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Supplementary Material for

Plant-soil feedbacks and mycorrhizal type influence temperate forest population dynamics

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This PDF file includes:

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Database S1

Materials and Methods

Experimental design

Species and population selection

We selected 55 tree species native to temperate North American forests (see Figures 1 and 2 in the main text for the distribution of populations and species identities). These species were selected because they were common and easily found in the field. They were also selected to include (a) those that form ectomycorrhizas (EM) and (b) those that do not (i.e., they form arbuscular mycorrhizas [AM] only). We note that most species that form ectomycorrhizas also form arbuscular mycorrhizas as well, and this was confirmed in our observations of field collected roots. From 2005-2011, multiple teams of field assistants identified 10 different populations for each tree species in the USA and Canada (Figure 1). Sites were selected to be structurally similar and the vast majority of populations were located within mixed forest with a productive understory. Within species, populations (sites) were located a minimum of 10 km apart. At each site, an individual mature tree was randomly selected, which was then used as the focal tree.

Soil and seed collection

Three soil samples (using a 1L bulb planter; 3L total) were collected from underneath the canopy of each focal tree. Samples were shipped back to the lab, pooled, and fine roots were separated and cleaned over a coarse sieve. To ensure that the roots belonged to the target species, we compared them to fine roots that were collected in the field that were attached to the focal tree. Roots were then processed to determine the presence of AM and EM. Prior to processing, roots were stored in 50% ethanol for at least 24 hours. For processing, roots were cleared by autoclaving for 20 min in 10% potassium hydroxide, bleached in 35% hydrogen peroxide for 30 min, acidified in 1% hydrochloric acid for 5 min, and stained using Chlorazol Black E (*29*). Roots were then observed under 200x magnification. As the initial focus of the study was on the potential for EM to protect trees from antagonists, trees were considered to be EM if EM structures (fungal mantle and Hartig net) were observed, regardless of the presence of AM structures (arbuscules and/or vesicles). Thus, species from typically dual mycorrhiza genera (*Salix, Populus, Quercus*) are classified as EM in this study. However, even species from predominately EM genera (e.g. *Pinus*) were also observed to form AM, which is not without precedent (e.g. *30*). Plants were only considered to be AM if AM structures were observed, but not EM structures. To ensure that root tips covered with a fungal mantle were mycorrhizal, a subsample of fine roots were sectioned to assess the presence of a Hartig net.

In addition to the soil samples mentioned above, we randomly collected (using 1L bulb planter) an additional 5 soil samples from underneath the canopy, and 5 soil samples from beneath a random heterospecific tree 5-10m from the canopy (and also at least 10 m from any other conspecific tree), for a total of 10 additional soil samples per site. At each field site we also collected seeds from each of the tree species. For seed collection, populations were typically visited by the teams of field assistants at multiple times in the summer/fall over a 2-year period to find adequate seeds. All populations within a species were sampled in the same year. For most species, seeds were collected from the ground,

with some additional collections directly from trees. For *Populus* and *Salix* spp. we collected stem cuttings as well, because of difficulties in seed germination for these species. All materials were shipped back to the lab and stored at 4°C. Seeds were cold-moist stratified for 2-16 weeks, depending on the species. When enough seed had germinated, they were used for one of the experiments described below (except for *Populus* and *Salix* spp., where we used stem cuttings). In each case, the seeds or cuttings were matched with soils from the same site. For each sample, the greenhouse trials were conducted in the year of seed/cutting collection. However, given the magnitude of the experiment, the greenhouse trials were conducted over a 7-year span.

Additional measurements were made within each population for ten of the focal species (five EM species - *Betula papyrifera, Gleditsia triacanthos, Pinus strobus, Populus deltoides, Quercus rubra*; and five AM species - *Acer saccharum, Fraxinus americana, Prunus serotina, Sassafras albidum, Thuja occidentalis*). These species were used for multiple additional aspects of our study (see below) and were selected based upon ease of access to the populations, the availability of seeds and soil, and ease of cultivation. The identity of the heterospecific tree was recorded for each population of these ten species. Under each of focal tree from these 10 species, we also measured soil chemistry, specifically, soil pH (determined on a 1:1 mixture of dried soil and H2O; *31*), total soil carbon (following dry combustion using a LECO CR-12 analyzer, Leco corp, St. Joseph, MI; *32*), total soil nitrogen (following dry combustion using a LECO FP-228 analyzer, Leco Corp, St. Joseph, MI, using manufacturer's protocol, and available soil phosphorus (using the Bray and Kurtz P1 test; *31*).

Three different, but complimentary, studies were conducted to determine the direction and strength of plant-soil feedback, its relationship to conspecific density dependence, and the mechanism behind the feedback.

Study 1: Greenhouse experiment

For each of the 55 species, we grew individual seedlings/cuttings in pots containing either conspecific soil or heterospecific soil. For the ten species selected for additional measurements, we added additional treatments where we inoculated pots with conspecific sterile soil, heterospecific sterile soil, sterile soil + conspecific roots, or sterile soil + heterospecific roots. Soil was sterilized by wet autoclaving at 121°C for 1 hour. For each population, we set up 5 pots per combination of soil source and inoculum type. Seeds were pre-germinated (or cuttings were dipped in 1% indole-3-butyric acid) and added to small pots (164 mL Cone-tainers^{TM}, Stuewe & Sons, Tangent, Oregon, USA) containing one of the previously described field soil treatments. Plants were not fertilized, but were watered every two days. Each plant was grown for 6 months (16-hr light/ 8-hr dark) at 25°C/15°C and then harvested. At harvest, we measured biomass (shoot +root) for all plants after drying the plants at 60°C for 48 hours.

For the ten species selected for additional measurements, we also measured focal species % mycorrhizal colonization and % root lesions [damaged parts of fine roots due to herbivory or microbial infection that was clearly not mycorrhizal (*34*)] using a subsample of the root system that was weighed, so that root biomass could also later be determined.. We recognize that lesions do not perfectly reflect antagonist damage as the precise cause of the damage is unknown and many pathogens are asymptomatic. Despite these flaws, lesion density provides additional information beyond that typically

presented in plant-soil feedback studies that can be used to infer the relative importance of antagonists between conspecific and heterospecific soils. For mycorrhizal colonization, roots were cleared and stained as described above. In AM plants, percent colonization was determined using the magnified intersections method (*35*). Percent colonization of EM plants was determined by counting the proportion of fine roots that were colonized with a fungal mantle. Percent root lesions was assessed using the magnified intersections method. All measurements within populations were averaged, resulting in N=1 per population, N=10 per tree species for each of the 6 treatments.

