assess the effects of fungicides on rare ectomycorrhizal fungal species or those that do not colonize seedlings in greenhouses. Second, Topas® may affect seedling physiology and/or other soil biota. These impacts are more difficult to identify and quantify by short term experiments in a greenhouse setting. Propiconazole has been shown to have growth-regulator effects on plants in the Solanacaeae family (Kendrick 2000), and it has also been shown to affect soil fauna, such as flagellates (Ekelund et al. 2000), as well as soil respiration (Elmholt 1992). Topas® is recommended for prevention of a variety of foliar fungal diseases, and its mode of action by preventing ergosterol synthesis makes it likely to also affect non-target saprotrophic and parasitic soil fungi. A change in this community would alter potential food substrates of soil fauna. In experiments where reduction of ectomycorrhizal fungi is of primary concern, and side-effects on the soil biota is unimportant, then applications of Topas® can be an effective treatment regime. Given that the active ingredient in Topas® is fungistatic, repeated applications may be required where there is high hyphal turnover, as would happen over a temperate growing season, or where there is high fungal propagule pressure; both of these conditions occur in field situations.

Mesh barrier effects on hyphal penetration

Our study indicates that mesh with pore size 0.2 µm is effective at reducing hyphal penetration and mycorrhizal colonization of neighboring seedlings. However we conclude that the threshold for restricting ectomycorrhizal hyphal penetration lies between 0.2 and 1 µm. Ectomycorrhizal richness tended to increase in sterilized compartments where mesh size equaled or exceeded 1 µm, suggesting hyphae from the source seedlings compartment penetrated the mesh and colonized the recipient seedlings growing in the sterilized compartment. Of even greater significance, ectomycorrhizal community similarity between source and recipient seedlings greatly increased in meshes \geq 1 µm. If the recipient seedlings were mycorrhiza-free, differences in richness alone should have indicated mesh effectiveness at restricting hyphal penetration, regardless of abundance, but the small number of morphotypes may have rendered richness as a measure with little resolving power.

The ectomycorrhizal community observed in our study was typical for interior Douglas-fir seedlings inoculated with field soil and grown in the greenhouse (Jones et al. 1997, Simard et al. 1997, Hagerman and Durall 2004, Teste et al. 2004). The six morphotypes formed on the source seedlings also represented a broad range of mantle types (texture and thickness), width of emanating hyphal forms (width and extension 3 to 7 μ m), as well as the presence or absence of rhizomorphs. Their presence allowed us to test the effectiveness of the pore sizes at preventing hyphal penetration by ectomycorrhizal fungi with different characteristics. We might predict, for example, that a mesh with a smaller pore size would be required to prevent penetration of single hyphae, compared to the size required to stop penetration of rhizomorphs. Our findings support this prediction since we found that the rhizomorph-forming *Rhizopogon/Suillus*- type morphotype was restricted by a mesh size between 1 to 20 μ m. We propose that meshes with pore sizes smaller than 1 μ m would be adequate in field situations.

Although mesh with 0.2 μ m pores was the most effective at reducing hyphal penetration, it was very fragile. This characteristic of nylon mesh with pore sizes smaller than 1 μ m has been noted previously (Tarafdar and Marschner 1994). Our results suggest that field experiments requiring fine mesh (0.2 μ m) should use more durable nylon (i.e. mesh thickness > 115 μ m) or metal based mesh.

Our finding that mesh with pore sizes between 0.2 μ m and 1 μ m are most effective at inhibiting ectomycorrhizal colonization must be interpreted cautiously because some ectomycorrhizas were found in sterilized soils with a 0.2 µm mesh barrier. Within the sterilized compartment of these pots, the ectomycorrhizal community was reduced but not eliminated. For example, Wilcoxina rehmii was on the recipient seedlings, regardless of the mesh barrier type, but was not observed in control pots, suggesting that hyphal penetration or spore dispersal may have occurred. We are uncertain why Wilcoxina rehmii was not found in the sterilized compartment of the control pots. Further research is warranted on Wilcoxina rehmii propagating strategies in nurseries (e.g., hyphal and spore) and morphological plasticity. We also found that Thelephora terrestris had colonized root tips in one seedling of the control treatment (i.e. sterilized soil with a full barrier), confirming previous studies that it is a common greenhouse contaminant. Statistical analyses were run without *Thelephora terrestris* (data not shown); however, results were similar, and did not change our conclusions about the hyphal restriction properties of the mesh treatments. MRA-type mycorrhizas were also only observed on source seedlings across all mesh treatments, suggesting that chemical changes induced by autoclaving may have inhibited this particular ectomycorrhizal fungus. Rhizomorphs were completely excluded from sterilized compartments separated by 1 or 0.2 µm mesh.

Conclusions

The use of mesh barriers versus fungicides for controlling ectomycorrhizal colonization depends on the ecological processes that must be maintained and those that can be compromised in the experiment. Future CMN research can benefit from the use of mesh barriers. Mesh barriers with a gradient of pore sizes have the potential to tease out carbon and nutrient pathways (soil-only, hyphal-only, rhizomorph-only, etc.) in

resource sharing CMN studies. However, installing mesh barriers will disrupt soil structure and potentially reduce water flow through small pore sizes. If the purpose of mesh is to exclude mycorrhizal hyphae, and maintain non-mycorrhizal status of the enclosed host, the soil contained in the mesh barrier compartment will require sterilization. Mesh with pore sizes < 1 μ m appear to reduce hyphal penetration, however care will be required to exclude fungal propagules arriving via air or water pathways. We suggest that mesh barriers, apart from their disruptive installment, are a more promising method than fungicides to completely exclude fungal.

Table 3.1: Analysis of variance for effect of fungicide type (F), concentration (C), and application frequency (A) on square root percent ectomycorrhizal colonization (%) and size of Douglas-fir (*Pseudotsuga menziesii* var. *glauca*) seedlings after five months.

			%			Height		S	shoot bion	nass	F	Root biom	ass
Source of variation	df	MS	F	р	MS	F	р	MS	F	р	MS	F	р
Control vs. all others	1	13.55	9.67	<.0001	0.03	0.00	0.98	0.01	0.01	0.90	0.03	0.32	0.57
Fungicide type	2	9.70	6.92	<.0001	69.40	2.06	0.13	0.29	0.60	0.55	0.08	1.01	0.37
Concentration	2	0.23	0.16	0.85	16.10	0.48	0.63	0.62	1.29	0.28	0.04	0.48	0.62
Application frequency	2	22.81	16.28	<.0001	46.00	1.37	0.26	0.74	1.55	0.22	0.11	1.47	0.23
FxC	4	1.56	1.11	0.35	22.90	0.68	0.61	0.36	0.75	0.56	0.06	0.77	0.55
FxA	4	1.99	1.42	0.23	47.90	1.42	0.23	0.15	0.32	0.87	0.05	0.68	0.61
СхА	4	0.25	0.18	0.95	8.32	0.25	0.91	0.73	1.52	0.20	0.16	2.11	0.08
FxCxA	8	1.44	1.03	0.42	17.90	0.53	0.83	0.43	0.90	0.52	0.02	0.29	0.97
Error	135	1.40			33.70			0.48	0.48		0.08		

Table 3.2: Description of morphological characteristics of ectomycorrhizas observed on Douglas-fir (*Pseudotsuga menziesii* var. *glauca*) seedlings grown in the fungicide (F) and mesh (M) study.

Morphotype and Blast match	Macroscopic description	Mante type(s)	Emanating hyphae	Rhizomorphs	Cystidia
<i>Rhizopogon/Suillus</i> -type (R/S); F and M	Unbranched to subtuberculate silvery white mycorrhiza with rough texture	Outer: felt prosenchyma, hyphae 3-4 µm smooth, and thick-walled; inner: net synenchyma, thin, hyphae 2 µm	3 µm wide; no clamps, crystalline ornamentation, and elbow-like bends	Compact brown with crystalline ornamentation and elbow-like bends	Absent
<i>Thelophora</i> -type (T) Blasted to <i>Thelephora terrestris</i> , Accession No. U83486, 619/627 base pairs = 99%; F and M	Unbranched or irregular bright orange to brown (sometimes whitish) mycorrhiza with smooth reflective texture	Outer: net synenchyma, hyphae 3 µm wide; inner: incomplete interlocking irregular synenchyma, hyphae 4-5 µm wide	Rare, 3 µm wide; clamps, smooth with occasional enlarged hyphal junctions	Absent	Common, 40-50 µm long and 3 µm wide with basal clamp

	Morphotype and Blast match	Macroscopic description	Mante type(s)	Emanating hyphae	Rhizomorphs	Cystidia
-	<i>Cenococcum geophilum</i> (Cg); F and M	Unbranched, black mycorrhiza with rough hairy texture	Outer: net synenchyma in a stellate pattern, hyphae 6 µm wide; inner: net synenchyma	5-6 µm wide black, straight	Absent	Absent
	<i>Wilcoxina-</i> type (W) Blasted to <i>Wilcoxina rehmii</i> Accession No: DQ069001, 510/519 base pairs = 98%	Irregular dark brown to orangish mycorrhiza, often wrinkled, also called E-strain	Outer: not seen; inner: patchy and incomplete net prosenchyma, hyphae 2 µm wide	Absent	Absent	Absent
• • • • • • • • • • • • • • • • • • • •	<i>Mycelium radicis atrovirens-</i> type (MRA); F and M	Unbranched black to brown mycorrhiza with curled hairy or very rough texture	Outer: felt prosenchyma, hyphae 3 µm wide; inner: net synenchyma, hyphae 2-3 µm wide	Rare, 5-7 µm wide, no clamps, smooth but becoming progressively more verrucose away from the mantle	Absent	Absent
	Undifferentiated (Undif); F and M	Young orange mycorrhiza with no distinct characters	Barely visible net synenchyma readily turning into Hartig net	Absent	Absent	Absent

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Morphotype and Blast match	Macroscopic description	Mante type(s)	Emanating hyphae	Rhizomorphs	Cystidia	
<i>Tomentella</i> -type (Tom); F	Swollen dark-brown sandy textured mycorrhiza	Outer: squarish incomplete interlocking irregular synenchyma with thick-walled hyphae; inner: net synenchyma	Absent	Absent	Absent	
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 Piloderma-type (P); F	Yellow coarsely felty mycorrhiza with abundant rhizomorphs	Not determined Absent	Finely verrucose, Absent septa common, not clamped, approximately 3 µm wide	

Table 3.3: Effect of sterilization on growth and ectomycorrhizal (EM) colonization of Douglas-fir (*Pseudotsuga menziesii* var. *glauca*) seedlings. A series of t-tests were used to determine differences among source (S) and recipient (R) seedlings grown for each mesh barrier treatment.

Mesh (µm) control	Soil S	n 10	Height increment (cm) 15	SEM* 2.6	p 0.0294	n 10	Shoot gain (g) 0.91	SEM 0.137	p 0.0061	n 9	Root gain (g) 0.32	SEM 0.056	p 0.6633
	R	12	10	2.6		12	0.42	0.137		10	0.29	0.056	
0.2	S	12	14	0.8	<.0001	12	0.97	0.084	<.0001	10	0.44	0.064	0.0055
	R	12	9	0.8		12	0.34	0.084		12	0.19	0.064	
1	S	11	20	2.4	0.0195	11	1.55	0.196	<.0001	8	0.61	0.123	0.0360
	R	11	14	2.4		11	0.70	0.196		9	0.31	0.123	
20	S	12	18	3.6	0.3541	12	1.23	0.379	0.4363	10	0.48	0.204	0.4843
	R	8	ຸ12	3.6		8	0.86	0.379		5	0.29	0.204	
500	S	12	21	4.1	0.0588	12	1.51	0.319	0.0333	11	0.50	0.074	0.0400
	R	9	11	4.1		[`] 9	0.61	0.319		9	0.30	0.074	

*SEM: standard error of the mean. Seedling growth is expressed as height and biomass measured after 5 months.

Table 3.4: (continued) Effect of sterilization on growth and ectomycorrhizal (EM) colonization of Douglas-fir (*Pseudotsuga menziesii* var. *glauca*) seedlings. A series of t-tests were used to determine differences among source (S) and recipient (R) seedlings grown for each mesh barrier treatment.

Mesh (µm)	Soil	Root: Shoot gain 0.33	SEM 0 155	р	n 9	Percent EM colonization (%) 50	SEM 7	р
control	R	0.88	0.155	0.0075	9	3	7	<0.0001
0.0	S	0.44	0.056	0.0675	7	43	12	0 0105
0.2	R	0.56	0.056	0.0075	9	11	12	0.0135
4	S	0.49	0.145	0 6007	9	57	8	0 0113
I	R	0.41	0.145	0.0007	9	33	8	0.0110
00	S	0.42	0.077	0 5220	10	47	9	0 1308
20	R	0.37	0.077	0.5529	5	29	9	0.1500
	S	0.35	0.083	0.0407	11	51	10	0.0424
500	R	0.57	0.083	0.0427	9	28	10	0.0434

*SEM: standard error of the mean. Seedling growth is expressed as height and biomass measured after 5 months.

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Table 3.5: Effect of mesh treatment on growth and ectomycorrhizal (EM) colonization of Douglas-fir (*Pseudotsuga menziesii* var. *glauca*) seedlings. Response differences between source and recipient seedlings were calculated for each pot. This single number was used in the ANOVA for each response variable. Statistically significant mesh treatment effects detected by a Bonferroni multiple comparison test are designated by different letters (p < 0.05).

Mesh (µm)	n	Height increment (cm)			SEM*	n	Shoot gain (g)			SEM	n	Root gain (g)			SEM
control	10	6	а	±	2.6	10	0.49	а	±	0.220	9	0.03	а	±	0.088
0.2	12	5	а	±	2.4	12	0.63	а	±	0.201	10	0.23	a	±	0.084
1	10	7	а	±	2.6	10	0.90	а	±	0.220	7	0.33	а	±	0.100
20	8	4	а	±	2.9	8	0.31	а	±	0.247	5	0.16	а	±	0.118
500	9	9	а	±	2.7	9	0.82	а	±	0.232	9	0.18	а	±	0.088

*SEM: standard error of the mean.

Table 3.6: (continued).Effect of mesh treatment on growth and ectomycorrhizal (EM) colonization of Douglas-fir (*Pseudotsuga menziesii* var. *glauca*) seedlings. Response differences between source and recipient seedlings were calculated for each pot. This single number was used in the ANOVA for each response variable. Statistically significant mesh treatment effects detected by a Bonferroni multiple comparison test are designated by different letters (p < 0.05).

Mesh		Root:Shoot					EM colonization			
(µm)	n	(g)			SEM	n	(%)			SEM
control	9	-0.55	а	±	0.105	9	47	а	±	8
0.2	10	-0.12	ab	±	0.100	7	30	а	±	9
1	7	0.08	b	±	0.120	8	26	а	±	9
20	5	0.05	b	±	0.142	5	6	а	±	11
500	8	-0.21	ab	±	0.112	9	29	а	Ŧ	8

*SEM: standard error of the mean.

Figure 3.1: Effect of a) fungicide type and b) application frequency on percent ectomycorrhizal colonization (determined by clearing and staining root tips) of Douglasfir (*Pseudotsuga menziesii* var. *glauca*) seedlings. Fungicide abbreviations: S =Senator® and T = Topas®. Frequency abbreviations: A = once upon commencement of the experiment, B = every two months, and C = once a month. Statistically significant fungicide treatment effects detected by a Bonferroni multiple comparison test are designated by different letters (p < 0.05). Error bars are one standard error of the mean.



Figure 3.2: Abundance of morphotypes (*Tomentella*-type (Tom) *Thelephora terrestris* (T); *Mycelium radicis atrovirens*-type (MRA); *Wilcoxina rehmii* (W); *Cenococcum geophilum* (Cg); *Rhizopogon/Suillus*-type (R/S); *Piloderma*-type (P) and Undifferentiated (Undif) found on morphotyped Douglas-fir (*Pseudotsuga menziesii* var. *glauca*) root systems grown in soil treated with different a) fungicide types and b) application frequency. Fungicide abbreviations: S = Senator® and T = Topas®. Frequency abbreviations: A = once upon commencement of the experiment, B = every two months, and C = once a month.

73

a)



Figure 3.2 (continued): Abundance of morphotypes (*Tomentella*-type (Tom) *Thelephora terrestris* (T); *Mycelium radicis atrovirens*-type (MRA); *Wilcoxina rehmii* (W); *Cenococcum geophilum* (Cg); *Rhizopogon/Suillus*-type (R/S); *Piloderma*-type (P) and Undifferentiated (Undif) found on morphotyped Douglas-fir (*Pseudotsuga menziesii* var. *glauca*) root systems grown in soil treated with different a) fungicide types and b) application frequency. Fungicide abbreviations: S = Senator® and T = Topas®. Frequency abbreviations: A = once upon commencement of the experiment, B = every two months, and C = once a month.



Figure 3.3: Abundance of *Wilcoxina rehmii* ectomycorrhizas, as a percentage of all root tips examined on Douglas-fir (*Pseudotsuga menziesii* var. *glauca*) grown in soil treated with fungicides. Fungicide abbreviations: S = Senator® and T = Topas®. Statistically significant fungicide type treatment effects detected by a Bonferroni multiple comparison test are designated by different letters (p < 0.05). Error bars are one standard error of the mean.



Figure 3.4: Abundance of morphotypes (*Thelephora terrestris* (T); *Mycelium radicis atrovirens*-type (MRA); *Wilcoxina rehmii* (W); *Cenococcum geophilum* (Cg); *Rhizopogon/Suillus*-type (R/S); and Undifferentiated (Undif), as a percentage of all root tips examined on recipient (R) and source (S) soil seedlings separated by a mesh barrier.



Figure 3.5: Ectomycorrhizal community differences. a) Steinhaus similarity index for ectomycorrhizal communities observed on source and recipient seedlings separated by a mesh barrier. b) Richness difference = number of morphotypes observed on source Douglas-fir (*Pseudotsuga menziesii* var. *glauca*) root systems minus morphotypes present on recipient Douglas-fir separated by a mesh barrier. Statistically significant mesh treatment effects detected by a Bonferroni multiple comparison test are designated by different letters (p < 0.05). Error bars are one standard error of the mean.





b)



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4 Ectomycorrhizal colonization and intraspecific variation in growth responses of lodgepole pine¹

Introduction

Phenotypic variation of any organism is a product of its genotype, environment and the interaction between these components. Both abiotic and biotic factors will be ecologically significant components of an organism's environment. Because many tree species rely on ectomycorrhizal fungi for establishment and survival, variation in the identity and abundance of ectomycorrhizal fungi can impact seedling growth (Dickie et al. 2002). Thus, the presence of ectomycorrhizal fungi in soils is a critical dimension to the biotic environment with which trees will interact.

Quantifying levels of colonization on root tips of host trees is one method to measure the extent of interaction with their ectomycorrhizal fungi; however, the relationship between host growth and colonization level is inconsistent (see Chapter 2). Because experiments on ectomycorrhizas have used different species (both phyto- and mycobiont) and substrates, it is difficult to untangle which factors contribute to the poor overall relationship between colonization level and plant response. Within a host species, however, we might expect the relationship between colonization level and host growth to be less variable, especially in homogenous environments. Furthermore, within more genetically similar groups nested within a species, the relationship between colonization level and host growth is expected to be even less variable.

Research approaches to study mycorrhizal fungi do not allow direct manipulation of the level of colonization of an individual plant. Here we present results from a greenhouse experiment with seedlings from seed families within the species *Pinus contorta* Dougl. ex Loud. var. *latifolia* Engelm., which naturally varied in ectomycorrhizal colonization levels; that is, colonization levels were not manipulated. We have analyzed the results to test the direction and consistency of the relationship between colonization level and growth responses across seed families. Earlier studies have considered the role of host genotype in determining level of colonization (Tagu et al. 2001, 2005; Gehring et al. 2006) and the composition of ectomycorrhizal fungal communities (Korkama et al. 2006), but to our knowledge this is the first study to test the relationship

¹A version of this chapter has been accepted by Canadian Journal of Botany as: Karst J, Jones MD, and Turkington R. Intraspecific variation in height of lodgepole pine is minimized with increased ectomycorrhizal colonization.

