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**Effects of mycorrhizal fungi on tree seedling growth: quantifying the
parasitism-mutualism transition along a light gradient**

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Abstract

Mycorrhizal fungi colonize tree seedlings shortly after germination, and the nature of this relationship (mutualistic to parasitic) has been reported to vary as a function of resources; but this transition has rarely been quantified. Using a light gradient, we grew seedlings of eight tree species in soils that were cultivated by several coexisting species of trees. We used data on mycorrhizal fungi on roots to quantify colonization along the gradient of light. We then analyzed plant growth as a function of both the light gradient and extent of mycorrhizae colonization. Mycorrhizal fungi colonization varied among species but was not correlated with the species' seed sizes or shade tolerances. Within a species, colonization varied among soil sources, but those differences followed neither the conspecific-heterospecific dichotomy, nor the soil host's arbuscular-ectomycorrhizal associations commonly reported. At high light, seedlings growth increased with increasing levels of colonization for seven species; and at low light the effect of colonization was negative for five species. We also quantified the light threshold at which the plant-mycorrhizal fungi relationship shifted from neutral to positive (four species), negative to neutral (one species), and neutral to negative (one species), documenting differences among species that could exacerbate competitive interactions during recruitment.

Keywords: *Acer rubrum*, *Acer saccharum*, *Carya glabra*, hierarchical Bayes, *Liriodendron tulipifera*, irradiance, *Prunus serotina*, *Quercus rubra*, *Quercus velutina*, *Robinia pseudoacacia*, soil nutrients, temperate forests

40 Introduction

41 The plant-mycorrhizal fungi symbiosis is one of the most ubiquitous inter-species relationships
42 in terrestrial ecosystems. Mycorrhizal fungi play a key role assisting plants in the acquisition of
43 soil nutrients and water by increasing the volume of soil explored for resources (e.g., Avolio et
44 al. 2009; Booth et al. 2010; Bingham and Simard 2012). Mycorrhizal fungi can also confer
45 protection from pathogens and root herbivores (Arya et al. 2010) and mediate the transfer of
46 carbon between plants (Simard et al. 1997; Lerat et al. 2002; Teste et al. 2009). In return plants
47 supply carbohydrates to the fungus. Many tree species have been reported as dependent
48 symbionts (e.g., Molina et al. 1992; Nuñez et al. 2009) while for others the symbiosis, if not
49 required for survival, still confers higher performance (e.g., Rayner 1930; Giri et al. 2005). Yet,
50 the plant-mycorrhizal fungi association is frequently hypothesized to develop within a continuum
51 that ranges from parasitism to commensalism to mutualism depending on the plant's surplus of
52 fixed carbon (e.g., Francis and Read 1995; Jones and Smith 2004; Grman et al. 2012). Despite
53 the potential implications of such shifts, e.g., changes in the plant's growth performance, and
54 consequently species coexistence and community structure (Lovelock et al. 1996, Sebastiana et
55 al. 2013), there is little documentation of the threshold.

56 The two mycorrhizal groups associated with tree species are arbuscular mycorrhizal fungi
57 (AM) and ectomycorrhizal fungi (EM). AM (*Glomeromycota*) constitute the most widespread
58 mycorrhizal group among all life forms of plant species (Azcón-Aguilar and Barea 1995), while
59 EM (*Basidiomycota* and *Ascomycota*) are commonly found associated with woody plants and
60 trees in temperate forests (Cairney and Burke 1994; Kernaghan 2013). Although most tree
61 species are associated with AM or EM, for some species, especially as seedlings, individuals can
62 be colonized by both AM and EM (Egerton-Warburton and Allen 2001). In addition, individual

plants' mycorrhizal fungi colonization can vary as a function of the plant's life history traits (e.g., seed size, shade tolerance, age; Gehring 2004; Diéhiou et al. 2005) and of the environmental conditions in which the symbiosis is taking place (e.g., soil fertility, light levels; Gehring 2003; Dehlin et al. 2004; Johnson et al. 2010, 2015). The nature of the mycorrhizal fungi, cultivated under conspecific adults vs. heterospecific plants, can influence the outcome too. Seedlings of *Quercus rubra* grown near EM *Quercus* adults had better performance, survival and growth, than seedlings planted near AM *Acer rubrum* trees (Dickie et al. 2002).

Seed size has been associated with mycorrhizal colonization with small seeded species being more dependent on the symbiosis than large seeded ones (Gehring 2004; Diéhiou et al. 2005). Differences between successional groups have too been reported. Zangaro et al. (2003) analyzed 80 woody species in a tropical forest and showed that late successional species (usually larger seeded and shade tolerant) had lower AM colonization than pioneer species (small seeded and shade intolerant). The degree of mycorrhizal colonization has also been linked to the level of soil resources, with reported increased colonization when soil fertility increases (Avolio et al. 2009) but also when fertility was low (Dehlin et al. 2004). In addition, several studies have documented an increase in mycorrhizal fungi colonization as light levels rise (Bereau et al. 2000; Turner et al. 2009; but also see Hurst et al. 2002). This trend is usually explained as a response to the plant's higher carbon assimilation capacity that can then maintain more fungal biomass (e.g., Bereau et al. 2000). However, even at low light levels seedlings can be colonized by mycorrhizal fungi (Whibeck 2001), and it is not clear if under such conditions, i.e., when carbon production is limited by low light, the mycorrhizal symbiont acts as a mutualist or as a parasite (Johnson et al. 1997).

The shift of the mycorrhizal symbiosis from negative or neutral to positive is usually a function of the environmental conditions (e.g., Zhou and Sharik 1997; Jonsson et al. 2001; Kennedy and Peay 2007). For example, seedlings of a tropical tree did not vary in their performance with or without mycorrhizal fungi inoculum at low light levels (neutral), but inoculated plants had higher growth performance (positive) at medium to high light (Bureau et al. 2000). In a grassland experiment Johnson et al. (2015) reported positive effects of mycorrhizal colonization when soil phosphorous was limiting plant growth, but they also found negative effects in phosphorous rich soils when light levels were low.

As these effects are not homogeneous among coexisting plant species, the interaction with mycorrhizal fungi can influence plants' competitive hierarchies, favoring some species over others (Gehring 2003). Moreover, if these uneven effects follow the lines of the species' life history traits, e.g., seed size or shade tolerance, then differential effects of the symbiosis could exacerbate competitive interactions (Turner et al. 2009) and consequentially alter community structure (Kiers et al. 2000). Thus, understanding the nature of the association with mycorrhizal fungi along resource gradients is essential to determine success in tree seedling recruitment since this is the stage likely most influenced by both the beneficial and detrimental effects of mycorrhizal fungi (e.g., Turjaman et al. 2006; Sebastiana et al. 2013).

In this study we grew seedlings of eight temperate tree species in a greenhouse experiment. Seedlings were planted in several soil sources and under several light levels. We hypothesized that plant species that differ in their seed sizes and shade tolerances may have different abilities to promote or avoid root colonization by mycorrhizal fungi when resources, i.e., light, are low. We also hypothesized that, since light availability is an integral factor in the seedlings carbon balance, the nature of the association, positive (mutualism), neutral (commensalism) or negative

(parasitism) will depend on this resource (Johnson et al. 2015). With those hypotheses in mind the main goals of our analyses were: (1) to investigate if mycorrhizal fungal colonization of establishing seedlings vary among coexisting seedling species, and if it does, to assess if this variation is associated with the species seed size or shade tolerance and/or with soil nutrients; (2) to estimate how mycorrhizal colonization vary along a light gradient; (3) to assess the effects of mycorrhizal colonization on tree seedling growth; and, (4) to document the nature of mycorrhizal symbiosis (e.g., positive, negative or neutral) along a light gradient. Addressing these objectives allowed us to quantify the context-dependent (i.e., light gradient) role of the plant-mycorrhizal fungi symbiosis in determining establishing seedlings performances in temperate forests.

Materials and Methods

Seed and Soil Sources

In Spring 2010 we planted recently germinated seeds of eight tree species in soils cultivated by adult trees of the same species. We specifically studied mycorrhizal fungi colonization of seedlings roots before they lignified, and thus assessed their effects on the plant during this most vulnerable stage. Unlike most plant-mycorrhizal fungi experiments we did not compare plants in sterile soils with and without mycorrhizal inoculum (an unrealistic setting in nature). Instead, for this experiment we only worked with seedlings growing in non-sterilized soils and compared seedlings' performance along a light gradient as a function of the degree of mycorrhizal colonization they displayed (we carried out a parallel study where soils were sterilized and reported how eliminating the entire soil microbial community affected plant performance [McCarthy-Neumann and Ibáñez 2012, 2013]). This particular set up allowed us to attribute differences in mycorrhizal colonization of the roots to features of the seedlings, i.e., seed size,

shade tolerance, or other, since conditions were the same in each combination of soil source and light level. We thus considered this to be an observational study where colonization by mycorrhizal fungi is determined by the features of the seedling.

We selected eight tree species that are dominant in eastern North American forests and commonly found in our study region, the Great Lakes. These species vary in their mycorrhizal fungal associations, their shade intolerance and their seed mass (Table 1). Seeds were collected from wild populations in SE Michigan (Wildtype, Mason, MI-USA). For one species, *Acer saccharum*, seeds were not available in the area that year and were purchased from a different region (Pennsylvania-USA; Sheffields Seed, Locke, NY-USA). Soils cultivated under the canopy of adult trees of each of the studied species were collected in the same region (42°28'N, 84°00'W). To test if there were regional differences within a soil source we also collected soils from a northern forest (45°36'N, 84°41'W) under the three studied species that are also common in the Northern Great Lakes (*A. rubrum*, *A. saccharum* and *Quercus rubra*). Soils were collected under the canopy of four adult trees of each species the fall before the experiment. We collected four soil cores per tree (30 cm diameter and 15 cm deep) that were within 1 m of the adult's bole. All trees sampled were at least two crown diameters away from adults of the other species. Soil samples of each species were aggregated, roots were diced, and soils were sifted through a 1 cm mesh. We follow the standard practice of storing the soils at 4°C (e.g., Owen et al. 2013) until the beginning of the experiment (~ two months later). We also measured nutrient content in each of the soils (McCarthy-Neumann and Ibáñez 2012; see Supplementary Material 1).

Experimental set up

Before stratifying and again before planting the seeds, we sterilized the seeds' surfaces with a 0.6% NaOCL solution. Germinating seeds were weighed and then planted in 6.4 cm diameter x

25 cm depth plots filled with the different soil sources. Field soils were combined in a 1:1:2 mixture of field soil, sterile field soil and sterile peat soil (Fafard Mix No. 2; Conrad Fafard, Agawam, MA-USA; gamma irradiation [~ 30 KGray; Sterigenics International, Schaumburg, Illinois, USA] was used to sterilize soils). Sterile soil was used to quantify seedlings' shade intolerances (McCarthy-Neumann and Ibáñez 2013). Due to lack of enough germination not all species were planted in all the soils (Table 1). Pots representing all combinations of seed and soil sources were distributed along 12 benches. Four benches were then randomly assigned a light treatment representing common values found in the region's forests (from dark canopies to forest canopy gaps, 1.3%, 3.8% and 29% full sun [~ 0.4 , 1.5 and 14 $\mu\text{mol photons/m}^2\text{s}$ respectively]; Schreeg et al. 2005). We planted ten replicates of each seed species x soil source x light level combination. We watered the seedlings every three days (50mL of deionized water), and measured soil moisture in two representative plots at each bench with two Soil Moisture Smart Sensors (20 cm probe, Onset Comp. Corp.) connected to HOBO Micro Station Data Loggers (Onset Comp. Corp.). Loggers recorded volumetric water content at 20-minute intervals over the course of the experiment. We also measured soil moisture in a random sub-sample ($\sim 20\%$) of pots as they were harvested using a moisture probe (Delta-T Moisture meter HH2). Light was recorded (average reading from 5 seconds every 20 minutes) at each bench with two Photosynthetic Light (PAR) Smart Sensors (Onset Comp. Corp.), attached to a HOBO Micro Station Data Logger (Onset Comp. Corp.). Estimated average PAR ($\mu\text{mol photons/m}^2\text{s}$) for each week was calculated for every bench and averaged light levels at each bench were used in the analyses. Greenhouse temperature was kept at $\sim 21^\circ\text{C}$.

At the end of ten weeks, surviving seedlings were harvested (N value in Table 1). Prior to drying we sectioned 5-10 root fractions (1 cm), and weighed and stained them with 5% Schaeffer

black ink in vinegar solution (Vierheilig et al. 1998). We followed standard practices of quantifying the percent of AM colonization in the roots (vesicles, arbuscules, coils and hyphae that were near but not at vesicles or arbuscules). We inspected 100 root intersections with a microscope eyepiece cross hair every 1 mm at 200X magnification (McGonigle and Fitter 1990). We also assessed percent EM colonization by counting the number of intact root tips (out of 100, every 2 mm at 100X magnification; a rather conservative estimate) with mantle and Hartig nets. Short roots were considered ectomycorrhizal when both a mantle and Hartig net were observed (Egerton-Warburton and Allen 2001). Seedlings, leaves, stems and remaining roots, were then oven-dried at 70°C and total biomass was weighed. We then standardized growth measurements by calculating daily growth rate (mg/day).

Analyses

Because we did not control the level of mycorrhizal fungi colonization we could not analyze the data using standard statistical techniques. In stead, we analyzed both percent root mycorrhizal colonization and daily growth rate as a saturating response to light availability (Table 2; the saturating relationship was inferred from exploratory analysis of the data for mycorrhizal fungi, or followed common practice in the case of growth [e.g., Ibáñez et al. 2009]). A graphical representation of the analytical approach and a list of all the parameters included are shown in Table 2, detail descriptions of equations are provided in Supplementary Material 2.

We analyzed the mycorrhizal fungal data and independently estimated AM and EM colonization using a zero-inflated Poisson model (Ibáñez and McCarthy-Neumann 2014). This model divides the likelihood into two components: 1) the probability of not detecting any colonization (used when count data have a large number of zero observations as occurred in our study for seedlings grown at low light; Table 1); and 2) the percent of mycorrhizal fungal

colonization. The probability of not detecting colonization was estimated as a function of soil source (ϖ_{soil}) nested within a species overall mean (ϖ_{mean} ; Table 2). The percent of mycorrhizal fungi colonization was estimated as a function of light using a saturating equation (Table 2). Parameters of the curve (α , β , γ) were estimated for each soil source nested within a species overall parameter, parameter β was also estimated as a function of seed size. We then used parameter estimates to predict mycorrhizal colonization as a function of soil source, seed size and light level.

Growth rates were analyzed as a saturating function of light but also as a function of the predicted mycorrhizal colonization (Table 2). With this approach we then assessed the role of mycorrhizal fungi on seedling performance at different light levels (δ -high, κ -low, μ -medium). For the *Quercus* species we included predicted estimates for both AM and EM since these species were colonized by both types of mycorrhizal fungi.

Given the number of parameters involved and the low number of replicates at each light level (not all seedlings survived the 10 week period) we used a hierarchical Bayesian framework in our analyses (Clark 2007); parameters were then estimated from non-informative prior distributions. We tried several combinations of fixed effects in addition of those we were interested in (e.g., nutrients, soil moisture, region) and of random effects (e.g., bench), but they did not improved the fit of the model (based on predictive loss [Gelfand and Gosh 1998]) and to aid with interpretations we did not include them in the final analyses.