Using the population averaged data, we calculated plant-soil feedback (PSF) for each population as log response ratios [ln(conspecific/heterospecific)]. PSF was calculated using plant biomass for each inoculum source (whole soil, sterilized soil, and roots only) and as effects on percent mycorrhizal colonization and root lesions. There were 55 species and 550 total populations when using whole soil inoculum. For the other inoculum sources and the root measurements, there were only 10 species (see above) and 100 total populations.

Data on plant-soil feedback and mycorrhiza type were also related to large-scale density dependence. Details can be found in the analysis section below.

Study 2: Field transplant

We hypothesized that if mycorrhizas protect plant roots from antagonists, a plant colonized by mycorrhizas prior to being transplanted into the field would have fewer lesions and increased survival. To experimentally test this hypothesis we transplanted pre-inoculated and uninoculated seedlings into the field to test for mycorrhizal effects on seedling survival and lesion densities. We used four species (two EM species – *Betula papyrifera, Pinus strobus*; and two AM species - *Acer saccharum, Fraxinus americana*); these species were selected for ease of access to populations, availability of seeds and fungal inoculum, and ease of cultivation. Seeds were germinated in petri dishes containing filter paper and sterile, distilled water. They were then planted in 400mL pots, containing sterilized field soil with or without mycorrhizal fungal inoculum under greenhouse conditions for 6 months. The inoculum was either a) field-collected *Glomus* spp. spores for AM trees or b) field-isolated *Cenoccocum geophilum* culture + field-collected *Glomus* spp. spores for EM trees. The *Glomus* spp. inoculum was constructed by extracting AM fungal spores from local field soil using a wet-sieving technique (*36*) and isolating *Glomus* morphotypes. 100 spores were added per plant. The *Cenoccocum geophilum* inoculum was isolated from locally collected EM roots and grown on a dialysis membrane that was placed on potato dextrose agar. When the dialysis membrane was colonized by the fungus, it was cut into 3x3 cm pieces, and one piece was added per plant.

At each of 5 sites, 10 seedlings of similar size were planted a) under the canopy, or b) 5-10m away beneath the canopy of a heterospecific tree. At each site, we identified gaps within the understory to avoid having the seedling strongly shaded. However, it remains possible that the understory may still have affected seedling survival. After a growing season, the number of surviving seedlings were counted and from the surviving seedlings, percent root lesions was determined as described above.

Study 3: Field survey

To test for small-scale density dependence under natural field conditions, we surveyed seedling densities beneath conspecific trees and beneath heterospecific trees 5-10 m away. For this study, we focus on the ten species selected for additional measurements and use all ten populations per species. For each focal tree, we constructed plots (7.5 m^2) beneath the canopy and 5-10m from canopy edge and counted the number of individuals with stems <2.54 cm in diameter (seedlings and saplings) within each plot. Data are reported as the number individuals m^{-2}. We also collected roots of these individuals and measured percent root lesions, as described above.

Data analysis

Study 1

To test for the effect of mycorrhiza type on PSF and incorporate variation among populations, we ran a series of phylogenetic generalized mixed models using the R package 'MCMCglmm' (*37*). We used PSF log response ratios as the response variables, mycorrhiza type as a fixed effect, and species identity and shared ancestry, expressed in terms of phylogenetic relationships among species, as random factors. To create a phylogeny for data analysis, we used the fossil calibrated seed plant phylogeny from Zanne et al. (*38*), which contained 51 of the 55 species used in this study. For the four remaining species (*Abies balsamea, Malus coronaria, Salix nigra*, and *Sorbus americana*), we substituted the nearest congeneric species (*Abies fraseri, Malus ioensis, Salix laevigata*, and *Sorbus scopulina*). We repeated this analysis for all five PSF related measures separately. PSF values using whole soil were power transformed $[(PSF+3)^{1.4} - 3^{1.4}]$ to eliminate left skew. The resultant distribution was leptokurtic, so we took the log of both tails [sign(PSF)*log(abs(PSF))] to reduce the influence of outliers. PSF effects on mycorrhizal colonization were right skewed, so we took the 2/3 root of these values $[(Myc + 2)^{2/3} - 2^{2/3}]$. To determine phylogenetic signal in PSF, we measured phylogenetic signal as Pagel's λ on the mean values for PSF using the r package phytools (*39*). To determine if mycorrhiza type was the driver of this phylogenetic signal, we also tested for phylogenetic signal in the residuals of a simple linear model with mycorrhiza type as the only predictor of mean PSF.

For the ten species with available data on heterospecific tree identity and soil chemistry, we conducted additional analyses. Specifically, we tested whether the match in mycorrhizal type, the phylogenetic distance between the focal and neighbouring heterospecific trees, or soil chemistry (pH, C, N, P) affected PSF. If a heterospecific tree was used as a focal species at other sites in the study, we assigned it the same mycorrhiza type as seen in this study. For heterospecific species not included in this study, we used published mycorrhiza types (Table S5). In all cases, this assessment was in agreement with our data for congeneric species. For these tests, we used PSF data from whole soil, focusing on PSF effects on plant growth, mycorrhizal colonization, and lesions. All models were phylogenetic generalized mixed models following the same procedures as above.

For the same 10 species, we tested whether soil chemistry varied between mycorrhiza types. We used the same phylogenetic generalized mixed model structure as before, but in these models, mycorrhiza type was the lone fixed factor. We ran separate

models for each of the soil chemistry variables (soil pH, total soil carbon, total soil nitrogen, and available soil phosphorus).