Methods

Greenhouse experimental set-up

The greenhouse experiment was set up to test the effects of five ectomycorrhizal fungal species, plus a non-mycorrhizal control treatment on the variation in growth responses of ten seed families of lodgepole pine seedlings. Each fungal species x family treatment was replicated twenty times. Seed was produced during controlled pollination trials by the British Columbia Ministry of Forests using trees from seed planning units in the central interior of British Columbia. Seed from within each family was full sib, i.e. genetic similarity was higher within than among families. Relative wood density was the primary trait for which seeds had been selected.

Seeds were soaked 24 hours in distilled water, then sterilized in 30% H₂O₂ for 15 minutes, and 3% H₂O₂ for a further 2 hours. All solutions were mixed constantly. The seeds were dried and kept at 4°C for 28 days. For each fungal species x family replicate, we sowed two seeds into a SC10R Super cell Ray Leach cone-tainer (Stuewe and Sons, Inc., Corvallis, Oregon, USA) measuring 3.8 cm in diameter and 21 cm in length, filled with 3:1 (v:v) autoclaved peat and perlite. All cone-tainers were sterilized previously in a 30% bleach solution for 30 minutes. The cone-tainers were held in RL98 trays (Stuewe and Sons, Inc., Corvallis, Oregon, USA) and randomized monthly. We covered the seeds with 0.5 cm of autoclaved sand and all seeds were watered every 4 days. Two weeks after germination, we thinned seedlings to one per cone-tainer. For the next eight months, we watered the seedlings as required and fertilized once every 2 weeks with ¼ strength Ingestad's solution (Pelham and Mason 1978). Natural daylight in the greenhouse was supplemented by 400 W high pressure sodium lamps for 18 hours daily. The average temperature ranged from 20 to 25°C and the average relative humidity was 53%.

At four weeks and again at four months we inoculated the seedlings with 5 mL of mycelial slurry of one of the five ectomycorrhizal fungi. The species of fungi used were: *Cenococcum geophilum, Rhizopogon roseolus, Wilcoxina mikolae, Hebeloma crustuliniforme* and *Paxillus involutus*. Cultures of these fungi were obtained from the Mycorrhiza Research Group, University of British Columbia Okanagan and maintained on solid modified Melin-Norkrans (MMN) media. To obtain the mycelium, we placed approximately twenty 0.5 cm³ cubes of actively growing mycelium in each flask of liquid

MMN media. Liquid cultures were grown under sterile conditions and shaken daily. No contamination occurred in liquid cultures. The mycelial slurry used to inoculate seedlings was produced by blending 150 mL of mycelium with 1850 mL of distilled water. We also produced a non-mycorrhizal slurry for control plants from solid MMN media that had not been inoculated.

When seedlings were harvested after nine months, visual observations of morphotypes under a dissecting scope showed that none of the inoculated fungi were present on the roots; however, seedlings were mycorrhizal with other fungi. Hence, we harvested 45 randomly selected seedlings per seed family in order to test the relationships among percent colonization, seed family and growth responses (height and biomass) of lodgepole pine. We measured the height of each harvested seedling and subsequently dried the shoots at 65°C for 72 hours. Roots were refrigerated at 4°C until examined (see below) and then were dried at 65°C for 72 hours.

Assessment of ectomycorrhizal fungal colonization

Seed families having less than 10% of seedlings survive were omitted from the analysis; thus, we examined eight of the initial ten families. Using these 360 seedlings (45 seedlings x 8 families), a power analysis performed in JMP IN 5.1 (Sall et al. 2005) determined that 64 seedlings were required to detect observed differences in height due to seed family, with a 97% probability of achieving a significance of 0.05. Since we could not estimate variation in mycorrhizal colonization in advance, we used variation in height to determine how many seedlings to examine for colonization. Consequently, we sub-sampled eight seedlings randomly from each family for which mycorrhizal colonization was measured. Entire root systems were carefully washed under running water and cut into approximately 1-cm pieces. All root fragments were placed in a baking dish containing water and a random sub-sample was then distributed into a Petri plate. We examined 300 (± 57) root tips per seedling under a stereomicroscope. Tips were classified as mycorrhizal if root hairs were absent. Examination of a sub-set of these roots under high magnification (400x) confirmed that this approach accurately distinguished mycorrhizal from non-mycorrhizal roots. Two morphotypes were distinguished based on the presence or absence of cystidia and on characteristics of the mantle and mycelial strands.

Molecular analyses

Total genomic DNA from three replicate tips of each morphotype identified was extracted by pulverizing the tips for 45 seconds at a speed of 5.0 units using a Bio101 Systems Fast Prep FP120 high frequency shaker (Q-biogene, Carlsbad, CA, USA). DNA was isolated using the procedure of Baldwin and Egger (1996). The final DNA pellet was dried using a speed vacuum concentrator and then re-suspended in 50 μ L EDTA-TE buffer.

Following DNA extraction and isolation, the internal transcribed spacer (ITS) region of the fungal nuclear rDNA was specifically amplified by the primers NSI1 and NLC2 (Martin and Rygiewicz, 2005). PCR reactions typically included 1 µL template DNA, 18.6 µL sterile purified water (Barnested Nanopure Diamond water purifier), 0.2 mM deoxyribonucleoties (dNTPs), 2.5 µL 10x PCR buffer, 2.0 mM MgCl₂, 0.48 mM each primer, 1.6 mg mL⁻¹ bovine serum albumin (BSA), and 0.25 U µL⁻¹ AmpliTaq Gold[™] (Applied Biosystems, Foster City, CA, USA). Samples were amplified using a PTC-200 thermal cycler (MJ Research Inc., Waltham, MA, USA). A 10 minute hot start was followed by PCR cycling as follows: 45 seconds at 94°C followed by 34 cycles of denaturation at 94°C for 45 seconds, annealing at 54°C for 45 seconds, ramping 72°C for 1 minute with a 1 second extension after each cycle, and extension at 72°C for 10 minutes, and then the temperature was held at 4°C. The PCR products were visualized on 1.5% agarose gels using a Gel Logics 440 (Kodak Instruments, Rochester, NY, USA). The PCR product was cleaned using the QIAquick PCR Purification kit (Qiagen Inc., Valencia, CA, USA).

Prior to sequencing, the large ITS fragment produced above, was re-amplified in a nested PCR reaction using the primers ITS 1 and ITS 4 (White et al. 1990). PCR products were quantified and then sequenced using a 3730 DNA Capillary Sequencer (Applied Biosystems) at the University of British Columbia Nucleic Acid and Protein Services Unit. All unique morphotypes were sequenced and then aligned using Sequencher software (Gene Codes Corporation, Ann Arbor, MI, USA). Taxonomic matches were based on BLAST results with \geq 97% sequence similarity.

Statistical analyses

We used an analysis of covariance (ANCOVA) to test the effect of seed family on seedling growth responses using level of ectomycorrhizal fungal colonization (% root

tips colonized) as a covariate regressor. We included an interaction term (seed family x % colonization) to determine if colonization interacted with seed family (i.e. whether the slope of the relationship between colonization and a given growth response differed by seed family). To meet ANCOVA assumptions, we ensured that colonization levels did not differ by seed family using an analysis of variance (see Results). We used a reciprocal transformation on shoot height to meet the assumption of homogeneity of variance. As shoot height was the only growth response to show unequal variance across seed families and Burgess and Malajczuk (1989) demonstrated decreases in variation of height among individuals of *Eucalyptus globulus* Labill. with inoculation by ectomycorrhizal fungi, we further explored the effects of colonization level on variation in shoot height. To do so, we used colonization level to predict the residuals in seedling height. Residuals were calculated by taking the absolute value of the deviation of each seedling from its mean family value, standardized by that particular family average:

seedling residual = $|y_{iF} - X_F| / X_F$

where y_{iF} is the value for the ith seedling from family F and X_F is the mean for that family. We used the family means in contrast to the overall mean because seed family had a significant effect in explaining variation in height among seedlings (see Results). In other words, we removed seed family effects to look at the independent contribution of colonization level on the height response of each individual seedling. All analyses were performed in JMP IN 5.1 (Sall et al. 2005). The relative abundance of each ectomycorrhizal fungal species was calculated as the percentage of the total number of ectomycorrhizal tips that were colonized by a given fungal species.

Results

All seedlings were mycorrhizal. The mean level of colonization was 85% (SD 15%), ranging from 39 to 100% per seedling. Mean colonization levels did not differ by seed family (df = 7, 56; F = 1.08; p = 0.39). The effect of colonization on root and shoot biomass varied by seed family (Table 4.1, Fig. 4.1). In particular, both positive and negative relationships between colonization level and shoot mass were observed, although seedlings in most families did not show any response to colonization levels (Fig. 4.1). For the majority of seed families no relationship was observed between

colonization level and root mass, however, two seed families showed negative relationships (Fig. 4.1). Shoot height differed only by seed family (Tables 4.1, 4.2).

Residual height variation across seedlings was weakly explained by colonization levels. In particular, there was a negative relationship between the magnitude of seedling deviation from its family mean and level of colonization (Fig. 4.2). Thus, increased colonization lessened height differences among seedlings within families. The mean coefficient of variation in height for each seed family was not related to mean colonization level (df = 1, 6; F = 0.0024; p = 0.96). Colonization levels were also not related to the deviations of mean family heights from the overall mean (df = 1, 6; F = 0.03; p = 0.87) indicating that colonization levels did not diminish differences among seed families.

The two morphotypes identified on seedling root tips had \geq 97% sequence matches of their ITS sequences to *Thelephora terrestris* and *Rhizopogon vulgaris* accessions in Genbank. Neither fungus had been inoculated onto seedlings, but rather were greenhouse contaminants. *Thelephora terrestris* was the most common ectomycorrhizal fungus to colonize seedlings. It was present on root tips of all seedlings and had a mean relative abundance of 98%. *Rhizopogon vulgaris* colonized roots of 5% of the seedlings, with a mean relative abundance of 60% on those seedlings. *R. vulgaris* was found on seedlings from two seed families (Table 4.2).

Discussion

Seed family effects on the relationship between colonization level and host growth

In this study the role of genetics was clear in determining seedling growth characteristics: seed family affected height and biomass of individual seedlings. Results from provenance trials of lodgepole pine in British Columbia, Canada indicate that differences in height of 20-yr trees are also, to some degree, under genetic control (Rehfeldt et al. 1999); adaptive differences among populations that were related to their climate of origin were demonstrated among populations that had been transplanted to various test sites across British Columbia. In our study, responses in seedling biomass were modified by colonization levels, representing a seed family x ectomycorrhizal colonization interaction. Because ectomycorrhizal fungi are part of the biotic environment, their presence should be viewed as a component within the more general

framework of assessing genotype x environment interactions influencing seedling growth.

Across different host plant species, the relationship between mycorrhizal colonization and host growth parameters varies (Jones et al. 1990, Thompson et al. 1994). Results from our study indicate that this inconsistency can be observed even at an intraspecific level. The environment of the seedlings in our experiment was homogeneous, indicating that the identity of seed family alone can be an important factor determining the relationship of ectomycorrhizal colonization to seedling biomass. Studies from other systems also confirm that genotypic effects can be such that they are as strong as species effects. For example, the effects of genotypic diversity of *Solidago altissima* on arthropod diversity and community structure living on their leaves are comparable to those from studies testing the effects of species diversity of seagrass (*Zostera marina*) showed that increasing genetic diversity results in increased invertebrate community resilience and decreased recovery time to disturbances caused by goose herbivory (Hughes and Stachowicz 2004); this finding mirrors those reported in experiments manipulating functional (species) diversity (Díaz and Cabido 2001).

Ectomycorrhizal colonization and host phenotypic variation

Ecological processes may be drivers of population differentiation and divergence (Schluter 2001). The role of ecological processes in population convergence has gained more attention with the introduction of neutral theory (Hubbell 2001, 2006); nonetheless, equalizing mechanisms are usually invoked in the context of explaining species coexistence (Chesson 2000). To our knowledge, ours is the first study to show that increases in colonization by ectomycorrhizal fungi tends to reduce intraspecific variability or, in other words, differences in height tend to be equalized among seedlings. Our results indicate that a mycorrhizal signal, albeit a weak one (9% of the variance in seedling height residuals was explained by colonization level), was observed at the seed family level. Such low r^2 values are not unusual given that the mean amount of variance explained in ecological experiments is only 2.5-5.4% (Møller and Jennions 2002).

Our results suggest that those seedlings able to escape ectomycorrhizal fungal colonization could benefit in terms of height gained. Nonetheless, roots of seedlings of

lodgepole pine occurring under natural conditions are heavily colonized by ectomycorrhizal fungi (Bradbury 1998; Kranabetter et al. 1999; Bothwell et al. 2001). We offer two reasons to explain high levels of colonization on seedlings in natural conditions. First, poorly colonized seedlings have an equal likelihood of growing shorter than the average seedlings. Hosts may invest more in the maintenance of ectomycorrhizas as a strategy analogous to insurance that buffers against extreme variation in performance. However, despite some theoretical developments (Kummel and Salant 2006), the amount of control a host has on the composition and abundance of its mycorrhizal fungal partners is uncertain. If host selection of a fungal partner is passive, our results would suggest that, in areas devoid of ectomycorrhizal fungi. stochasticity will influence seedling growth more so than in areas replete with ectomycorrhizal fungal inoculum. Second, there may be no advantage per se to reduced intraspecific variation. It may be present only as a byproduct of selection pressures on hosts for ectomycorrhizal colonization, which in turn, is selected for to increase plant survival in low nutrient conditions. Host benefits received from increased ectomycorrhizal colonization in terms of nutrient uptake may outweigh the costs (e.g. carbon) of supporting ectomycorrhizal fungi.

We observed a negative relationship between colonization level and intraspecific variation within, but not among families. Other studies have reported that phenotypic variation among families is minimized in the presence of ectomycorrhizal fungi. For example, thirty open-pollinated families of *Picea abies* grown with or without *Laccaria bicolor* showed striking reductions in variance of shoot and root dry weight among families when ectomycorrhizas were present (Mari et al. 2003). Variation in root architecture, an important trait for nutrient acquisition, also declined when ectomycorrhizas with *Paxillus involutus* were present on *Picea abies* (Boukcim and Plassard 2003). In particular, the number of lateral roots per seedling differed when the two families when non-mycorrhizal, but not when they were mycorrhizal. Our results are an advance over these earlier studies, which considered colonization as a categorical variable only (i.e., presence or absence). Colonization levels of seedlings in the field are more likely to be continuous rather than a discrete property as commonly employed in experiments. As such, results from our study may be more reflective of naturally occurring colonization levels.

Our results differ from experiments that treat ectomycorrhizal colonization level as a response variable. We found that colonization levels did not differ by seed families; a power analysis indicated that at least 220 seedlings would be required to detect significant differences (α =0.05) in colonization levels among families 97% of the time. Progeny obtained from crosses between two species, *Populus deltoides* and *P. trichocarpa* differed in the extent to which they were colonized by *Laccaria bicolor* (Tagu et al. 2001). Hence, Tagu et al. (2005) concluded that the ability to form ectomycorrhizas (measured by colonization levels) is a quantitative trait under polygenic control. The few measures of broad sense heritability calculated for levels of ectomycorrhizal colonization range from 0.09 to 0.81 (Rosado et al. 1994; Tagu et al. 2001, 2005) indicating possibly high involvement of environmental factors in determining the level of colonization, depending on the host and fungal species. The genetic basis to the response by hosts to ectomycorrhizal colonization levels deserves further study.

The prevalence of contamination on seedlings

None of the target fungi were successful in colonizing seedlings. Although we inoculated seedlings twice in the experiment, it is likely that the aggressive colonization abilities of those ectomycorrhizal fungi common to greenhouses facilitated their early establishment on seedlings. Contamination of seedlings used in ectomycorrhizal experiments is not uncommon. Nearly half of all studies extracted from papers used in the meta-analysis (Chapter 2) reported contamination of seedlings. While levels of contamination are lower in experiments performed in growth chambers, the small size of growth chambers necessitates the use of young seedlings, or running experiments for short durations. Clearly, the presence of contamination is problematic in experiments where maintaining non-ectomycorrhizal controls is required.

Conclusions

The role of the environment in determining plant phenotypes is undisputed in ecology. Our results suggest that mycorrhizal fungi should be considered as a component of the environment that can influence the amount of phenotypic variation in a population. Moreover, we highlight the importance of intraspecific differences in determining the sensitivity between symbionts involved in mycorrhizal associations. As such, models of intraspecific interactions should consider ectomycorrhizal associations when assessing phenotypic variability. Since we are unable to manipulate colonization levels directly, future research should examine the effects of the presence, absence and species of ectomycorrhizal fungi on the variance among seed families screened for high differentiation in growth traits. Additionally, the ecological relevance of decreased intraspecific variation through mycorrhizal colonization deserves further study. Table 4.1: Analysis of covariance for effects of seed family, percent ectomycorrhizal fungal colonization of root tips (% colonization) and their interaction on growth responses of *Pinus contorta* Dougl. ex Loud. var. *latifolia* Engelm. seedlings.

		Shoot h	eight (cm) †	Shoo	t mass (g)	Root mass (g)		
Source	df	F	р	F	р	F	р	
Family	7	2.20	0.051	1.31	0.26	3.44	0.0046	
% colonization	Í	0.65	0.43	0.48	0.49	2.42	0.13	
Family x	7	0.70	0.67	2.33	0.039	3.084	0.0091	
% colonization								

† A reciprocal transformation was used on shoot height to meet homogeneity of variance assumption.

Table 4.2: Mean shoot height of full sib families of *Pinus contorta* Dougl. ex Loud. var. *latifolia* Engelm. Seedlings grown for 36 weeks (n=8). British Columbia Ministry of Forests seed family identification follows in brackets seed family designation.

	Shoot h	eight (cm)
Seed family	Mean	SD .
A (2094 x 2065 CP RD5)	5.3 ^b	0.54
B (354 x 468 BV RD2) †	5.2 ^b	0.79
C (1659 x 479 BV RD2) †	6.2 ^a	1.01
D (268 x 1631 BV RD1)	5.1 ^b	0.54
E (1817 x 220 PG RD5)	6.2 ^a	0.76
F (253 x 236 PG RD2)	4.8 ^c	0.87
G (466 x 502 BV RD2)	5.1 ^b	1.24
H (2076 x 1620 CP RD2)	5.3 ^b	0.67

* Family effects sharing the same letter are not statistically different (P< 0.05 Tukey-Kramer multiple comparison test).

†Root tips of seedlings colonized by *Thelephora terrestris* and *Rhizopogon vulgaris*; all other seedlings colonized by *Thelephora terrestris* only.

Figure 4.1: The effect of ectomycorrhizal fungal colonization by seed family on shoot (top panel) and root mass (bottom panel) of *Pinus contorta* var. *latifolia* seedlings. Regression lines are shown for only those seed families showing a significant relationship between shoot or root mass and level of colonization. See Table 4.2 for British Columbia Ministry of Forests seed family identification.


Figure 4.2: The contribution of ectomycorrhizal fungal colonization to height variation in seedlings of *Pinus contorta* Dougl. ex Loud. var. *latifolia* Engelm., independent of seed family effects.