Model simulations were run in OpenBUGS (Thomas et al. 2006; see Supplementary Material 2 for model code). Parameters' estimates were calculated after the convergence of three chains by calculating the Gelman-Rubin statistic (Brooks and Gelman 1998). We then used parameter estimates, species level parameters and soil-specific parameters to simulate seedlings overall

growth (all soils combined) and soil-specific growth for seedlings grown with and without mycorrhizal fungi along the light gradient. We first simulated mycorrhizal fungal colonization for each soil type and light level and then used that estimate to simulate growth (growth without mycorrhizal fungi was simulated by setting up mycorrhizal fungal colonization to zero).

Predicted growth data, based on soil-level parameters had a high goodness of fit for most species ($R^2 > 0.85$ for six of the eight species). We then felt confident about using soil-level parameter estimates from our models to simulate seedling growth along the light gradient. However, for most species the percent of seedlings colonized while growing at high light was large, thus our predictions of seedling performance at high light without mycorrhizal fungi are based on a few seedlings only. Still, the multilevel structure of our models allowed us to make predictions for combination of soils sources and mycorrhizal fungi colonization scenarios (with and without mycorrhizal colonization) for which we had few observations (Clark 2007).

For parameters estimated at the species level, we ran correlations (Pearson product moment correlation coefficient r) with their average species seed weight and shade intolerance to determine if these functional traits could explain the differences observed among species (McCarthy-Neumann and Ibáñez 2013; Table 1). Shade intolerance and average seed weight were correlated across our study species (r : 0.61). For all the parameter values estimated for each soil source we also calculated correlations with soil nutrient levels (total nitrogen and phosphorus) to assess if soil differences in mycorrhizal fungi colonization could have been due to nutrient availability rather than the soil community associated with each soil. We only report correlations that were ≥ 0.5 , and fixed effects coefficients that were statistically significant (95% credible interval did not overlap zero) for all correlations see Figs. 1 and 2, for a list of all the parameter values estimated see the Supplementary Material 3.

Results

Mycorrhizal fungi colonization

The probability of mycorrhizal colonization (species level parameter $[1-\text{logit}(\omega_{mean})]$) varied among the different species in magnitude and variability and for *Q. velutina* whether they were colonized by AM or EM fungi (Fig. 1a). Within a species, parameters estimated for each soil source ($1-\text{logit}(\omega_{soil})$) were correlated with nitrogen for *Q. rubra* EM (r : -0.85) and with phosphorus for *A. saccharum* (r : 0.54) and *Q. rubra* EM (r : 0.63). The maximum level of mycorrhizal colonization, parameter α_{mean} , also varied among species (Fig. 1b), ranging from $43 \pm 2.9\%$ (mean $\pm$ SD) for *Robinia pseudoacacia* to $18 \pm 2.3\%$ for *Prunus serotina*. In this case the only species that had a high correlation between the soil-specific parameters, α_{soil} , and nitrogen was *Liriodendron tulipifera* (r : -0.65). The minimum amount of light necessary to observe mycorrhizal colonization (at an average seed weight) also varied among species (βI_{mean} ; Fig. 1c). Among soil-specific parameters, βI_{soil} , correlations with soil phosphorus were high for *Carya glabra* (r : 0.5) and for *Q. rubra* AM (r : 0.51). Seed size within a species also affected the minimum amount of light at which colonization was observed (β_2 ; Fig. 1d), larger seeds increased the level of light needed for colonization in *C. glabra*, *L. tulipifera*, *P. serotina*, and *Q. rubra* AM, and reducing it for *A. rubrum*, *Q. rubra* EM and *Q. velutina* EM. The light level necessary to reach half of maximum colonization was relatively low, varied among species and for *Q. velutina* seedlings it differed between AM and EM colonization (γ_{mean} ; Fig. 1e). The soil-specific parameters, γ_{soil} , were correlated with nutrients for *A. saccharum* (nitrogen r : -0.73, phosphorus r : 0.88) and for *C. glabra* (phosphorous r : 0.57).

268 Seedling growth

269 The performance of the growth model, assessed as a function of goodness of fit, R^2 predicted vs
 270 observed, was very high among the five small seeded species (R^2 : 0.99) and varied considerably
 271 among the rest (0.87 for *C. glabra*, 0.61 for *Q. rubra* and 0.15 for *Q. velutina*). Our estimates of
 272 maximum growth reflect the seedlings potential to grow given their species-specific average seed
 273 sizes. Thus the maximum growth rate parameter, δI_{mean} , was highly correlated with species
 274 average seed weight (Fig. 2a). The soil-level parameters were correlated with nitrogen in *L.*
 275 *tulipifera* (r : -0.54). The effect of AM and EM colonization on maximum growth rate ($\delta 2$; i.e., at
 276 high light) was positive for seven of the eight species and only negative for *Q. velutina* AM (Fig.
 277 2b). The minimum amount of light at which growth starts without mycorrhizal colonization,
 278 κI_{mean} , also varied among species (Fig. 2c), and the soil-specific parameters, κI_{soil} , were
 279 correlated with nutrient content for *A. rubrum* (phosphorous r : -0.55), *L. tulipifera* (phosphorous
 280 r : -0.59), and for *Q. velutina* (nitrogen r : -0.55). The effects of mycorrhizal colonization on the
 281 minimum amount of light required to start growth ($\kappa 2$) varied among species and for five of the
 282 eight species more light was required to start growth as their level of colonization increased, and
 283 only one required less (Fig. 2d). The amount of light necessary to reach the half of the maximum
 284 growth rate in the absence of mycorrhizal colonization was relatively low and varied among
 285 species (μI_{mean} ; Fig. 2e). For soil-specific parameters, μI_{soil} , levels of soil nutrients were
 286 correlated with nitrogen for *L. tulipifera* (r : 0.7) and with phosphorus for *C. glabra* (r : -0.52) and
 287 *L. tulipifera* (r : -0.83). Seedlings of four species required greater light to reach half of the
 288 maximum growth rate when colonized by mycorrhizae ($\mu 2$; Fig. 2f), and this parameter was
 289 correlated with shade intolerance (r : -0.52) and average seed weight (r : 0.52).

290 Simulations of seedling growth along the light gradient

Predicted growth curves from the species-level parameters (all soils combined) reflect the large variability of growth rates we found in the data (see Supplementary Material 4). Simulations of seedling growth under their conspecific soils (soils where most seeds germinate) show that for four species, *A. rubrum*, *A. saccharum*, *P. serotina* and *R. pseudoacacia*, there is a light level at which the mycorrhizal interaction shifted from neutral to beneficial (95% predicted intervals did not overlap; Fig. 3). We also identified the light threshold at which the relationship shifted from negative to neutral in one species, *A. saccharum*, and unexpectedly from neutral to negative in another, *Q. rubra* (Fig. 3). For three species, *C. glabra*, *L. tulipifera*, and *Q. velutina* the effect was neutral along the light gradient, although for *L. tulipifera* growth performance was substantially higher with mycorrhizal fungi (Fig. 3; simulations for other soil sources can be found in Supplementary Material 4).

Discussion

Most tree seedlings benefit from the interactions with mycorrhizal fungi (e.g., Turjaman et al. 2006; Sánchez-Zabala et al. 2013), but the nature of this relationship, positive to negative, greatly depends on the environmental conditions the plant is growing under (e.g., Hengari et al. 2004; Misbahuzzaman and Newton 2006; Ishaq et al. 2013). To assess the isolated effects of the fungal symbiont on plants most plant-mycorrhizal fungi experiments use sterile soils to which a mycorrhizal inoculum is then added. However, sterilization also eliminates the entire soil microbial community (e.g., fungal pathogens, beneficial bacteria) that might also affect plant performance. In our experiment by using intact (non-sterile) soils we were able to compare growth among seedlings that naturally developed or did not an association with mycorrhizal fungi, while still being exposed to the entire soil microbial community. Thus we assumed that

differences in colonization within each soil source and light level treatments were due to characteristics of the seedlings. In particular, we assessed the effects of mycorrhizal fungi before the roots lignified, the most susceptible stage of the seedling, but we are aware that the effects of mycorrhizal fungi will continue along their life spans and their effects and impacts will likely change. Our results document how not only the abiotic environment, i.e., light, can drive seedling performance, but also how the interaction between the light environment and the biotic association with soil mycorrhizal fungi plays a role determining seedling growth (Table 2). Specifically we quantified the effects of AM and EM fungal colonization on seedling growth along the light gradient commonly found in temperate forests. Our simulations provided us with the information necessary to quantify the light threshold at which the plant-mycorrhizal fungi relationship shifted from neutral to positive (in four species), negative to neutral (in one species), and neutral to negative (in one species). Our results indicate that the nature of this relationship (e.g., neutral, positive, or negative), depends on the light context and can significantly affect seedling performance, and thus potentially determine patterns of tree species recruitment.

Investigating variations, and potential drivers, in mycorrhizal fungal colonization of seedling roots among coexisting species

Although most tree seedlings are associated with mycorrhizal fungi, and in many cases benefit from this association, not all species have the same propensity to stimulate mycorrhizal colonization (Smith and Read 1997). Our results illustrate how the probability of colonization varied among species, in their magnitude and variability (Fig. 1a). Within a species there were also differences in this parameter among soil sources, but those differences followed neither the conspecific *vs.* heterospecific dichotomy, nor the AM *vs.* EM host division that has been reported in other studies (e.g., Dickie et al. 2002; Supplementary Material 3).

The degree of maximum mycorrhizae colonization also varied among species (Fig 1b), but within a species it was relatively similar among soil sources (Supplementary Material 3). Several studies have documented that the level of soil resources may influence the extent of the symbiosis (e.g., Dehlin et al. 2004; Avolio et al. 2009). However, in our study soil nutrients could only explain the variability found on maximum colonization rates among soils in two species. For *Q. rubra*, soils with more nitrogen were correlated with less EM, however for *A. saccharum* (AM) and *Q. rubra* (EM) the association with soil phosphorus was unexpectedly positive. This pattern could be explained by the fact that in these forests soil nitrogen is a more limiting resource than phosphorus (Baribault et al. 2010). Also, the species with the highest degree of colonization, *R. pseudoacacia*, also formed symbiotic nodules with nitrogen-fixing *Rhizobium*. Thus, in our study system we cannot associate the differences we observed in mycorrhizal colonization among soils with the availability of these two nutrients.

Estimating how mycorrhizal colonization varied along a light gradient

We also quantified the initiation of the mycorrhizal colonization process with respect to the light levels that seedlings were exposed to. The amount of light necessary to start colonization varied among species and was correlated with species-specific shade intolerance and average seed weight, with small-seeded and more shade-intolerant species starting colonization at lower light levels (Fig. 1c). This pattern may be reflecting a lack of control by the small-seeded species to prevent the symbiosis at low light levels even when it may not be entirely beneficial for the plant (Zangaro et al. 2003). Alternatively, small-seeded shade-intolerant species may have evolved to promote the association with the mycorrhizal fungi regardless of light availability to rapidly enhance seedling performance if the conditions for growth become optimal (Kiers et al. 2000; Whitbeck 2001). However inferring which of these two mechanisms dominated in our study was

complicated. Intra-specific differences in seed weight also affected this parameter. Our results show four species requiring more light to start colonization for larger seeds, supporting the first mechanism, that within a species large seedlings could be preventing colonization at low light levels. Nevertheless, three species showed the opposite trend, larger seedlings reduced the amount of light necessary to start colonization (Fig. 1d), supporting the second mechanism that larger seedlings could be promoting colonization. As these trends were not highly correlated with either species shade intolerance or average seed weight we cannot resolve this issue with our data.

There were also species differences on how colonization rates would respond to an increase in light levels (half saturation parameter; Fig. 1e); and this parameter was also negatively correlated with soil nitrogen for *A. saccharum* (i.e., soils with more nutrients required less light to reach half of maximum percent colonization). Soil source also affected these two parameters (amount of light necessary to start colonization, and half saturation; Supplementary Material 3) illustrating differential mycorrhizal colonization dynamics among soils along the light gradient; differences that could potential contribute to the unequal success in seedling recruitment in forest stands (McCarthy-Neumann and Ibáñez 2012, 2013).

Assessing the effects of mycorrhizal colonization on tree seedlings growth

Mycorrhizal fungi hyphal networks can considerably extend the soil surface from which water and nutrients can be uptaken and transported to the plant, and consequently affect plant performance (e.g., Giri et al. 2005; Bingahm and Simard 2012). The mycorrhizal fungi symbiosis can also enable the transfer of carbohydrates from adult trees to seedlings, greatly affecting the chances of recruitment when light levels in the forest floor are very low (e.g., van der Heijden and Horton 2009; Booth and Hoeksema 2010; but see Gehring and Connell 2006; Teste et al.

2009). Nevertheless, this symbiosis comes at a cost as the plant allocates carbon to the fungus at the expense of its own growth. In the case of seedlings, growing in the forest floor (and in our experiment without connections with adult individuals) the enhancement of nutrient and water uptake may not compensate for the loss of limited carbohydrates (e.g., Hengari et al. 2004).

We had originally hypothesized that the effects of mycorrhizal fungi on seedlings growth would likely be positive at high to intermediate light levels, and negative when light was limited. Our results confirm these patterns for most species. At high light levels, maximum growth rate overwhelmingly increased with increasing levels of mycorrhizal colonization for seven species (Fig. 2b). Only the colonization of *Q. velutina* by AM fungi had a detrimental effect at high light, which is likely an opportunistic event during this younger stage as this species will be dominated by EM fungal colonization at later stages. At low light levels, the amount of light necessary to start growth increased with the level of mycorrhizal colonization for five of the eight species, illustrating the negative nature of the association under these conditions (Fig. 2d). These are trends that could exacerbate species differences during the establishment period, especially at low light levels (Turner et al. 2009; Zangaro et al. 2003).

Documenting the nature of the mycorrhizal fungi symbiosis, positive, negative or neutral, along a light gradient

The environmental conditions under which the plant-mycorrhizal fungi symbiosis develops, i.e., the balance between access to scarce soil resources vs. loss of carbohydrates, play a key role determining the overall effect on the plant (e.g., Bereau et al. 2005). Thus, the level of mycorrhizal colonization experienced by a particular seedling, given a particular environment, could greatly influence the outcome during recruitment; and in the case of several coexisting species it could also contribute to determining the assemblage of species in that community. In

our experiment, the effects of mycorrhizal colonization were estimated for seedlings still exposed to the entire microbial community associated with each soil. Thus any effects on plant performance caused by other soil organisms (McCarthy-Neumann and Ibáñez 2012, 2013) were accounted for in both types of seedlings, those that developed and those that did not develop mycorrhizal fungi associations.