To examine the broader significance of PSFs, we related PSF for plant growth in whole soil to published estimates of conspecific density dependence by Johnson et al. (*3*). Johnson et al. calculated density dependence by regressing conspecific seedling densities against conspecific mature tree densities within the U.S. Forest Service Forest Inventory and Analysis (FIA) database (http://fia.fs.fed.us/). Johnson et al. (*3*) define trees as individuals with diameter at breast height > 12.7 cm and seedlings as individuals with stems < 2.54 cm in diameter and height > 30.5 cm (or 12.24 cm for conifers). From these data, we selected only species that matched ours and that had $N \geq 5$. This resulted in estimates of conspecific density dependence for 38 of the 55 species. To make the estimates of conspecific density dependence and plant-soil feedback comparable, we calculated standardized effect sizes for both. For density dependence, we divided the mean estimate of density dependence by the standard deviation of that estimate. For PSF, we calculated the standardized effect size for each species as (mean Conspecific – mean Heterospecific)/pooled standard deviation. With these data, we used a phylogenetic generalized linear model in the R package 'caper' (*40*), with the same phylogeny as before (*38*), which included mycorrhiza type and PSF as fixed effects. Due to a strong relationship between mycorrhiza type and PSF (see results), we repeated the analysis with each variable on its own.

Study 2

To test whether mycorrhizas caused differences in distance dependence, we used the data from the transplantation and inoculation experiment. With these data, we tested whether seedling survival following transplantation and lesion density responded to a factorial combination of mycorrhiza type, location, and inoculation treatment (inoculated / uninoculated) using phylogenetic generalized mixed models. Lesion densities could only be measured on surviving seedlings, resulting in a reduced sample size. As with the previous models, species identity, population nested within species, and phylogenetic relatedness were included as random effects. Lesion densities were square root transformed to normalize the residuals.

Study 3

We tested whether AM and EM associated plants differed in distance dependence under natural conditions and whether this was associated with variation in lesion densities by comparing seedling and lesion densities under conspecifics with densities 5-10 m away under heterospecifics. Here, we used separate phylogenetic generalized mixed models (*37*) for seedlings and lesions. The models included mycorrhizal functional group and location (conspecific or heterospecific) as fixed effects, with species identity, population nested within species, and phylogenetic relatedness as random effects. To achieve normality of the residuals, seedling densities were log transformed and lesion densities power transformed ($\text{lesions}^{0.8}$).

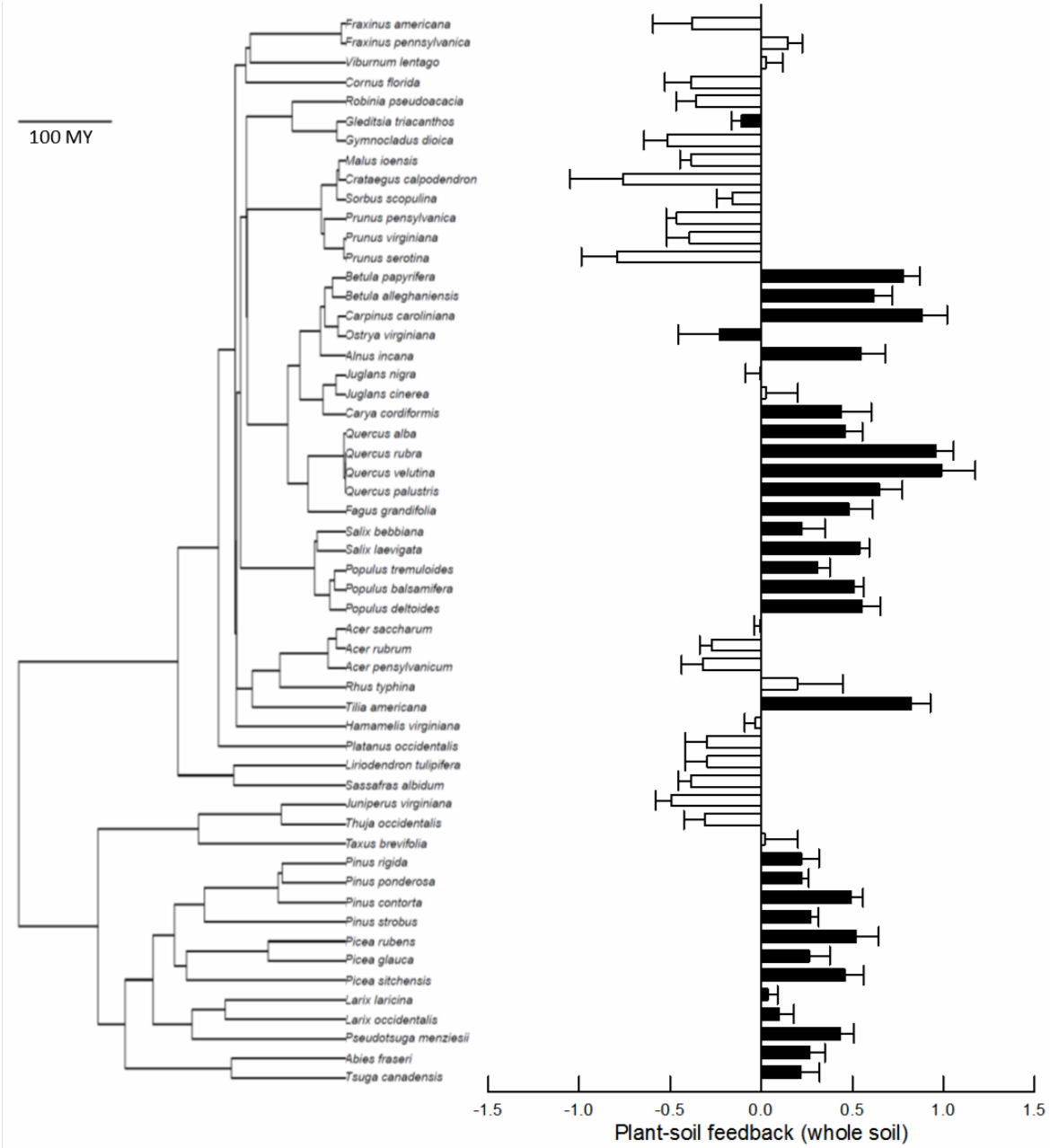

Fig. S1.