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5 Interactions among soil characteristics, host intraspecific variation and ectomycorrhizal fungal communities

Introduction

Partner species in coevolved interactions are expected to be sensitive to intraspecific variation of each partner due to the intimate and interdependent nature of their interactions (Thompson 1994). Ectomycorrhizal associations are of particular interest because individual trees host communities of fungi, and whether the composition of these communities is sensitive to intraspecific variation in hosts is poorly understood. Previous research has shown that host individuals provide a range, or gradient, of biotic variation, and that this gradient produces changes in ectomycorrhizal fungal communities. For example, variation among host individuals induced by defoliation (Saikkonen et al. 1999, Cullings et al. 2005a) or varying levels of parasitism will change the composition of ectomycorrhizal fungal communities (Cullings et al. 2005b, Mueller and Gehring 2006). Communities of ectomycorrhizal fungi have also been reported to segregate depending on the associated growth rate of their host (Korkama et al. 2006).

In addition to the variation provided by properties of host species, variation in soil characteristics can structure ectomycorrhizal fungal communities. For example, differences in soil nitrogen (Lilleskov et al. 2002) and nutrient and moisture status (Gehring et al. 1998, Robertson et al. 2006) have been shown to alter the composition of ectomycorrhizal fungal communities. Similarly, the ecological amplitude of host plants (measured by height and biomass performance) is clearly dependent on soil properties such as nutrient and moisture availability (Burns and Honkala 1990). Thus, variation in soil characteristics acts in parallel to influence both the composition of ectomycorrhizal fungal communities and intraspecific variation in hosts. This process alone should create a correlation between the composition of ectomycorrhizal fungal communities and intraspecific variation for ectomycorrhizal fungal communities and intraspecific variation of ectomycorrhizal fungal communities and intraspecific variation among hosts, independent of a direct interaction between the two components.

Identification of a correlation between environmentally-induced intraspecific variation in hosts and composition of their associated ectomycorrhizal fungal community is key to understanding how environmental gradients structure ectomycorrhizal fungal communities. A correlation not only indicates that variation in one symbiont is synchronous with variation in the other, but also that the environmental properties influencing host variation may act indirectly to affect the composition of ectomycorrhizal fungal communities. The possible sources of variation that influence ectomycorrhizal fungal communities would have to be extended to include those that affect host intraspecific variation. Because host and ectomycorrhizal fungal communities are interdependent (Kernaghan 2005), covariance between host intraspecific variation and the composition of the ectomycorrhizal community cannot be used to infer causation. Regardless, the presence of a correlation between the two components offers a way of determining the ecological relevance to ectomycorrhizal fungal communities of variation present within both a host species and the abiotic environment.

The objective of this study was to identify environmental factors that directly influence composition of ectomycorrhizal fungal communities, as well as those that may act indirectly through host intraspecific variation. We characterized "the environment" by measuring variation in soil characteristics related to fertility and moisture. Host intraspecific variation was measured by properties including shoot height, total biomass and root:shoot ratio. The composition of ectomycorrhizal communities was quantified in two distinct ways: 1) categorical; the presence or absence of individual ectomycorrhizal fungal species comprising a community and 2) continuous; the relative abundance of each species.

Materials and methods

Overview

We grew Douglas-fir (*Pseudotsuga menziesii* var. *glauca* (Beissn.) Franco) seedlings in pots containing soils that varied naturally in fertility. We also implemented an artificial gradient of soil moisture on replicate subsamples of these soils. Seedlings became colonized with the ectomycorrhizal fungi present in the soils and both the seedlings and fungi were subject to the variation in soil fertility and moisture. We then used multivariate analyses to correlate variation in soil fertility and moisture to variation in host growth and ectomycorrhizal fungal community composition.

Origin of soils

Soil was collected from the Thompson and Okanagan Valleys of the southern interior plateau of British Columbia, Canada. This area has a continental climate, with warm, dry summers and cool winters. In valley bottoms, the average daily minimum for the winter months is -5°C; for the summer months, the average daily maximum is 25°C (Environment Canada 2004). There is a strong elevational gradient in annual precipitation ranging from 300 mm at lower elevations (300-800 masl) to greater than 1000 mm at montane (1200-1400 masl) elevations (Meidinger and Pojar 1991). Open forests of Douglas-fir mixed with Ponderosa pine (*Pinus ponderosa* Dougl. Ex P. & C. Lawa.) and several species of grasses (*Koeleria macrantha* [Ledeb.] J. A. Schultes f., *Poa pratensis* L. and *Calamagrostis rubescens* Buckl.) occur at lower elevations, whereas at higher elevations, Douglas-fir grades into hybrid spruce (*Picea engelmanni* Parry ex Engelm. x *Picea glauca* [Moench] Voss) and lodgepole pine (*Pinus contorta* Dougl. Ex. Loud. var. *latifolia* Engelm.) (Meidinger and Pojar 1991).

Soil collection

Sampling locations were distributed over a distance of 140 km and ranged in elevation from 360 to 1390 masl (Table 5.1). This elevational range coincides with that of Douglas-fir in this region of British Columbia. After removing loose litter or moss, we collected 50 x 50 x 10 cm deep volumes of soil from six locations within the rooting zones of Douglas-fir trees at each of six approximately 400 m² sites. We sieved the soil through a 2.5 cm² mesh in the field to remove woody debris and stones and afterwards refrigerated the soil at 4°C in plastic tubs. By removing soil from the field, only those fungal species able to survive through resistant propagules will be retained in soil samples. The species pool of ectomycorrhizal fungi evaluated in this assay will be substantially less than what occurs in the field because those species requiring mycelial connections will be absent.

To determine the nutrient status of soils, one subsample of mixed soil from each of the six sites was analyzed (Soilcon Laboratories Ltd., Richmond, British Columbia, Canada) for pH, % organic matter measured by loss on ignition, total organic C, ammonium N, nitrate and nitrite N, total N, available P, and estimated C:N (Table 5.2). Analyses were performed using procedures described in Carter (1993) and McKeague (1978).

Plant material

In mid-November, 2003, non-mycorrhizal Douglas-fir seedlings were grown in a greenhouse at the University of British Columbia, Vancouver, from seeds (seedlot #48520, collected at 850-950 masl) obtained from the BC Ministry of Forest Tree Seed Center (Surrey, British Columbia, Canada). Seeds were moist-stratified at 4°C for 21 days, then sterilized in 3% H_2O_2 and mixed constantly for 2 hours. We sowed the seeds into #1206 bedding inserts (Kora Products, Bramalea, Ontario, Canada) filled with an autoclaved 3:1 (v:v) mixture of peat and perlite. Two seeds were placed into each cavity and covered with 0.5 cm of sterilized sand. The trays were misted each day for six weeks, after which seedlings were transplanted into 1.5 L pots. Just prior to transplanting, a random subsample of twenty seedlings was harvested to determine the initial mass of seedlings. We also cleared and stained roots from fifteen additional seedlings to confirm their non-mycorrhizal status. Throughout the experiment, natural daylight in the greenhouse was supplemented by 400 W high pressure sodium lamps for 18 hours daily. The temperature ranged from 20 to 24°C and the relative humidity was maintained at 60%.

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Maintenance of soil moisture

In December 2003, the field soil was removed from cold storage and mixed with perlite (3:1 v:v). Soils from each sampling site were crossed with three levels of watering (10, 20, and 30% volumetric soil moisture). The range in watering levels was based on field measurements of soil at 450 and 1200 masl taken over one week in July 2003 using a CS620 Hydrosense soil moisture probe (Campbell Scientific, Inc., Utah, USA). In total, 200 pots were prepared into which the seedlings were transplanted. One hundred and eighty pots were prepared for the treatments (6 sites x 3 watering levels x 10 replicates = 180) and 20 were prepared to establish allometric relationships between seedling height and biomass to adjust the total pot weight due to increased seedling biomass (based on seedling height) over the course of the experiment. Dry soil was determined to be equivalent to 3% soil moisture using a CS620 Hydrosense soil moisture probe (Campbell Scientific, Inc., Utah, USA). The weight of a pot required to maintain the designated soil moisture levels was then calculated based on this initial measurement.

The seedlings were transplanted on January 6, 2004 and during the 8 months of the experiment we regularly weighed pots and added enough water to bring the pot weight up to the appropriate weight for the watering treatment imposed. It was not feasible to maintain the pots at constant soil moisture; we let the pots dry to 10% below their designated soil moisture level before adding water. This required that the seedlings be watered every three days at the beginning of the experiment and each day by the end of the experiment.

Final harvest

A final harvest was done August 18, 2004. Shoots were dried at 65°C for 48 hours and weighed. Roots were bagged along with their surrounding soil and refrigerated at 4°C. For processing, entire root systems were carefully washed under running water and then cut into approximately 1-cm pieces. All root fragments were placed in a baking dish containing water and a random subsample was then distributed into a Petri plate. We aimed to count at least 100 root tips per individual seedling. In cases where seedlings had fewer than 100 root tips, all tips were counted. Generally, ectomycorrhizal tips were turgid and smooth, had emanating hyphae or rhizomorphs, and a Hartig net. A root tip that was dark and wrinkled, or was somewhat hollow and fragmented under minimal pressure was classified as dead. Gross morphology of ectomycorrhizal roots and rhizomorphs was determined under a stereomicroscope while Hartig net, mantle, emanating hyphae, and other such features were observed with a compound microscope under 400 or 1000x magnification. When possible, mantle peels were made by separating the fungal tissue from the root with fine forceps and microscalpels. Morphological descriptions were made with reference primarily to Ingleby et al. (1990) and Goodman et al. (1996). Once processed, roots were dried at 65°C for 48 hours and weighed.

Two root tips representing each morphotype were lyophilized, and total genomic DNA was extracted from single ectomycorrhizal tips following the methods of Teste et al. (2006) (Chapter 3). We were successful in amplifying fungal DNA from only one morphotype out of seven (see Results), possibly due to lyophilization techniques. Thus, we relied on morphological characteristics to differentiate among ectomycorrhizal types.

104

Statistical analyses

Four response variables were measured or calculated for each seedling at the end of the experiment: percentage of root tips that were mycorrhizal, total dry weight, shoot height, and root:shoot ratios. Data were aggregated to obtain a mean for each site x watering level treatment. We used the actual soil moisture content measured in each pot and treated it as a continuous variable because the soil moisture values of the initially designated categories overlapped.

We used multivariate analyses to test for correlations among seedling growth, soil characteristics and the ectomycorrhizal fungal community. In particular, canonical correspondence analysis (CANOCO 4 - ter Braak and Smilaurer 1998) was used to correlate variation in (i) seedling growth traits, (ii) soil moisture, and (iii) soil fertility with variation in fungal community composition. Fungal community composition was considered in two, multivariate forms. Columns in each matrix represented individual morphotypes and rows represented soils of the various treatment combinations. We first assessed individual morphotypes in a categorical nature which resulted in a matrix of 0s and 1s indicating presence (1) or absence (0) of each individual morphotype. Next, we assessed the abundance of individual morphotypes; this resulted in a matrix of cells with values ranging from 0 to 100 (% relative abundance). This type of analysis assumes that species have unimodal distributions along environmental gradients. Values for soil moisture and soil fertility were in two separate matrices due to asymmetrical units of replication (soil moisture: n = 16; soil fertility: n = 6). We also used redundancy analyses, which assume linear relationships between response and explanatory variables, to correlate (i) soil moisture and (ii) fertility with seedling growth traits (total biomass, root:shoot ratio and seedling height). Values for seedling growth traits were centered and standardized. The significance level for all ordinations was determined by Monte Carlo permutation tests (999 permutations).

Results

Soil properties affected shoot growth (Table 5.3). Specifically, 32% of the variance in seedling traits was explained by soil moisture (p = 0.018); both height and biomass increased with soil moisture (Fig. 5.1). A substantial amount of variance in seedling traits was explained by the ratio of carbon to nitrogen in the soil ($r^2 = 0.63$, p = 0.0090). When examined individually, only height was positively correlated to C:N (Fig.

5.2). On average seedlings were 11.5 (\pm 3.08 SD) cm tall, weighed 2.2 (\pm 1.03 SD) g and had root:shoot of 1.2 (\pm 0.31 SD).

In total, seven morphotypes were identified on the roots of the seedlings (Fig. 5.3) with two *Wilcoxina* morphotypes being the most frequent. Fungal DNA from *Wilcoxina* mycorrhizas with abundant, smooth emanating hyphae matched that of *Wilcoxina mikolae* in a BLAST search of Genbank (99% match; expected = 0.0). A second type of *Wilcoxina* mycorrhiza, which we refer to as *Wilcoxina* II, was clearly distinguishable from the first because it had few, roughly verrucose emanating hyphae. Those matching descriptions of mycorrhizas formed by *Rhizopogon, Amphinema, Piloderma* spp. as well as *Mycelium radicis atrovirens* (MRA)–type mycorrhizas, as described by Jones et al. (1997) and Hagerman et al. (1999), were less frequent.

The presence or absence of each of the seven morphotypes was independent of variation in shoot growth traits (p = 0.27) (Table 5.3). Likewise, variation in soil moisture levels did not explain variation in the presence or absence of the seven ectomycorrhizal fungal morphotypes (p = 0.34) (Table 5.3). Of the soil fertility characteristics measured, only total amount of nitrogen explained significant amounts (31%) of the variance in the presence or absence of ectomycorrhizal fungal morphotypes (p = 0.012) (Table 5.3). Piloderma, Rhizopogon and Amphinema- type morphotypes were present in low nitrogen soils, and both Wilcoxina morphotypes and Cenococcum geophilum occurred in soils with mid-range values of nitrogen (Fig. 5.4). The MRA-type morphotype was present only in high nitrogen soils (Fig. 5.4). No other soil fertility variables (i.e. pH, % organic matter, % organic C, mg kg⁻¹ of NH₄, NO₃/NO₂ and P, or C:N) correlated with presence or absence of morphotypes (minimum $p \ge 0.41$). Total amount of nitrogen was not correlated to C:N ratio in these samples (p = 0.084). Variation in total colonization (i.e., abundance measured by percent colonization of all morphotypes combined) for each site x watering level combination was not correlated to seedling biomass or height (minimum p = 0.95), but was positively correlated to root:shoot ratio (p = 0.048, r = 0.52; Fig. 5.4). Total colonization was not related to the soil moisture level (p = 0.090).

While neither soil moisture levels nor variation in seedling growth covaried with the presence or absence of the individual fungal morphotypes, variation in seedling traits was related to the relative abundance of each of the seven morphotypes (Table 5.3). Specifically, *Wilcoxina mikolae* and *Rhizopogon*-type morphotypes were more abundant on tall seedlings compared to other morphotypes ($r^2 = 0.22$, p = 0.024) (Fig.

5.5). The abundances of each morphotype, however, were not related to soil moisture (p= 0.45) or any of the soil fertility variables (minimum p \geq 0.074).

Discussion

In our study, the composition of the ectomycorrhizal fungal community was influenced both directly and indirectly by variation in the soil environment. The presence or absence of each of the seven morphotypes was correlated with total soil nitrogen, but this community metric was not correlated to any host shoot growth responses. In other words, of the pool of morphotypes sampled in our assay, occurrence of each morphotype was influenced by the soil environment. When morphotypes were measured by their relative abundance, we found that the abundance of specific morphotypes did not respond directly to any of the soil variables, but instead was mediated by growth characteristics in the host. Because host growth was affected by soil moisture and C:N ratios, we suggest that the abundance of morphotypes sampled were indirectly affected by soil conditions.

It is to be expected that the presence or absence of individual morphotypes correlated directly to soil nitrogen. Because we did not measure nitrogen status of host individuals, we cannot distinguish whether fungi responded directly to nitrogen levels in the soil or indirectly via nitrogen status of the host (e.g. Nilsson and Wallander 2003). However, there have been numerous studies showing that in culture, ectomycorrhizal fungal species show distinct preferences for different forms and levels of nitrogen (e.g. Lilleskov et al. 2002 and references therein). Niche segregation along nitrogen gradients has also been demonstrated in the field (see reviews by Wallenda and Kottke 1998, Treseder and Allen 2000). Interestingly, those factors that affected the presence or absence of individual morphotypes did not affect seedling growth traits. Nantel and Neumann (1992) also reported that factors affecting fungal species distribution were different from those affecting the distribution of their tree hosts, namely humus characteristics. More recently, Toljander et al. (2006) demonstrated that despite variation in host identity along a nutrient gradient, most variation in the ectomycorrhizal fungal community was attributable to soil characteristics such as extractable ammonium and base saturation. Overall, findings from previous literature suggest that beta diversity in ectomycorrhizal fungal communities is somewhat controlled by the presence or

absence of particular host species, but soil environmental heterogeneity is a more important factor maintaining ectomycorrhizal fungal diversity.

Our results were based on the responses of seedlings grown from open pollinated seeds in which the effect of genetic diversity is expected to be consistent across treatments. Thus, the nearly three-fold difference in seedling heights we observed was probably mostly due to soil environmental variation. The range of soil variation coincides with the elevational range of Douglas-fir in this study area. However, because we had few samples (n = 6) of soils within the study area, the resolving power of seedling sensitivity to variation in soil characteristics is low. Nonetheless, this difference in seedling heights is more than that reported by Korkama et al. (2006) who observed dissimilar ectomycorrhizal fungal communities between fast and slow-growing clones of *Picea abies*. In our study the phenotypic gradient, as measured by variation in shoot biomass, height and root: shoot ratios, was not sufficient to promote partitioning among fungal morphotypes. It is possible that phenotypic variation expressed belowground could be amplified to the extent that the composition of the ectomycorrhizal community would be affected. In particular, variation in quantity and quality of exudates, should be tested as possible determinants of membership within ectomycorrhizal fungal communities.

The environmental gradients did not influence host intraspecific variation sufficiently to determine membership within the fungal community, however they were important in modifying the abundance of morphotypes present. Because it is unlikely that colonization levels of individual morphotypes influence host intraspecific variation to the same extent as variation in soil characteristics (e.g. C:N ratios explained 63% of the variance in seedling growth traits whereas only 22% was related to morphotype abundance), we suggest that C:N ratios and soil moisture levels may act indirectly to modify the abundance of individual morphotypes. Högberg et al. (2007) also reported the importance of indirect effects of soil chemistry (C:N ratio) on abundance of ectomycorrhizal fungi as measured by PLFA biomarkers.

Of the soil characteristics measured, it was surprising how little impact variation in soil moisture had on the ectomycorrhizal fungal community. Soil moisture has been shown to induce changes in the species composition of ectomycorrhizal fungal communities surveyed in intact forests (Shi et al. 2002; Swaty et al. 2004) and in part this is thought to reflect differences in the drought tolerance of ectomycorrhizal fungi (Parke et al. 1983; Boyle and Hellenbrand 1991). The relationship between ectomycorrhizal colonization and soil moisture has been previously reported but the direction of the response varies (Lodge 1989; Gehring and Whitham 1994; Runion et al. 1997; Nilsen et al. 1998; Swaty et al. 1998; Valdes et al. 2006). The portion of the soil moisture gradient studied clearly influences the response of ectomycorrhizas to soil moisture, but despite a four-fold difference in imposed soil moisture values, ectomycorrhizal fungi did not sort along this particular gradient. Possibly, plasticity of colonization levels present at a fungal species level accommodates variation in soil moisture.

Because we removed soils from the field, the available ectomycorrhizal fungal species pool should have been similar across soils as we sampled only those species with resistant propagules. Results from both the field (e.g. Bidartondo et al. 2001) and greenhouse studies document that the resistant propagule community (sensu Taylor and Bruns [1999]) is often spatially homogeneous. For example, *Wilcoxina* spp. and *Cenococcum geophilum* were reported to be abundant and spatially homogeneous in soils collected from mixed-conifer forest bioassayed with two host species (Izzo et al. 2006). Cline et al. (2005) demonstrated that ectomycorrhizal fungal communities on Douglas-fir seedlings planted at various distances outside mycelium networks were similar to those on greenhouse seedlings grown in field soil. We cannot rule out however, that those fungal species widely distributed via resistant propagules may also be "generalists" when responding to intraspecific host variation and soil moisture.