Overall, our simulations indicate that when carbon fixation is seriously limited by light availability, maintaining the association with mycorrhizal fungi may result in a net negative effect on the plant. This scenario, and the shift in nature of the relationship along a resource gradient, is often theorized, but has rarely been quantified in terms of resource availability. We used parameter estimates from our analyses, their means, variances and covariances, to simulate seedling growth as a function of not only light but also of the level of mycorrhizal colonization associated with that light level. This exercise enabled us to illustrate shifts in the nature of this relationship along increasing light levels. When grown in their conspecific soils, we found several trends (Fig. 4), e.g., neutral to positive (*A. rubrum*, *P. serotina*, *R. pseudoacacia*), always neutral (*C. glabra*, *L. tulipifera*, *Q. velutina*), negative to neutral to positive (*A. saccharum*), and neutral to negative (*Q. rubra*; this unexpected result could be due to the potential negative effect of being colonized by both AM and EM during the first year [Egerton-Warburton and Allen 2001]). Light thresholds at which these shifts took place differed among the study species (Fig. 4). In our prior analysis of this experiment we have found that the majority of temperate tree species experience negative plant-soil feedbacks with decreased survival in conspecific relative to heterospecific soils (McCarthy-Neumann & Ibáñez 2012). These feedbacks are stronger and/or restricted to low light environments and are positively correlated with shade intolerance and adult rarity (McCarthy-Neumann & Ibáñez 2013). Our current results, suggest

that soil source can affect the probability of mycorrhizal colonization and/or the effect of mycorrhizal colonization on growth rates for some species. However, those subtle differences followed neither the conspecific *vs.* heterospecific dichotomy, nor the soil host's arbuscular mycorrhizal fungi *vs.* ectomycorrhizal fungi associations commonly reported. Shade intolerant (and smaller seeded) species do seem to be more likely to experience negative responses in their growth at low light levels when colonized by mycorrhizal fungi. Our results clearly emphasize differences among coexisting species, differences that at this stage could be critical determining seedlings performance and ultimately community composition. However, to truly quantify the impact of these differences seedling measurements of photosynthetic performance and carbon allocation patterns would be necessary to elucidate the actual mechanisms driving differential seedling performance. Also, we studied establishing seedlings without lignified roots and without connections with adults trees that could have provided carbohydrates via the mycorrhizal hyphae network, thus we are documenting effects of mycorrhizae that will likely change in magnitude and direction as the plants become older. In summary, the species-specific effects we have documented could ameliorate or exacerbate differences among species in their recruitment abilities and potentially could contribute to the community's recruitment patterns.

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Supplementary Material

Supplementary Material 1. Soils nutrient contents.

Supplementary Material 2. Detailed description of the analyses and OpenBUGS code.

Supplementary Material 3. Full array of parameter estimates (posterior means+95%CI).

Supplementary Material 4. Seedling growth predictions all soils combined and for eac soil source.

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Table 1. Species used in this study (code name used in figures; number of seedlings analyzed [N] and percentage of seedlings colonized by mycorrhizal fungi [%M]); the different soil sources in which were planted; their mycorrhizal fungi association; shade intolerance (Barnes and Wagner 2007); and average seed mass (Burns and Honkala 1990). A: arbuscular mycorrhizal fungi; E: ectomycorrhizal fungi

Species (code; N; %M)	Soil sources (conspecific in bold)	Mycorrhizal association	Shade intolerance*	Average seed mass (mg)
<i>Acer rubrum</i> (Acru; 190; 79%)	Acsa, Acru , Cagl, Prse, Quru, Quve, Rops	A	tolerant, 8.6 (5.3)	19.6
<i>Acer saccharum</i> (Acsa; 88; 78%)	Acru, Acsa , Quru	A	very tolerant	64.9
<i>Carya glabra</i> (Cagl; 122; 32%)	Acru, Acsa, Cagl , Quru	E	intermediate, 0 (1.6)	2272.0
<i>Liriodendron tulipifera</i> (Litu; 65; 77%)	Acru, Acsa, Litu , Quru	A	intolerant 17.5 (11.7)	40.0
<i>Prunus serotina</i> (Prse; 97; 90%)	Acru, Acsa, Prse , Quru, Quve, Rops	A	intolerant, 20.1 (10.6)	94.3
<i>Quercus rubra</i> (Quru; 243; 61%)	Acsa, Acru, Prse, Quru , Quve, Rops	A & E	intermediate, 0.2 (1.6)	4127.0
<i>Quercus velutina</i> (Quve; 278; 54%)	Acsa, Acru, Prse, Quru, Quve , Rops	A & E	intolerant, 0 (0.8)	1570.0
<i>Robinia pseudoacacia</i> (Rops; 155; 90%)	Acsa, Acru, Cagl, Quru, Quve, Rops	A, E & NFB**	intolerant, 50.5 (13.2)	18.9

*Shade intolerance was also estimated for seven species as the difference in percent survival between seedlings grown in sterile potting soil in high vs. low light (mean(SD); McCarthy-Neuman and Ibáñez 2013. Not enough seedlings of *A. saccharum* survived to estimate its shade tolerance using this method, but survival rates for these species were lower than those for the large seeded species).

**Both, A and E have been reported for *R. pseudoacacia*. In our seedlings we only observed AM colonization. This species also is associated with nitrogen-fixing bacteria (NFB) and a few of our seedlings had developed NFB nodules.

Table 2. Graphical representation of the analyses performed and list of parameters included in the analyses. Light directly affects mycorrhizal percent colonization (%M) and seedling growth (solid arrows; saturating curves) and indirectly affects seedling growth (dashed arrow) through the effects of mycorrhizal fungi on seedlings (parameters $\delta 2$, $\kappa 2$, $\mu 2$). Soil source directly affects all the parameters of the mycorrhizal colonization and seedling growth models (solid arrows; parameters α , $\beta 1$, γ , $\delta 1$, $\kappa 1$, $\mu 1$).

<p>The diagram shows the following relationships and equations:</p> <ul style="list-style-type: none"> Mycorrhizal colonization equation: $M = \alpha \frac{\text{light} - \beta}{\text{light} + \gamma}$ Seedling growth equation: $\text{growth} = \delta \frac{\text{light} - \kappa}{\text{light} + \mu}$ Parameters for Mycorrhizal colonization: <ul style="list-style-type: none"> - detection: ϖ_{soil} - percent colonization: M - $\alpha: \alpha_{\text{soil}}$ - $\beta: \beta 1_{\text{soil}} + \beta 2 \cdot \text{SeedSize}$ - $\gamma: \gamma_{\text{soil}}$ Parameters for Seedling growth: <ul style="list-style-type: none"> - $\delta: \delta 1_{\text{soil}} + \delta 2 \cdot M$ - $\kappa: \kappa 1_{\text{soil}} + \kappa 2 \cdot M$ - $\mu: \mu 1_{\text{soil}} + \mu 2 \cdot M$ <p>Two graphs are included: one for %M vs light and one for growth vs light, both showing saturating curves.</p>	
Mycorrhizal fungi model:	Parameter
- Probability of detecting mycorrhizal colonization	<ul style="list-style-type: none"> • $\text{logit}(1 - \varpi_{\text{mean}})$ species overall • $\text{logit}(1 - \varpi_{\text{soil}})$ each soil source
- Maximum mycorrhizal colonization at high light	<ul style="list-style-type: none"> • α_{mean} species overall • α_{soil} each soil source
- Minimum amount of light necessary to observe colonization at average seed size Effects of seed size on this parameter	<ul style="list-style-type: none"> • $\beta 1_{\text{mean}}$ species overall • $\beta 1_{\text{soil}}$ each soil source • $\beta 2$

- Light required to reach half of maximum colonization	<ul style="list-style-type: none">• γ_{mean} species overall• γ_{soil} each soil source
Seedling growth model:	Parameter
- Maximum growth rate at high light levels Effects of mycorrhizal colonization on this parameter	<ul style="list-style-type: none">• $\delta 1_{\text{mean}}$ species overall• $\delta 1_{\text{soil}}$ each soil source• $\delta 2$
- Minimum amount of light necessary to start growth Effects of mycorrhizal colonization on this parameter	<ul style="list-style-type: none">• $\kappa 1_{\text{mean}}$ species overall• $\kappa 1_{\text{soil}}$ each soil source• $\kappa 2$
- Light required to reach half of the maximum growth rate Effects of mycorrhizal colonization on this parameter	<ul style="list-style-type: none">• $\mu 1_{\text{mean}}$ species overall• $\mu 1_{\text{soil}}$ each soil source• $\mu 2$

Figure 1. Results from the analysis of mycorrhizal colonization along a light gradient (species-level responses). A: arbuscular mycorrhizal fungi, E: ectomycorrhizal fungi. Different lower case letters indicate significant differences between species (95% credible intervals [CI] do not overlap, panels a, b, c and e). Asterisks indicate statistically significant fixed effect coefficients (95%CI does not include zero, panel d). r_{SI} : correlation between the species level parameter and the species shade intolerant value; r_{SW} : correlation between the species level parameter and the species average seed weight. Species are sorted by their shade tolerance (lowest to highest; Table 1), as we do not have a measurement for *A. saccharum*, a shade tolerant species, we ranked it as the most shade tolerant among the small-seeded species.

Figure 2. Results from the analysis of seedling growth as a function of mycorrhizal colonization along a light gradient (species-level responses). A: arbuscular mycorrhizal fungi, E: ectomycorrhizal fungi. Different lower case letters among species indicate significant differences between species (95% CI do not overlap, panels a, c and d). Asterisks indicate statistically significant fixed effect coefficients (95%CI does not include zero, panels b, d and f). r_{SI} : correlation between the species level parameter and the species shade intolerant value; r_{SW} : correlation between the species level parameter and the species average seed weight. Species are sorted by their shade tolerance (lowest to highest; Table 1).

Figure 3. Simulated growth (mean $\pm$ 95%PI) for each species when grown in their conspecific soils with (solid lines) and without (dashed lines) mycorrhizal fungi. Vertical lines mark the light level at which the predicted intervals do not overlap indicating shifts in the plant-fungi relationship. Black dotted vertical lines: growth with mycorrhizal fungi is higher than without; gray dotted vertical lines: growth with mycorrhizal fungi is lower than without. A: arbuscular

mycorrhizal fungi, E: ectomycorrhizal fungi. Horizontal lines indicate the overall effect for growing with mycorrhizal fungi along the light gradient.

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FIGURE 1.

FIGURE 2.

FIGURE 3.

SUPPLEMENTARY MATERIAL 1

Soils nutrient content: Soils from each soil source (5 g) were shaken for 30 minutes in 2 M KCl to extract inorganic nitrogen (N), and then NH_4^+ and NO_3^- were measured with an Alpkem Series 500 autoanalyzer (OI Analytical Alpkem, College Station, TX). Magnesium, Ca^{2+} , K^+ and phosphate (PO_4^-) were extracted from 5-g sub samples with a Mehlich III solution. Concentrations of Mg^{2+} , Ca^{2+} , and K^+ in extracts were measured with Direct Current Plasma (DCP, SMI Corp., Gloucestershire, UK) atomic emission spectrometry, and the Alpkem Series 500 autoanalyzer was used to measure PO_4^- . Total soil carbon (C) and N ($\text{NO}_3^- + \text{NH}_4^+$) content were measured from 5-g sub samples that were ground into powder by a pestle and mortar. Duplicate 25-mg secondary sub samples were compared against atropine standard by combustion in a C-N analyzer (Carlo Erba NA 1500 Series 2, Lakewood, NJ). Soil pH was determined using a glass and reference electrode with a pH meter on a 1:1 suspension (5 gram of soil to 5 milliliters water).

Soil source	pH	Total organic N (mg/L)	Total organic C (mg/L)	C:N	$\text{NO}_3^- + \text{NH}_4^+$ (mg/Kg ⁻¹)	Mg (ppm)	Ca (ppm)	K (ppm)	PO_4 (ppm)
AcruN	5.26 ± 0.09	0.19 ± 0.06	2.77 ± 0.27	15.75 ± 2.97	96.98 ± 29.87	1239.68 ± 407.43	889.92 ± 267.45	763.24 ± 131.83	168.50 ± 45.36
AcsaN	4.93 ± 0.09	0.23 ± 0.05	1.30 ± 0.24	10.09 ± 2.56	140.84 ± 29.87	873.85 ± 407.43	868.12 ± 267.45	850.85 ± 131.83	290.72 ± 45.36
QuruN	4.96 ± 0.09	0.11 ± 0.05	1.74 ± 0.24	16.44 ± 2.56	165.20 ± 29.87	1513.99 ± 407.43	930.42 ± 267.45	1140.86 ± 131.83	262.82 ± 45.36
AcruS	5.08 ± 0.09	0.16 ± 0.05	1.53 ± 0.24	12.65 ± 2.56	156.46 ± 29.87	1382.66 ± 407.43	1066.56 ± 267.45	875.21 ± 131.83	168.42 ± 45.36
AcsaS	4.93 ± 0.09	0.08 ± 0.05	1.13 ± 0.24	14.11 ± 2.56	172.97 ± 29.87	2148.86 ± 407.43	1360.17 ± 267.45	1134.06 ± 131.83	212.15 ± 45.36
CaglS	4.26 ± 0.09	0.10 ± 0.05	1.11 ± 0.24	13.32 ± 2.56	225.30 ± 29.87	878.27 ± 407.43	555.25 ± 267.45	698.17 ± 131.83	163.89 ± 45.36
LituS	5.79 ± 0.09	0.15 ± 0.05	1.25 ± 0.24	11.12 ± 2.56	104.81 ± 29.87	2224.99 ± 407.43	1454.23 ± 267.45	1262.30 ± 131.83	246.36 ± 45.36
PrseS	5.11 ± 0.09	0.06 ± 0.05	0.76 ± 0.24	13.29 ± 2.56	165.20 ± 29.87	1124.33 ± 407.43	699.30 ± 267.45	885.63 ± 131.83	237.83 ± 45.36

						407.43	267.45	131.83	
QuruS	5.33 ± 0.09	0.16 ± 0.05	1.11 ± 0.24	11.98 ± 2.56	149.04 ± 29.87	889.49 ± 407.43	665.44 ± 267.45	829.57 ± 131.83	253.15 ± 45.36
QuveS	4.16 ± 0.09	0.19 ± 0.05	1.26 ± 0.24	11.30 ± 2.56	83.61 ± 29.87	1725.99 ± 407.43	802.23 ± 267.45	905.05 ± 131.83	149.78 ± 45.36
RopsS	5.10 ± 0.09	0.05 ± 0.05	0.64 ± 0.24	12.65 ± 2.56	98.95 ± 29.87	1999.21 ± 407.43	1290.98 ± 267.45	1173.89 ± 131.83	208.04 ± 45.36

[†] For species code key, see Table 1 in the main text. N = northern soils, S = southern soils.

