# Science

AAAS

## Supplementary Materials for

## Shifting microbial communities can enhance tree tolerance to changing climates

Cassandra M. Allsup, Isabelle George, Richard A. Lankau

Corresponding author: Richard A. Lankau, lankau@wisc.edu

*Science* **380**, 835 (2023)
DOI: 10.1126/science.adf2027

**The PDF file includes:**

Material and Methods
Figs. S1 to S6
Tables S1 to 16
References

**Materials and Methods**

To test whether pre-inoculation with microbial communities sourced from areas with different climates affected seedling survival in field conditions, we performed a field transplant experiment in two forest sites (northern Wisconsin, central Illinois) over a four year period (2018-2021). We collected live soil from 6 forested locations in Wisconsin and 6 in Illinois in fall 2017 (Fig 1). Soil was stored at 4°C for 3 months to simulate winter conditions. We procured seeds for 12 native tree species, either through our own field collections or from commercial sources (Table S1). After cold stratification for up to 90 days (dependent on species), we then germinated seedlings from each species in sterilized potting mix. Once germinated, we planted seedlings into 0.5 L Conetainers (Stuewe and Sons, Inc, Tanget, OR, USA) filled with soil from one of the 12 sources and allowed the them to grow for eight weeks in greenhouse conditions prior to transplanting into a field site. To prevent introduction of unknown microbial taxa across political and ecological boundaries, we restricted the experiment such that seedlings planted in our Wisconsin site received one of the six soils sourced from Wisconsin, while seedlings planted in our Illinois site received one of the six soils sourced from Illinois (Fig 1). We chose an eight week period as this has been shown to be sufficient time to develop symbiotic associations with either arbuscular or ectomycorrhizal fungi, along with other microbes (*21*).

At each site, seedlings were planted into three replicated plots per initial soil inoculum. Each plot contained one seedling of each species, all with the same soil inoculum (to prevent spread of inoculated microbes from different sources among transplanted seedlings). For two species (*Acer negundo* and *Quercus rubra*), we planted up to six seedlings per plot that each represented a different seed population – however, for all subsequent analyses these populations were lumped into a generalized species level response. Plots were paired such that half of the seedlings experienced ambient rainfall conditions, while the other half had rainfall reduced (Fig. 1). Each sub-plot measured 1.21 x 3.05 meters and were covered with four 0.61 x 1.21 m transparent plastic sheets. For rainfall reduction plots, the plastic sheets were angled to cause run-off of intercepted rainfall. For ambient rainfall plots, mock shelters were created to account for any non-target effects

of the plastic sheeting, but sheets were installed level with 28 holes (1.27 cm diameter each) in each sheet to allow passage of rainfall through to the experimental seedlings. Shelters were put in place by July of each growing season and removed by October, to allow natural levels of snowfall in each plot. To document the effectiveness of our rainfall reduction treatment, we installed soil moisture probes in three paired ambient and rainfall reduction plots at each site (2 years in the northern site, 3 years in the southern site). In our northern site, the rainfall reduction treatment reduced soil moisture by 28.0% $\pm$ 0.065% SE on average during the July-September period over the two measured growing seasons (see Table S17). In our southern site, the rainfall reduction treatment reduced soil moisture by 22.3% $\pm$ 0.06% SE on average during the July-October period over the three measured growing seasons (see Table S17).

Seedlings were planted in two cohorts (2018 and 2019), with independent soil collections from the same 12 sites for each cohort. Seedlings were planted into field sites in July 2018 (cohort 1) and June 2019 (cohort 2). Each experimental plot had 24 predetermined seedling planting locations, with each seedling position a minimum of 20 cm from each other seedling and the edge of a plastic sheet. Seedlings in cohort 2 were planted into the same experimental plots in locations that were never planted or where a seedling from the previous cohort had died (generally from transplant shock or browsing), again ensuring that all seedlings in a plot shared the same microbial inoculation source site. Seedling survival was monitored for three growing seasons (2018-2020 for cohort 1, and 2019-2021 for cohort 2). We checked all seedlings for survival two weeks after planting – any mortality in this two week period was considered potentially a result of transplant shock, and these seedlings were not analyzed further. For the remaining seedlings, survival was checked an additional five times over the next three years – in the fall of year 1, late spring of year 2, fall of year 2, late spring of year 3, and fall of year 3. Once per season, in August, we surveyed all seedlings for signs of mammalian browsing, insect damage, foliar disease symptoms, and wilting and browning of leaves, in an attempt to identify potential causes of mortality. However, given the time between survival surveys, for the vast majority of seedlings it was not possible to assign cause of death. Some of our target species can lose all aboveground tissue and still resprout in

later seasons. If a seedling was marked dead but later grew new leaves, our records were corrected. After the third fall survival check for each cohort, any remaining surviving seedlings were harvested. We collected all aboveground tissue and as much belowground tissue as possible without disrupting other target seedlings. Approximately 100 mg of fine root tissue from each collected seedling was stored at -80° C for characterization of root-associated fungal communities.