In conclusion, individuals of a host species and species within their associated ectomycorrhizal fungal community respond to different environmental gradients. While host traits were controlled mostly by variation in soil moisture and C:N ratio, the occurrence of particular ectomycorrhizal morphotypes was structured by levels of total nitrogen. Host variation did not directly affect the presence or absence of individual ectomycorrhizal fungal morphotypes. However, host variaiton was correlated to the relative abundance of each of the ectomycorrhizal fungal morphotypes, suggesting that the abundance of morphotypes may be modified by those gradients affecting intraspecific host variation. At the seedling stage, soil nitrogen and host growth characteristics influence composition of ectomycorrhizal fungal communities.

Table 5.1: Site coordinates and elevation of soil sampling locations.

Site Label	Latitude	Longitude	Elevation (masl)
BB	50°01.918N	119°21.526W	724
BT	50°02.325N	119°15.994W	1318
OB	49°46.737N	119°36.203W	360
ОТ	49°42.792N	119°36.101W	1396
RB	50°44.477N	120°32.409W	648
RT	50°49.064N	120°42.524W	1387

Table 5.2: Fertility characteristics of soils collected from six sites from the Thompson-Okanagan region of British Columbia. Values are from a composite of 6 samples per site.

							Р	
		Organic					(Bray-	
Site		matter	Organic	NH₄	NO ₃ /NO ₂	Total	P1)	
Label	pН	(LOI) (%)	C (%)	(mg/kg)	(mg/kg)	N (%)	(mg/kg)	C:N
BB	7.3	8.4	4.2	10	6	0.30	44.3	14
вт	6.0	11.7	5.8	9	0.1	0.15	25.9	40
OB	5.0	16.8	8.4	20	0.1	0.22	86.9	38
ОТ	4.7	18.2	9.1	19	. 0.1	0.21	51.9	44
RB	6.2	11.0	5.5	22	16.5	0.19	100.0	29
RT	5.6	9.8	4.9	9	0.5	0.14	57.7	35

111

Table 5.3: Types of statistical analyses (canonical correspondence analysis [CCA] or redundancy analysis [RA]) used and significance of explanatory variables tested to explain measures of ectomycorrhizal fungal community composition or seedling growth traits. Only those soil aspects of soil fertility found to be significant are reported in table. Numbers in brackets represent percentage of variance explained by each significant explanatory factor.

Explanatory variable*	Response variable		
	Presence/absence of	Abundance of	
	individual	individual	
	morphotypes	morphotypes	
	р	р	
Soil moisture	0.34	0.45	
Seedling growth traits∞	0.27	0.024 (22%)	
Soil fertility (% total N)	0.012 (31%)	≥ 0.074†	
	Explanatory variable* Soil moisture Seedling growth traits∞ Soil fertility (% total N)	ResponseExplanatory variable*Presence/absence of individual morphotypesDistributionPresence/absence of individual morphotypesSoil moisture0.34Seedling growth traits∞0.27Soil fertility (% total N)0.012 (31%)	

RA

	Seedling growth
	traits
Soil moisture	0.018 (32%)
Soil fertility (C:N)	0.0090 (63%)

* Variables are categorized as explanatory, however it should be recognized that in both analyses, causation cannot be inferred.

 \dagger none of the measures of soil fertility (pH, % organic matter, % organic C, % total N, mg kg⁻¹ of NH₄, NO₃/NO₂ and P, and C:N) were significant in explaining variation in abundance of individual morphotypes. The minimum p-value across all measures is given.

∞seedling growth traits include shoot height, total biomass and root:shoot

Figure 5.1: Relationships between soil moisture (%) and seedling height, biomass and root:shoot ratio.





Figure 5.2: Relationships between soil C:N and seedling height, biomass and root:shoot.

Figure 5.3: Frequency of ectomycorrhizal morphotypes observed across seedlings of *Pseudotsuga menziesii* var. *glauca*.



Figure 5.4: Canonical correspondence analysis of ectomycorrhizal morphotypes observed on seedlings of *Pseudotsuga menziesii* var. *glauca* ordinated along gradient of % total soil nitrogen.



Figure 5.5: Relationship between percent ectomycorrhizal colonization and root:shoot ratio of *Pseudotsuga menziesii* var. *glauca* seedlings.



Figure 5.6: Canonical correspondence analysis of ectomycorrhizal morphotypes observed on seedlings of *Pseudotsuga menziesii* var. *glauca* ordinated along gradient of seedling height.



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6 Conclusions

Ectomycorrhizal associations represent interactions among species that are tightly linked, both physically and physiologically. We therefore expect organisms involved in ectomycorrhizal associations to be more sensitive to variation within each partner than organisms involved in free-living associations (e.g. predator-prey relationships). In this thesis, I used meta-analysis and experimental approaches to consider how variation in one partner of the ectomycorrhizal symbiosis affected the other. In particular, my objectives were to evaluate:

- i. how colonization levels, regardless of ectomycorrhizal fungal taxon, correlated with host growth
- ii. how ectomycorrhizal fungi differentially influenced growth of different genera of plant hosts, and
- iii. how variation in growth of a single host species was correlated to the composition of ectomycorrhizal fungal communities in various soil environments.

Because some of my conclusions relied on comparisons of inoculated and noninoculated seedlings, I also tested the efficacy of two methods to control colonization by ectomycorrhizal fungi on host plants. These results are of practical significance because prior to our experiment, no one had tested whether it was possible to reduce ectomycorrhizal colonization in unsterilized field soil.

My thesis objectives can be distilled into one summary question: to what level of organization of ectomycorrhizal fungi does the growth of host plants respond? I considered several levels of organization: 1. colonization levels regardless of ectomycorrhizal fungal taxon, 2. taxonomic identity of ectomycorrhizal fungi, and 3. communities of ectomycorrhizal fungi. By conducting a meta-analysis on a large body of previously published work, and by applying multivariate analyses to my experimental data, I was able to evaluate the contribution of the three levels of organization to variation in growth responses of host plants. Three main conclusions emerged.

The relationship between colonization level and host growth response is inconsistent

When considering individuals of a particular species of host plant, variation in host growth varied with the abundances of different morphotypes of ectomycorrhizal fungi (Chapter 5). In other words, colonization levels of some fungi increased with seedling height, and decreased for other fungal morphotypes. The relationship between total colonization level and seedling growth differed among seed families of a host species (Chapter 4). When considered across many host genera, I detected no relationship between colonization level and host growth response, regardless of fungal taxon (Chapter 2). These findings suggest that for the most part, host growth response to colonization level is unpredictable.

In order to study the effects of ectomycorrhizal fungi on plants, it is helpful to have control plants that are completely free of ectomycorrhizal contamination. However, this can be challenging in the lab (Chapter 2), and almost impossible in non-sterile field soils (Chapters 3). My experiments demonstrated that fungicides or mesh have the potential to reduce colonization, but this may be of little value if host growth responses do not consistently scale with colonization levels. If plants sometimes respond to very low levels of colonization, this raises the question of whether reductions in colonization levels are meaningful treatments to assess host response to ectomycorrhizas.

There is little sensitivity in growth responses of host plants to variation in the identity of ectomycorrhizal fungi

Seedlings across multiple host genera increased in biomass and shoot height when inoculated with ectomycorrhizal fungi regardless of the identity of the fungal associate (Chapter 2). When ectomycorrhizas were considered in a multi-specific context (i.e. one host species associated with a community of ectomycorrhizal fungi), variation in host shoot properties did not correlate with species composition of the community of ectomycorrhizal fungi on their roots but rather appeared to be more tightly coupled to edaphic conditions (Chapter 5). Thus, the variation a host plant perceives and selects for in ectomycorrhizal fungi may be of a discrete rather than continuous nature, i.e., host plants respond to the presence or absence of ectomycorrhizal fungi but not to variation in their identity. A consequence of the coevolution among organisms in multi-specific systems may be that reciprocal specialization is unlikely, therefore host plants tend to be generalists in their responses to variation in the identity of ectomycorrhizal fungi.

Publication bias exists in the ectomycorrhizal literature

The meta-analysis investigating the mutualism-parasitism continuum in ectomycorrhizas represents a significant advance in the field of ectomycorrhizal research because it statistically evaluates and summarizes nearly four decades of research on inoculation trials. I demonstrated that publication bias has clouded our ability to determine general principles of host response to ectomycorrhizal inoculation. In the past, mycorrhizas were synonymous with mutualisms, and the tendency to publish results congruent with this perception has resulted in the under representation of studies reporting contrary results demonstrating a more parasitic role for ectomycorrhizas.

Future research directions

The approaches used in my thesis represent initial tests to determine the importance of symbiotic variation to host growth. I suggest several avenues of further research. While the effects of host genotype on colonization level have been documented (Tagu et al. 2001, 2005, Gehring et al. 2006), we are far from understanding host genotype x ectomycorrhiza interactions. Research is necessary to determine the relative importance of host genetics versus the presence, absence and species of ectomycorrhizal fungi on intraspecific variation in growth among individual host plants. This type of research would clarify the importance of interactions between hosts and ectomycorrhizal fungi in influencing seedling growth. I have contributed to this particular topic in Chapter 4 with evidence that the relationship between colonization level and host growth can be positive or negative, depending on plant genotype, within a host species. However, the weakness of this experiment is that the seedlings were not colonized by target fungi. Implementing other inoculation techniques, such as submerging root systems of seedlings in slurries of inoculum or use solid inoculum, may increase the success of inoculation.

It is also critical that future research explores the magnitude of specialization between host taxa and communities of ectomycorrhizal fungi. Multi-specific rather than pairwise interactions have been recognized to be the norm for coevolved organisms (Stanton 2003, Strauss and Irwin 2004) and those organisms involved in ectomycorrhizal associations are no exception – individual trees frequently host communities of ectomycorrhizal fungi. In other study systems, the role of host plant morphological variation has been shown to be important in determining the composition of dependent communities (Whitham et al. 2006). Until very recently, we have known virtually nothing about how host plants influence the composition of ectomycorrhizal communities. Two pioneering studies have finally addressed this question and found that the relative growth rates (Korkama et al. 2006) and taxonomic identity (Ishida et al. 2007) of hosts alter the composition of their ectomycorrhizal fungal communities, yet much more research is required to adequately assess the sensitivity of host plants to changes in membership within ectomycorrhizal fungal communities and vice versa.

Although the meta-analysis in Chapter 2 is powerful in synthesizing decades of research, it is limited by the features of the studies included in the analysis. In particular, pair-wise host-fungal combinations were the norm, thus conclusions on the sensitivity of hosts to variation in the identity of ectomycorrhizal fungi may change if interactions among species of ectomycorrhizal fungi were to be present. Co-inoculation of hosts by several fungi is challenging and sampling in the field may yield more information on the specificity between hosts and communities of ectomycorrhizal fungi. For example, surveying the taxonomic affinities between various host taxa and their ectomycorrhizal fungal communities, complimented by field experiments that manipulate host characteristics would be a useful initial approach to address this question.

That hosts perceive ectomycorrhizal fungi as functionally redundant, as suggested by the meta-analysis in Chapter 2, may indicate that edaphic conditions are more important than the presence and/or variation in composition of ectomycorrhizal fungal communities in determining seedling growth. In addition, results from Chapter 5 indicate that host growth is coupled to edaphic conditions. Variation in edaphic conditions takes many forms and, compared to descriptions of vegetative variation, our understanding of variation in soil characteristics is poor (but see Bell and Lechowicz 1991, Bell et al. 1993, Farley and Fitter 1999). In particular, the role of spatial structure in the edaphic environment will be critical to understanding the role of ectomycorrhizal associations to host growth given the strong spatial covariance between the composition of ectomycorrhizal fungal communities and soil characteristics. This feature makes it difficult to untangle the ecological importance of either to host plant growth.

The strength of the analytical approach taken in Chapter 5 is that it identifies and statistically parses the variation in host growth due to variation in the composition of fungal communities and soil characteristics – a conceptually novel framework. The weaknesses of the experiment presented in Chapter 5 are that no causation can be inferred and the low number of soils sampled effectively shortens the environmental gradient that might influence host growth and membership within ectomycorrhizal fungal communities. While the contribution of abiotic and symbiotic factors in structuring ectomycorrhizal fungal communities has been evaluated (Nantel and Neumann 1992, Kernaghan et al. 2003, Gehring et al. 2006, Toljander et al. 2006, Hogberg et al. 2007, Taniguchi et al. 2007), it has rarely been posed from a host perspective (but see Dickie et al. 2007). An experimental design for the field that renders changes in the composition of ectomycorrhizal fungal communities independent from variation in soil characteristics remains elusive yet stands as an important challenge in mycorrhizal research.

Final conclusion

Numerous opportunities now exist to investigate the distribution and abundance of plant species in the context of ectomycorrhizal associations. In particular, the degree to which host plants and ectomycorrhizal fungal communities are specialized will be relevant information for forecasts of species' shifts with climate change. As ranges of symbionts are unlikely to change concordantly, it will be crucial to understand the basis and consequences of coevolution between hosts and fungi to predict their future distributions.

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Appendices

A. Identity of host plant and fungal species pairings and effect sizes (Ln R) for seedling biomass, shoot height and shoot:root ratio for each study used in meta-analysis.

				Ln R	
Authors	Host species	Fungal species	Biomass	Height	Shoot:root
			n=459	n=329	n=235
Baum et al. 2000	Populus trichocarpa	Laccaria bicolor	-0.518	-0.334	-0.522
Baum et al. 2000	Populus trichocarpa	Laccaria bicolor	0.856	0.529	1.627
Baum et al. 2000	Populus trichocarpa	Paxillus involutus	-0.319	-0.401	-0.895
Baum et al. 2000	Populus trichocarpa	Paxillus involutus	0.797	0.485	1.600
Baum et al. 2002	Populus trichocarpa	Laccaria laccata		0.305	
Baum et al. 2002	Populus trichocarpa	Laccaria laccata		0.101	
Baum et al. 2002	Populus trichocarpa	Laccaria laccata		0.005	
Baumann et al. 2005	Pinus sylvestris	Paxillus involutus	0.251		-0.198
Baumann et al. 2005	Pinus sylvestris	Paxillus involutus	-0.111		0.358
Baumann et al. 2005	Pinus sylvestris	Paxillus involutus	0.064		-0.087
Baumann et al. 2005	Pinus sylvestris	Paxillus involutus	0.066		-0.399
Baumann et al. 2005	Pinus sylvestris	Paxillus involutus	0.292		0.048
Baumann et al. 2005	Pinus sylvestris	Paxillus involutus			
Beyeler & Heyser 1997	Fagus sylvatica	Lactarius subdulcis	0.272		
Bougher et al. 1990	Eucalyptus diversicolor	Descolea maculata	0.894		
Bougher et al. 1990	Eucalyptus diversicolor	Descolea maculata	0.368		
Bougher et al. 1990	Eucalyptus diversicolor	Laccaria laccata	0.575		
Browning & Whitney 1991	Pinus banksiana	Pisolithus tinctorius	-0.031		0.236
Browning & Whitney 1991	Pinus banksiana	Cenococcum geophilum	0.000		0.086
Browning & Whitney 1991	Pinus banksiana	Laccaria proxima	-0.014		0.114
Browning & Whitney 1991	Pinus banksiana	Hebeloma cylindrosporum	-0.030		-0.150
Browning & Whitney 1991	Pinus banksiana	Tricholoma pessundatum	-0.065		0.233

130

Authors Browning & Whitney 1991 Burgess & Malajczuk 1989 Burgess & Malajczuk 1989 Burgess & Malajczuk 1989 Burgess et al. 1994 Burgess et al. 1994 Burgess et al. 1994 Burgess et al. 1994

Host species Pinus banksiana Picea mariana Eucalyptus globulus Eucalyptus globulus Eucalyptus globulus Eucalyptus grandis Eucalyptus grandis Eucalyptus grandis Eucalyptus grandis

		Ln R			
Fungal species	Biomass	Height	Shoot:root		
Thelephora terrestris	-0.046		0.231		
Suillus granulatus	-0.058		0.242		
Hebeloma cylindrosporum	0.126		-0.022		
Pisolithus tinctorius	0.163		-0.004		
Laccaria proxima	0.198		0.034		
Tricholoma pessundatum	0.138		0.143		
Cenococcum geophilum	0.129		-0.056		
Laccaria bicolor	-0.099		0.186		
Laccaria proxima	0.037		0.307		
Pisolithus tinctorius	-0.092		0.313		
Tricholoma pessundatum	-0.020		0.336		
Hebeloma cylindrosporum	-0.007		0.275		
Thelephora terrestris	0.030		0.374		
Cenococcum geophilum	0.020		0.306		
Suillus granulatus	0.020		0.234		
Laccaria bicolor	-0.104		0.153		
Hebeloma cylindrosporum	-0.005		0.329		
Pisolithus tinctorius	0.010		0.058		
Laccaria proxima	0.172		0.320		
Tricholoma pessundatum	-0.005		0.015		
unknown	0.813				
unknown	0.957				
unknown	1.253				
Pisolithus sp	0.511	0.303			
Pisolithus sp	0.863	0.493			
Pisolithus sp	1.111	0.614			
Pisolithus sp	1.215	0.650			
				Ln R	
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Authors	Host species	Fungal species	Biomass	Height	Shoot:root
Burgess et al. 1994	Eucalyptus grandis	Pisolithus sp	1.804	1.249	
Burgess et al. 1994	Eucalyptus grandis	Pisolithus sp	1.956	1.308	
Burgess et al. 1994	Eucalyptus grandis	Pisolithus sp	2.408	1.434	
Burgess et al. 1994	Eucalỳptus grandis	Pisolithus sp	2.576	1.531	
Burgess et al. 1994	Eucalyptus grandis	Pisolithus sp	2.650	1.590	
Burgess et al. 1994	Eucalyptus grandis	Pisolithus sp	2.696	1.632	
Burgess et al. 1994	Eucalyptus grandis	Pisolithus sp	2.802	1.646	
Burgess et al. 1994	Eucalyptus grandis	Pisolithus sp	2.824	1.686	
Burgess et al. 1994	Eucalyptus grandis	Pisolithus sp	3.086	1.762	
Burgess et al. 1994	Eucalyptus grandis	Pisolithus sp	3.116	1.809	
Burgess et al. 1994	Eucalyptus grandis	Pisolithus sp	3.173	1.843	
Burgess et al. 1994	Eucalyptus grandis	Pisolithus sp	3.173	1.842	
Burgess et al. 1994	Eucalyptus grandis	Pisolithus sp	3.189	1.886	
Burgess et al. 1994	Eucalyptus grandis	Pisolithus sp	3.202	1.896	
Burgess et al. 1994	Eucalyptus grandis	Pisolithus sp	3.305	1.928	
Burgess et al. 1994	Eucalyptus grandis	Pisolithus sp	3.566	2.099	
Chakravarty & Unestam 1987	Pinus sylvestris	Laccaria laccata	0.489	0.143	
Chakravarty & Unestam 1987	Pinus sylvestris	Hebeloma crustulinforme	0.032	0.000	
Chakravarty & Unestam 1987	Pinus sylvestris	Pisolithus tinctorius	0.614	0.208	
Chakravarty & Unestam 1987	Pinus sylvestris	unknown	0.643	0.268	
Chakravarty & Unestam 1987	Pinus sylvestris	Laccaria laccata	0.489	0.143	
Chakravarty & Unestam 1987	Pinus sylvestris	Hebeloma crustulinforme	0.032	0.000	
Chakravarty & Unestam 1987	Pinus sylvestris	Pisolithus tinctorius	0.614	0.208	
Chakravarty & Unestam 1987	Pinus sylvestris	unknown	0.643	0.268	
Chen et al. 2006	Eucalyptus globulus	Scleroderma cepa	0.000	0.248	
Chen et al. 2006	Eucalyptus globulus	Scleroderma cepa	0.000	0.686	
Chen et al. 2006	Eucalyptus globulus	Scleroderma cepa	0.000	0.598	