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SUPPLEMENTARY MATERIAL 2

Mycorrhizal fungi data was analyzed using a zero-inflated Poisson model. This model divides the likelihood into two components: 1) the probability of not detecting any colonization, parameter ϕ (used when count data have a large number of zero observations as occurred in our study); and 2) the percent of mycorrhizal fungi colonization, parameter λ . Thus, for seedling i with percent colonization M_i we have a Poisson likelihood with probability density function:

$$P(M_i = m_i) = \begin{cases} \phi_i + (1 - \phi_i)e^{-\lambda_i} & \text{if } m_i = 0 \\ (1 - \phi_i) \frac{1}{m_i!} \lambda_i^{m_i} e^{-\lambda_i} & \text{if } m_i > 0 \end{cases}$$

The probability of zero colonization, ϕ , was estimated as a function of soil source, with mean ω_{soil} , and of individual random effects with variance σ_ϕ^2 .

$$\phi_i \sim \text{Normal}(\text{logit}(\omega_{soil(i)}), \sigma_\phi^2) \text{ where } \omega_{soil} \sim \text{Normal}(\omega_{mean}, \sigma_\omega^2) \text{ and}$$

$$\omega_{mean} \sim \text{Normal}(0, 100)$$

The percent of mycorrhizal fungi colonization, λ , was estimated as a function of light using a saturating equation, with parameters M_{max} , M_o and M_s . M_{max} represents maximum colonization at high light and was estimated for each soil source. M_o indicates minimum amount of light necessary to observe colonization, and was estimated for each soil source and as a function of standardized seed weight because within a species seedlings of different sizes may have had different requirements. M_s estimates the amount of light required to reach half of maximum colonization and was estimated for each soil source.

$$\lambda_i = M_{max_i} \frac{(\text{light}_i - M_o_i)}{(\text{light}_i + M_s_i)}$$

$M_{max_i} \sim \text{Normal}(\alpha_{soil(i)}, \sigma_{M_{max}}^2)$ where $\alpha_{soil} \sim \text{Normal}(\alpha_{mean}, \sigma_{\alpha}^2)$ and

$$\alpha_{mean} \sim \text{Normal}(0, 1000)$$

$M_{o_i} = \beta 1_{soil(i)} + \beta 2 \cdot seed\ weight_i$ where $\beta 1_{soil} \sim \text{Normal}(\beta 1_{mean}, \sigma_{\beta 1}^2)$, and

$$\beta 2, \beta 1_{mean} \sim \text{Normal}(0, 100)$$

$M_{s_i} \sim \text{Normal}(\gamma_{soil(i)}, \sigma_{M_s}^2)$ where $\gamma_{soil} \sim \text{Normal}(\alpha_{\gamma_{mean}}, \sigma_{\gamma}^2)$ and $\gamma_{mean} \sim \text{Normal}(0, 1000)$

We then used parameter estimates to predict mycorrhizal colonization in each seedling,

$M_i^{predicted}$, as a function of soil source, seed size and light level.

Growth rates were also analyzed as a saturating function of light but also as a function of mycorrhizal colonization. As part of the Bayesian framework of our analysis we included the predicted percent of mycorrhizal fungi colonization in the estimation of the growth parameters to allow the growth data also inform the mycorrhizal colonization model (Clark 2005, 2007). G_{max} estimated the maximum growth rate of each seedlings at high light levels, parameter G_o accounted for the minimum amount of light necessary to start growth (i.e., photosynthesis > respiration), and G_s reflected the amount of light required to reach half of the maximum growth rate. The three parameters were estimated as a function of soil source, mycorrhizal colonization and individual random effects. This approach, incorporating predicted mycorrhizal colonization in the estimation of each parameter, allowed us to assess the role of mycorrhizal fungi on seedling performance at different light levels (G_{max} -high, G_o -low, G_s -medium). For the *Quercus* species we included predicted estimates for both AM and EM since these species were colonized by both types of mycorrhizal fungi. To aid with the simulations, some parameters were constrained to their biological limits (e.g., maximum growth rates can only be positive, and as a

prior value for this parameter we used the maximum rate observed for each species, $Gmax^{obs}$), or to the limits of the data (e.g., light ranged from values 0-18 $\mu\text{mol photons/m}^2\text{s}$).

$$Growth\ rate_i \sim Normal\left(Gmax_i \frac{(light_i - Go_i)}{(light_i + Gs_i)}, \sigma_{growth}^2\right)$$

$$Gmax_i \sim Normal(\delta1_{soil(i)} + \delta2 \cdot M_i^{predicted}, \sigma_{Gmax}^2) \text{ where } \delta1_{soil} \sim Normal(\delta1_{mean}, \sigma_{\delta1}^2),$$

$$\delta2 \sim Normal(0, 1000) \text{ and } \delta1_{mean} \sim Normal(Gmax^{obs}, 1000) \text{ limited to be positive}$$

$$Go_i \sim Normal(\kappa1_{soil(i)} + \kappa2 \cdot M_i^{predicted}, \sigma_{Go}^2) \text{ where } \kappa1_{soil} \sim Normal(\kappa1_{mean}, \sigma_{\kappa1}^2),$$

$$\kappa2 \sim Normal(0, 1000) \text{ and } \kappa1_{mean} \sim Uniform(0, 18)$$

$$Gs_i \sim Normal(\mu1_{soil(i)} + \mu2 \cdot M_i^{predicted}, \sigma_{Gs}^2) \text{ where } \mu1_{soil} \sim Normal(\mu1_{mean}, \sigma_{\mu1}^2),$$

$$\mu2 \sim Normal(0, 1000) \text{ and } \mu1_{mean} \sim Uniform(0, 18)$$

All variances were estimated from non-informative prior distributions,

$$1/\sigma_*^2 \sim Gamma(0.01, 0.01).$$

OpenBUGS code for the mycorrhizal fungi colonisation and seedling growth models.

Sample code for species with both AM and EM fungi. *i*: individual, *spp*: species, *e*: individual random effects, *tau*: precision (1/variance)

```

model{

#standarizing variables,
#seed weights

seedS[i]<-(seed[i]-mseedw[sppM[i]])/(2*sdseedw[sppM[i]])
}

for(i in 1:N){          #per seedling
#AM data
delta0[i]<-equals(AM[i],0) # =1 if AMF = 0
logL[i]<-delta0[i]*log(phi[i]+(1- phi [i])*exp(-ab[i]))+(1-delta0[i])*(log(1- phi
[i])+AM[i]*log(ab[i])-ab[i]-logfact(AM[i]))

phi0[i]<--logL[i]
phi [i]<-max(0, phi 0[i])
logit(phi 0[i])<-o1[sppM[i],soil[i]]+eo[i]
eo[i]~dnorm(0,tau[sppM[i],3])

zeros[i]<- 0
zeros[i]~dpois(phi0[i])
pm[i]<-(1- phi[i])
AM.h[i]<-ab[i]*pm[i] #expected value

ab[i]<-MAmax[i]*(light[i]-MAlo[i])/(light[i]+MAtheta[i])
MAmax[i]~dnorm(alpha[sppM[i],soil[i]],tau[sppM[i],3])
MAlo[i]<-beta1[sppM[i],soil[i]]+beta2[sppM[i]]*seedS[i]
MAtheta[i]~dnorm(th[sppM[i],soil[i]],tau[sppM[i],4])
e[i]~dnorm(0,tau[sppM[i],1])

#EM data
deltaE0[i]<-equals(EM[i],0) # =1 if ECTO = 0
logLE[i]<-deltaE0[i]*log(phiE[i]+(1-phiE[i])*exp(-abE[i]))+(1-deltaE0[i])*(log(1-
phiE[i])+EM[i]*log(abE[i])-abE[i]-logfact(EM[i]))

```

```

phiE0[i]<--logLE[i]
phiE[i]<-max(0, phi0E[i])
logit(phi0E[i])<-o1E[sppM[i],soil[i]]+eoE[i]
eoE[i]~dnorm(0,tau[sppM[i],6])

zerosE[i]<- 0
zerosE[i]~dpois(phiE0[i])
pmE[i]<-(1-phiE[i])
EM.h[i]<-abE[i]*pmE[i] #expected value

abE[i]<-MEmax[i]*(light[i]-MElo[i])/(light[i]+MEtheta[i])
MEmax[i]~dnorm(alphaE[sppM[i],soil[i]],tau[sppM[i],7])
MElo[i]<-betaE1[sppM[i],soil[i]]+betaE2[sppM[i]]*seedS[i]
MEtheta[i]~dnorm(thE[sppM[i],soil[i]],tau[sppM[i],8])
eE[i]~dnorm(0,tau[sppM[i],5])

}

for(s in 1:2){          #per species
  for(i in 1:23){tau[s,i]~dgamma(0.01,0.01)
    var[s,i]<-1/tau[s,i]
  }

  for(i in 1:10){      # per soil
    o1[s,i]~dnorm(om[s],tau[s,9])
    o1E[s,i]~dnorm(omE[s],tau[s,10])
    alpha[s,i]~dnorm(am[s],tau[s,11])
    alphaE[s,i]~dnorm(aEm[s],tau[s,12])
    beta1[s,i]~dnorm(b1m[s],tau[s,13])
    betaE1[s,i]~dnorm(b1Em[s],tau[s,14])
    th[s,i]~dnorm(thm[s],tau[s,15])
    thE[s,i]~dnorm(thEm[s],tau[s,16])
  }

  om[s]~dnorm(0,0.01)
  omE[s]~dnorm(0,0.01)
  am[s]~dnorm(0,0.001)
  aEm[s]~dnorm(0,0.001)
  b1m[s]~dnorm(0,0.001)
  b1Em[s]~dnorm(0,0.001)

```

```

beta2[s]~dnorm(0,0.01)
betaE2[s]~dnorm(0,0.01)
thm[s]~dnorm(0,0.001)
thEm[s]~dnorm(0,0.001)

```

```

}

```

```

#####Growth model

```

```

for(i in 1:521){          #per seedling
GR[i]~dnorm(TG[i],tau[sppM[i],17]) #likelihood
GR.h[i]~dnorm(TG[i],tau[sppM[i],17]) #predicted

```

```

TG[i]<-Gmax[i]*(light[i]-Glo[i])/(light[i]+Gtheta[i])
Gmax[i]~dnorm(gmaxm[i],tau[sppM[i],18])
gmaxm[i]<-(delta[sppM[i],soil[i]]+ d1[sppM[i]]*AM.h[i]+ d2[sppM[i]]*EM.h[i])
Glo[i]~dnorm(Glom[i],tau[sppM[i],19])C(0,)
Glom[i]<-(kappa[sppM[i],soil[i]]+k1[sppM[i]]*AM.h[i]+k2[sppM[i]]*EM.h[i])
Gtheta[i]~dnorm(Gthetam[i],tau[sppM[i],20])
Gthetam[i]<-(mu[sppM[i],soil[i]]+mu1[sppM[i]]*AM.h[i]+mu2[sppM[i]]*EM.h[i])

```

```

}

```

```

for(sp in 1:2){          #per species
  for(so in 1:10){        #per soil
    delta[sp,so]~dnorm(deltam[sp],tau[sp,21])
    kappa[sp,so]~dnorm(km[sp],tau[sp,22])
    mu[sp,so]~dnorm(mum[sp],tau[sp,23])

```

```

}

```

#observed maximum growth
rate; limited to be positive

```

deltam[sp]~dnorm(gmaxobs[sp],0.001)
km[sp]~dunif(0,18)      #light range 0-18
mum[sp]~dunif(0,18)    #light range 0-18
d1[sp]~dnorm(0,0.001)
d2[sp]~dnorm(0,0.001)
k1[sp]~dnorm(0,0.001)
k2[sp]~dnorm(0,0.001)
mu1[sp]~dnorm(0,0.001)

```

```
mu2[sp]~dnorm(0,0.001)
}
}
```

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SUPPLEMENTARY MATERIAL 3

Full array of parameter estimates for the mycorrhizal fungi colonization and seedling growth models.

Mycorrhizal Colonization Model

1) Probability of not detecting mycorrhizal fungi colonization. Parameters' means and 95% credible intervals (below). Code for species and soil sources abbreviations can be found in Table 1 in the main text. A: arbuscular mycorrhizal fungi, E: ectomycorrhizal fungi.

	Aclu A	Aclu A	Cagl E	Litu A	Prse A	Quru A	Quru E	Quve A	Quve E	Rops A
ω_{mean}	0.50 0.15,0.72	0.04 0.01,0.09	$8E^{-5}$ $2E^{-8}$,0.08	0.49 0.28,0.67	0.01 $2E^{-8}$,0.43	0.35 0.26,0.45	0.39 0.32,0.45	0.51 0.49,0.54	0.16 0.13,0.20	0.20 0.01,0.66
ω_{AcluS}	-1.8 -2.5,-1.0	0.28 0.13,0.43	25.25 10.2,39.7	-1.69 -2.50,-0.92	-34.4 -75.2,-3.7	0.05 -0.1,0.16	1.56 1.35,1.80	-0.04 -0.09,0.09	0.34 0.23,0.51	-2.99 -4.55,-1.39
ω_{AcluN}	-16.35 -35.9,-5.8	-0.10 -0.33,0.09	8.20 0.5,15.4	0.50 0.1,0.78	-29.22 -62.9,-0.28	-0.16 -0.36,0.03	0.59 0.36,0.79	-0.083 -0.08,-0.01	-0.09 -0.12,-0.06	-2.63 -2.43,-0.69
ω_{AcluS}	-1.74 -2.4,-0.8	1.10 1.00,1.21	2.43 -1.1,12.6	0.58 0.3,0.89	-2.58 -4.4,-0.84	1.02 0.89,1.21	0.07 -0.16,0.23	-0.04 -0.17,0.04	-0.06 -0.1,-0.03	-1.22 -1.58,-0.14
ω_{AcluN}	-1.72 -2.4,-0.75	0.96 0.88,1.16	4.50 -0.35,6.8	-0.70 -2.15,0.37	-1.54 -3.1,-0.47	0.36 0.21,0.5	0.38 0.07,0.55	-0.04 -0.16,0.10	-0.26 -0.29,-0.08	-13.76 -12.8,-2.07
ω_{CaglS}	-2.22 -5.8,-0.57	-	9.82 2.9,15.6	-	-	-0.16 -0.3,-0.04	0.95 0.62,1.10	0.04 -0.13,0.32	0.50 0.47,0.52	-
ω_{LituS}	-	-	-	1.72 1.02,2.42	-	-	-	-	-	-
ω_{PrseS}	-1.46 -2.2,-0.25	-	-	-	-42.40 -93,-1.89	0.05 -0.09,0.20	-0.12 -0.29,0.10	-0.09 -0.16,0.09	0.10 -0.05,0.2	-
ω_{QuruS}	-2.04 -2.5,-1.1	-0.65 -0.85,-0.30	14.1 4.3,27.0	1.36 0.89,1.67	-50.48 -89.5,-1.91	-0.09 -0.25,0.02	-0.01 -0.14,0.05	-0.08 -0.15,0.05	0.17 0.12,0.21	-3.27 -2.02,-0.57
ω_{QuruN}	-1.56 -2.7,-0.52	0.34 0.21,0.44	14.02 4.4,20.1	-0.45 -0.75,-0.18	-4.05 -7.9,-0.99	0.71 0.54,0.88	0.07 -0.05,0.26	-0.09 -0.15,-0.01	0.17 0.16,0.2	-13.83 -11.6,-1.90

ω_{QuveS}	-1.94 -2.9,-0.51	-	-	-	-40.33 -79.6,-2.9	-0.07 -0.25,0.05	0.91 0.66,1.16	-0.08 -0.25,0.07	0.53 0.47,0.72	-13.23 -6.78,-2.01
ω_{RopsS}	-1.03 -1.5,-0.50	-	-	-	-0.78 -1.76,0.1	0.20 0.11,0.30	0.03 -0.39,0.15	-0.01 -0.12,0.03	0.01 -0.01,0.04	-1.74 -2.61,-0.8
σ_{φ}^2	0.57 0.42,0.72	0.4 0.26,0.55	0.11 0.05,0.16	0.02 0.008,0.03	0.01 0.003,0.02	1.78 1.11,2.44	3.53 2.93,4.13	3.23 0.25,6.21	0.03 0,0.07	1.94 1.24,2.6
σ_{ω}^2	21.5 2.69,111	0.42 0.35,0.49	57 15,117	1.44 1.24,1.99	416 1.66,1678	0.43 0,0.92	1.26 0,2.66	0.001 2E ⁻⁴ ,0.008	0.066 0.06,0.07	34.2 20.04,55.4

2) Percent of mycorrhizal fungi colonization model. Parameters’ means and 95% credible intervals (below). Code for species and soil sources abbreviations can be found in Table 1 in the main text. A: arbuscular mycorrhizal fungi, E: ectomycorrhizal fungi.