*Statistical analysis*: To test whether pre-inoculation with microbes adapted to specific climate conditions could enhance the tolerance seedlings facing those conditions, we analyzed three-year seedling survival rates at each site using generalized linear models which included quantitative measures of climate conditions of the microbial inocula source as predictor variables, along with field rainfall treatment and the interactions between microbial source climate and rainfall treatment. Note that our use of the term tolerance simply refers to greater survival rate under a particular condition, and does not imply any particular physiological, phenological, or ontogenetic mechanism. We considered two aspects of the climate at each soil inocula source: temperature and aridity. To quantify aridity, we used the Aridity Index (AI) calculated over the growing season (May – September) prior to soil sampling. The Aridity Index is the ratio of total precipitation to potential evapotranspiration. This index measures the predicted ratio of moisture inputs to losses; higher values indicate wetter conditions, while lower values indicate increasing drought stress for plants. We estimated potential evapotranspiration using the Hargreave approximation method with the spei package in R, using latitude and month to predict external radiation (*44*).

We considered three ways to represent the temperature of the microbial source site: the mean annual temperature, the minimum temperature, and the maximum temperature, all measured over of the 12 months prior to soil sampling. Mean annual temperature was measured as the daily mean temperature averaged over the twelve months prior to soil sampling. Minimum temperature was measured as the daily minimum temperature averaged over the coldest month in the 12-month period prior to soil sampling. Maximum temperature was

measured as the daily maximum temperature averaged over the warmest month in the 12-month period prior to soil sampling. We obtained climate data for each site and year from the PRISM database (*45*).

We used phylogenetic generalized linear mixed models with three-year survival rates as a binomially distributed dependent variable. We included rainfall treatment, and soil inocula source climate variables as fixed effects, along with the interactions between rainfall treatment and soil inocula source climate variables (aridity and temperature). We included the height of each seedling measured just prior to transplanting in the field as an additional covariate, to control for any growth differences induced during the eight week pre-planting period. We used the pglmm function in the phyr package in R to fit models that included random effects to address two potential sources of non-independence among samples –experimental plots, nested within cohort year, as a grouping variable, and the phylogenetic covariance among seedling species (*46*). We used the V.Phylomaker package in R (*47*) to prune the "GBTOB.extended" phylogeny of vascular plants to our set of 21 total tree species. The "GBTOB.extended" combines mega-trees from (*48*) and (*49*) to cover all families of extant vascular plants. We ran separate models for each of the two field sites.

Prior to modeling, we explored the intercorrelation between our climate variables to ensure models did not include highly co-linear predictors. The three measures of temperature (mean, maximum, and minimum) were reasonably correlated within the six source sites for each experiment ($0.46 < r < 0.91$, $0.13 > P > 0.00001$ for WI; $0.71 < r < 0.90$, $0.01 > P > 0.00001$ for IL). Aridity Index was not substantially correlated with either temperature variable for the Wisconsin sites ($r < 0.46$, $P > 0.13$ for all). For the Illinois sites, AI was negatively correlated with minimum temperature ($r = -0.64$, $P = 0.02$), but not with mean annual temperature or maximum temperature ($r > -0.20$, $P > 0.49$). To avoid collinearity in models, we first compared three alternative models with AIC. Each model followed the structure described above with the AI and one of the three temperature variables. For each experimental site, we chose the model with the lowest AIC value for subsequent analysis and interpretation. For the northern site, this was the model including minimum temperature (AIC = 526.93, versus 531.26 and 533.28 for models including mean and maximum temperature, respectively). For the southern

site, this was the model including maximum temperature (AIC = 722.86, versus 724.79 and 722.93 for models including mean and minimum temperature, respectively).