Plant-soil feedback as a function of mycorrhizal type (arbuscular mycorrhizal in white and ectomycorrhizal in black). These are the same data as presented in Fig. 1 in the main text; however, the plant-soil feedback estimates are now ordered along a phylogeny. There was significant phylogenetic signal in PSF ($\lambda = 0.772$, $P < 0.001$); however, this signal was lost after accounting for the effect of mycorrhiza type ($\lambda = 0.221$, $P = 0.241$).

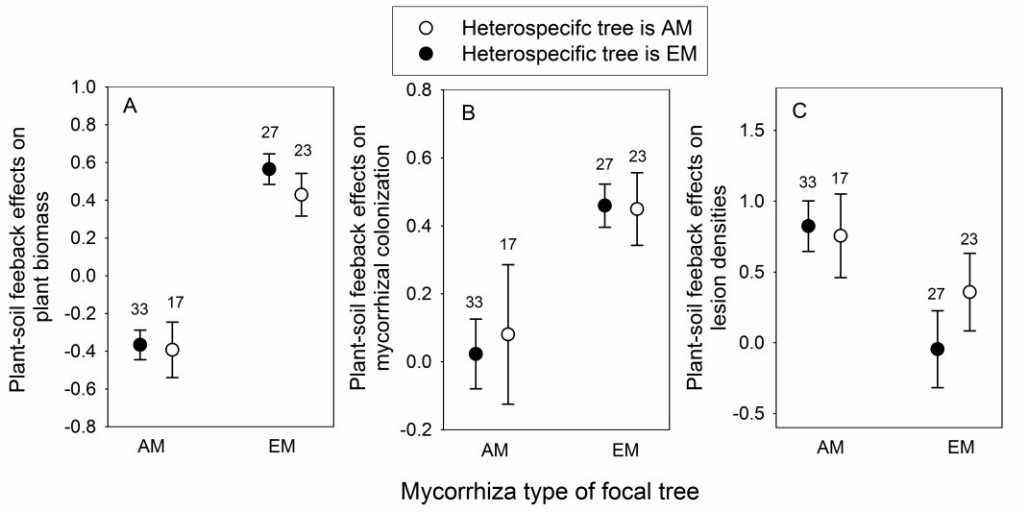

Fig. S2

Plant-soil feedback effects on plant growth (A), mycorrhizal colonization (B), and lesion density (C) as a function of the mycorrhiza types (arbuscular (AM) or ectomycorrhizal (EM)) of the focal tree species and the heterospecific tree species used for comparison. We found no significant effect of matching mycorrhizal types between conspecific and heterospecific trees on any measure of plant-soil feedback (Table S1). All plant-soil feedback effects were calculated as ln (conspecific / heterospecific). Error bars represent one standard error and numbers above error bars represent the number of cases.

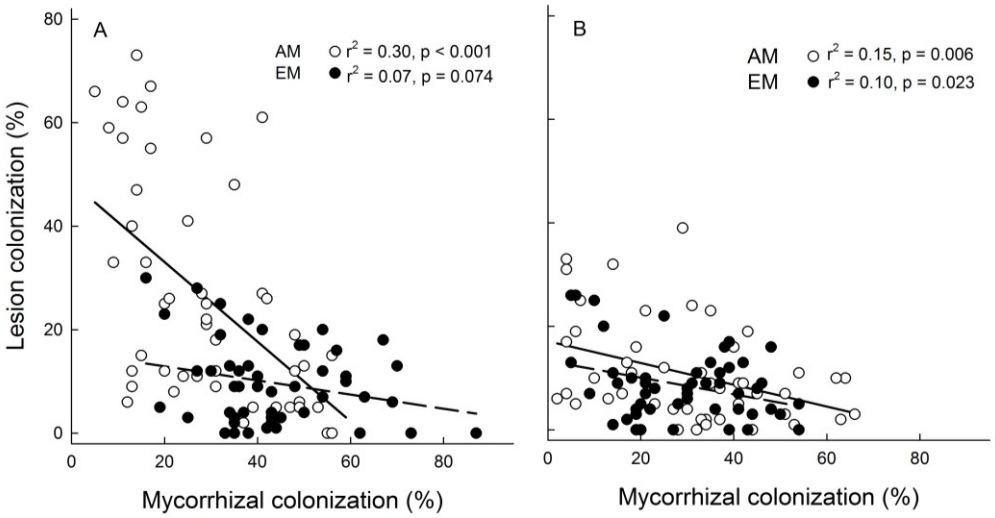

Fig. S3

The relationship between mycorrhizal colonization and lesion densities in (A) conspecific soil and (B) heterospecific soil for ectomycorrhizal species (N = 10 populations by five species; black dots dashed lines) and arbuscular mycorrhizal species (N = 10 populations by five species; white dots solid lines). Lines and statistics represent linear regression fit.