	Acru A	Acsa A	Cagl E	Litu A	Prse A	Quru A	Quru E	Quve A	Quve E	Rops A
α_{mean}	41.5 39.4,42.5	35.7 34.6,36.9	26.6 23.8,28.8	21.3 18.3,24.9	18.1 13.5,23.4	29.5 16.4,40.2	37.1 34,40.2	33.7 31.45,35.6	33.7 31.4,35.7	43.7 38,54.4
α_{Acrus}	41.5 40.9,42.3	35.7 34.6,37.1	26.6 23.7,28.3	21.3 19.9,21.9	18.1 14.2,22	15.3 14.1,17.1	36.5 32.6,38.9	38.4 38,38.7	39.3 38.8,39.8	43.7 38,45.4
α_{AcrusN}	41.55 39.4,42.2	35.7 34.6,36.9	26.6 23.6,28.5	21.3 19.6,20.7	18.1 14.2,22	38.6 37.2,40.9	37.1 35.4,39.4	39.7 39.6,40.7	39.5 39,39.9	43.8 38,44.7
α_{AcsaS}	41.5 40.8,42.2	35.8 34.6,36	26.6 24.2,28.3	21.3 20.5,22.4	18.1 14.3,22	41.8 40.8,43	37.6 33.8,39.5	30.5 30.4,32.1	39.4 38.9,39.4	43.8 38.1,45.5
α_{AcsaN}	41.5 39.3,41.9	35.7 34.9,38	26.6 24.2,27.5	21.3 19.4,22.7	18.1 13.8,21	18.8 16.4,25.5	37.1 35.2,40.5	36.4 34.2,38	39.2 37.9,40.2	-
α_{Cagls}	41.5 41.3,42.3	-	26.7 23.8,28.9	-	-	13.3 15.3,18.05	37 33.8,41.2	31.4 29.4,33.1	39.8 39,40.9	-
α_{Litus}	-	-	-	21.3 18.3,22.9	-	-	-	-	-	-
α_{PrseS}	41.56 39.6,42.1	-	-	-	18.1 14.3,21.6	38.5 35.4,38.9	37.3 36.7,39.9	31.6 30.5,32.5	39.7 39.2,40.3	-
α_{Qurus}	41.5 41.1,41.2	35.7 34.5,37.1	26.6 23.7,28.2	21.3 18.3,22.9	18.1 14.4,21.3	50.5 51.6,53.8	39 35.8,43.6	31.04 28.8,33.2	39.4 38.7,40	43.7 38,44.7
α_{QurusN}	41.5 41.1,42.2	35.7 34.5,37	26.6 23.9,28.4	21.3 19.2,21.5	18.1 14.1,22	39.8 37.2,41.2	37.4 34.8,40.8	31.3 30.7,32.2	39.5 39.3,39.8	43.7 38,45.8
α_{QuveS}	41.5, 41,41.7	-	-	-	18.1 14.1,21.3	42.7 41.9,44.5	36.8 35.2,38.8	30.3 29.7,31.7	39.3 38.9,40.1	43.7 38,44.5

α_{RopsS}	41.8 41.5,42.1	-	-	-	18.1 14.1,21.7	46.3 45.3,47.8	37.3 35.5,40.1	40.6 39.7,41.8	39.6 39.2,40	43.7 38,45.6
βI_{mean}	0.55 0.26,0.74	0.72 0.4,0.96	0.54 0.36,0.72	0.25 0.1,0.43	0.19 0.06,0.31	0.37 0.21,0.53	0.87 0.61,0.99	0.39 0.12,0.64	0.31 0.04,0.67	0.19 0.1,0.27
βI_{AcrusS}	0.3 0.08,0.43	0.67 0.46,0.98	0.59 0.26,0.98	0.24 0.07,0.43	0.18 0.03,0.32	1.36 0.9,1.6	0.72 0.49,0.84	0.08 0.05,0.11	1.04 0.9,1.08	0.24 0.1,0.42
βI_{AcrusN}	0.35 0.22,0.48	0.7 0.6,0.79	0.44 0.14,0.69	0.2 0.04,0.35	0.22 0.06,0.36	0.58 0.44,0.73	0.11 0.04,0.17	0.01 1E ⁻⁴ ,0.03	0.05 0.04,0.06	0.22 0.1,0.34
βI_{AcsaS}	0.4 0.2,0.6	0.46 0.33,0.81	0.56 0.38,0.73	0.13 0.01,0.27	0.13 0.02,0.26	0.11 0.01,0.25	0.11 0.007,0.17	0.06 0.01,0.11	0.06 0.04,0.08	0.18 0.06,0.31
βI_{AcsaN}	0.77 0.57,0.89	0.68 0.54,0.92	0.55 0.35,0.72	0.33 0.08,0.51	0.16 0.03,0.27	1.24 0.84,1.69	0.3 0.18,0.38	1.29 0.82,1.6	1.33 1.13,1.39	0.17 0.09,0.27
βI_{CagIS}	0.53 0.39,0.72	-	0.51 0.24,0.68	-	-	1.37 1.01,1.86	0.62 0.38,0.8	0.8 0.75,1.02	0.18 0.16,0.19	-
βI_{LituS}	-	-	-	0.22 0.03,0.41	-	-	-	-	-	-
βI_{PrseS}	0.77 0.42,0.97	-	-	-	0.17 0.02,0.37	1.34 1.21,1.61	0.38 0.31,0.43	0.05 0.001,0.09	0.52 0.47,0.62	-
βI_{QuruS}	0.53 0.27,0.76	0.67 0.27,1.23	0.61 0.32,1.04	0.2 0.04,0.38	0.21 0.04,0.37	1.54 1.21,1.61	0.31 0.25,0.39	0.73 0.41,1.14	0.24 0.2,0.28	0.16 0.03,0.27
βI_{QuruN}	1.18 0.91,1.44	0.79 0.64,0.94	0.65 0.28,1	0.35 0.15,0.51	0.22 0.05,0.38	0.21 0.06,0.51	0.34 0.3,0.51	0.03 -0.004,0.07	0.01 -0.004,0.03	0.21 0.03,0.27
βI_{QuveS}	0.26 0.02,0.46	-	-	-	0.19 0.02,0.33	0.95 0.77,1.19	0.06 0.004,0.13	0.17 0.06,0.34	0.07 0.06,0.09	0.19 0.1,0.29
βI_{RopsS}	0.22 0.07,0.36	-	-	-	0.21 0.02,0.46	1.17 0.99,1.59	0.79 0.67,0.89	0.07 0.009,0.12	0.08 0.06,0.1	0.21 0.07,0.37
$\beta 2$	-0.53 -0.7,-0.33	-0.006 -0.04,0.03	0.33 0.06,0.49	0.41 0.32,0.49	0.02 0.004,0.03	0.7 0.24,1.13	-0.11 -0.15,-0.06	0.13 -0.16,0.17	-0.077 -0.09,0.07	0.016 -0.31,0.34
γ_{mean}	0.72 0.54,0.9	1.8 1.5,2.09	1.51 0.69,2.33	1.7 1.4,2.1	1.21 0.75,1.88	1.08 0.82,1.35	1.7 1.23,2.32	0.64 0.53,0.74	1.55 0.96,2.14	1.63 0.95,1.98
γ_{AcrusS}	0.73 0.54,0.98	1.35 0.62,1.92	1.56 0.95,2.15	1.84 1.32,2.64	1.85 0.74,1.32	0.44 0.14,0.69	0.84 0.81,0.92	6.38 5.94,7.31	0.68 0.55,0.79	2.59 1.49,3.35
γ_{AcrusN}	0.78 0.6,1.11	2.05 1.69,2.4	1.58 1.06,2.05	1.15 0.58,1.54	1.95 0.73,1.32	2.33 1.78,2.79	0.9 0.79,1.05	4.55 4.45,6.01	0.74 0.79,0.83	0.85 0.2,1.24
γ_{AcsaS}	0.73 0.55,1.09	2.84 1.24,3.05	1.54 1.06,2.05	1.29 1.06,2.57	1.47 0.69,1.11	5.52 4.65,6.2	0.82 0.77,0.94	7.97 7.3,8.54	0.65 0.59,0.7	1.11 0.34,1.42
γ_{AcsaN}	0.76 0.59,1.18	2.56,2.21,3. 06	1.48 0.94,2.07	1.88 1.34,2.94	0.51 0.69,1.22	0.39 0.12,0.71	0.74 0.62,0.86	9.09 7.19,10.5	0.5 0.4,0.53	4.31 2.59,4.19
γ_{CagIS}	0.62	-	1.47	-	-	0.97	0.94	9.9	0.58	-

	0.36,0.96		0.88,1.96			0.69,1.26	0.81,1.01	8.5,10.9	0.51,0.67	
γ_{LituS}	-	-	-	0.69 0.31,1.43	-	-	-	-	-	-
γ_{PrseS}	0.73 0.42,1.02	-	-	-	1.17 0.69,1.64	2.05 0.8,2.71	0.88 0.8,0.93	5.63 4.56,6.55	0.58 0.51,0.64	-
γ_{QuruS}	0.64 0.39,0.98	3.37 2.76,3.71	1.55 0.83,2.08	0.72 0.17,1.51	1.25 0.76,1.72	4.91 4.4,5.79	0.79 0.69,0.88	3.02 2.02,3.46	0.57 0.45,0.71	1.06 0.62,1.51
γ_{QuruN}	0.7 0.49,0.9	3.96 2.9,4.7	1.65 1.15,2.47	1.66 1.17,2.96	1.31 0.73,1.75	3.8 2.22,4.31	0.86 0.76,0.97	5.23 4.06,5.27	0.6 0.57,0.65	3.1 1.68,3.8
γ_{QuveS}	0.7 0.57,1.04	-	-	-	1.13 0.63,1.63	5.16 4.37,5.68	0.91 0.79,0.99	10.48 9.06,12.4	0.59 0.51,0.7	1.94 1.2,2.35
γ_{RopsS}	0.68 0.44,0.98	-	-	-	1.22 0.74,1.75	5.04 3.52,5.81	0.86 0.76,1.07	9.56 9.12,11.2	0.49 0.4,0.55	2.02 1.3,2.39
σ_{α}^2	0.01 0.004,0.018	0.015 0.008,0.02	0.4 0.25,0.54	0.03 0.009,0.05	0.06 0.01,0.1	169 156,180	4.8 0,12.3	12.8 1.87,23.8	1.004 0,2.26	0.01 0.007,0.02
$\sigma_{\beta 1}^2$	0.12 0,0.27	0.03 0,0.08	0.02 0,0.05	0.05 0,0.13	0.006 0,0.02	0.26 0,0.58	0.05 0,0.11	0.17 0,0.42	0.35 0,0.73	0.03 3E ⁻⁴ ,0.005
σ_{γ}^2	0.008 0,0.017	0.03 0,0.08	0.02 0,0.06	0.06 0,0.16	0.02 0,0.04	6.18 0,13.1	0.02 0,0.06	37.1 0,89	0.007 0,0.01	0.62 0,1.25

Seedling Growth Model

3) Seedling growth model results. Parameters’ means and 95% credible intervals (below). Code for species and soil sources abbreviations can be found in Table 1 in the main text. A: arbuscular mycorrhizal fungi, E: ectomycorrhizal fungi.

	Aclu A	Aclu A	Cagl E	Litu A	Prse A	Quru A & E	Quve A & E	Rops A
δI_{mean}	5.34 4.92,5.86	14.4 10.1,17	22.04 20.3,23.5	0.51 0.06,1.23	6.63 5.11,8.14	76.8 71.6,81.2	9.76 9.41,10.1	7.99 4.73,12.4
δI_{AcluS}	5.47 4.42,6.13	8.28 7.3,9.3	22.2 20.5,23.7	2.69 1.62,3.5	6.2 3.96,7.91	73.7 69.8,76.8	11.7 11.5,11.9	8.29 6.79,9.56
δI_{AcluN}	5.6 4.4,6.1	12.4 10.5,13.7	21.9 20.1,23.3	2.78 2.25,3.53	5.93 3.8,7.52	91.67 78.4,86.4	12.09 12,12.1	2.79 0.36,4.39
δI_{AcluS}	5.7 4.9,6.8	4.44 3.7,5.1	21.9 19.7,23.6	4.22 3.49,4.98	7.26 5.52,8.67	72.06 64.5,70.7	4.2 4.18,4.3	6.06 5.21,8.04

δI_{AcsaN}	6.27 5.46,7.1	7.1 6.1,7.8	22.01 19.4,23.7	3.24 2.27,3.8	7.5 5.58,8.73	76.2 71.09,78.1	8.13 7.98,8.24	9.72 7.31,10.9
δI_{CagIS}	4.89 4.1,5.2	-	22.5 20.7,24.6	-	-	71.3 66.4,75.9	10.88 10.6,10.9	-
δI_{LituS}	-	-	-	0.91 0.29,1.82	-	-	-	-
δI_{PrseS}	5.04 4.14,5.83	-	-	-	6.54 4.68,9.03	84.4 77,85.9	12.8 12.6,12.9	-
δI_{QuruS}	5.92 4.9,6.6	8.69 6.79,9.9	21.98 19.8,23.5	4.39 4.16,4.34	6.12 4.68,9.03	70.7 67,73.2	9.99 9.64,10.1	10.7 8.85,13.09
δI_{QuruN}	4.68 3.91,5.16	6.62 5.05,7.8	22.4 20.3,23.6	2.28 1.89,3.16	67.65 5.8,9.31	84.03 75.5,85.1	6.06 6.03,6.11	12.1 9.59,13.1
δI_{QuveS}	5.14 4.54,5.5	-	-	-	6.59 4.55,8.04	71.7 68.8,74.2	8.57 8.59,8.62	11.9 7.76,13
δI_{RopsS}	6.44 5.32,6.6	-	-	-	6 4.46,7.87	76.7 67.8,78.4	11.8 11.7,12	6.88 4.93,7.55
$\delta 2_A$	0.16 0.14,0.18	0.94 0.89,1.003	-	0.11 0.09,0.13	0.16 0.12,0.2	0.75 0.2,1.3	-0.03 -0.11,-0.003	0.18 0.13,0.25
$\delta 2_E$	-	-	0.12 -0.01,0.26	-	-	0.96 0.84,1.07	0.02 0.007,0.04	-
κI_{mean}	0.02 0.001,0.05	0.029 0.0007,0.08	0.11 0.05,0.17	0.18 0.09,0.26	0.13 0.06,0.2	0.06 0.02,0.1	0.15 0.1,0.18	0.02 0.0008,0.09
κI_{Acrus}	0.18 0.11,0.3	0.06 0.033,0.12	0.14 0.07,0.24	0.18 0.08,0.31	0.15 0.06,0.26	0.049 0.008,0.1	0.12 0.03,0.18	0.26 0.18,0.41
κI_{AcrusN}	0.13 0.06,0.2	0.07 0.02,0.13	0.12 0.05,0.2	0.2 0.09,0.27	0.18 0.08,0.3	0.057 0.006,0.11	0.12 0.02,0.16	0.07 0.01,0.15
κI_{AcsaS}	0.13 0.06,0.23	0.08 0.01,0.13	0.1 0.04,0.17	0.19 0.08,0.3	0.15 0.08,0.24	0.049 0.006,0.12	0.14 0.08,0.18	0.21 0.15,0.31
κI_{AcsaN}	0.23 0.16,0.35	0.15 0.06,0.23	0.12 0.05,0.21	0.22 0.12,0.35	0.14 0.06,0.22	0.073 0.01,0.14	0.13 0.03,0.2	0.24 0.15,0.32
κI_{CagIS}	0.25 0.17,0.35	-	0.14 0.07,0.21	-	-	0.097 0.05,0.15	0.19 0.15,0.26	-
κI_{LituS}	-	-	-	0.2 0.07,0.34	-	-	-	-
κI_{PrseS}	0.32 0.21,0.5	-	-	-	0.16 0.05,0.28	0.06 0.01,0.13	0.19 0.12,0.28	0.23 0.14,0.36
κI_{QuruS}	0.24 0.17,0.32	0.06 0.01,0.14	0.11 0.05,0.18	0.12 0.02,0.22	0.16 0.05,0.23	0.04 0.004,0.09	0.14 0.06,0.24	0.26 0.18,0.32
κI_{QuruN}	0.23	0.09	0.14	0.22	0.15	0.067	0.12	0.24