Following statistically significant estimates for the main effects of climate variables or interactions between climate variables and the rainfall treatment, we ran separate models for ambient and rainfall reduced conditions. We additionally tested whether the effects of microbial source climate on seedling survival depended on the mycorrhizal category of the seedling species. Tree species were assigned to arbuscular or ectomycorrhizal types based on (50). We ran phylogenetic generalized linear models as described above, but included mycorrhizal type as a fixed variable along with its one- and two-way interactions with rainfall treatment and microbial inocula source climate variables. As before, if the main or interactive effects of mycorrhizal type were significant, we ran separate models for each mycorrhizal type, and for each mycorrhizal type by rainfall treatment combination.

*Survival analysis of seedlings*. As an alternative means to analyze seedling survival, we used a mixed model Cox regression to analyze survival time for each seedling, using a model structure identical to that described above, except that we used tree seedling genus and species as grouping random effects as phylogenetic error structures were not available in the coxme package in R (51). Survival time was determined by the six census dates described above (spring and fall censuses for each of three growing seasons). Cox regression models a constant probability of mortality per unit time, as a function of model parameters, while accounting for censored data for individuals who do not die during the course of the experiment (52).

*Seedling survival by season.* To further investigate when during the three year experiment the effect of microbial inoculum source climate was most pronounced, we used our spring and fall sampling to estimate survival across distinct seasonal periods. Specifically, we calculated the survival of each seedling across five periods – summer 1, winter 1, summer 2, winter 2, and summer 3. A seedling was determined to have survived a summer period if it was alive in both the spring (May or June) sampling and the fall sampling (September or

October) of a given year. A seedling was determined to have survived a winter period if it was alive in both the Fall sampling of one year and the Spring sampling of the following year. To test how the microbial inoculum source climate affected seasonal survival, we used the phylogenetic generalized linear modeling structure described above, separately for survival across each of the five distinct season periods. Sample size for each model declines for each progressive seasonal period, as survival probabilities can only be calculated based on seedlings alive at the start of each seasonal period. As before, if we detected statistically significant main or interactive effects of microbial inoculum source climate, we ran separate models for each rainfall condition.

*Greenhouse experiment:* To confirm the effects of microbial source climate under controlled conditions, we performed a pot experiment in greenhouse conditions over three years in which seedlings were grown with soil microbes from the same 12 sources, in all combinations of ambient and elevated summer temperatures and sufficient vs. restricted watering frequency. To mimic our field experiment, we established separate pot experiments to represent each field site. For the northern WI experiment, we filled 1.6 L Mini-treepots (Stuewe and Sons, Inc, Tangent, OR, USA) with a 50/50% mixture of river sand and sterilized field soil collected from the Kemp Natural Resource Station (KNRS, northern WI site). Pots were then inoculated with 50 mL of live soil from one of the six WI soil sources used in the field experiment. For each soil source, we inoculated four pots for each seedling species. Pots were split into two greenhouse units, one set to the average summer temperature at KNRS (26.1° C day/ 15° C night), and the other set at an elevated temperature (29.4°C day/ 18.3°C night). Within each greenhouse unit, pots were watered every 5 days (sufficient) or 10 days (restricted). Because we manipulated temperature at the scale of greenhouse units, to provide replication we repeated this experiment over three summers, switching the temperature of greenhouse units each time. In each repetition, we grew between 5-10 seedling species, dependent on availability of germinated seedlings, with one pot per species per combination of temperature × watering frequency × microbial inocula source. For each repetition, seedlings grew for 4 months, and then above- and belowground biomass was harvested, dried, and weighed.

We performed a similar experiment reflecting our central IL site, with an identical design with the following exceptions: 1) background soil was taken from the Allerton Park site, mixed 50/50% with river sand, 2) microbial inocula came from the six sites in IL, 3) pots were grown at 29.4°C day/ 18.3°C night vs. 32.2°C day/ 21.1°C night. Seedling species varied by repetition and between the WI and IL experiment to some degree due to seedling availability (see Table S1 for full list).

*Statistical Analysis*: Our experiments included a diversity of seedling species with highly divergent growth rates and patterns. Therefore, to allow for meaningful comparisons across species, prior to analysis we accounted for species differences by taking the residuals of a linear model that regressed seedling total biomass against categorical predictors for repetition and species, a continuous predictor of initial height at planting, and the interaction of species and initial height. We controlled for initial height because seedlings were germinated in sterilized soil flats prior to planting in the experiment and grew to different sizes in that time due to variation in germination time and intrinsic growth rates. We included the species by initial height interaction to account for differential dependence of final biomass on initial seedling size across species. By taking the residuals of this model, we created a new outcome variable that ranged from positive values (seedling biomass larger than expected for that species in that repetition given its initial size) to negative values (seedling biomass smaller than expected for that species in that repetition given its initial size).