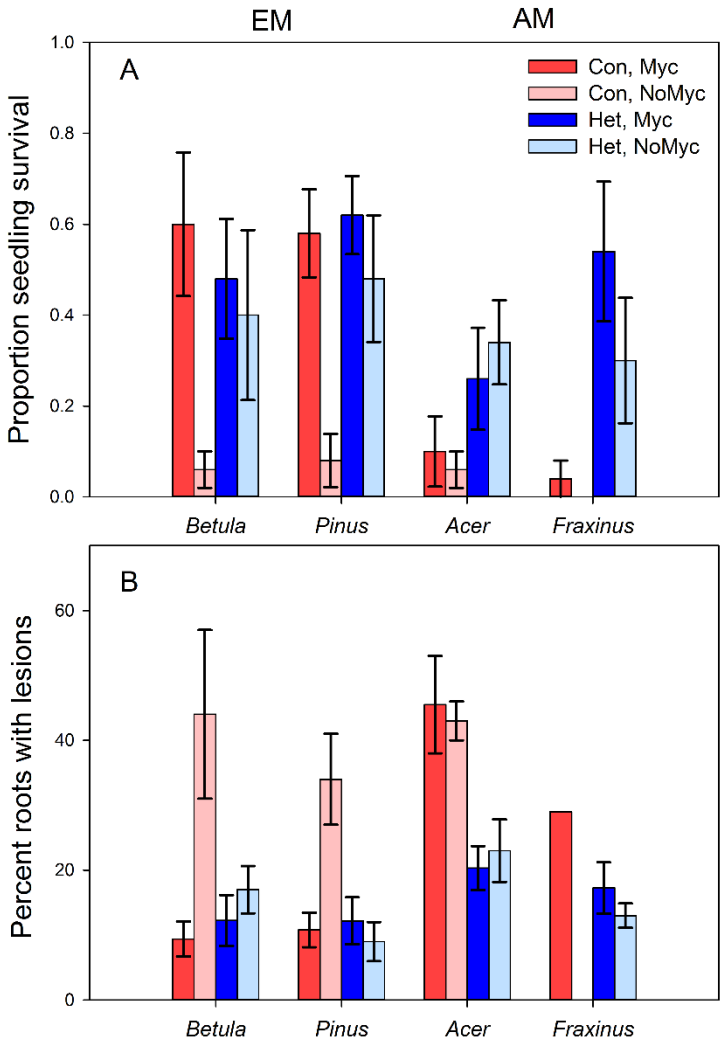

Fig. S4

Seedling survival and lesion densities as a function of proximity to conspecific or heterospecific trees and mycorrhizal inoculation. Ten seedlings were transplanted per treatment for five populations per species. Error bars represent standard errors. For *Fraxinus*, only one seedling survived near conspecific trees, so error was not estimable.

Table S1.

Results of phylogenetic generalized mixed models testing the effect of mycorrhizal type on plant-soil feedback (PSF). Expanded data for additional analyses were only available for 10 species. Heterospecific mycorrhiza type is abbreviated as myc. type match, and the phylogenetic distance to the heterospecific species as het. phylogeny. All posterior means compare ectomycorrhizal trees relative to arbuscular mycorrhizal trees. As the models were Bayesian, CI refers to credible intervals. Species and phylogeny were included as random effects; consequently, no significance values are assigned.

Data used	Model	Factor	Posterior mean	Lower 95% CI	Upper 95% CI	Effective samples	P
All 55 species	Whole soil PSF	Mycorrhizal type	0.433	0.478	0.992	900	<0.001
		Species	0.322	0.103	0.595	900	
		Phylogeny	0.206	0.182	0.233	900	
10 species with data on colonization, heterospecific identity, and soil chemistry	Mycorrhizal colonization	Mycorrhizal type	0.430	0.172	0.736	900	0.004
		Species	0.049	0.002	0.169	559	
		Phylogeny	0.314	0.236	0.412	741	
	Lesion densities	Mycorrhizal type	-0.743	-1.221	-0.078	900	0.013
		Species	0.132	0.0002	0.479	623	
		Phylogeny	1.545	1.117	1.965	857	
	Sterile soil PSF	Mycorrhizal type	-0.016	-0.136	0.084	900	0.760
		Species	0.009	0.002	0.025	900	
		Phylogeny	0.038	0.028	0.051	900	
	Rhizosphere fraction PSF	Mycorrhizal type	0.525	0.228	0.834	678	0.011
		Species	0.128	0.018	0.286	466	
		Phylogeny	0.054	0.038	0.069	1404	
	Whole soil PSF	Mycorrhizal type	1.070	0.401	1.773	1000	0.007
		Myc. type match	0.103	-0.086	0.259	900	0.249
		Het. phylogeny	-0.0001	-0.0006	0.0003	900	0.616
		pH	0.106	-0.022	0.248	1004	0.118
		Carbon	-0.001	-0.015	0.013	900	0.900
		Nitrogen	0.002	-0.084	0.088	1030	0.973
		Phosphorus	0.002	-0.001	0.007	900	0.282
		Species	0.703	0.147	1.704	900	
		Phylogeny	0.139	0.101	0.186	797	
	Mycorrhizal colonization	Mycorrhizal type	1.070	0.401	1.773	1000	<0.001
		Myc. type match	0.006	-0.102	0.118	900	0.940
		Het. phylogeny	0.0001	-0.0001	0.0004	900	0.404
		pH	0.106	-0.022	0.248	1004	0.118
		Carbon	-0.001	-0.015	0.013	900	0.896
		Nitrogen	0.002	-0.084	0.088	1030	0.973
		Phosphorus	0.002	-0.001	0.007	900	0.282
		Species	0.001	0.000	0.001	185	
		Phylogeny	0.085	0.060	0.110	900	
	Lesion densities	Mycorrhizal type	-0.650	-1.261	-0.147	900	0.029
		Myc. type match	-0.274	-0.791	0.209	1041	0.298
		Het. phylogeny	0.0004	-0.0009	0.0017	900	0.493
		pH	-0.007	-0.495	0.554	849	0.982
		Carbon	0.021	-0.035	0.084	900	0.500
		Nitrogen	-0.087	-0.474	0.244	900	0.609
		Phosphorus	0.013	-0.005	0.030	900	0.127
		Species	0.017	0.000	0.075	230	
		Phylogeny	1.504	1.069	1.947	739	

Table S2.

Results from phylogenetic generalized mixed models testing for differences in soil chemistry between soils taken from beneath trees of different mycorrhiza types. Ten populations of ten tree species were used for these analyses, although samples were lost for three populations. In all cases, the reported posterior means compare the effects of EM to AM soils. CI refers to credible intervals. Species and phylogeny were random effects; consequently, no significance values are assigned.

Model	Factor	Posterior mean	Lower 95% CI	Upper 95% CI	Effective samples	P
Soil pH	Mycorrhizal type	-0.283	-0.644	0.150	900	0.118
	Species	0.165	0.017	0.417	900	
	Phylogeny	0.172	0.119	0.224	1087	
Total soil carbon (g/kg)	Mycorrhizal type	-1.679	-4.323	0.550	900	0.164
	Species	4.384	0.012	13.050	900	
	Phylogeny	15.980	11.510	21.480	900	
Total soil nitrogen (g/kg)	Mycorrhizal type	0.134	-0.489	0.810	900	0.649
	Species	0.546	0.057	1.333	546	
	Phylogeny	0.415	0.288	0.531	1000	
Available soil phosphorus (mg/kg)	Mycorrhizal type	7.230	-1.429	14.961	900	0.100
	Species	57.400	0.004	195.000	580	
	Phylogeny	192.000	142.300	252.600	900	

Table S3

Results from phylogenetic generalized mixed models testing A) the effect of mycorrhizal type and mycorrhizal inoculation on transplant survival and lesion densities in conspecific and heterospecific soil and B) variation in seedling and lesion densities as a function of mycorrhizal type and location (conspecific vs. heterospecific soils). All posterior means compare ectomycorrhizal trees relative to arbuscular mycorrhizal trees, conspecific soils to heterospecific soils, or uninoculated to inoculated, depending on the factor. CI refers to credible intervals. Species and phylogeny were random effects; consequently, no significance values are assigned.