				Ln R	
Authors	Host species	Fungal species	Biomass	Height	Shoot:root
Chen et al. 2006	Eucalyptus globulus	Scleroderma cepa	0.000	1.152	
Chen et al. 2006	Eucalyptus globulus	Scleroderma cepa	0.000	1.152	
Chen et al. 2006	Eucalyptus globulus	Scleroderma citrinum	0.000	0.092	
Chen et al. 2006	Eucalyptus globulus	Scleroderma citrinum	0.000	0.430	
Chen et al. 2006	Eucalyptus globulus	Scleroderma citrinum	0.000	0.213	
Chen et al. 2006	Eucalyptus globulus	Scleroderma citrinum	0.000	1.021	
Chen et al. 2006	Eucalyptus globulus	Scleroderma citrinum	0.000	1.510	
Chen et al. 2006	Eucalyptus urophylla	Scleroderma cepa	0.000	0.666	
Chen et al. 2006	Eucalyptus urophylla	Scleroderma cepa	0.000	0.759	
Chen et al. 2006	Eucalyptus urophylla	Scleroderma cepa	0.000	1.275	
Chen et al. 2006	Eucalyptus urophylla	Scleroderma cepa	0.000	1.214	*. :
Chen et al. 2006	Eucalyptus urophylla	Scleroderma cepa	0.000	0.319	
Chen et al. 2006	Eucalyptus urophylla	Scleroderma citrinum	0.000	0.093	
Chen et al. 2006	Eucalyptus urophylla	Scleroderma citrinum	0.000	0.378	
Chen et al. 2006	Eucalyptus urophylla	Scleroderma citrinum	0.000	1.491	
Chen et al. 2006	Eucalyptus urophylla	Scleroderma citrinum	0.000	0.903	
Chen et al. 2006	Eucalyptus urophylla	Scleroderma citrinum	0.000	0.325	
Chen et al. 2006	Eucalyptus globulus	Scleroderma albidum	0.034	0.198	
Chen et al. 2006	Eucalyptus globulus	Scleroderma albidum	0.128	0.168	
Chen et al. 2006	Eucalyptus globulus	Scleroderma areolatum	0.128	0.104	
Chen et al. 2006	Eucalyptus globulus	Scleroderma areolatum	-0.116	0.059	
Chen et al. 2006	Eucalyptus globulus	Scleroderma areolatum	0.476	0.329	
Chen et al. 2006	Eucalyptus globulus	Scleroderma cepa	-0.065	0.021	
Chen et al. 2006	Eucalyptus globulus	Scleroderma cepa	0.049	0.238	
Chen et al. 2006	Eucalyptus globulus	Scleroderma cepa	0.311	0.104	
Chen et al. 2006	Eucalyptus globulus	Scleroderma citrinum	-0.112	0.104	
Chen et al. 2006	Eucalyptus globulus	Scleroderma citrinum	0.171	0.168	

				Ln R	
Authors	Host species	Fungal species	Biomass	Height	Shoot:root
Chen et al. 2006	Eucalyptus globulus	Scleroderma flavidum	0.153	0.147	
Chen et al. 2006	Eucalyptus globulus	Scleroderma flavidum	0.430	0.329	
Chen et al. 2006	Eucalyptus globulus	Scleroderma paradoxum	0.125	0.389	
Chen et al. 2006	Eucalyptus globulus	Scleroderma sp	0.220	0.247	
Chen et al. 2006	Eucalyptus globulus	Scleroderma verrucosum	0.155	0.168	
Chen et al. 2006	Eucalyptus urophylla	Scleroderma albidum	0.714	0.294	
Chen et al. 2006	Eucalyptus urophylla	Scleroderma albidum	0.042	0.216	
Chen et al. 2006	Eucalyptus urophylla	Scleroderma areolatum	0.300	0.152	
Chen et al. 2006	Eucalyptus urophylla	Scleroderma areolatum	0.005	0.184	
Chen et al. 2006	Eucalyptus urophylla	Scleroderma areolatum	0.123	0.205	
Chen et al. 2006	Eucalyptus urophylla	Scleroderma cepa	-0.079	0.108	
Chen et al. 2006	Eucalyptus urophylla	Scleroderma cepa	0.612	0.275	
Chen et al. 2006	Eucalyptus urophylla	Scleroderma_cepa	-0.165	0.085	
Chen et al. 2006	Eucalyptus urophylla	Scleroderma citrinum	-0.214	-0.013	
Chen et al. 2006	Eucalyptus urophylla	Scleroderma citrinum	0.327	0.426	
Chen et al. 2006	Eucalyptus urophylla	Scleroderma flavidum	0.419	0.375	
Chen et al. 2006	Eucalyptus urophylla	Scleroderma flavidum	0.750	0.483	
Chen et al. 2006	Eucalyptus urophylla	Scleroderma paradoxum	0.451	0.393	
Chen et al. 2006	Eucalyptus urophylla	Scleroderma sp	0.559	0.536	
Chen et al. 2006	Eucalyptus urophylla	Scleroderma verrucosum	0.507	0.331	
Chen et al. 2006	Pinus elliottii	Scleroderma albidum	0.400	0.270	,
Chen et al. 2006	Pinus elliottii	Scleroderma albidum	0.253	0.277	
Chen et al. 2006	Pinus elliottii	Scleroderma areolatum	-0.102	0.178	
Chen et al. 2006	Pinus elliottii	Scleroderma areolatum	-0.150	0.109	
Chen et al. 2006	Pinus elliottii	Scleroderma areolatum	0.302	0.034	
Chen et al. 2006	Pinus elliottii	Scleroderma cepa	-0.221	0.079	
Chen et al. 2006	Pinus elliottii	Scleroderma cepa	0.270	0.134	

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Authors	Host species	Fungal species	Biomass	Height	Shoot:root
Chen et al. 2006	Pinus elliottii	Scleroderma cepa	-0.326	0.100	
Chen et al. 2006	Pinus elliottii	Scleroderma citrinum	-0.312	-0.007	
Chen et al. 2006	Pinus elliottii	Scleroderma citrinum	0.558	0.205	
Chen et al. 2006	Pinus elliottii	Scleroderma flavidum	0.438	0.297	
Chen et al. 2006	Pinus elliottii	Scleroderma flavidum	0.236	0.170	
Chen et al. 2006	Pinus elliottii	Scleroderma paradoxum	0.224	0.146	
Chen et al. 2006	Pinus elliottii	Scleroderma sp	0.224	0.170	
Chen et al. 2006	Pinus elliottii	Scleroderma verrucosum	-0.262	0.021	
Chen et al. 2006	Pinus radiata	Scleroderma albidum	0.959	0.342	
Chen et al. 2006	Pinus radiata	Scleroderma albidum	1.260	0.302	
Chen et al. 2006	Pinus radiata	Scleroderma areolatum	1.134	0.164	
Chen et al. 2006	Pinus radiata	Scleroderma areolatum	0.895	0.146	
Chen et al. 2006	Pinus radiata	Scleroderma areolatum	0.794	0.312	
Chen et al. 2006	Pinus radiata	Scleroderma cepa	1.080	0.165	
Chen et al. 2006	Pinus radiata	Scleroderma cepa	0.830	0.255	
Chen et al. 2006	Pinus radiata	Scleroderma cepa	0.959	0.176	
Chen et al. 2006	Pinus radiata	Scleroderma citrinum	0.391	0.070	
Chen et al. 2006	Pinus radiata	Scleroderma citrinum	0.717	0.213	
Chen et al. 2006	Pinus radiata	Scleroderma flavidum	0.935	0.435	
Chen et al. 2006	Pinus radiata	Scleroderma flavidum	0.717	0.266	
Chen et al. 2006	Pinus radiata	Scleroderma paradoxum	0.830	0.400	
Chen et al. 2006	Pinus radiata	Scleroderma sp	0.747	0.422	
Chen et al. 2006	Pinus radiata	Scleroderma verrucosum	0.623	0.198	
Choi et al. 2005	Pinus densiflora	Pisolithus tinctorius			
Choi et al. 2005	Pinus densiflora	Pisolithus tinctorius			
Conjeaud et al. 1996	Pinus pinaster	Hebeloma cylindrosporum			-
Diedhiou et al. 2005	Afzelia africana	Scleroderma dictyosporum	0.303		-0.518 -1 35 5

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Authors	Host species	Fungal species	Biomass	Height	Shoot:root
Diedhiou et al. 2005	Afzelia africana	Scleroderma verrucosum	0.175		-0.535
Diedhiou et al. 2005	Afzelia africana	Pisolithus sp	0.288		-0.417
Diedhiou et al. 2005	Afzelia africana	Thelephora sp	0.281		-0.461
Diedhiou et al. 2005	Afzelia bella	Scleroderma dictyosporum	0.571		-0.976
Diedhiou et al. 2005	Afzelia bella	Scleroderma verrucosum	0.595		-0.939
Diedhiou et al. 2005	Afzelia bella	Pisolithus sp	0.360		-1.182
Diedhiou et al. 2005	Afzelia bella	Thelephora sp	0.358		-0.973
Diedhiou et al. 2005	Anthonotha macrophylla	Scleroderma dictyosporum	0.081		0.181
Diedhiou et al. 2005	Anthonotha macrophylla	Scleroderma verrucosum	-0.010		0.214
Diedhiou et al. 2005	Anthonotha macrophylla	Pisolithus sp	0.199		-0.088
Diedhiou et al. 2005	Anthonotha macrophylla	Thelephora sp	0.186		0.235
Diedhiou et al. 2005	Cryptosepalum tetraphylum	Scleroderma dictyosporum	0.741		-0.380
Diedhiou et al. 2005	Cryptosepalum tetraphylum	Scleroderma verrucosum	0.302		-0.510
Diedhiou et al. 2005	Cryptosepalum tetraphylum	Pisolithus sp	0.474		-0.492
Diedhiou et al. 2005	Cryptosepalum tetraphylum	Thelephora sp	0.489		-1.063
Diedhiou et al. 2005	Paramacrolobium coeruleum	Scleroderma dictyosporum	0.456		-0.624
Diedhiou et al. 2005	Paramacrolobium coeruleum	Scleroderma verrucosum	0.426		-0.650
Diedhiou et al. 2005	Paramacrolobium coeruleum	Pisolithus sp	0.375		-0.749
Diedhiou et al. 2005	Paramacrolobium coeruleum	Thelephora sp	0.358		-0.744
Diedhiou et al. 2005	Uapaca somon	Scleroderma dictyosporum	2.209		-0.726
Diedhiou et al. 2005	Uapaca somon	Scleroderma verrucosum	2.035		-0.434
Diedhiou et al. 2005	Uapaca somon	Pisolithus sp	2.242		-0.642
Diedhiou et al. 2005	Uapaca somon	Thelephora sp	1.984		-0.688
Dixon et al. 1981	Quercus velutina	Pisolithis tinctorius	1.244	0.598	
Dixon et al. 1981	Quercus velutina	Pisolithis tinctorius	-0.850	-0.405	
Dixon et al. 1983	Quercus velutina	Pisolithus tinctorius		0.162	
Dixon et al. 1983	Quercus velutina	Pisolithus tinctorius		-0.015	
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Authors	Host species	Fungal species	Biomass	Height	Shoot:root
Dixon et al. 1984	Quercus robur	Pisolithuis tinctorius	0.711	0.397	-0.443
Dixon et al. 1984	Quercus robur	Pisolithus tinctorius	0.657	0.451	-0.335
Dixon et al. 1984	Quercus robur	Suillus granulatus	0.249	0.323	-0.074
Dixon et al. 1984	Quercus robur	Thelephora terrestris	0.601	0.420	-0.357
Dixon et al. 1984	Quercus robur	Suillis luteus	0.477	0.307	-0.206
Dixon et al. 1984	Quercus robur	Cenococcum geophilum	0.601	0.411	-0.267
Dixon et al. 1984	Quercus velutina	Pisolithuis tinctorius	0.443	0.209	0.129
Dixon et al. 1984	Quercus velutina	Pisolithus tinctorius	0.246	0.222	0.352
Dixon et al. 1984	Quercus velutina	Suillus granulatus	0.413	0.265	0.163
Dixon et al. 1984	Quercus velutina	Thelephora terrestris	0.443	0.162	-0.042
Dixon et al. 1984	Quercus velutina	Suillis luteus	0.282	0.241	0.311
Dixon et al. 1984	Quercus alba	Pisolithuis tinctorius	0.288	0.211	0.208
Dixon et al. 1984	Quercus alba	Pisolithus tinctorius	0.201	0.305	0.154
Dixon et al. 1984	Quercus alba	Suillus granulatus	0.065	0.141	0.312
Dixon et al. 1984	Quercus alba	Thelephora terrestris	0.105	0.148	0.087
Dixon et al. 1984	Quercus alba	Suillis luteus	0.201	0.205	0.154
Dixon et al. 1987	Pinus taeda	Pisolithus tinctorius	0.095	0.136	
Dixon et al. 1987	Pinus taeda	Pisolithus tinctorius	0.000	0.109	
Dixon et al. 1987	Pinus taeda	Pisolithus tinctorius	0.501	0.331	
Dixon et al. 1987	Pinus taeda	Pisolithus tinctorius	0.071	0.134	
Dixon et al. 1987	Pinus taeda	Pisolithus tinctorius	-0.025	0.080	
Dixon et al. 1987	Pinus taeda	Pisolithus tinctorius	0.476	0.305	
Dixon et al. 1987	Pinus taeda	Pisolithus tinctorius	0.048	0.152	
Dixon et al. 1987	Pinus taeda	Pisolithus tinctorius	0.024	0.138	
Dixon et al. 1987	Pinus taeda	Pisolithus tinctorius	0.491	0.352	
Dixon et al. 1987	Pinus taeda	Pisolithus tinctorius	0.000	0.088	
Dixon et al. 1987	Pinus taeda	Pisolithus tinctorius	0.000	0.111	

. 137

			Ln R	
Host species	Fungal species	Biomass	Height	Shoot:root
Pinus taeda	Pisolithus tinctorius	0.243	0.211	
Pinus taeda	Pisolithus tinctorius	0.023	0.080	۰.
Pinus taeda	Pisolithus tinctorius	0.190	0.095	
Pinus taeda	Pisolithus tinctorius	0.171	0.203	
Pinus taeda	Pisolithus tinctorius	0.023	0.088	
Pinus taeda	Pisolithus tinctorius	0.151	0.095	
Pinus taeda	Pisolithus tinctorius	0.190	0.196	
Pinus taeda	Pisolithus tinctorius	0.223	0.010	
Pinus taeda	Pisolithus tinctorius	0.377	-0.095	
Pinus taeda	Pisolithus tinctorius	0.583	0.310	
Pinus taeda	Pisolithus tinctorius	0.298	0.049	
Pinus taeda	Pisolithus tinctorius	0.391	-0.106	
Pinus taeda	Pisolithus tinctorius	0.649	0.303	
Pinus taeda	Pisolithus tinctorius	0.189	0.010	
Pinus taeda	Pisolithus tinctorius	0.318	-0.062	
Pinus taeda	Pisolithus tinctorius	0.606	0.307	
Pinus radiata	Rhizopogon luteolus		0.075	
Pinus radiata	Rhizopogon roseolus		0.206	
Pinus radiata	Scleroderma citrinum		0.079	
Pinus radiata	Rhizopogon luteolus		0.023	
Pinus radiata	Rhizopogon roseolus		0.143	
Pinus radiata	Scleroderma citrinum		0.175	
Acacia holosericea	Pisolithus tinctorius	0.621		0.715
Eucalyptus urophylla x E. kirtoniana	Pisolithus tinctorius		0.215	
Eucalyptus urophylla x E. kirtoniana	Scleroderma texense		0.148	
Eucalyptus urophylla x E. kirtoniana	Scleroderma aurantium		0.000	
Eucalyptus urophylla x E. kirtoniana	Hebeloma cylindrosporum		-0.041	
	Host species Pinus taeda Pinus radiata Pinus radiata	Host speciesFungal speciesPinus taedaPisolithus tinctoriusPinus radiataRhizopogon luteolusPinus radiataScleroderma citrinumPinus radiataScleroderma citrinumPinus radiataScleroderma citrinumAcacia holosericeaPisolithus tinctoriusEucalyptus urophylla x E. kirtonianaScleroderma aurantiumEucalyptus urophylla x E. kirtonianaScleroderma aurantium	Host speciesFungal speciesBiomassPinus taedaPisolithus tinctorius0.243Pinus taedaPisolithus tinctorius0.023Pinus taedaPisolithus tinctorius0.190Pinus taedaPisolithus tinctorius0.171Pinus taedaPisolithus tinctorius0.023Pinus taedaPisolithus tinctorius0.023Pinus taedaPisolithus tinctorius0.023Pinus taedaPisolithus tinctorius0.151Pinus taedaPisolithus tinctorius0.190Pinus taedaPisolithus tinctorius0.223Pinus taedaPisolithus tinctorius0.233Pinus taedaPisolithus tinctorius0.190Pinus taedaPisolithus tinctorius0.233Pinus taedaPisolithus tinctorius0.223Pinus taedaPisolithus tinctorius0.377Pinus taedaPisolithus tinctorius0.391Pinus taedaPisolithus tinctorius0.391Pinus taedaPisolithus tinctorius0.649Pinus taedaPisolithus tinctorius0.318Pinus taedaPisolithus tinctorius0.606Pinus radiataRhizopogon roseolus189Pinus radiataScleroderma citrinumPinus radiataPinus radiataScleroderma citrinum0.621Eucalyptus urophylla x E. kirtonianaScleroderma exense0.621Eucalyptus urophylla x E. kirtonianaScleroderma aurantium1.621	Ln RHost speciesFungal speciesBiomassHeightPinus taedaPisolithus tinctorius0.2430.211Pinus taedaPisolithus tinctorius0.0230.080Pinus taedaPisolithus tinctorius0.1900.095Pinus taedaPisolithus tinctorius0.1710.203Pinus taedaPisolithus tinctorius0.1710.203Pinus taedaPisolithus tinctorius0.1510.095Pinus taedaPisolithus tinctorius0.1900.196Pinus taedaPisolithus tinctorius0.1900.196Pinus taedaPisolithus tinctorius0.2230.010Pinus taedaPisolithus tinctorius0.377-0.095Pinus taedaPisolithus tinctorius0.377-0.095Pinus taedaPisolithus tinctorius0.391-0.106Pinus taedaPisolithus tinctorius0.391-0.106Pinus taedaPisolithus tinctorius0.391-0.106Pinus taedaPisolithus tinctorius0.318-0.062Pinus taedaPisolithus tinctorius0.318-0.062Pinus taedaPisolithus tinctorius0.3030.010Pinus taedaPisolithus tinctorius0.3030.016Pinus taedaPisolithus tinctorius0.3060.307Pinus taedaPisolithus tinctorius0.6060.307Pinus taedaPisolithus tinctorius0.6060.307Pinus taedaPisolithus tinctorius0.0160.023Pin