	0.09,0.33	0.04,0.12	0.06,0.23	0.09,0.34	0.05,0.24	0.004,0.16	0.08,0.18	0.11,0.32
κl_{QuveS}	0.2 0.1,0.28	-	-	-	0.15 0.05,0.25	0.049 0.004,0.1	0.12 0.06,0.21	0.24 0.11,0.32
κl_{RopsS}	0.18 0.13,0.28	-	-	-	0.2 0.1,0.33	0.07 0.01,0.13	0.24 0.11,0.26	0.32 0.13,0.5
$\kappa 2_A$	0.001 0.0004,0.002	0.305 0.29,0.31	-	0.095 0.091,0.1	0.001 -0.0003,0.003	0.205 0.19,0.22	0.002 -0.01,0.01	0.015 0.007,0.02
$\kappa 2_E$	-	-	0.005 -9E ⁻⁵ ,0.01	-	-	-0.0036 -0.007,-9E ⁻⁴	0.389 0.382,0.397	-
μl_{mean}	1.83 1.42,2.24	1.71 1.27,2.14	0.46 0.36,0.57	1.1 0.72,1.48	1.83 1.37,1.99	1.91 1.79,2.02	0.5 0.45,0.55	1.8 1.42,1.99
μl_{Acrus}	7.87 5.64,8.91	1.42 1.21,1.63	0.46 0.3,0.66	1.61 0.59,1.63	1.83 1.26,2.34	1.28 1.15,1.52	0.53 0.42,0.66	2.05 1.22,2.62
μl_{AcrusN}	12.03 907,13.9	2.35 1.96,2.61	0.43 0.28,0.6	1.41 0.99,1.49	2 1.38,2.7	0.59 0.08,0.97	0.49 0.4,0.57	2.62 1.64,2.79
μl_{AcsaS}	11.14 7.7,11.6	1.11 0.8,1.57	0.42 0.26,0.56	1.29 1.11,1.42	1.9 1.21,2.45	0.36 0.14,0.55	0.41 0.34,0.44	2.05 1.42,2.53
μl_{AcsaN}	4.37 2.7,4.51	2.17 1.64,2.59	0.44 0.27,0.62	1.05 0.54,1.38	1.68 1.16,2.09	0.57 0.07,0.83	0.44 0.34,0.51	1.98 1.4,2.48
μl_{CagIS}	4.83 2.98,5.74	-	0.47 0.32,0.59	-	-	0.78 0.51,1.07	0.44 0.42,0.54	-
μl_{LituS}	-	-	-	1.17 0.65,1.58	-	-	-	-
μl_{PrseS}	2.59 1.8,2.97	-	-	-	1.85 1.14,2.55	1.19 0.36,1.42	0.48 0.38,0.61	-
μl_{QuruS}	4.89 4.15,6.27	1.98 1.67,2.22	0.4 0.22,0.55	0.76 0.5,0.99	1.97 1.22,2.61	0.62 0.2,0.84	0.48 0.39,0.59	2.45 1.39,2.86
μl_{QuruN}	8.66 5.77,10.4	1.91 1.69,2.12	0.45 0.29,0.59	0.9 0.46,1.11	1.6 0.97,2.14	1.08 0.85,1.87	0.58 0.55,0.62	1.98 1.29,2.79
μl_{QuveS}	1.86 1.27,3.15	-	-	-	1.87 1.22,2.49	0.49 0.11,0.65	0.5 0.44,0.58	2.19 1.48,3.19
μl_{RopsS}	7.78 5.76,9.97	-	-	-	2.03 1.35,2.81	0.7 0.13,0.65	0.59 0.54,0.64	2.04 1.43,2.81
$\mu 2_A$	0.13 0.1,0.15	-3E ⁻⁴ -0.01,0.01	-	0.007 -4E ⁻⁴ ,0.01	0.08 0.07,0.088	0.34 0.33,0.35	0.98 0.97,0.99	-0.002 -0.03,0.02
$\mu 2_E$	-	-	-0.001 -0.005,0.001	-	-	0.47 0.45,0.49	0.835 0.831,0.84	-
σ^2_{growth}	0.005 0.002,0.007	0.04 0.01,0.06	13.4 9.1,17.8	0.005 0.004,0.007	0.03 0.01,0.04	112 93,131	140 119,161	0.006 0.002,0.009

$\sigma_{\delta 1}^2$	26.5 21.3,31.7	13.8 9.13,18.4	39.2 29.4,48.9	5.06 3.676,45	19.02 14.03,24.02	0.55 0.32,0.79	0.052 0.03,0.06	31.04 25.4,36.6
$\sigma_{\kappa 1}^2$	0.0019 0.0015,0.002	0.005 0.002,0.008	0.004 0.0009,0.007	0.0019 0.001,0.002	0.003 0.002,0.004	0.004 0.002,0.005	0.006 0.004,0.009	0.003 0.001,0.005
$\sigma_{\mu 1}^2$	0.68 0.32,1.05	0.25 0.17,0.33	0.01 0.006,0.018	0.013 0.006,0.019	0.15 0,0.31	0.06 0.04,0.07	0.04 0.02,0.05	0.06 0.04,0.08

Draft

SUPPLEMENTARY MATERIAL 4

Figure SM-4. Daily growth rates (data-dots and predictions-lines [mean±95%PI]) along the light gradient for seedlings growing with (black triangles and solid lines) and without (white circles and dashed lines) mycorrhizal fungi. Predictive curves are for all soil sources combined (species-level parameters). A: arbuscular mycorrhizal fungi, E: ectomycorrhizal fungi.

Seedling growth predictions for all soil sources as a function of light levels, with (left columns) and without (right columns) mycorrhizal fungi colonization, predicted mean and 95% predicted intervals (mean, low, upper). Code for species and soil sources abbreviations can be found in Table 1 in the main text. Light values (PAR) are in $\mu\text{mol photons/m}^2\text{s}$. Growth rates are in mg/day.

Seedling	Soil	Light	With Mycorrhizal fungi			Without Mycorrhizal fungi		
			mean	lower	upper	mean	lower	upper
Acru	acruS	0	0.045	0.001	0.133	0.045	0.001	0.132
Acru	acruS	2	1.559	0.647	2.608	1.315	1.039	1.635
Acru	acruS	5	3.984	2.521	5.424	2.442	2.210	3.316
Acru	acruS	8	5.903	3.943	7.831	3.053	2.854	3.769
Acru	acruS	11	7.550	4.207	10.440	3.444	3.245	4.075
Acru	acruS	15	8.238	4.969	10.740	3.789	3.468	4.285
Acru	acruS	18	9.842	7.053	12.210	3.974	3.492	4.485
Acru	acruN	0	0.045	0.002	0.131	0.045	0.001	0.135
Acru	acruN	2	1.265	0.528	2.112	0.811	0.635	1.044
Acru	acruN	5	3.347	2.232	4.412	1.668	1.371	1.974
Acru	acruN	8	5.040	2.950	7.040	2.220	1.835	2.570
Acru	acruN	11	6.716	4.452	8.421	2.607	2.128	2.936
Acru	acruN	15	8.165	5.289	10.510	2.977	2.387	3.270
Acru	acruN	18	8.047	5.294	10.370	3.183	2.522	3.525
Acru	acsaS	0	0.045	0.002	0.135	0.045	0.001	0.134
Acru	acsaS	2	1.332	0.561	2.299	1.083	0.853	1.573
Acru	acsaS	5	3.552	1.563	4.762	2.096	1.834	2.754
Acru	acsaS	8	5.168	2.268	6.821	2.689	2.408	3.347
Acru	acsaS	11	6.759	3.748	8.808	3.089	2.818	3.681
Acru	acsaS	15	7.686	3.387	9.899	3.458	3.079	3.983
Acru	acsaS	18	8.561	6.102	12.420	3.661	3.263	4.171
Acru	acsaN	0	0.045	0.001	0.134	0.045	0.001	0.135
Acru	acsaN	2	2.271	0.763	3.431	2.350	1.694	3.498
Acru	acsaN	5	4.720	2.401	6.524	3.803	3.369	4.747
Acru	acsaN	8	6.096	4.175	8.651	4.445	4.164	5.207
Acru	acsaN	11	7.633	5.226	9.458	4.812	4.574	5.416
Acru	acsaN	15	9.805	6.806	12.480	5.115	4.848	5.450
Acru	acsaN	18	10.800	8.201	13.880	5.268	4.946	5.718
Acru	cagl	0	0.045	0.001	0.134	0.045	0.001	0.134
Acru	cagl	2	1.928	0.741	3.239	1.545	1.258	2.139

Acru	cagl	5	4.220	2.414	5.779	2.637	2.312	3.441
Acru	cagl	8	5.745	3.287	7.936	3.148	2.765	4.012
Acru	cagl	11	7.257	4.211	8.785	3.448	3.046	4.336
Acru	cagl	15	8.834	4.546	12.510	3.698	3.270	4.583
Acru	cagl	18	9.218	7.042	12.230	3.826	3.398	4.693
Acru	prse	0	0.045	0.001	0.133	0.045	0.002	0.134
Acru	prse	2	1.767	0.382	3.035	1.901	1.623	2.387
Acru	prse	5	4.474	2.503	5.739	3.073	2.727	3.504
Acru	prse	8	5.542	3.141	7.922	3.550	3.126	4.267
Acru	prse	11	7.414	5.098	9.082	3.807	3.315	4.223
Acru	prse	15	10.620	6.824	12.240	4.013	3.473	4.612
Acru	prse	18	9.710	5.778	11.580	4.113	3.540	4.259
Acru	quruS	0	0.045	0.001	0.132	0.045	0.001	0.133
Acru	quruS	2	1.945	0.756	3.346	1.781	1.427	2.434
Acru	quruS	5	5.021	2.689	7.256	3.108	2.698	3.861
Acru	quruS	8	6.287	3.694	8.148	3.751	3.261	4.474
Acru	quruS	11	7.683	3.771	9.723	4.135	3.675	4.814
Acru	quruS	15	9.443	4.157	11.030	4.458	4.010	5.109
Acru	quruS	18	10.190	5.243	12.230	4.624	4.157	5.273
Acru	quruN	0	0.045	0.001	0.135	0.045	0.002	0.135
Acru	quruN	2	1.437	0.516	2.925	1.040	0.806	0.919
Acru	quruN	5	3.714	2.123	5.432	2.033	1.721	2.357
Acru	quruN	8	5.321	2.967	7.202	2.591	2.293	3.413
Acru	quruN	11	6.184	4.479	8.023	2.954	2.671	3.314
Acru	quruN	15	8.838	4.687	10.590	3.278	3.016	3.714
Acru	quruN	18	9.009	7.012	11.810	3.453	3.187	4.057
Acru	quve	0	0.046	0.002	0.135	0.045	0.001	0.134
Acru	quve	2	3.286	0.989	3.792	2.107	1.512	3.013
Acru	quve	5	4.375	2.490	5.486	3.232	2.582	4.189
Acru	quve	8	6.168	2.664	7.725	3.699	3.021	4.567
Acru	quve	11	8.247	5.879	10.100	3.958	3.258	4.760
Acru	quve	15	9.445	7.298	11.890	4.162	3.490	4.961
Acru	quve	18	10.610	7.181	12.060	4.264	3.620	5.022
Acru	rops	0	0.045	0.001	0.136	0.045	0.001	0.132
Acru	rops	2	1.604	0.733	2.610	1.310	1.072	1.698
Acru	rops	5	3.899	2.437	5.048	2.559	2.212	3.065
Acru	rops	8	5.372	3.623	7.108	3.273	2.855	3.815
Acru	rops	11	7.753	4.701	9.688	3.741	3.269	4.261
Acru	rops	15	7.948	6.341	10.540	4.160	3.628	4.680
Acru	rops	18	9.302	7.081	10.980	4.386	3.849	4.918
Acsa	acruS	0	0.143	0.005	0.453	0.143	0.005	0.456
Acsa	acruS	2	0.143	0.006	0.459	4.786	3.842	5.486
Acsa	acruS	5	0.144	0.005	0.467	6.422	5.338	7.325

Acsa	acruS	8	0.162	0.005	0.525	7.008	5.275	7.954
Acsa	acruS	11	0.190	0.005	0.551	7.308	6.188	8.307
Acsa	acruS	15	2.949	0.026	5.263	7.535	6.350	8.589
Acsa	acruS	18	13.120	9.999	17.110	7.643	6.346	8.679
Acsa	acruN	0	0.144	0.005	0.454	0.143	0.005	0.457
Acsa	acruN	2	0.162	0.005	0.533	5.652	4.726	6.809
Acsa	acruN	5	0.144	0.005	0.463	8.187	6.810	9.293
Acsa	acruN	8	0.144	0.005	0.459	9.201	7.704	10.480
Acsa	acruN	11	0.163	0.005	0.518	9.746	8.078	11.240
Acsa	acruN	15	1.983	0.008	4.242	10.170	8.422	11.480
Acsa	acruN	18	6.292	0.047	10.960	10.380	8.567	11.750
Acsa	acsaS	0	0.143	0.005	0.461	0.144	0.005	0.458
Acsa	acsaS	2	1.155	0.021	2.173	3.022	2.344	3.809
Acsa	acsaS	5	1.605	0.009	4.338	4.046	3.300	5.169
Acsa	acsaS	8	2.634	0.019	3.918	4.399	3.626	5.627
Acsa	acsaS	11	7.581	4.101	10.460	4.581	3.769	6.003
Acsa	acsaS	15	11.520	7.993	15.630	4.714	3.888	6.138
Acsa	acsaS	18	14.800	11.020	18.520	4.779	3.881	6.198
Acsa	acsaN	0	0.143	0.005	0.459	0.144	0.005	0.455
Acsa	acsaN	2	1.766	0.036	3.643	3.223	2.453	4.108
Acsa	acsaN	5	1.842	0.020	4.455	4.905	3.853	6.239
Acsa	acsaN	8	3.398	0.055	5.700	5.583	4.403	6.993
Acsa	acsaN	11	6.488	2.458	9.537	5.953	4.728	7.408
Acsa	acsaN	15	11.240	8.193	13.360	6.241	4.994	7.757
Acsa	acsaN	18	14.200	10.720	18.170	6.384	5.116	7.972
Acsa	quruS	0	0.143	0.005	0.462	0.144	0.005	0.458
Acsa	quruS	2	0.142	0.005	0.475	4.226	3.315	5.295
Acsa	quruS	5	0.146	0.005	0.468	6.053	4.686	7.331
Acsa	quruS	8	0.142	0.005	0.455	6.771	5.115	8.108
Acsa	quruS	11	0.144	0.005	0.454	7.153	5.364	8.632
Acsa	quruS	15	1.321	0.018	3.131	7.455	5.502	8.982
Acsa	quruS	18	1.792	0.010	5.328	7.601	5.618	9.175
Acsa	quruN	0	0.144	0.005	0.465	0.144	0.005	0.453
Acsa	quruN	2	1.845	0.032	2.951	3.557	2.719	4.981
Acsa	quruN	5	1.878	0.043	3.577	5.045	3.964	6.508
Acsa	quruN	8	1.761	0.015	4.607	5.615	4.445	7.076
Acsa	quruN	11	2.196	0.009	7.113	5.923	4.754	7.446
Acsa	quruN	15	6.312	3.621	10.440	6.159	4.830	7.750
Acsa	quruN	18	8.367	4.277	12.550	6.275	5.011	7.919
Cagl	acruS	0	2.950	0.101	8.739	2.935	0.106	8.802
Cagl	acruS	2	16.780	5.491	28.720	16.790	9.006	24.390
Cagl	acruS	5	19.550	7.362	31.740	19.610	11.870	27.420
Cagl	acruS	8	20.430	7.445	33.570	20.400	12.750	28.140