Study	Model	Factor	Posterior mean	Lower 95% CI	Upper 95% CI	Effective samples	P
A) Field transplants	Transplant survival	Mycorrhizal type	1.485	-0.736	4.036	900	0.216
		Location	-3.292	-5.404	-0.984	900	0.004
		Inoculation	-0.775	-3.140	1.235	900	0.020
		MycTyp *Location	3.623	0.571	6.493	900	0.020
		MycTyp *Inoc.	-0.297	-3.194	2.803	900	0.836
		Loc.*Inoc.	0.378	-2.69	3.283	900	0.782
		MycTyp *Loc.*Inoc	-4.429	-8.491	0.154	900	0.049
		Species	0.769	0.003	2.667	521	
		Population/Species	0.181	0.003	0.705	900	
		Phylogeny	5.871	3.849	7.735	900	
	Transplant lesions	Mycorrhizal type	-0.920	-3.302	0.625	600	0.202
		Location	2.001	0.529	3.445	1019	0.004
		Inoculation	-0.109	-1.053	0.909	1195	0.838
		MycTyp *Location	-2.269	-4.037	-0.637	1059	0.009
		MycTyp *Inoc.	0.260	-1.188	1.657	900	0.720
		Loc.*Inoc.	0.185	-2.013	2.449	1166	0.882
		MycTyp *Loc.*Inoc	2.753	0.073	5.429	961	0.047
		Species	6.913	0.004	6.733	183	
		Population/Species	0.080	0.002	0.268	900	
		Phylogeny	1.109	0.680	1.610	900	
B) Field survey	Seedling density	Mycorrhizal type	-0.373	-1.244	0.476	900	0.360
		Location	-0.334	-0.467	-0.191	1145	<0.001
		MycTyp*Location	0.523	0.313	0.715	1116	<0.001
		Species	1.093	0.225	2.379	900	
		Population/Species	0.030	0.005	0.076	900	
		Phylogeny	0.134	0.107	0.161	900	
	Lesion density	Mycorrhizal type	0.586	-3.664	5.075	900	0.709
		Location	5.151	3.364	6.897	900	<0.001
		MycTyp *Location	-4.985	-7.546	-2.346	900	<0.001
		Species	20.870	1.655	52.280	900	
		Population/Species	0.221	0.002	0.814	900	
		Phylogeny	21.210	16.900	25.960	900	

Table S4

Results from phylogenetic generalized linear models testing the relationship between mycorrhizal type, plant-soil feedback (PSF), and large-scale density dependence. PSF is for trees throughout North America (Fig. 1) and density dependence is for trees throughout the eastern USA (*3*). Initially both PSF and mycorrhizal type were included in the same model, but the variables were highly collinear, so we repeated the analysis with each variable on its own. Also included are estimates of lambda (λ) returned from the model.

Model	Fixed factor	t	d.f.	P	λ	P
Combined	Mycorrhizal type	0.83	35	0.411	0.430	0.029
	Plant-soil feedback	0.74	35	0.465		
Separate	Mycorrhizal type	2.25	36	0.031	0.432	0.041
	Plant-soil feedback	2.21	36	0.033	0.382	0.016

Table S5

Mycorrhiza types of trees that were used as heterospecific trees for the 10 focal species in study 1 where we collected additional information.

Species	Mycorrhiza type	Source
Abies balsamea	EM	This study
Acer rubrum	AM	This study
Acer saccharinum	AM	Bainard et al. 2011 (*41*)
Acer saccharum	AM	This study
Alnus incana	EM	This study
Betula alleghaniensis	EM	This study
Betula lenta	EM	Comas and Eissenstat 2004 (*42*)
Betula papyrifera	EM	This study
Carya cordiformis	EM	This study
Carya glabra	EM	Comas and Eissenstat 2004 (*42*)
Carya ovata	EM	Comas and Eissenstat 2004 (*42*)
Carya tomentosa	EM	Taylor et al 2016 (*43*)
Cornus florida	AM	This study
Fagus grandifolia	EM	This study
Fraxinus americana	AM	This study
Juniperus virginiana	AM	This study
Larix lacricina	EM	This study
Liriodendron tulipifera	AM	This study
Ostrya virginiana	EM	This study
Picea glauca	EM	This study
Picea mariana	EM	Stein et al 1990 (*44*)
Picea rubens	EM	This study
Pinus monticola	EM	Molina and Trappe 1982 (*45*)
Pinus resinosa	EM	Wilcox 1968 (*46*)
Pinus strobus	EM	This study
Pinus taeda	EM	This study
Pinus virginiana	EM	Comas and Eissenstat 2004 (*42*)
Platanus occidentalis	AM	This study
Populus grandidentata	EM	Bainard et al. 2011 (*41*)
Prunus pensylvanica	AM	This study
Pseudotsuga menziesii	EM	This study
Quercus alba	EM	This study
Quercus macrocarpa	EM	Dickie et al 2004 (*47*)
Quercus palustris	EM	This study
Quercus velutina	EM	This study
Robinia pseudoacacia	AM	This study
Tilia americana	EM	This study
Tsuga canadensis	EM	This study

Additional Data table S1 (separate file)

All data associated with studies one through three.