We again used phylogenetic generalized linear mixed models (with Gaussian error distribution) to test whether the residual seedling biomass increased when pots were inoculated with microbial communities that matched the temperature or soil moisture conditions in the experiment. While we manipulated greenhouse temperature and watering frequency factorially, we chose to model the four treatment combinations as a single factor with four levels (cool wet, cool dry, hot wet, hot dry) because air temperature and watering frequency combined to determine the soil moisture experienced by the seedlings (highest soil moisture in the cool wet treatment and lowest in the hot dry treatment, see Fig. S1). Our models included this four-level factor along

with microbial source AI and maximum temperature, along with their interactions, as fixed effects. We included greenhouse unit ID and experimental repetition as random effects, to account for non-independence of samples sharing the same greenhouse unit and grown in the same year. We included phylogenetic error covariance to account for non-independence among tree species. When the main or interactive effect of a microbial inocula source climate variable was significant, we ran separate models for each treatment combination. Results did not differ when restricting the analysis to only those seedling species that were also present in the field experiments.

If we found evidence that microbial source climate affected seedling growth in either greenhouse experiment, we again tested whether these effects differed between seedlings of contrasting mycorrhizal types. We used similar phylogenetic generalized linear mixed models as described above but including seedling mycorrhizal type and all interactions with temperature and watering frequency treatments and microbial inocula source climate variables. If the main or interactive effects of mycorrhizal type were significant, we ran separate models within each temperature and watering frequency treatment combination, as well as within each mycorrhizal type.


*Characterization of fungal communities on soils and roots:* We used metabarcoding of the fungal ITS2 gene region to characterize fungal community composition in the bulk soils used as microbial inocula for the field and greenhouse experiment, as well as on the roots of surviving seedlings from the field experiments. Library preparation and sequencing protocols followed (*53*). For bulk soils, 1 g of the soil used to inoculate Conetainers (for field transplanted seedlings) and greenhouse pots was stored at -30°C until DNA extraction. Soil DNA extractions were performed on 1 g of frozen soil using the Omega Bio-tek E.Z.N.A. Soil DNA kit following the manufacturer's protocol. For roots of surviving seedlings, we harvested as much belowground biomass as possible of the seedling from the field plots and froze a representative sample of fine roots from each seedling (~1 g) for later analysis. From this subsample, we extracted DNA from 25 mg of root using the Omega Bio-tek E.Z. 96 Plant DNA kit using the manufacturer's protocol.

The fungal ITS2 region was amplified, and Illumina read primers and adaptors added in a two-step PCR protocol. We used the ITS3-KYO2 (*54*) and ITS4 (*55*) primers with added Nextera read primer sequences for the first reaction. External fusion PCR primers contained a 14-bp overlap to the trailing end of the initial primers followed by either an 8-bp i7 index and P7 flow cell adapter sequence or an 8-bp i5 index, 7-bp spacer, and P5 flow cell adapter (See Lankau and Keymer 2015 for more details).

The first round of PCR amplified the ITS2 marker along with priming regions for the Nextera read primers. PCR was performed in 10 µl reactions using 0.2 µL of a hot-start, high fidelity polymerase (Clonetech Prime Star GLX) with 2 µL of its 5X buffer, 0.8 µL dNTPs (at 10 nM concentration), 0.25 µL of each primer (at 10 nM), 0.7 µg T4 gene 32 protein, and 10 ng of template DNA. Thermal cycling conditions included a 5-minute hot start at 98°C, 35 cycles of denaturing (98°C, 0:30), annealing (50°C, 0:45), and extension (68°C, 1:00) and a final extension of 15 minutes at 68°C. Successful amplification was verified using agarose gel electrophoresis.