Cagl	acruS	11	20.840	7.959	33.780	20.880	13.100	28.600
Cagl	acruS	15	21.230	7.799	34.510	21.120	13.610	29.080
Cagl	acruS	18	21.320	8.156	34.710	21.290	12.940	28.850
Cagl	acruN	0	2.920	0.107	8.464	2.955	0.109	8.405
Cagl	acruN	2	16.760	5.086	28.320	16.970	9.420	24.430
Cagl	acruN	5	19.840	7.439	32.700	19.590	11.640	26.840
Cagl	acruN	8	21.070	7.748	34.330	20.350	12.500	28.100
Cagl	acruN	11	21.520	7.926	35.610	20.670	12.850	28.550
Cagl	acruN	15	21.900	8.451	35.830	20.960	13.240	29.380
Cagl	acruN	18	22.000	8.560	35.890	21.110	13.260	28.840
Cagl	acsaS	0	2.956	0.112	8.829	2.931	0.112	8.878
Cagl	acsaS	2	17.650	6.251	29.160	17.200	9.486	24.670
Cagl	acsaS	5	21.800	8.043	34.310	19.730	11.900	27.240
Cagl	acsaS	8	24.150	10.770	39.510	20.490	12.600	28.180
Cagl	acsaS	11	25.110	9.882	42.400	20.840	12.930	28.360
Cagl	acsaS	15	25.600	10.210	42.490	21.060	13.320	28.690
Cagl	acsaS	18	25.830	11.070	43.040	21.140	13.540	28.720
Cagl	acsaN	0	2.922	0.112	9.037	2.951	0.116	9.050
Cagl	acsaN	2	17.000	5.634	28.950	16.880	9.247	24.640
Cagl	acsaN	5	20.160	7.375	32.930	19.530	11.860	26.960
Cagl	acsaN	8	21.530	8.159	34.640	20.350	12.780	27.860
Cagl	acsaN	11	21.930	8.415	36.150	20.750	12.700	28.690
Cagl	acsaN	15	22.360	8.996	36.270	20.970	13.100	28.520
Cagl	acsaN	18	22.340	9.159	36.000	21.120	13.390	28.950
Cagl	cagl	0	2.941	0.111	8.706	2.954	0.117	8.614
Cagl	cagl	2	17.050	5.784	28.470	16.810	9.017	24.180
Cagl	cagl	5	19.990	7.953	32.380	19.800	11.970	27.610
Cagl	cagl	8	20.880	7.595	33.510	20.680	12.900	28.350
Cagl	cagl	11	21.060	7.978	34.240	21.090	13.340	28.570
Cagl	cagl	15	21.270	8.114	34.890	21.330	13.560	29.180
Cagl	cagl	18	21.600	8.125	35.110	21.500	13.870	29.090
Cagl	quruS	0	2.932	0.116	8.697	2.950	0.118	8.890
Cagl	quruS	2	17.210	5.382	29.250	17.310	9.724	24.800
Cagl	quruS	5	20.140	7.618	33.000	19.740	12.210	27.410
Cagl	quruS	8	20.610	7.496	34.160	20.520	12.740	27.490
Cagl	quruS	11	21.000	7.842	34.240	20.870	13.030	28.590
Cagl	quruS	15	21.250	8.229	34.870	21.110	12.970	29.100
Cagl	quruS	18	21.490	8.037	35.490	21.200	13.360	28.870
Cagl	quruN	0	2.918	0.108	8.568	2.932	0.107	8.667
Cagl	quruN	2	17.050	5.449	28.670	16.930	9.954	24.430
Cagl	quruN	5	19.980	7.264	31.920	19.810	11.990	27.720
Cagl	quruN	8	20.650	7.681	33.550	20.660	12.820	28.330
Cagl	quruN	11	21.160	8.168	34.630	21.130	13.340	28.930

Cagl	quruN	15	21.360	8.249	34.560	21.390	13.330	29.450
Cagl	quruN	18	21.480	8.193	34.300	21.530	13.870	28.910
Litu	acruS	0	0.064	0.002	0.198	0.064	0.002	0.195
Litu	acruS	2	1.047	0.023	2.589	1.525	0.748	2.139
Litu	acruS	5	1.680	0.202	4.109	2.035	1.210	2.724
Litu	acruS	8	2.218	0.089	4.878	2.213	1.266	2.953
Litu	acruS	11	3.528	1.505	5.799	2.305	1.408	3.077
Litu	acruS	15	4.981	2.848	6.475	2.375	1.454	3.159
Litu	acruS	18	5.613	3.131	7.846	2.410	1.452	3.218
Litu	acruN	0	0.065	0.002	0.199	0.064	0.002	0.196
Litu	acruN	2	0.935	0.041	2.269	1.258	0.517	1.707
Litu	acruN	5	1.762	0.252	3.794	1.702	0.747	2.249
Litu	acruN	8	2.905	1.138	5.421	1.858	0.608	2.439
Litu	acruN	11	3.100	1.321	5.696	1.935	0.672	2.510
Litu	acruN	15	4.177	2.087	7.195	1.996	0.711	2.581
Litu	acruN	18	5.190	2.537	8.216	2.024	0.644	2.581
Litu	acsaS	0	0.064	0.002	0.194	0.064	0.002	0.197
Litu	acsaS	2	1.529	0.078	3.651	2.324	1.784	2.817
Litu	acsaS	5	2.706	0.776	5.109	3.128	2.273	3.716
Litu	acsaS	8	3.943	1.391	6.207	3.406	2.440	3.969
Litu	acsaS	11	4.791	2.361	7.172	3.543	2.518	4.049
Litu	acsaS	15	5.908	3.947	8.625	3.650	2.568	4.258
Litu	acsaS	18	6.370	4.090	9.227	3.700	2.584	4.292
Litu	acsaN	0	0.064	0.002	0.197	0.065	0.002	0.199
Litu	acsaN	2	1.289	0.090	3.441	1.576	0.867	2.113
Litu	acsaN	5	2.225	0.210	4.093	2.112	1.211	2.845
Litu	acsaN	8	2.890	0.995	5.262	2.290	1.297	3.091
Litu	acsaN	11	3.790	1.139	6.117	2.380	1.337	3.270
Litu	acsaN	15	4.942	2.747	7.238	2.448	1.392	3.331
Litu	acsaN	18	5.526	3.368	8.022	2.480	1.393	3.462
Litu	quruS	0	0.064	0.002	0.198	0.064	0.002	0.198
Litu	quruS	2	2.148	0.037	5.039	3.663	3.240	5.248
Litu	quruS	5	3.630	1.286	6.757	4.540	3.869	6.410
Litu	quruS	8	5.036	2.969	7.695	4.821	3.681	6.743
Litu	quruS	11	5.543	2.938	9.408	4.959	3.940	6.872
Litu	quruS	15	6.654	4.163	11.130	5.060	4.146	6.926
Litu	quruS	18	7.391	4.968	10.470	5.109	4.214	7.074
Litu	quruN	0	0.064	0.002	0.198	0.064	0.002	0.198
Litu	quruN	2	1.397	0.041	3.871	1.441	0.742	2.019
Litu	quruN	5	1.854	0.145	4.887	1.854	1.029	2.600
Litu	quruN	8	2.627	0.678	5.446	1.984	1.079	2.782
Litu	quruN	11	3.607	1.140	5.733	2.046	1.112	2.876
Litu	quruN	15	5.383	2.932	7.824	2.094	1.086	2.955

Litu	quruN	18	5.926	3.610	8.251	2.117	1.087	2.989
Litu	litu	0	0.064	0.002	0.196	0.064	0.002	0.196
Litu	litu	2	1.024	0.046	2.603	0.798	0.219	1.504
Litu	litu	5	1.743	0.130	3.722	1.037	0.310	1.927
Litu	litu	8	2.753	0.260	5.138	1.115	0.372	2.102
Litu	litu	11	2.491	0.331	5.465	1.153	0.361	2.149
Litu	litu	15	2.390	0.328	4.918	1.183	0.353	2.177
Litu	litu	18	3.446	0.695	6.347	1.197	0.405	2.240
Prse	acruS	0	0.202	0.007	0.621	0.202	0.007	0.620
Prse	acruS	2	3.263	0.611	6.103	3.001	1.773	4.087
Prse	acruS	5	6.296	3.058	10.000	4.401	2.789	5.750
Prse	acruS	8	9.006	4.686	13.050	4.949	3.143	6.429
Prse	acruS	11	10.890	6.626	15.790	5.241	3.308	6.863
Prse	acruS	15	12.810	8.088	17.860	5.468	3.514	7.027
Prse	acruS	18	13.600	9.031	18.810	5.577	3.579	7.245
Prse	acruN	0	0.201	0.007	0.612	0.200	0.007	0.613
Prse	acruN	2	2.953	0.534	5.593	2.702	1.521	3.822
Prse	acruN	5	5.995	2.251	9.512	4.081	2.513	5.571
Prse	acruN	8	8.712	4.842	12.700	4.635	2.973	6.241
Prse	acruN	11	10.570	6.097	14.880	4.935	3.220	6.553
Prse	acruN	15	11.950	6.060	17.140	5.166	3.425	6.833
Prse	acruN	18	13.270	8.072	18.280	5.281	3.364	6.965
Prse	acsaS	0	0.201	0.007	0.616	0.201	0.007	0.623
Prse	acsaS	2	3.412	0.832	6.197	3.443	2.474	4.330
Prse	acsaS	5	6.574	3.115	9.728	5.094	3.788	6.265
Prse	acsaS	8	9.398	5.428	13.490	5.746	4.259	7.074
Prse	acsaS	11	11.330	7.346	16.070	6.097	4.542	7.419
Prse	acsaS	15	12.890	7.644	18.290	6.373	4.730	7.707
Prse	acsaS	18	13.960	8.852	19.250	6.507	4.828	7.939
Prse	acsaN	0	0.200	0.007	0.615	0.201	0.007	0.625
Prse	acsaN	2	3.798	0.970	7.016	3.796	2.696	4.905
Prse	acsaN	5	6.810	2.854	10.660	5.457	3.993	6.926
Prse	acsaN	8	9.517	5.181	13.820	6.089	4.518	7.625
Prse	acsaN	11	11.300	6.844	15.780	6.422	4.758	8.035
Prse	acsaN	15	13.060	8.229	18.800	6.682	4.950	8.458
Prse	acsaN	18	13.880	7.884	18.970	6.808	5.079	8.450
Prse	prse	0	0.203	0.008	0.624	0.201	0.007	0.614
Prse	prse	2	3.296	0.836	6.088	3.135	2.048	4.277
Prse	prse	5	6.587	3.034	10.150	4.613	3.204	6.196
Prse	prse	8	9.362	5.150	13.010	5.196	3.632	6.942
Prse	prse	11	11.200	7.075	15.520	5.508	3.850	7.365
Prse	prse	15	12.810	7.899	17.390	5.750	4.026	7.612
Prse	prse	18	13.900	9.535	18.760	5.868	4.133	7.882

Prse	quruS	0	0.201	0.007	0.624	0.200	0.007	0.611
Prse	quruS	2	3.126	0.613	6.057	2.852	1.685	3.990
Prse	quruS	5	6.223	2.796	9.579	4.253	2.777	5.546
Prse	quruS	8	9.125	5.551	12.830	4.812	3.119	6.205
Prse	quruS	11	10.770	6.731	14.880	5.114	3.423	6.492
Prse	quruS	15	12.630	7.757	17.560	5.349	3.532	6.796
Prse	quruS	18	13.560	8.348	18.910	5.467	3.700	6.880
Prse	quruN	0	0.202	0.007	0.619	0.201	0.007	0.610
Prse	quruN	2	3.881	0.971	6.738	3.932	2.787	4.955
Prse	quruN	5	6.789	3.349	10.490	5.612	4.133	6.961
Prse	quruN	8	9.646	5.385	13.630	6.244	4.644	7.645
Prse	quruN	11	11.650	6.713	16.330	6.579	4.889	8.057
Prse	quruN	15	13.650	8.349	18.440	6.835	5.094	8.331
Prse	quruN	18	14.360	8.981	20.060	6.960	5.163	8.515
Prse	quve	0	0.201	0.007	0.619	0.199	0.007	0.619
Prse	quve	2	3.310	0.843	5.971	3.145	2.079	4.222
Prse	quve	5	6.576	2.935	10.040	4.641	3.184	6.053
Prse	quve	8	9.297	5.799	13.470	5.232	3.616	6.730
Prse	quve	11	11.190	7.119	15.450	5.544	3.702	7.122
Prse	quve	15	13.030	8.800	17.890	5.794	3.850	7.429
Prse	quve	18	13.750	8.910	18.630	5.911	3.930	7.542
Prse	rops	0	0.202	0.008	0.621	0.200	0.007	0.612
Prse	rops	2	2.981	0.529	6.041	2.697	1.739	4.047
Prse	rops	5	5.643	1.870	9.566	4.107	2.778	5.801
Prse	rops	8	8.090	3.370	12.770	4.673	3.192	6.406
Prse	rops	11	9.526	4.880	14.600	4.979	3.446	6.738
Prse	rops	15	10.720	5.978	16.200	5.220	3.657	7.153
Prse	rops	18	11.680	6.989	17.670	5.337	3.700	7.336
Quru	acruS	0	8.089	0.332	22.410	8.145	0.307	22.960
Quru	acruS	2	12.120	0.521	30.610	45.580	25.200	65.850
Quru	acruS	5	8.126	0.309	21.710	58.580	38.350	79.240
Quru	acruS	8	8.123	0.319	23.600	63.180	41.540	83.640
Quru	acruS	11	8.938	0.382	25.120	65.560	44.500	85.160
Quru	acruS	15	14.980	1.156	34.360	67.280	47.370	87.560
Quru	acruS	18	24.830	4.589	45.330	68.070	48.160	88.450
Quru	acruN	0	8.070	0.311	23.030	8.139	0.328	22.360
Quru	acruN	2	8.726	0.366	24.400	67.670	44.840	93.150
Quru	acruN	5	8.108	0.323	22.970	75.470	50.580	104.500
Quru	acruN	8	8.185	0.342	22.390	77.760	52.380	102.000
Quru	acruN	11	9.158	0.359	25.360	78.880	54.550	98.230
Quru	acruN	15	16.560	1.557	35.050	79.620	55.020	98.770
Quru	acruN	18	14.120	0.858	36.100	80.200	71.400	103.000
Quru	acsaS	0	8.063	0.313	22.300	8.112	0.307	23.190