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Authors	Host species	Fungal species	Biomass	Height	Shoot:root
Garbave et al. 1988	Eucalyptus urophylla x E. kirtoniana	Scleroderma dictysporum		-0.083	
Garbave et al. 1988	Eucalyptus urophylla x E. kirtoniana	Pisolithis tinctorius		-0.083	
Grandcourt et al. 2004	Dicorynia guianensis	unknown	0.342		
Grandcourt et al. 2004	Eperua falcata	unknown	-0.209		
Heinrich et al. 1988	Eucalyptus pilularis	Pisolithus tinctorius	1.188		
Hung & Molina 1986	Pseudotsuga menziesii	Laccaria laccata	0.352	0.154	0.158
Hung & Molina 1986	Pseudotsuga menziesii	Laccaria laccata	0.388	0.373	0.412
Hung & Molina 1986	Pseudotsuga menziesii	Laccaria laccata	0.385	0.270	0.312
Hung & Molina 1986	Pseudotsuga menziesii	Laccaria laccata	0.384	0.194	0.297
Hung & Molina 1986	Pseudotsuga menziesii	Laccaria laccata	0.277	0.223	0.260
Hung & Molina 1986	Pseudotsuga menziesii	Laccaria laccata	0.390	0.305	0.420
Hung & Molina 1986	Pseudotsuga menziesii	Laccaria laccata	0.298	0.134	0.283
Hung & Molina 1986	Pseudotsuga menziesii	Laccaria laccata	-0.039	0.046	0.162
Hung & Molina 1986	Pseudotsuga menziesii	Laccaria laccata	0.104	0.097	0.121
Hung & Molina 1986	Pseudotsuga menziesii	Laccaria laccata	-0.137	0.000	0.119
Hung & Molina 1986	Pseudotsuga menziesii	Laccaria laccata	-0.136	-0.074	0.001
Hung & Molina 1986	Pseudotsuga menziesii	Laccaria laccata	-0.193	-0.133	0.539
Hung & Molina 1986	Pseudotsuga menziesii	Laccaria laccata	-0.266	-0.166	0.163
Hung & Molina 1986	Pseudotsuga menziesii	Laccaria laccata	-0.029	-0.017	-0.511
Hung & Molina 1986	Pseudotsuga menziesii	Laccaria laccata	0.021	-0.082	-0.106
lvorv & Munga 1983	Pinus caribaea	Pișolithis tinctorius		-0.130	
lvory & Munga 1983	Pinus caribaea	Rhizopogon nigrescens		-0.130	
Ivory & Munga 1983	Pinus caribaea	Scleroderma bovista		-0.109	
Ivory & Munga 1983	Pinus caribaea	Scleroderma texense		0.048	
Ivory & Munga 1983	Pinus caribaea	Thelephora terrestris		0.065	
Lamhamedi et al. 1990	Pinus pinaster	Pisolithus arhizus	-0.261		-0.129
Lambamedi et al. 1990	Pinus pinaster	Pisolithus arhizus	-0.061		-0.294

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Authors	Host species	Fungal species	Biomass	Height	Shoot:root
Authors	Pinus pinaster	Pisolithus arhizus	-0.361		-0.294
Lamhamedi et al. 1990	Pinus pinaster	Pisolithus arhizus	-0.319		0.133
	Pinus pinaster	Pisolithus arhizus	-0.334		-0.217
	Pinus pinaster	Pisolithus arhizus	0.013		-0.224
	Dinus pinaster	Pisolithus arhizus	-0.410		0.096
Lamhamedi et al. 1990	Pinus pinaster	Pisolithus arhizus	-0.022		-0.121
Lamhamedi et al. 1990	Pinus pinaster	Pisolithus arhizus	-0.280		-0.197
Lamhamedi et al. 1990	Pinus pinaster	Pisolithus arhizus	-0.335		-0.370
Lamhamedi et al. 1990	Pinus pinaster	Pisolithus arhizus	-0.242		0.072
Lamhamedi et al. 1990	Pinus pinaster	Pisolithus arhizus	-0.277		-0.198
Lamhamedi et al. 1990	Pinus pinaster	Pisolithus arhizus	0.076		0.035
Lamhamedi et al. 1990	Pinus pinaster	Pisolithus arhizus	-0.300		-0.254
Lamhamedi et al. 1990	Pinus pinaster	Pisolithus arhizus	-0 247		-0.229
Lamhamedi et al. 1990	Pinus pinaster	Pisolithus arhizus	0.247		0.033
Lamhamedi et al. 1990	Pinus pinaster	Pisolithus arhizus	0.001		-0.167
Lamhamedi et al. 1990	Pinus pinaster	Pisolitnus arhizus	-0.230		-0.121
Lamhamedi et al. 1990	Pinus pinaster	Pisolithus arhizus	-0.270		-0 166
Lamhamedi et al. 1990	Pinus pinaster	Pisolithus arhizus	-0.337		0.079
Lamhamedi et al. 1990	Pinus pinaster	Pisolithus arhizus	0.141		0.073
Lamhamedi et al. 1990	Pinus pinaster	Pisolithus arhizus	-0.220		0.064
Lamhamedi et al. 1990	Pinus pinaster	Pisolithus arhizus	-0.329		-0.143
Lamhamedi et al. 1990	Pinus pinaster	Pisolithus arhizus	-0.149		-0.279
Lamhamedi et al. 1990	Pinus pinaster	Pisolithus arhizus	-0.166		0.025
Lamhamedi et al. 1990	Pinus pinaster	Pisolithus arhizus	-0.172		0.026
Lamhamedi et al. 1990	Pinus pinaster	Pisolithus arhizus	0.053		0.139
Lambamedi et al. 1990	Pinus pinaster	Pisolithus arhizus	-0.364		-0.066 140
Lambamedi et al. 1990	Pinus pinaster	Pisolithus arhizus	-0.346		0.095
Lamhamedi et al. 1990	Pinus pinaster	Pisolithus arhizus	-0.194		0.043

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Authors	Host species	Fungal species	Biomass	Height	Shoot:root
Lambamedi et al. 1990	Pinus pinaster	Pisolithus arhizus	-0.337		0.093
Lamhamedi et al. 1990	Pinus pinaster	Pisolithus arhizus	-0.276		-0.142
Lambamedi et al. 1990	Pinus pinaster	Pisolithus arhizus	-0.321		0.010
Lamhamedi et al. 1990	Pinus pinaster	Pisolithus arhizus	-0.119		0.004
Lamhamedi et al. 1990	Pinus pinaster	Pisolithus arhizus	-0.222		0.120
Lambamedi et al. 1990	Pinus pinaster	Pisolithus arhizus	0.098		0.006
Lamhamedi et al. 1990	Pinus pinaster	Pisolithus arhizus	-0.136		-0.045
Lambamedi et al. 1990	Pinus pinaster	Pisolithus arhizus	-0.170		0.011
Lambamedi et al. 1990	Pinus pinaster	Pisolithus arhizus	-0.232		0.021
Lamhamedi et al. 1990	Pinus pinaster	Pisolithus arhizus	0.058		0.017
Lamhamedi et al. 1990	Pinus pinaster	Pisolithus arhizus	-0.018		-0.009
Lamhamedi et al. 1990	Pinus pinaster	Pisolithus arhizus	-0.268		0.059
Lamhamedi et al. 1990	Pinus pinaster	Pisolithus arhizus	-0.332		0.067
Lamhamedi et al. 1990	Pinus pinaster	Pisolithus arhizus	-0.312		0.032
Lamhamedi et al. 1990	Pinus pinaster	Pisolithus arhizus	-0.067		0.108
Lamhamedi et al. 1990	Pinus pinaster	Pisolithus arhizus	-0.029		0.072
Lamhamedi et al. 1990	Pinus pinaster	Pisolithus arhizus	-0.130		0.057
Lamhamedi et al. 1990	Pinus pinaster	Pisolithus arhizus	0.002		0.238
Lamhamedi et al. 1990	Pinus pinaster	Pisolithus arhizus	-0.269		0.073
Lamhamedi et al. 1990	Pinus pinaster	Pisolithus arhizus	-0.131		-0.040
Lambamedi et al. 1990	Pinus pinaster	Pisolithus arhizus	-0.039		-0.213
Lambamedi et al. 1990	Pinus pinaster	Pisolithus arhizus	0.051		0.051
Lamhamedi et al. 1990	Pinus pinaster	Pisolithus arhizus	-0.050		0.054
Lamhamedi et al. 1990	Pinus pinaster	Pisolithus arhizus	0.010		0.103
Lamhamedi et al. 1990	Pinus pinaster	Pisolithus arhizus	-0.144		0.058
Lamhamedi et al. 1990	Pinus pinaster	Pisolithus arhizus	-0.370		-0.199
Lamhamedi et al. 1990	Pinus pinaster	Pisolithus arhizus	-0.235		0.008

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Authors	Host species	Fungal species	Biomass	Height	Shoot:root
Lamhamedi et al. 1990	Pinus pinaster	Pisolithus arhizus	-0.337		0.093
Lamhamedi et al. 1990	Pinus pinaster	Pisolithus arhizus	-0.276		-0.142
Lamhamedi et al. 1990	Pinus pinaster	Pisolithus arhizus	-0.321		0.010
Lamhamedi et al. 1990	Pinus pinaster	Pisolithus arhizus	-0.119		0.004
Lamhamedi et al. 1990	Pinus pinaster	Pisolithus arhizus	-0.222		0.120
Lamhamedi et al. 1990	Pinus pinaster	Pisolithus arhizus	0.098		0.006
Lamhamedi et al. 1990	Pinus pinaster	Pisolithus arhizus	-0.136		-0.045
Lamhamedi et al. 1990	Pinus pinaster	Pisolithus arhizus	-0.170		0.011
Lamhamedi et al. 1990	Pinus pinaster	Pisolithus arhizus	-0.232		0.021
Lamhamedi et al. 1990	Pinus pinaster	Pisolithus arhizus	0.058		0.017
Lamhamedi et al. 1990	Pinus pinaster	Pisolithus arhizus	-0.018		-0.009
Lamhamedi et al. 1990	Pinus pinaster	Pisolithus arhizus	-0.268		0.059
Lamhamedi et al. 1990	Pinus pinaster	Pisolithus arhizus	-0.332		0.067
Lamhamedi et al. 1990	Pinus pinaster	Pisolithus arhizus	-0.312		0.032
Lamhamedi et al. 1990	Pinus pinaster	Pisolithus arhizus	-0.067		0.108
Lamhamedi et al. 1990	Pinus pinaster	Pisolithus arhizus	-0.029		0.072
Lamhamedi et al. 1990	Pinus pinaster	Pisolithus arhizus	-0.130		0.057
Lamhamedi et al. 1990	Pinus pinaster	Pisolithus arhizus	0.002		0.238
Lamhamedi et al. 1990	Pinus pinaster	Pisolithus arhizus	-0.269		0.073
Lamhamedi et al. 1990	Pinus pinaster	Pisolithus arhizus	-0.131		-0.040
Lamhamedi et al. 1990	Pinus pinaster	Pisolithus arhizus	-0.039		-0.213
Lamhamedi et al. 1990	Pinus pinaster	Pisolithus arhizus	0.051		0.051
Lamhamedi et al. 1990	Pinus pinaster	Pisolithus arhizus	-0.050		0.054
Lamhamedi et al. 1990	Pinus pinaster	Pisolithus arhizus	0.010		0.103
Lamhamedi et al. 1990	Pinus pinaster	Pisolithus arhizus	-0.144		0.058
Lamhamedi et al. 1990	Pinus pinaster	Pisolithus arhizus	-0.370		-0.199
Lamhamedi et al. 1990	Pinus pinaster	Pisolithus arhizus	-0.235		0.008

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Authors	Host species	Fungal species	Biomass	Height	Shoot:root
Luetal 1998	Eucalvptus globulus	Hydnangium submellatum		-0.026	
Luetal 1998	Eucalyptus globulus	Hdynotrya sp		-0.042	
	Eucalyptus globulus	Hydnum repandum		-0.030	
Lu et al. 1998	Eucalvptus globulus	Laccaria lateritia		-0.002	
Luetal 1998	Eucalyptus globulus	Laccaria lateritia		0.000	
Luetal 1998	Eucalyptus globulus	Laccaria laccata		-0.007	
Lu et al. 1998	Eucalyptus globulus	Laccaria sp		0.021	
Lu et al. 1998	Eucalyptus globulus	Leucopaxillus lilacinus		-0.023	
Lu et al. 1998	Eucalyptus globulus	Mesophellia		-0.144	
	Eucalyptus globulus	Mesophellia		-0.023	
Lu et al. 1990	Eucalyptus globulus	Paxillus muelleri		-0.014	
Lu et al. 1990	Eucalyptus globulus	Paxillus sp		-0.062	
Lu et al. 1998	Eucalyptus globulus	Pisolithus albus		-0.055	
	Eucalyptus globulus	Pisolithus microcarpus		-0.035	
	Eucalyptus globulus	Pisolithus tinctorius		-0.199	
	Eucalyptus globulus	Pisolithus sp		-0.007	
	Fucalyptus globulus	Pisolithus sp		-0.030	
	Fucalyptus globulus	Scleroderma cepa		-0.026	
	Eucalyptus globulus	Scleroderma cepa		0.016	
	Eucalyptus globulus	Scleroderma cepa		-0.112	
	Eucalyptus globulus	Scleroderma sp		-0.123	
	Eucalyptus globulus	Scleroderma sp		-0.125	·
	Eucalyptus globulus	Tricholoma sp		0.016	
Lu el al. 1990 MaaFall & Slack 1001	Pinus resinosa	Thelephora terrestris			
MacFall & Slack 1991	Pinus resinosa	Pisolithus tinctorius			
MacFall & Slack 1991	Pinus resinosa	Hebeloma arenosa			
	Dinus resinosa	Hebeloma arenosa	0.398	0.070	-0.425
Machall & Slack 1991	riius i toinusa	11000101110 0101000			

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Authors	Host species	Fungal species	Biomass	Height	Shoot:root
MacFall & Slack 1991	Pinus resinosa	Hebeloma arenosa	0.171	0.050	-0.386
MacFall & Slack 1991	Pinus resinosa	Hebeloma arenosa	0.398	0.050	0.086
MacFall & Slack 1991	Pinus resinosa	Hebeloma arenosa	0.023	0.017	0.038
MacFall & Slack 1991	Pinus resinosa	Hebeloma arenosa	0.134		-0.013
MacFall & Slack 1991	Pinus resinosa	Hebeloma arenosa	0.266		0.042
MacFall & Slack 1991	Pinus resinosa	Hebeloma arenosa	0.294		0.045
MacFall & Slack 1991	Pinus resinosa	Hebeloma arenosa	0.132		0.058
MacFall & Slack 1991	Pinus resinosa	Pisolithus tinctorius	0.149		-0.112
MacFall & Slack 1991	Pinus resinosa	Hebeloma arenosa	0.069		-0.072
MacFall & Slack 1991	Pinus resinosa	Pisolithus tinctorius	0.233		-0.024
MacFall & Slack 1991	Pinus resinosa	Hebeloma arenosa	0.285		-0.017
MacFall & Slack 1991	Pinus resinosa	Pisolithus tinctorius	0.304		0.163
MacFall & Slack 1991	Pinus resinosa	Hebeloma arenosa	0.318		0.199
MacFall & Slack 1991	Pinus resinosa	Pisolithus tinctorius			
MacFall & Slack 1991	Pinus resinosa	Hebeloma arenosa			
MacFall et al. 1991	Pinus resinosa	Hebeloma arenosa	2.187		-0.802
Marx et al. 1976	Pinus clausa	Pisolithus tinctorius	0.284		
Marx et al. 1976	Pinus clausa	Pisolithus tinctorius	0.464		
Marx et al. 1976	Pinus taeda	Pisolithus tinctorius	0.035		
Marx et al. 1976	Pinus taeda	Pisolithus tinctorius	0.063		
Marx et al. 1976	Pinus elliottii	Pisolithus tinctorius	0.144		
Marx et al. 1976	Pinus elliottii	Pisolithus tinctorius	0.165		
Marx et al. 1976	Pinus strobus	Pisolithus tinctorius	0.693	0.261	0.000
Marx et al. 1976	Pinus strobus	Pisolithus tinctorius	0.118	0.044	0.028
Marx et al. 1976	Pinus taeda	Pisolithus tinctorius	0.877	0.348	-0.208
Marx et al. 1976	Pinus taeda	Pisolithus tinctorius	0.603	0.206	-0.321
Marx et al. 1976	Pinus virginiana	Pisolithus tinctorius	0.732	0.231	-0.455

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Authors	Host species	Fungal species	Biomass	Height	Shoot:root
Marx et al. 1976	Pinus virginiana	Pisolithus tinctorius	0.177	0.022	-0.245
Mason et al. 2000	Eucalyptus globulus	Laccaria fraterna			
Mason et al. 2000	Eucalyptus globulus	Laccaria fraterna			
Mason et al. 2000	Eucalyptus globulus	Pisolithus tinctorius			
Morte et al. 2001	Pinus halapensis	Suillus mediterraneansis	0.105	-0.006	
Morte et al. 2001	Pinus halapensis	Suillus mediterraneansis	0.103	-0.006	
Muhsin & Zwiazek 2002	Picea glauca	Hebeloma crustuliniforme	0.125		0.017
Nylund & Wallander 1989	Pinus sylvestris	Hebeloma crustuliniforme	-0.515		
Nylund & Wallander 1989	Pinus sylvestris	Laccaria laccata	-0.599		
Osonubi et al. 1991	Acacia auriculiformis	Boletus suillus	0.726		0.303
Osonubi et al. 1991	Albizia lebbeck	Boletus suillus	-1.526		-1.282
Osonubi et al. 1991	Leucaena leucocephala	Boletus suillus	1.127		-0.062
Osonubi et al. 1991	Gliricidia sepium	Boletus suillus	0.683		-0.404
Repac 1996	Picea abies	Suillus bovinus	0.000	-0.032	-0.238
Repac 1996	Picea abies	Suillus bovinus	0.112	0.023	-0.136
Repac 1996	Picea abies	Suillus bovinus	-0.070	-0.040	-0.107
Repac 1996	Picea abies	Suillus bovinus	0.050	0.012	-0.076
Repac 1996	Picea abies	Inocybe lacera	0.157	-0.018	-0.153
Repac 1996	Picea abies	Inocybe lacera	0.136	0.021	-0.037
Riffle & Tinus 1982	Pinus ponderosa	Rhizopogon roseolus	0.936	0.095	
Riffle & Tinus 1982	Pinus ponderosa	Suillis granulatus	0.771	0.013	
Riffle & Tinus 1982	Pinus ponderosa	Thelephora terrestris	0.736	-0.076	
Riffle & Tinus 1982	Pinus ponderosa	Pisolithus tinctorius	0.805	0.020	
Riffle & Tinus 1982	Pinus ponderosa	Cenococcum geophilum	0.906	0.204	
Riffle & Tinus 1982	Pinus ponderosa	unknown	0.794	0.052	
Riffle & Tinus 1982	Pinus ponderosa	unknown	0.724	0.026	
Riffle & Tinus 1982	Pinus sylvestris	Suillus cothurnatus	0.039	-0.055	0.147

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Authors	Host species	Fungal species	Biomass	Height	Shoot:root	
Riffle & Tinus 1982	Pinus sylvestris	Rhizopogon roseolus	0.136	0.026	0.256	
Riffle & Tinus 1982	Pinus sylvestris	Suillus granulatus	0.122	0.037	0.088	
Riffle & Tinus 1982	Pinus svlvestris	Thelephora terrestris	-0.028	-0.124	0.146	
Difflo & Tinus 1982	Pinus sylvestris	Pisolithus tinctorius	-0.082	-0.083	0.060	
Riffle & Tinus 1982	Pinus sylvestris	Cenococcum geophilum	0.146	-0.011	0.196	
Riffle & Tinus 1982	Pinus sylvestris	unknown	0.039	-0.055	0.190	
Diffle & Tinus 1982	Pinus sylvestris	unknown	0.230	0.016	0.283	
Riffle & Tinus 1982	Pinus ponderosa	Rhizopogon roseolus				
Piffle & Tinus 1982	Pinus ponderosa	Suillis granulatus				
Diffle & Tinus 1982	Pinus ponderosa	Thelephora terrestris				
Diffle & Tinus 1982	Pinus ponderosa	Pisolithus tinctorius				
Diffle & Tinus 1982	Pinus ponderosa	Cenococcum geophilum				
Riffle & Tinus 1982	Pinus ponderosa	unknown				
Riffle & Tinus 1982	Pinus ponderosa	unknown				
Riffle & Tinus 1982	Pinus svlvestris	Suillus cothurnatus				
Riffle & Tinus 1982	Pinus svlvestris	Rhizopogon roseolus				
Riffle & Tinus 1982	Pinus svlvestris	Suillus granulatus				
Riffle & Tinus 1982	Pinus svlvestris	Thelephora terrestris				
Riffle & Tinus 1982	Pinus svlvestris	Pisolithus tinctorius				
Riffle & Tinus 1982	Pinus sylvestris	Cenococcum geophilum				
Riffle & Tinus 1982	Pinus sylvestris	unknown				
Riffle & Tinus 1982	Pinus sylvestris	unknown				
Rincon et al. 2001	Pinus pinea	Hebeloma crustulinforme	-0.125	-0.008		
Rincon et al. 2001	Pinus pinea	Hebeloma crustulinforme	0.000	-0.058		
Rincon et al. 2001	Pinus pinea	Hebeloma crustulinforme	-0.092	-0.071		740
Rincon et al. 2001	Pinus pinea	Hebeloma crustulinforme	-0.030	0.039		0
Rincon et al. 2001	Pinus pinea	Hebeloma crustulinforme	-0.061	-0.049		