References and Notes

1. K. Nadrowski, C. Wirth, M. Scherer-Lorenzen, Is forest diversity driving ecosystem function and service? *Curr. Opin. Environ. Sustain.* **2**, 75–79 (2010). doi:10.1016/j.cosust.2010.02.003

2. L. Gamfeldt, T. Snäll, R. Bagchi, M. Jonsson, L. Gustafsson, P. Kjellander, M. C. Ruiz-Jaen, M. Fröberg, J. Stendahl, C. D. Philipson, G. Mikusiński, E. Andersson, B. Westerlund, H. Andrén, F. Moberg, J. Moen, J. Bengtsson, Higher levels of multiple ecosystem services are found in forests with more tree species. *Nat. Commun.* **4**, 1340 (2013). doi:10.1038/ncomms2328 Medline

3. D. J. Johnson, W. T. Beaulieu, J. D. Bever, K. Clay, Conspecific negative density dependence and forest diversity. *Science* **336**, 904–907 (2012). doi:10.1126/science.1220269 Medline

4. L. S. Comita, H. C. Muller-Landau, S. Aguilar, S. P. Hubbell, Asymmetric density dependence shapes species abundances in a tropical tree community. *Science* **329**, 330–332 (2010). doi:10.1126/science.1190772 Medline

5. J. A. LaManna, M. L. Walton, B. L. Turner, J. A. Myers, Negative density dependence is stronger in resource-rich environments and diversifies communities when stronger for common but not rare species. *Ecol. Lett.* **19**, 657–667 (2016). doi:10.1111/ele.12603 Medline

6. W. H. van der Putten, M. A. Bradford, E. Pernilla Brinkman, T. F. J. van de Voorde, G. F. Veen, Where, when and how plant-soil feedback matters in a changing world. *Funct. Ecol.* **30**, 1109–1121 (2016). doi:10.1111/1365-2435.12657

7. L. S. Comita, S. A. Queenborough, S. J. Murphy, J. L. Eck, K. Xu, M. Krishnadas, N. Beckman, Y. Zhu, L. Gómez-Aparicio, Testing predictions of the Janzen-Connell hypothesis: A meta-analysis of experimental evidence for distance- and density-dependent seed and seedling survival. *J. Ecol.* **102**, 845–856 (2014). doi:10.1111/1365-2745.12232 Medline

8. A. Packer, K. Clay, Soil pathogens and spatial patterns of seedling mortality in a temperate tree. *Nature* **404**, 278–281 (2000). doi:10.1038/35005072 Medline

9. E. Laliberté, H. Lambers, T. I. Burgess, S. J. Wright, Phosphorus limitation, soil-borne pathogens and the coexistence of plant species in hyperdiverse forests and shrublands. *New Phytol.* **206**, 507–521 (2015). doi:10.1111/nph.13203 Medline

10. J. H. Connell, M. D. Lowman, Low-diversity tropical rain forests: Some possible mechanisms for their existence. *Am. Nat.* **134**, 88–119 (1989). doi:10.1086/284967

11. J. N. Klironomos, Feedback with soil biota contributes to plant rarity and invasiveness in communities. *Nature* **417**, 67–70 (2002). doi:10.1038/417067a Medline

12. W. H. van der Putten, R. D. Bardgett, J. D. Bever, T. M. Bezemer, B. B. Casper, T. Fukami, P. Kardol, J. N. Klironomos, A. Kulmatiski, J. A. Schweitzer, K. N. Suding, T. F. J. Van de Voorde, D. A. Wardle, Plant-soil feedbacks: The past, the present and future challenges. *J. Ecol.* **101**, 265–276 (2013). doi:10.1111/1365-2745.12054

13. A. Kulmatiski, K. H. Beard, J. R. Stevens, S. M. Cobbold, Plant-soil feedbacks: A meta-analytical review. *Ecol. Lett.* **11**, 980–992 (2008). doi:10.1111/j.1461-0248.2008.01209.x Medline

14. B. A. Sikes, K. Cottenie, J. N. Klironomos, Plant and fungal identity determines pathogen protection of plant roots by arbuscular mycorrhizas. *J. Ecol.* **97**, 1274–1280 (2009). doi:10.1111/j.1365-2745.2009.01557.x

15. R. L. Vannette, S. Rasmann, Arbuscular mycorrhizal fungi mediate below-ground plant–herbivore interactions: A phylogenetic study. *Funct. Ecol.* **26**, 1033–1042 (2012). doi:10.1111/j.1365-2435.2012.02046.x

16. M. G. A. van der Heijden, T. R. Horton, Socialism in soil? The importance of mycorrhizal fungal networks for facilitation in natural ecosystems. *J. Ecol.* **97**, 1139–1150 (2009). doi:10.1111/j.1365-2745.2009.01570.x

17. R. Aerts, in *Mycorrhizal Ecology*, M. G. A. van der Heijden, I. R. Sanders, Eds. (Springer Berlin Heidelberg, 2003), pp. 117–133.

18. A. Corrales, S. A. Mangan, B. L. Turner, J. W. Dalling, An ectomycorrhizal nitrogen economy facilitates monodominance in a neotropical forest. *Ecol. Lett.* **19**, 383–392 (2016). doi:10.1111/ele.12570 Medline

19. D. H. Marx, Ectomycorrhizae as biological deterrents to pathogenic root infections. *Annu. Rev. Phytopathol.* **10**, 429–454 (1972). doi:10.1146/annurev.py.10.090172.002241 Medline

20. K. L. McGuire, Common ectomycorrhizal networks may maintain monodominance in a tropical rain forest. *Ecology* **88**, 567–574 (2007). doi:10.1890/05-1173 Medline

21. Materials and methods are available as supplementary materials.

22. B. L. Anacker, J. N. Klironomos, H. Maherali, K. O. Reinhart, S. Y. Strauss, Phylogenetic conservatism in plant-soil feedback and its implications for plant abundance. *Ecol. Lett.* **17**, 1613–1621 (2014). doi:10.1111/ele.12378 Medline

23. M. Brundrett, Mycorrhizal associations and other means of nutrition of vascular plants: Understanding the global diversity of host plants by resolving conflicting information and developing reliable means of diagnosis. *Plant Soil* **320**, 37–77 (2009). doi:10.1007/s11104-008-9877-9

24. J. A. Bennett, J. F. Cahill Jr., Fungal effects on plant-plant interactions contribute to grassland plant abundances: Evidence from the field. *J. Ecol.* **104**, 755–764 (2016). doi:10.1111/1365-2745.12558