Quru	acsaS	2	12.790	0.744	31.640	56.490	36.730	77.610
Quru	acsaS	5	14.090	0.926	31.210	63.870	41.720	86.110
Quru	acsaS	8	16.170	1.305	34.480	66.210	44.900	86.740
Quru	acsaS	11	19.240	1.720	38.510	67.110	49.310	88.170
Quru	acsaS	15	21.680	2.790	43.180	67.960	47.190	87.950
Quru	acsaS	18	35.820	16.230	56.240	68.200	51.960	89.040
Quru	acsaN	0	8.094	0.301	20.840	8.092	0.288	23.170
Quru	acsaN	2	9.328	0.403	26.500	56.590	32.860	79.550
Quru	acsaN	5	8.059	0.308	22.930	64.860	44.480	82.730
Quru	acsaN	8	8.387	0.307	23.270	67.400	50.970	90.120
Quru	acsaN	11	10.150	0.489	26.360	68.560	48.040	86.130
Quru	acsaN	15	17.820	1.637	35.750	69.410	52.470	90.620
Quru	acsaN	18	23.980	5.924	46.280	69.820	46.880	90.810
Quru	cagl	0	8.160	0.359	20.590	8.114	0.301	22.380
Quru	cagl	2	15.110	0.907	32.550	49.820	29.570	71.300
Quru	cagl	5	8.232	0.336	22.970	60.760	40.650	81.290
Quru	cagl	8	8.531	0.349	23.570	64.210	43.130	84.790
Quru	cagl	11	8.171	0.312	23.000	65.750	45.320	86.170
Quru	cagl	15	12.510	0.707	31.090	67.040	46.590	87.780
Quru	cagl	18	17.240	1.353	37.030	67.560	50.420	87.930
Quru	prse	0	8.117	0.297	22.690	8.076	0.318	22.730
Quru	prse	2	9.853	0.444	25.520	52.850	29.460	75.980
Quru	prse	5	8.185	0.344	22.620	65.560	43.600	86.780
Quru	prse	8	8.085	0.322	22.950	69.850	50.400	90.680
Quru	prse	11	11.370	0.604	28.980	72.040	48.570	91.680
Quru	prse	15	13.240	0.749	30.740	73.560	53.820	94.910
Quru	prse	18	21.470	3.165	43.340	74.340	52.260	94.740
Quru	quruS	0	8.078	0.328	21.750	8.035	0.309	22.380
Quru	quruS	2	15.870	1.170	36.740	57.580	36.140	81.880
Quru	quruS	5	9.846	0.467	26.050	64.320	44.500	82.350
Quru	quruS	8	8.570	0.371	23.690	66.410	46.110	86.750
Quru	quruS	11	8.529	0.333	23.550	67.470	47.060	87.350
Quru	quruS	15	13.180	0.879	30.090	68.100	49.420	88.840
Quru	quruS	18	14.450	1.123	34.990	68.290	47.790	88.660
Quru	quruN	0	8.201	0.303	22.690	8.097	0.297	22.880
Quru	quruN	2	9.961	0.422	27.610	45.670	24.170	71.580
Quru	quruN	5	9.516	0.462	24.970	60.540	36.570	84.220
Quru	quruN	8	10.390	0.474	26.430	65.690	41.450	87.390
Quru	quruN	11	14.880	0.901	36.210	68.360	43.300	91.420
Quru	quruN	15	23.130	3.970	42.380	70.490	57.460	90.160
Quru	quruN	18	27.200	7.616	44.950	71.410	45.580	90.150
Quru	quve	0	8.120	0.304	23.090	8.026	0.292	21.430
Quru	quve	2	9.229	0.378	25.050	55.870	34.730	80.410

Quru	quve	5	9.269	0.390	25.620	63.860	43.440	84.560
Quru	quve	8	11.720	0.561	28.470	66.220	44.270	85.970
Quru	quve	11	12.190	0.690	27.630	67.340	45.120	87.730
Quru	quve	15	12.480	0.612	29.350	68.190	47.700	88.340
Quru	quve	18	15.290	0.992	35.060	68.660	48.350	88.650
Quru	rops	0	8.163	0.327	20.390	8.003	0.306	20.860
Quru	rops	2	14.560	1.059	33.280	55.120	33.910	76.240
Quru	rops	5	10.930	0.501	32.830	64.800	44.110	85.650
Quru	rops	8	9.158	0.375	24.820	67.730	45.880	88.750
Quru	rops	11	9.717	0.413	24.760	69.320	54.180	89.330
Quru	rops	15	19.170	2.322	38.920	70.430	48.740	92.100
Quru	rops	18	17.480	1.641	34.520	71.100	50.180	92.960
Quve	acruS	0	9.513	0.387	26.810	9.607	0.364	26.630
Quve	acruS	2	9.538	0.361	26.540	13.610	0.788	33.920
Quve	acruS	5	9.645	0.372	27.040	14.500	0.853	34.690
Quve	acruS	8	9.498	0.368	27.210	14.770	0.874	35.680
Quve	acruS	11	9.562	0.394	26.620	14.960	0.991	36.200
Quve	acruS	15	9.598	0.386	27.010	14.840	0.946	35.860
Quve	acruS	18	9.700	0.388	27.270	15.040	0.945	36.540
Quve	acruN	0	9.527	0.370	26.570	9.541	0.382	27.120
Quve	acruN	2	9.553	0.384	26.670	13.850	0.710	33.870
Quve	acruN	5	9.551	0.351	26.270	14.860	0.939	35.170
Quve	acruN	8	9.559	0.352	26.710	15.070	0.946	35.630
Quve	acruN	11	9.480	0.365	26.530	15.320	1.005	36.240
Quve	acruN	15	9.375	0.338	26.360	15.330	0.996	36.230
Quve	acruN	18	9.550	0.367	26.950	15.460	1.031	35.700
Quve	acsaS	0	9.591	0.347	26.360	9.616	0.357	27.010
Quve	acsaS	2	9.487	0.391	26.740	11.010	0.455	28.920
Quve	acsaS	5	9.465	0.355	26.660	11.230	0.534	29.740
Quve	acsaS	8	9.501	0.362	26.600	11.410	0.541	30.020
Quve	acsaS	11	9.561	0.375	26.870	11.430	0.521	29.960
Quve	acsaS	15	9.443	0.379	26.820	11.450	0.518	30.000
Quve	acsaS	18	9.501	0.345	26.980	11.420	0.540	30.070
Quve	acsaN	0	9.567	0.377	26.700	9.524	0.372	26.670
Quve	acsaN	2	9.556	0.374	26.790	11.940	0.564	31.290
Quve	acsaN	5	9.593	0.378	26.650	12.470	0.697	32.030
Quve	acsaN	8	9.514	0.388	26.950	12.500	0.615	32.260
Quve	acsaN	11	9.539	0.344	26.990	12.500	0.560	31.950
Quve	acsaN	15	9.560	0.373	26.820	12.660	0.660	32.130
Quve	acsaN	18	9.413	0.345	26.440	12.780	0.667	32.510
Quve	cagl	0	9.520	0.379	27.070	9.487	0.391	26.880
Quve	cagl	2	9.588	0.385	26.680	13.320	0.750	33.000
Quve	cagl	5	9.484	0.404	26.570	14.070	0.712	34.480

Quve	cagl	8	9.516	0.348	26.200	14.290	0.793	34.350
Quve	cagl	11	9.424	0.370	26.510	14.400	0.807	34.970
Quve	cagl	15	9.536	0.354	26.260	14.540	0.927	35.470
Quve	cagl	18	9.606	0.393	26.970	14.560	0.801	34.980
Quve	prse	0	9.493	0.367	26.490	9.463	0.355	27.030
Quve	prse	2	9.518	0.331	26.600	14.110	0.776	33.250
Quve	prse	5	9.536	0.339	27.240	15.200	0.994	36.060
Quve	prse	8	9.509	0.325	26.880	15.610	0.942	35.590
Quve	prse	11	9.536	0.342	26.690	15.750	1.072	34.130
Quve	prse	15	9.489	0.383	26.810	15.890	1.063	36.300
Quve	prse	18	9.408	0.370	26.610	15.950	1.099	36.570
Quve	quruS	0	9.531	0.365	26.960	9.551	0.378	26.690
Quve	quruS	2	9.531	0.397	26.610	12.710	0.621	32.270
Quve	quruS	5	9.598	0.391	27.040	13.570	0.740	33.700
Quve	quruS	8	9.547	0.367	27.100	13.740	0.799	33.730
Quve	quruS	11	9.515	0.358	26.740	13.800	0.719	33.910
Quve	quruS	15	9.440	0.365	26.130	13.830	0.784	33.940
Quve	quruS	18	9.527	0.382	26.660	14.010	0.806	34.480
Quve	quruN	0	9.618	0.386	27.250	9.528	0.399	26.780
Quve	quruN	2	9.512	0.389	26.660	11.330	0.526	30.160
Quve	quruN	5	9.442	0.350	26.590	11.920	0.604	31.030
Quve	quruN	8	9.602	0.394	26.750	11.860	0.569	29.960
Quve	quruN	11	9.542	0.372	26.920	12.080	0.604	31.310
Quve	quruN	15	9.496	0.409	25.780	12.130	0.581	31.450
Quve	quruN	18	9.548	0.359	26.800	12.020	0.566	31.210
Quve	quve	0	9.497	0.367	26.910	9.493	0.350	26.730
Quve	quve	2	9.584	0.392	26.220	12.300	0.642	31.740
Quve	quve	5	9.457	0.371	26.480	12.750	0.619	32.500
Quve	quve	8	9.499	0.389	26.010	13.060	0.664	32.420
Quve	quve	11	9.480	0.377	27.130	13.110	0.701	33.240
Quve	quve	15	9.589	0.376	26.700	13.110	0.684	32.650
Quve	quve	18	9.568	0.402	26.990	13.210	0.721	33.070
Quve	rops	0	9.483	0.333	27.020	9.469	0.363	26.200
Quve	rops	2	9.613	0.379	26.980	13.460	0.713	33.900
Quve	rops	5	9.559	0.415	26.930	14.380	0.869	35.050
Quve	rops	8	9.494	0.334	26.570	14.660	0.853	35.080
Quve	rops	11	9.569	0.366	26.890	14.840	0.967	35.490
Quve	rops	15	9.468	0.359	26.620	14.940	0.953	35.920
Quve	rops	18	9.558	0.363	26.420	15.130	0.961	35.850
Rops	acruS	0	0.071	0.003	0.219	0.071	0.003	0.219
Rops	acruS	2	3.245	0.908	6.590	2.672	2.132	4.104
Rops	acruS	5	7.671	3.954	12.900	4.562	3.900	6.144
Rops	acruS	8	13.500	6.906	19.600	5.474	4.731	7.085

Rops	acruS	11	16.210	7.432	22.230	6.020	5.220	7.590
Rops	acruS	15	16.290	12.100	22.890	6.484	5.597	7.921
Rops	acruS	18	20.120	13.930	25.140	6.723	5.735	8.119
Rops	acruN	0	0.071	0.003	0.220	0.071	0.003	0.220
Rops	acruN	2	1.913	0.065	3.720	0.699	0.114	1.279
Rops	acruN	5	7.756	3.166	12.890	1.240	0.190	2.479
Rops	acruN	8	9.990	7.207	15.100	1.551	0.216	2.407
Rops	acruN	11	12.520	7.969	20.000	1.757	0.262	3.222
Rops	acruN	15	11.020	4.891	16.880	1.943	0.258	3.409
Rops	acruN	18	14.510	8.646	21.520	2.043	0.261	3.329
Rops	acsaS	0	0.071	0.003	0.218	0.071	0.003	0.219
Rops	acsaS	2	2.780	0.351	5.010	2.115	1.571	3.469
Rops	acsaS	5	7.583	2.859	11.770	3.494	2.909	5.077
Rops	acsaS	8	10.410	5.049	17.000	4.141	3.508	5.824
Rops	acsaS	11	11.700	4.416	17.970	4.523	3.981	6.237
Rops	acsaS	15	15.770	8.059	18.950	4.844	4.184	6.580
Rops	acsaS	18	13.970	7.713	20.730	5.008	4.362	6.746
Rops	acsaN	0	0.071	0.003	0.219	0.071	0.003	0.220
Rops	acsaN	2	3.957	0.973	6.712	3.705	2.924	4.602
Rops	acsaN	5	9.429	4.523	14.050	6.000	4.901	7.003
Rops	acsaN	8	16.530	10.280	20.810	7.011	5.527	7.982
Rops	acsaN	11	18.470	13.900	25.960	7.587	5.878	8.566
Rops	acsaN	15	21.410	14.450	25.440	8.057	6.517	9.171
Rops	acsaN	18	20.360	15.710	27.520	8.294	6.477	9.385
Rops	quruS	0	0.071	0.003	0.221	0.071	0.003	0.218
Rops	quruS	2	3.886	0.870	7.353	3.777	3.456	5.045
Rops	quruS	5	11.130	5.020	15.400	6.273	5.942	7.551
Rops	quruS	8	14.680	8.885	20.190	7.429	6.875	8.989
Rops	quruS	11	15.870	9.811	22.380	8.105	7.393	9.609
Rops	quruS	15	20.070	12.060	25.270	8.666	7.715	10.180
Rops	quruS	18	19.910	14.630	29.660	8.950	7.896	10.510
Rops	quruN	0	0.071	0.003	0.218	0.071	0.003	0.218
Rops	quruN	2	4.192	1.532	7.310	3.847	3.352	5.617
Rops	quruN	5	9.340	6.251	14.500	6.568	6.105	7.979
Rops	quruN	8	15.790	9.540	20.730	7.898	7.265	9.133
Rops	quruN	11	20.430	14.080	25.730	8.703	7.901	10.020
Rops	quruN	15	21.030	15.350	28.980	9.391	8.353	10.770
Rops	quruN	18	21.320	15.450	25.770	9.746	8.503	11.220
Rops	quve	0	0.071	0.003	0.217	0.071	0.003	0.217
Rops	quve	2	3.287	1.340	5.754	3.481	3.015	4.632
Rops	quve	5	11.010	5.755	16.730	6.087	5.377	7.016
Rops	quve	8	16.900	9.883	22.770	7.425	6.137	8.413
Rops	quve	11	19.290	14.100	26.920	8.256	6.553	9.398

Rops	quve	15	19.880	11.930	25.280	8.978	6.856	10.490
Rops	quve	18	20.120	12.180	27.190	9.358	7.024	11.100
Rops	rops	0	0.071	0.003	0.218	0.071	0.003	0.217
Rops	rops	2	2.986	0.505	6.119	2.056	1.463	3.161
Rops	rops	5	8.650	4.483	13.720	3.610	2.795	4.849
Rops	rops	8	10.890	6.471	16.080	4.367	3.489	5.487
Rops	rops	11	14.800	7.544	21.040	4.830	3.836	5.974
Rops	rops	15	15.560	11.590	25.370	5.230	4.151	6.427
Rops	rops	18	17.190	12.960	24.760	5.438	4.189	6.711

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