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Authors	Host species	Fungal species	Biomass	Height	Shoot:root
Rinnen et al. 2001	Pinus pinea	Laccaria laccata	0.000	0.166	
Rincon et al. 2001	Pinus pinea	Laccaria laccata	0.000	-0.070	
Rincon et al. 2001	Pinus pinea	Laccaria laccata	0.027	0.119	
Rincon et al. 2001	Pinus pinea	Laccaria laccata	0.154	0.005	
Rincon et al. 2001	Pinus pinea	Laccaria laccata	0.027	0.027	
Rincon et al. 2001	Pinus pinea	Pisolithus tinctorius	-0.121	-0.020	
Rincon et al. 2001	Pinus ninea	Pisolithus tinctorius	-0.154	0.044	
Rincon et al. 2001	Pinus pinea	Melanogaster ambiguus	-0.208	-0.311	
Rincon et al. 2001	Pinus pinea	Melanogaster ambiguus	-0.043	-0.100	
Rincon et al. 2001	Pinus pinea	Rhizopogon luteolus	-0.262	0.134	
Rincon et al. 2001	Pinus pinea	Rhizopoaon luteolus	-0.230	0.064	
Rincon et al. 2001	Pinus pinea	Rhizopogon luteolus	-0.108	-0.012	
Rincon et al. 2001	Pinus pinea	Rhizopogon luteolus	-0.080	-0.012	
Rincon et al. 2001	Pinus pinea	Rhizopogon luteolus	-0.080	0.160	
Rincon et al. 2001	Pinus pinea	Rhizopogon luteolus	-0.026	0.248	
Rincon et al. 2001	Pinus pinea	Rhizopogon roseolus	-0.241	0.180	
Rincon et al. 2001	Pinus pinea	Rhizopogon roseolus	-0.241	0.222	
Rincon et al. 2001	Pinus pinea	Rhizopogon roseolus	-0.241	0.155	
Rincon et al. 2001	Pinus pinea	Rhizopogon roseolus	-0.304	0.166	
Rincon et al. 2001	Pinus pinea	Rhizopogon roseolus	-0 182	0.158	
Rincon et al. 2001	Pinus pinea	Rhizopogon rospolus	-0 304	0 121	
Rincon et al. 2001	Pinus pinea	Rinzopogon Toseolus	-0.004	-0.120	
Rincon et al. 2001	Pinus pinea		-0.211	-0 159	
Rincon et al. 2001	Pinus pinea	Pisolithus tinctonus	-0.102	-0.100	
Rincon et al. 2001	Pinus pinea	Pisolithus tinctorius	-0.049	-0.200	
Rincon et al. 2001	Pinus pinea	Scleroderma verrucosum	-0.207	-0.040	
Rincon et al. 2001	Pinus pinea	Scleroderma verrucosum	-0.384	0.000	
Rincon et al. 2001	Pinus pinea	Scleroderma verrucosum	-0.187	0.120	

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Ln R

А	uthors	Host species	Fungal species	Biomass	Height
R	tincon et al. 2001	Pinus pinea	Scleroderma verrucosum	-0.239	0.028
R	lincon et al. 2005	Pseudotsuga menziesii	Rhizopogon luteolus	-0.363	-0.038
·F	Rincon et al. 2005	Pseudotsuga menziesii	Rhizopogon roseolus	-0.363	0.000
F	Rincon et al. 2005	Pseudotsuga menziesii	Scleroderma verrucosum	-0.245	-0.099
F	Rouhier & Read 1998	Pinus sylvestris	Paxillus involutus	-0.067	
F	Rouhier & Read 1998	Pinus sylvestris	Suillus bovinus	-0.120	
S	Scagel & Linderman 1998	Pseudotsuga menziesii	Laccaria laccata	0.236	0.167
S	Scagel & Linderman 1998	Pseudotsuga menziesii	Laccaria laccata	0.217	0.131
S	Scagel & Linderman 1998	Pseudotsuga menziesii	Laccaria laccata	0.090	0.200
S	Scagel & Linderman 1998	Pseudotsuga menziesii	Rhizopogon vinicolor	0.612	0.382
S	Scagel & Linderman 1998	Pseudotsuga menziesii	Rhizopogon vinicolor	0.390	0.305
S	Scagel & Linderman 1998	Pseudotsuga menziesii	Rhizopogon vinicolor	0.242	0.243
ç	Scagel & Linderman 1998	Pinus contorta	Laccaria laccata	0.084	0.111
ę	Scagel & Linderman 1998	Pinus contorta	Laccaria laccata	0.032	0.093
S	Scagel & Linderman 1998	Pinus contorta	Laccaria laccata	0.136	0.048
ę	Scagel & Linderman 1998	Pinus contorta	Laccaria laccata	0.215	0.327
5	Scagel & Linderman 1998	Pinus contorta	Laccaria laccata	0.370	0.367
:	Scagel & Linderman 1998	Pinus contorta	Laccaria laccata	0.218	0.283
:	Scagel & Linderman 1998	Pseudotsuga menziesii	Laccaria laccata	0.530	0.296
:	Scagel & Linderman 1998	Pseudotsuga menziesii	Laccaria laccata	0.485	0.216
	Scagel & Linderman 1998	Pseudotsuga menziesii	Laccaria laccata	0.007	0.244
	Scagel & Linderman 1998	Pseudotsuga menziesii	Rhizopogon vinicolor	0.599	0.132
	Scagel & Linderman 1998	Pseudotsuga menziesii	Rhizopogon vinicolor	0.457	0.210
	Scagel & Linderman 1998	Pseudotsuga menziesii	Rhizopogon vinicolor	0.319	0.263
	Scagel & Linderman 1998	Pinus ponderosa	Laccaria laccata	0.167	0.262
	Scagel & Linderman 1998	Pinus ponderosa	Laccaria laccata	0.192	0.225
	Scagel & Linderman 1998	Pinus ponderosa	Laccaria laccata	0.245	-0.016
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0.042 -0.070 -0.227

Ln R

Shoot:root

0.320 0.380 0.051 0.138 0.182 -0.305 -0.428 -0.234 -0.277 -0.447 -0.756 -0.373 0.102 -0.155 -0.931 -0.573 -0.019 -0.377 -0.809 -0.630

				Ln R	
Authors	Host species	Fungal species	Biomass	Height	Shoot:root
Scagel & Linderman 1998	Pinus ponderosa	Laccaria laccata	0.240	0.260	0.212
Scagel & Linderman 1998	Pinus ponderosa	Laccaria laccata	0.194	0.172	0.198
Scagel & Linderman 1998	Pinus ponderosa	Laccaria laccata	-0.037	0.050	-0.082
Schier & McQuattie 1995	Pinus strobis	Pisolithus tinctorius	0.304	0.109	0.700
Schier & McQuattie 1996	Pinus rigida	Pisolithus tinctorius	0.654		0.193
Schier & McQuattie 1996	Pinus rigida	Pisolithus tinctorius	0.270		0.171
Tam & Griffiths 1994	Castanopsis fissa	Pisolithis tinctorius	0.117		-0.480
Tam & Griffiths 1994	Castanopsis fissa	Cenococcum geophilum	0.256		-0.256
Tam & Griffiths 1994	Castanopsis fissa	Thelephora terrestris	-0.094		-0.561
Tam & Griffiths 1994	Castanopsis fissa	Hymenogaster	0.033		-0.623
Tam & Griffiths 1994	Castanopsis fissa	Sclerodema sp	-0.158		-0.674
Thomson et al. 1994	Eucalyptus globulus	Protubera	-0.223		
Thomson et al. 1994	Eucalyptus globulus	unknown	0.148		
Thomson et al. 1994	Eucalyptus globulus	Chondrogaster	0.336		
Thomson et al. 1994	Eucalyptus globulus	Cortinarius	-0.174		
Thomson et al. 1994	Eucalyptus globulus	Cortinarius			-
Thomson et al. 1994	Eucalyptus globulus	Cortinarius			
Thomson et al. 1994	Eucalyptus globulus	Cortinarius			
Thomson et al. 1994	Eucalyptus globulus	Cortinarius			
Thomson et al. 1994	Eucalyptus globulus	Cortinarius			
Thomson et al. 1994	Eucalyptus globulus	Cortinarius			
Thomson et al. 1994	Eucalyptus globulus	Hysterangium	0.039		
Thomson et al. 1994	Eucalyptus globulus	Hysterangium			
Thomson et al. 1994	Eucalyptus globulus	^ Hysterangium			
Thomson et al 1994	Eucalyptus globulus	Hysterangium			
Thomson et al. 1994	Eucalyptus globulus	Amanita sp	-1.022		
Thomson et al. 1994	Eucalyptus globulus	Amanita sp			

			Ln R		
Authors	Host species	Fungal species	Biomass	Height	Shoot:root
Thomson et al. 1994	Eucalyptus globulus	Amanita sp			
Thomson et al. 1994	Eucalyptus globulus	Amanita sp			
Thomson et al. 1994	Eucalyptus globulus	Hydnangium	0.336		
Thomson et al. 1994	Eucalyptus globulus	Hydnangium			
Thomson et al. 1994	Eucalyptus globulus	Hydnangium			
Thomson et al. 1994	Eucalyptus globulus	Zelleromyces	0.307		
Thomson et al. 1994	Eucalyptus globulus	Zelleromyces			
Thomson et al. 1994	Eucalyptus globulus	Zelleromyces			
Thomson et al. 1994	Eucalyptus globulus	Hymenogaster	0.278		
Thomson et al. 1994	Eucalyptus globulus	Hymenogaster			
Thomson et al. 1994	Eucalyptus globulus	"Hymenogaster			
Thomson et al. 1994	Eucalyptus globulus	Hymenogaster			
Thomson et al. 1994	Eucalyptus globulus	Thaxterogaster sp	0.542		
Thomson et al. 1994	Eucalyptus globulus	Thaxterogaster sp			
Thomson et al. 1994	Eucalyptus globulus	Scleroderma sp	0.000		
Thomson et al. 1994	Eucalyptus globulus	Scleroderma sp			
Thomson et al. 1994	Eucalyptus globulus	Scleroderma sp			
Thomson et al. 1994	Eucalyptus globulus	Scleroderma sp			
Thomson et al. 1994	Eucalyptus globulus	Scleroderma sp			
Thomson et al. 1994	Eucalyptus globulus	Setchelliogaster sp	0.732		
Thomson et al. 1994	Eucalyptus globulus	Pisolithus sp	0.307		
Thomson et al. 1994	Eucalyptus globulus	Pisolithus sp			
Thomson et al. 1994	Eucalyptus globulus	Pisolithus sp			
Thomson et al. 1994	Eucalyptus globulus	Pisolithus sp			
Thomson et al. 1994	Eucalyptus globulus	Laccaria	0.365		15(
Thomson et al. 1994	Eucalyptus globulus	Laccaria			0
Thomson et al. 1994	Eucalyptus globulus	Laccaria			

				Ln R	
Authors	Host species	Fungal species	Biomass	Height	Shoot:root
Thomson et al. 1994	Eucalyptus globulus	Laccaria			
Thomson et al. 1994	Eucalyptus globulus	Hebeloma	1.138		
Thomson et al. 1994	Eucalyptus globulus	Descolea	1.151		
Thomson et al. 1994	Eucalyptus globulus	Descolea			
Turjaman et al. 2005	Shorea pinanga	Pisolithus arhizus	1.099	0.619	
Turjaman et al. 2005	Shorea pinanga	Scleroderma sp	0.930	0.533	
Wallander 2000	Pinus sylvestris	Suillus variegatus	0.288		
Wallander 2000	Pinus sylvestris	Suillus variegatus	0.431		
Wallander 2000	Pinus sylvestris	Suillus variegatus	0.693		
Wallander 2000	Pinus sylvestris	Suillus variegatus	0.526		
Wallander 2000	Pinus sylvestris	unknown	1.386		
Wallander 2000	Pinus sylvestris	unknown	0.932		
Wallander et al. 1997	Pinus sylvestris	Piloderma croceum			
Wallander et al. 1997	Pinus sylvestris	Paxillus involutus			
Wallander et al. 1997	Pinus sylvestris	Suillus variegatus			
Wallander et al. 1997	Pinus sylvestris	Suillus variegatus			
Yazid et al. 1994	Hopea odorata	Pisolithus tinctorius	2.122	0.617	0.155
Yazid et al. 1994	Hopea helferi	Pisolithus tinctorius	1.215	0.496	0.239

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158

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159

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B. Identity of host plant and fungal species pairings with associated effect sizes (Ln R) for seedling biomass.

Authors	Host species	Fungal species	P addition	Ln R
Autions		•	mg kg -1	Biomass
Bougher et al. 1990	Eucalyptus diversicolor	Descolea maculata	0	0.894
Bougher et al. 1990	Eucalyptus diversicolor	Descolea maculata	0	0.368
Bougher et al. 1990	Eucalyptus diversicolor	Laccaria laccata	0	0.575
Bougher et al. 1990	Eucalyptus diversicolor	Descolea maculata	2	1.170
Bougher et al. 1990	Eucalyptus diversicolor	Descolea maculata	2	1.170
Bougher et al. 1990	Eucalyptus diversicolor	Laccaria laccata	2	2.335
Bougher et al. 1990	Eucalyptus diversicolor	Descolea maculata	4	2.197
Bougher et al. 1990	Eucalyptus diversicolor	Descolea maculata	4	2.147
Bougher et al. 1990	Eucalyptus diversicolor	Laccaria laccata	4	3.050
Bougher et al. 1990	Eucalyptus diversicolor	Descolea maculata	8	1.603
Bougher et al. 1990	Eucalyptus diversicolor	Descolea maculata	8	1.518
Bougher et al. 1990	Eucalyptus diversicolor	Laccaria laccata	8	1.937
Bougher et al. 1990	Eucalyptus diversicolor	Descolea maculata	12	0.360
Bougher et al. 1990	Eucalyptus diversicolor	Descolea maculata	12	0.754
Bougher et al. 1990	Eucalyptus diversicolor	Laccaria laccata	12	0.873
Bougher et al. 1990	Eucalyptus diversicolor	Descolea maculata	16	0.182
Bougher et al. 1990	Eucalyptus diversicolor	Descolea maculata	16	0.416
Bougher et al. 1990	Eucalyptus diversicolor	Laccaria laccata	16	0.341
Bougher et al. 1990	Eucalyptus diversicolor	Descolea maculata	20	-0.259
Bougher et al. 1990	Eucalyptus diversicolor	Descolea maculata	20	-0.288
Bougher et al. 1990	Eucalyptus diversicolor	Laccaria laccata	20	-0.386
Bougher et al. 1990	Eucalyptus diversicolor	Descolea maculata	28	-0.062
Bougher et al. 1990	Eucalyptus diversicolor	Descolea maculata	28	-0.023

	Authors	Host species	Fungal species	P addition	Ln R
	Autors		-	mg kg -1	Biomass
	Bougher et al. 1990	Eucalyptus diversicolor	Laccaria laccata	28	-0.150
- '	Bougher et al. 1990.	Eucalyptus diversicolor	Descolea maculata	36	-0.168
	Bougher et al. 1990	Eucalyptus diversicolor	Descolea maculata	36	-0.002
	Bougher et al. 1990	Eucalyptus diversicolor	Laccaria laccata	36	0.013
	Bougher et al. 1990	Eucalyptus diversicolor	Descolea maculata	48 ⁻	-0.056
	Bougher et al. 1990	Eucalyptus diversicolor	Descolea maculata	48	0.047
	Bougher et al. 1990	Eucalyptus diversicolor	Laccaria laccata	48	-0.064
	Browning & Whitney 1992	Picea mariana	Laccaria bicolor	1.5	0.275
· · ·	Browning & Whitney 1992	Picea mariana	Laccaria bicolor	1.5	0.389
· · · ·	Browning & Whitney 1992	Pinus banksiana	Laccaria bicolor	1.5	0.512
	Browning & Whitney 1992	Pinus banksiana	Laccaria bicolor	1.5	0.144
	Browning & Whitney 1992	Picea mariana	Laccaria bicolor	7.2	-0.089
	Browning & Whitney 1992	Picea mariana	Laccaria bicolor	7.2	-0.131
	Browning & Whitney 1992	Pinus banksiana	Laccaria bicolor	7.2	0.331 🧠
	Browning & Whitney 1992	Pinus banksiana	- Laccaria bicolor	7.2	0.134
· · · · ·	Burgess et al. 1993	Eucalyptus globulus	Cortinarius globuliformis	4	0.560
	Burgess et al. 1994	Eucalyptus globulus	Paxillus muelleri	4	0.560
	Burgess et al. 1995	Eucalyptus globulus	Hysterangium inflatum	4	0.118
	Burgess et al. 1996	Eucalyptus globulus	Hysterangium inflatum	4	0.629
· .	Burgess et al. 1997	Eucalyptus globulus	Thaxterogaster sp	4	0.694
	Burgess et al. 1998	Eucalyptus globulus	Amanita xanthocephala	4	0.755
	Burgess et al. 1999	Eucalyptus globulus	Hymenogaster zeylanicus	4	0.694
	Burgess et al. 2000	Eucalyptus globulus	Hymenogaster viscidus	4	1.057
	Burgess et al. 2001	Eucalyptus globulus	Hymenogaster zeylanicus	4	1.355
	Burgess et al. 2002	Eucalyptus globulus	Setchelliogaster sp	4	1.099
·	Burgess et al. 2003	Eucalyptus globulus	Descolea maculata	4	1.771
	Burgess et al. 2004	Eucalyptus globulus	Hydnangium carneum	4	1.682