25. H. L. Reynolds, A. Packer, J. D. Bever, K. Clay, Grassroots ecology: Plant-microbe-soil interactions as drivers of plant community structure and dynamics. *Ecology* **84**, 2281–2291 (2003). doi:10.1890/02-0298

26. O. Godoy, M. Rueda, B. A. Hawkins, Functional determinants of forest recruitment over broad scales. *Glob. Ecol. Biogeogr.* **24**, 192–202 (2015). doi:10.1111/geb.12241

27. P. J. Ke, T. Miki, T.-S. Ding, The soil microbial community predicts the importance of plant traits in plant-soil feedback. *New Phytol.* **206**, 329–341 (2015). doi:10.1111/nph.13215 Medline

28. W. Chen, R. T. Koide, T. S. Adams, J. L. DeForest, L. Cheng, D. M. Eissenstat, Root morphology and mycorrhizal symbioses together shape nutrient foraging strategies of temperate trees. *Proc. Natl. Acad. Sci. U.S.A.* **113**, 8741–8746 (2016). doi:10.1073/pnas.1601006113 Medline

29. M. C. Brundrett, Y. Piché, R. L. Peterson, A new method for observing the morphology of vesicular–arbuscular mycorrhizae. *Can. J. Bot.* **62**, 2128–2134 (1984). doi:10.1139/b84-290

30. C. Wagg, M. Pautler, H. B. Massicotte, R. L. Peterson, The co-occurrence of ectomycorrhizal, arbuscular mycorrhizal, and dark septate fungi in seedlings of four members of the Pinaceae. *Mycorrhiza* **18**, 103–110 (2008). doi:10.1007/s00572-007-0157-y Medline

31. W. Hendershot, H. Lalande, M. Duquette, in *Soil Sampling and Methods of Analysis*, M. Carter, Ed. (Lewis Publishers, 1993).

32. D. Wang, D. W. Anderson, Direct measurement of organic carbon content in soils by the Leco CR-12 carbon analyzer. *Commun. Soil Sci. Plant Anal.* **29**, 15–21 (1998). doi:10.1080/00103629809369925

33. J. T. Sims, in *Methods of Phosphorus Analysis for Soils, Sediments, Residuals, and Waters*, G. M. Pierzynski, Ed. (North Carolina State University, 2000), pp. 13–14.

34. J. L. Maron, J. Klironomos, L. Waller, R. M. Callaway, Invasive plants escape from suppressive soil biota at regional scales. *J. Ecol.* **102**, 19–27 (2014). doi:10.1111/1365-2745.12172

35. T. P. McGonigle, M. H. Miller, D. G. Evans, G. L. Fairchild, J. A. Swan, A new method which gives an objective-measure of colonization of roots by vesicular arbuscular mycorrhizal fungi. *New Phytol.* **115**, 495–501 (1990). doi:10.1111/j.1469-8137.1990.tb00476.x

36. J. N. Klironomos, P. Moutoglis, B. Kendrick, P. Widden, A comparison of spatial heterogeneity of vesicular-arbuscular mycorrhizal fungi in two maple-forest soils. *Can. J. Bot.* **71**, 1472–1480 (1993). doi:10.1139/b93-178

37. J. D. Hadfield, MCMC methods for multi-response generalized linear mixed models: The MCMCglmm R package. *J. Stat. Softw.* **33**, 1–22 (2010). doi:10.18637/jss.v033.i02 Medline

38. A. E. Zanne, D. C. Tank, W. K. Cornwell, J. M. Eastman, S. A. Smith, R. G. FitzJohn, D. J. McGlinn, B. C. O'Meara, A. T. Moles, P. B. Reich, D. L. Royer, D. E. Soltis, P. F. Stevens, M. Westoby, I. J. Wright, L. Aarssen, R. I. Bertin, A. Calaminus, R. Govaerts, F. Hemmings, M. R. Leishman, J. Oleksyn, P. S. Soltis, N. G. Swenson, L. Warman, J. M. Beaulieu, Three keys to the radiation of angiosperms into freezing environments. *Nature* **506**, 89–92 (2014). doi:10.1038/nature12872 Medline

39. L. J. Revell, phytools: An R package for phylogenetic comparative biology (and other things). *Methods Ecol. Evol.* **3**, 217–223 (2012). doi:10.1111/j.2041-210X.2011.00169.x

40. D. Orme *et al.*, "caper: Comparative Analyses of Phylogenetics and Evolution in R," R package version 0.5.2. (2013).

41. L. D. Bainard, J. N. Klironomos, A. M. Gordon, The mycorrhizal status and colonization of 26 tree species growing in urban and rural environments. *Mycorrhiza* **21**, 91–96 (2011). doi:10.1007/s00572-010-0314-6 Medline

42. L. H. Comas, D. M. Eissenstat, Linking fine root traits to maximum potential growth rate among 11 mature temperate tree species. *Funct. Ecol.* **18**, 388–397 (2004). doi:10.1111/j.0269-8463.2004.00835.x

43. M. K. Taylor, R. A. Lankau, N. Wurzburger, Mycorrhizal associations of trees have different indirect effects on organic matter decomposition. *J. Ecol.* **104**, 1576–1584 (2016). doi:10.1111/1365-2745.12629

44. A. Stein, J. A. Fortin, G. Vallée, Enhanced rooting of *Picea mariana* cuttings by ectomycorrhizal fungi. *Can. J. Bot.* **68**, 468–470 (1990). doi:10.1139/b90-062

45. R. Molina, J. M. Trappe, Patterns of ectomycorrhizal host specificity and potential among Pacific Northwest conifers and fungi. *For. Sci.* **28**, 423–458 (1982).

46. H. E. Wilcox, Morphological studies of the roots of red pine, *Pinus resinosa*. Ii. Fungal colonization of roots and the development of mycorrhizae. *Am. J. Bot.* **55**, 688–700 (1968). doi:10.2307/2440526

47. I. A. Dickie, R. C. Guza, S. E. Krazewski, P. B. Reich, Shared ectomycorrhizal fungi between a herbaceous perennial (*Helianthemum bicknellii*) and oak (*Quercus*) seedlings. *New Phytol.* **164**, 375–382 (2004). doi:10.1111/j.1469-8137.2004.01177.x