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Authors	Host species	Fungal species	P addition	Ln R	
, all or o			mg kg -1	Biomass	
Burgess et al. 2005	Eucalyptus globulus	Laccaria laccata	4	1.505	
Burgess et al. 2006	Eucalyptus globulus	Laccaria laccata	. 4	1.853	
Burgess et al. 2007	Eucalyptus globulus	Sclerodema verrucosum	4	1.771	
Burgess et al. 2008	Eucalyptus globulus	Pisolithis tinctorius	4	2.421	
Burgess et al. 2009	Eucalyptus diversicolor	Cortinarius globuliformis	4	0.516	· · ·
Burgess et al. 2010	Eucalyptus diversicolor	Paxillus muelleri	4	0.921	
Burgess et al. 2011	Eucalyptus diversicolor	Hysterangium inflatum	4	0.307	
Burgess et al. 2012	Eucalyptus diversicolor	Hysterangium inflatum	4	0.429	. "
Burgess et al. 2013	Eucalyptus diversicolor	Thaxterogaster sp	4	0.997	
Burgess et al. 2014	Eucalyptus diversicolor	Amanita xanthocephala	4	0.544	
Burgess et al. 2015	Eucalyptus diversicolor	Hymenogaster zeylanicus	4	1.119	
Burgess et al. 2016	- Eucalyptus diversicolor	Hymenogaster viscidus	4	0.806	
Burgess et al. 2017	Eucalyptus diversicolor	Hymenogaster zeylanicus	4	1.444	2 - 2 - 2 - 2 2 - 3 - 2
Burgess et al. 2018	Eucalyptus diversicolor	Setchelliogaster sp	4	1.365 🗠	بالمين منعان
Burgess et al. 2019	Eucalyptus diversicolor	Descolea maculata	4	1.805	· *0
Burgess et al. 2020	Eucalyptus diversicolor	Hydnangium carneum	4	1.371	4 _ ¹
Burgess et al. 2021	Eucalyptus diversicolor	Laccaria laccata	4	1.959	
Burgess et al. 2022	Eucalyptus diversicolor	Laccaria laccata	4	2.208	
Burgess et al. 2023	Eucalyptus diversicolor	Sclerodema verrucosum	4	1.914	1 .
Burgess et al. 2024	Eucalyptus diversicolor	Pisolithis tinctorius	4	2.714	
Burgess et al. 2025	Eucalyptus globulus	Cortinarius globuliformis	12	0.055	
Burgess et al. 2026	Eucalyptus globulus	Paxillus muelleri	12	0.042	
Burgess et al. 2027	Eucalyptus globulus	Hysterangium inflatum	12	0.002	
Burgess et al. 2028	Eucalyptus globulus	Hysterangium inflatum	12	0.017	
Burgess et al. 2029	Eucalyptus globulus	Thaxterogaster sp	12	0.045	
Burgess et al. 2030	Eucalyptus globulus	Amanita xanthocephala	12	0.005	,
Burgess et al. 2031	Eucalyptus globulus	Hymenogaster zeylanicus	12	-0.008	162 2
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Authors	Host species	Fungal species	P addition	Ln R
			mg kg -1	Biomass
Burgess et al. 2032	Eucalyptus globulus	Hymenogaster viscidus	12	0.034
Burgess et al. 2033	Eucalyptus globulus	Hymenogaster zeylanicus	12	-0.007
Burgess et al. 2034	Eucalyptus globulus	Setchelliogaster sp	12	-0.034
Burgess et al. 2035	Eucalyptus globulus	Descolea maculata	12	0.023
Burgess et al. 2036	Eucalyptus globulus	Hydnangium carneum	12	0.089
Burgess et al. 2037	Eucalyptus globulus	Laccaria laccata	12	-0.061
Burgess et al. 2038	Eucalyptus globulus	Laccaria laccata	12	0.065
Burgess et al. 2039	Eucalyptus globulus	Sclerodema verrucosum	12	0.012
Burgess et al. 2040	Eucalyptus globulus	Pisolithis tinctorius	12	0.040
Burgess et al. 2041	Eucalyptus diversicolor	Cortinarius globuliformis	12	-0.317
Burgess et al. 2042	Eucalyptus diversicolor	Paxillus muelleri	12	-0.380
Burgess et al. 2043	Eucalyptus diversicolor	Hysterangium inflatum	12	-0.379
Burgess et al. 2044	Eucalyptus diversicolor	Hysterangium inflatum	12	-0.178
Burgess et al. 2045	Eucalyptus diversicolor	Thaxterogaster sp	12	-0.124
Burgess et al. 2046	Eucalyptus diversicolor	Amanita xanthocephala	12	-0.106
Burgess et al. 2047	Eucalyptus diversicolor	Hymenogaster zeylanicus	12	-0.541
Burgess et al. 2048	Eucalyptus diversicolor	Hymenogaster viscidus	12	-0.156
Burgess et al. 2049	Eucalyptus diversicolor	Hymenogaster zeylanicus	12	-0.007
Burgess et al. 2050	Eucalyptus diversicolor	Setchelliogaster sp	12	-0.119
Burgess et al. 2051	Eucalyptus diversicolor	Descolea maculata	12	-0.101
Burgess et al. 2052	Eucalyptus diversicolor	Hydnangium carneum	12	0.097
Burgess et al. 2053	Eucalyptus diversicolor	Laccaria laccata	12	-0.205
Burgess et al. 2054	Eucalyptus diversicolor	Laccaria laccata	12	-0.065
Burgess et al. 2055	Eucalyptus diversicolor	Sclerodema verrucosum	12	-0.081
Burgess et al. 2056	Eucalyptus diversicolor	Pisolithis tinctorius	12	-0.001
Chen et al. 2000	Eucalyptus globulus	Laccaria lateritia	5	0.368
Chen et al. 2000	Eucalyptus urophylla	Laccaria lateritia	5	2.048

Authors	Host species	Fungal species	P addition	Ln R	
			mg kg -1	Biomass	
Conieaud et al. 1996	. Pinus pinaster	Hebeloma cylindrosporum	0		
Grandcourt et al. 2004	Dicorynia guianensis	unknown	0	0.342	
Grandcourt et al. 2004	Eperua falcata	unknown	0	-0.209	
Grandcourt et al. 2004	Dicorynia guianensis	- unknown	8	1.228	
Grandcourt et al. 2004	Eperua falcata	unknown	8	0.312	
Grandcourt et al. 2004	Dicorynia guianensis	unknown	40	1.226	
Grandcourt et al. 2004	Eperua falcata	unknown	40	0.344	
Khasa et al. 2001	Pinus contorta	Hebeloma longicaudum	18	0.902	
Khasa et al. 2001	Pinus contorta	Laccaria bicolor	18	0.853	
Khasa et al. 2001	Pinus contorta	Paxillus involutus	18	0.936	
Khasa et al. 2001	Pinus contorta	Pisolithis tinctorius	18	0.964	
Khasa et al. 2001	Pinus contorta	Rhizopogon vinicolor	18	-0.015	
Khasa et al. 2001	Pinus contorta	Suillis tomentosus	18	0.014	
Khasa et al. 2001	Picea glauca	Hebeloma longicaudum	18	0.764 🕤	
Khasa et al. 2001	Picea glauca	Laccaria bicolor	18	0.852	
Khasa et al. 2001	Picea glauca	Paxillus involutus	18	1.246	
Khasa et al. 2001	Picea glauca	Pisolithis tinctorius	18	1.222	
Khasa et al. 2001	Picea glauca	Rhizopogon vinicolor	18	0.109	
Khasa et al. 2001	Picea glauca	Suillis tomentosus	18	0.016	
Khasa et al. 2001	Picea mariana	Hebeloma longicaudum	18	0.976	
Khasa et al. 2001	Picea mariana	Laccaria bicolor	18	1.152	
Khasa et al. 2001	Picea mariana	Paxillus involutus	18	1.677	
Khasa et al. 2001	Picea mariana	Pisolithis tinctorius	18	1.366	
Khasa et al. 2001	Picea mariana	Rhizopogon vinicolor	18	0.298	
Khasa et al. 2001	Picea mariana	Suillis tomentosus	18	0.328	
Khasa et al. 2001	Pinus sylvestris	Hebeloma longicaudum	18	0.066	
Khasa et al. 2001	Pinus sylvestris	Laccaria bicolor	18	-0.040	

164

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Authors	Host species	Fungal species	P addition	Ln R
			mg kg -1	Biomass
Khasa et al. 2001	Pinus sylvestris	Paxillus involutus	18	0.176
Khasa et al. 2001	Pinus sylvestris	Pisolithis tinctorius	18	0.152
Khasa et al. 2001	Pinus sylvestris	Rhizopogon vinicolor	18	-0.034
Khasa et al. 2001	Pinus sylvestris	Suillis tomentosus	18	1.615
Khasa et al. 2001	Larix sibirica	Hebeloma longicaudum	18	0.074
Khasa et al. 2001	Larix sibirica	Laccaria bicolor	18	0.148
Khasa et al. 2001	Larix sibirica	Paxillus involutus	18	0.099
Khasa et al. 2001	Larix sibirica	Pisolithis tinctorius	18	0.084
Khasa et al. 2001	Larix sibirica	Rhizopogon vinicolor	18	0.027
Khasa et al. 2001	Larix sibirica	Suillis tomentosus	18	0.043
Khasa et al. 2001	Pinus contorta	Hebeloma longicaudum	37	0.781
Khasa et al. 2001	Pinus contorta	Laccaria bicolor	37	0.755
Khasa et al. 2001	Pinus contorta	Paxillus involutus	37	0.908
Khasa et al. 2001	Pinus contorta	Pisolithis tinctorius	37	0.862
Khasa et al. 2001	Pinus contorta	Rhizopogon vinicolor	37	0.016
Khasa et al. 2001	Pinus contorta	Suillis tomentosus	37	0.128
Khasa et al. 2001	Picea glauca	Hebeloma longicaudum	37	0.982
Khasa et al. 2001	Picea glauca	Laccaria bicolor	37	1.061
Khasa et al. 2001	Picea glauca	Paxillus involutus	37	1.281
Khasa et al. 2001	Picea glauca	Pisolithis tinctorius	37	1.135
Khasa et al. 2001	Picea glauca	Rhizopogon vinicolor	37	0.140
Khasa et al. 2001	Picea glauca	Suillis tomentosus	37	0.131
Khasa et al. 2001	Picea mariana	Hebeloma longicaudum	37	0.688
Khasa et al. 2001	Picea mariana	Laccaria bicolor	37	1.025
Khasa et al. 2001	Picea mariana	Paxillus involutus	37	1.217
Khasa et al. 2001	Picea mariana	Pisolithis tinctorius	37	1.134
Khasa et al. 2001	Picea mariana	Rhizopogon vinicolor	37	0.057

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Authors	Host species	Fungal species	P addition	Ln R
			mg kg -1	Biomass
Khasa et al. 2001	Picea mariana	Suillis tomentosus	37	0.075
Khasa et al. 2001	Pinus sylvestris	Hebeloma longicaudum	37	-0.010
Khasa et al. 2001	Pinus sylvestris	- Laccaria bicolor	37	0.044
Khasa et al. 2001	Pinus sylvestris	Paxillus involutus	37	0.334
Khasa et al. 2001	Pinus sylvestris	Pisolithis tinctorius	37	0.334
Khasa et al. 2001	Pinus sylvestris	Rhizopogon vinicolor	37	0.039
Khasa et al. 2001	Pinus sylvestris	Suillis tomentosus	37	0.034
Khasa et al. 2001	Larix sibirica	Hebeloma longicaudum	37	-0.585
Khasa et al. 2001	Larix sibirica	Laccaria bicolor	37	-0.522
Khasa et al. 2001	Larix sibirica	Paxillus involutus	37	-0.531
Khasa et al. 2001	Larix sibirica	Pisolithis tinctorius	37	-0.531
Khasa et al. 2001	Larix sibirica	Rhizopogon vinicolor	37	-0.648
Khasa et al. 2001	Larix sibirica	Suillis tomentosus	37	-0.618
Khasa et al. 2001	Pinus contorta	Hebeloma longicaudum	55	0.505
Khasa et al. 2001	Pinus contorta	Laccaria bicolor	55	0.485
Khasa et al. 2001	Pinus contorta	Paxillus involutus	55	0.729
Khasa et al. 2001	Pinus contorta	Pisolithis tinctorius	55	0.662
Khasa et al. 2001	Pinus contorta	Rhizopogon vinicolor	55	0.076
Khasa et al. 2001	Pinus contorta	Suillis tomentosus	55	0.086
Khasa et al. 2001	Picea glauca	Hebeloma longicaudum	55	0.670
Khasa et al. 2001	Picea glauca	Laccaria laccata	55	0.716
Khasa et al. 2001	Picea glauca	Paxillus involutus	55	0.849
Khasa et al. 2001	Picea glauca	Pisolithis tinctorius	55	0.911
Khasa et al. 2001	Picea glauca	Rhizopogon vinicolor	55	0.105
Khasa et al. 2001	Picea glauca	Suillis tomentosus	55	0.156
Khasa et al. 2001	Picea mariana	Hebeloma longicaudum	55	0.579
Khasa et al. 2001	Picea mariana	Laccaria bicolor	55	0.608

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Authors		Host species	Fungal species	P addition	Ln R
				mg kg -1	Biomass
Khasa et al. 2001		Picea mariana	Paxillus involutus	55	0.795
Khasa et al. 2001		Picea mariana	Pisolithis tinctorius	55	0.793
Khasa et al. 2001		Picea mariana	Rhizopogon vinicolor	55	0.034
Khasa et al. 2001		Picea mariana	Suillis tomentosus	. 55	0.045
Khasa et al. 2001		Pinus sylvestris	Hebeloma longicaudum	55	0.066
Khasa et al. 2001		Pinus sylvestris	Laccaria bicolor	55	0.086
Khasa et al. 2001	Ξ.	Pinus sylvestris	Paxillus involutus	55	0.395
Khasa et al. 2001		Pinus sylvestris	Pisolithis tinctorius	55	0.398
Khasa et al. 2001		Pinus sylvestris	Rhizopogon vinicolor	55	0.021
Khasa et al. 2001	-	Pinus sylvestris	Suillis tomentosus	55	0.031
Khasa et al. 2001		Larix sibirica	Hebeloma longicaudum	55	0.045
Khasa et al. 2001		Larix sibirica	Laccaria bicolor	55	0.058
Khasa et al. 2001	-	Larix sibirica	Paxillus involutus	55	0.120
Khasa et al. 2001		Larix sibirica	Pisolithis tinctorius	55	0.058
Khasa et al. 2001		Larix sibirica	Rhizopogon vinicolor	55	0.036
Khasa et al. 2001		Larix sibirica	Suillis tomentosus	55	0.031
MacFall et al. 1991		Pinus resinosa	Hebeloma arenosa	0	2.187
MacFall et al. 1991		Pinus resinosa	Hebeloma arenosa	. 17	1.222
MacFall et al. 1991		Pinus resinosa	Hebeloma arenosa	34	0.488
MacFall et al. 1991		Pinus resinosa	Hebeloma arenosa	68	0.175
MacFall et al. 1991		Pinus resinosa	Hebeloma arenosa	136	0.105
Tyminski et al. 1986		Pinus sylvestris	Laccaria laccata	1	-0.566
Tyminski et al. 1986		Pinus sylvestris	Hebeloma crustliniforme	1	-0.714
- Tyminski et al. 1986		Pinus sylvestris	Laccaria laccata	3.1	-0.392
- Tyminski et al. 1986		Pinus sylvestris	Hebeloma crustliniforme	3.1	-0.287
- Tyminski et al. 1986		Pinus sylvestris	Laccaria laccata	10	-0.349
- Tyminski et al. 1986		Pinus sylvestris	Hebeloma crustliniforme	10	-0.392

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Authors	Host species	, Fungal species	P addition	Ln R
			mg kg -1	Biomass
Tyminski et al. 1986	Pinus sylvestris	Laccaria laccata	31	-0.128
Tyminski et al. 1986	Pinus sylvestris	Hebeloma crustliniforme	31	-0.566
Walker 2001	Pinus lambertiana	Pisolithis tinctorius	0	0.053
Walker 2001	Pinus jeffreyi	Pisolithis tinctorius	0	0.063
Walker 2001	Pinus lambertiana	Pisolithis tinctorius	8	-0.075
Walker 2001	Pinus jeffreyi	Pisolithis tinctorius	8	-0.328
Walker 2001	Pinus lambertiana	Pisolithis tinctorius	12	-0.038
Walker 2001	Pinus jeffreyi	Pisolithis tinctorius	12	0.167
Walker 2001	Pinus lambertiana	Pisolithis tinctorius	16	-0.413
Walker 2001	Pinus jeffreyi	Pisolithis tinctorius	16	-0.064
Walker 2001	Pinus lambertiana	Pisolithis tinctorius	20	-0.145
Walker 2001	Pinus jeffreyi	Pisolithis tinctorius	20	0.321
Walker 2001	Pinus lambertiana	Pisolithis tinctorius	24	-0.037
Walker 2001	Pinus lambertiana	Pisolithis tinctorius	24	-0.147
Walker 2001	Pinus jeffreyi	Pisolithis tinctorius	24	-0.019
Walker 2001	Pinus jeffreyi	Pisolithis tinctorius	24	0.000
Walker 2001	Pinus lambertiana	Pisolithis tinctorius	36	-0.197
Walker 2001	Pinus jeffreyi	Pisolithis tinctorius	36	0.071
Walker 2001	Pinus lambertiana	Pisolithis tinctorius	40	-0.103
Walker 2001	Pinus jeffreyi	Pisolithis tinctorius	40	0.174
Walker 2001	Pinus lambertiana	Pisolithis tinctorius	60	0.012
Walker 2001	Pinus ieffrevi	Pisolithis tinctorius	60	0.629

168

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Full citation of each study used in the meta-analysis examining the effects of phosphorus addition on the outcome of ectomycorrhizal associations.

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Study Bougher et al. 1990	Full citation Bougher NL, Grove TS, Malajczuk N. 1990. Growth and phosphorus acquisition of Karri (<i>Eucalyptus diversicolor</i> F-Muell) seedlings inoculated with ectomycorrhizal fungi in relation to phosphorus supply. New Phytologist 114: 77-85
Browning & Whitney 1992	Browning MHR, Whitney RD. 1991. Responses of jack pine and black spruce seedlings to inoculation with selected species of ectomycorrhiza fungi. Canadian Journal of Forest Research 21: 701-706
Burgess et al. 1993	Burgess TI, Malajczuk N, Grove TS. 1993. The ability of 16 ectomycorrhizal fungi to increase growth and phosphorus uptake of <i>Eucalyptus globulus</i> Labill and <i>E. diversicolor</i> F. Muell. Plant and Soil 153: 155-164
Chen et al. 2000	Chen YL, Brundrett MC, Dell B. 2000. Effects of ectomycorrhizas and vesicular-arbuscular mycorrhizas, alone or in competition, on root colonization and growth of <i>Eucalyptus globulus</i> and <i>E. urophylla</i> . New Phytologist 146: 545-556
Conjeaud et al. 1996	Conjeaud C, Scheromm P, Mousain D. 1996. Effects of phosphorus and ectomycorrhiza on maritime pine seedlings (<i>Pinus pinaster</i>). New Phytologist 133: 345-351

169

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	Study	Full citation
	Grandcourt et al. 2004	de Grandcourt A, Epron D, Montpied P, Louisanna E, Bereau M, Garbaye J, Guehl JM . 2004.
·		Contrasting responses to mycorrhizal inoculation and phosphorus availability in seedlings of
		two tropical rainforest tree species. New Phytologist 161: 865-875
	Khasa et al. 2001	Khasa PD, Sigler L, Chakravarty P, Dancik BP, Erikson L, McCurdy D. 2001. Effect of
		fertilization on growth and ectomycorrhizal development of container-grown and bare-root
n an	an a	nursery conifer seedlings. New Forests 221: 179-197
	8-1	Maefall J. Slack SA, lyor J. 1991. Effects of Hebeloma arenosa and phosphorus fertility on
		growth of red pine (Pinus resinosa) seedlings. Canadian Journal of Botany 69: 372-379
	÷ -	growin of red pine (r mus reamond secondings: edited and edution beams of beamy est and and
· . · ·	Tyminski et al. 1986	Tyminski A, le Tacon F, Chadoeuf J. 1986. Effect of three ectomycorrhizal fungi on growth and
·*	a a second a	phosphorus uptake of Pinus silvestris seedlings at increasing phosphorus levels. Canadian
	the second second	Journal of Botany 64: 2753-2757
	Walker 2001	Walker RF. 2001. Growth and nutritional responses of containerized sugar and Jeffrey pine
	.*	seedlings to controlled release fertilization and induced mycorrhization. Forest Ecology and
· · · ·	· .	Management 149: 163-179