The second round of PCR added the P5 and P7 flow cell adapters to prepare the library for sequencing on an Illumina MiSeq, along with an external set of sample barcodes located between the flow cell adaptors and read primers. PCR was performed in 25 µl reactions using 0.5 µL of a hot-start, high fidelity polymerase (Clonetech Prime Star GLX, location) with 5 µL of its 5X buffer, 2 µL dNTPs (at 10 nM concentration), 1 µL of each primer (at 10 nM), and 1 µL of product from the first PCR as template. Amplicons were cleaned with the Omega BioTek E-Z 96 Cycle Pure kit. Purified products were quantified using a Qubit 2.0 fluorometer with the Qubit dsDNA HS assay (Thermo Scientific, Grand Island, NY). Amplicons were pooled at equal concentration and sequenced on an Illumina MiSeq using V3 chemistry using paired-end sequencing (300 cycles).

Sequences were separated by barcode sequences by the University of Wisconsin-Biotechnology center, then filtered for quality and assigned to amplicon sequence variants (ASV's, equivalent to 100% identity operational taxonomic units) using the DADA2 program (*56*) as implemented in the QIIME2 pipeline. Non-

singleton ASVs were identified to the lowest confident taxonomic level using the naïve Bayesian classifier RDP using the UNITE database for ITS reads (*57*). Since exact sequence variants are not appropriate biological units for fungi (*58*), we agglomerated ASVs to species level based on taxonomic identification. We used the FungalTraits database to assign fungal species to functional groups (*59*). We assigned all fungal species to one of six broad putative categories: AMF, EMF, plant pathogens/endophytes, saprotrophs, other, and unassigned. The "other" category consisted of species assigned to rarer categories (lichenized fungi, animal pathogens, etc.). We made no attempt to separate plant pathogens from other, non-pathogenic plant endophytes because even individual fungal strains can switch between these lifestyles based on plant host and environmental conditions. For species assigned to multiple categories, for analytical purposes we assigned them to a single guild with the following priority (EMF > plant pathogen/endophyte > saprotroph).

We used permutation MANOVA to test whether the initial microbial inocula source had a statistically significant effect on Bray-Curtis dissimilarities among the root fungal communities of surviving seedlings. Because the mycorrhizal type of the seedling (AM or EM) had a very strong effect on fungal composition, we performed this analysis separately for seedlings of each mycorrhizal type in each field site. perMANOVA models included tree genus and rainfall treatment as factors.

Additionally, we tested whether certain summary metrics of the fungal community on surviving seedling roots correlated with the initial microbial source climate variables. We analyzed the Shannon-Weaver diversity, species richness (after rarefaction to a set sequence depth) and relative abundance of three functional guilds (AM fungi, EM fungi, and pathogenic/endophytic fungi), as well as the S-W diversity and rarefied richness of the full fungal community. These metrics were tested against microbial source climate, field rainfall treatments, and their interactions using phylogenetic generalized linear models as described above for seedling outcomes. For AM fungi and EM fungi, models only included samples from seedlings species of the appropriate mycorrhizal type.

We used the fungal community composition data to explore whether the diversity and richness of the full fungal community, or functional guilds, could explain effects on seedling performance. For the field experiments, we used data on fungal communities of surviving seedlings. Since we do not have data on the fungal communities of seedlings that died during the experiment, we instead analyzed the data at the level of the microbial inocula source. For each microbial inocula source (12 total per field site, since each cohort year involved a separate soil collection from each source site), we calculated the average Shannon-Weiner diversity and rarefied richness of 1) the total fungal community among surviving seedlings , 2) either the ectomycorrhizal fungal community (for EM associating seedling species) or the arbuscular mycorrhizal fungal community (for AM associated seedling species), and 3) the pathogenic/endophytic fungal community (all seedlings). We first calculated the diversity index and richness value for each individual surviving seedling. Then, to calculate the average diversity values, we used the least square estimated means of the diversity index or richness value for each microbial inocula source from a linear model that included microbial inocula source as a fixed categorical variable, as well as the rainfall reduction treatment, tree seedling genus and total fungal sequencing depth as fixed covariates and field plot as a random effect. We then used a generalized linear model to calculate the survival probability for seedlings in each microbial inocula source by rainfall reduction treatment and mycorrhizal type. We used the emmeans package in R to extract survival probabilities and standard errors for each microbial inocula source from the GLM. Finally, we regressed the estimated survival probabilities against the averaged fungal diversity/richness metrics for microbial inocula sources, in models including the rainfall reduction treatment and its interaction with diversity/richness metics, as well as separately for each rainfall reduction treatment, using a generalized linear model with a binomial error distribution.

Fig. S1
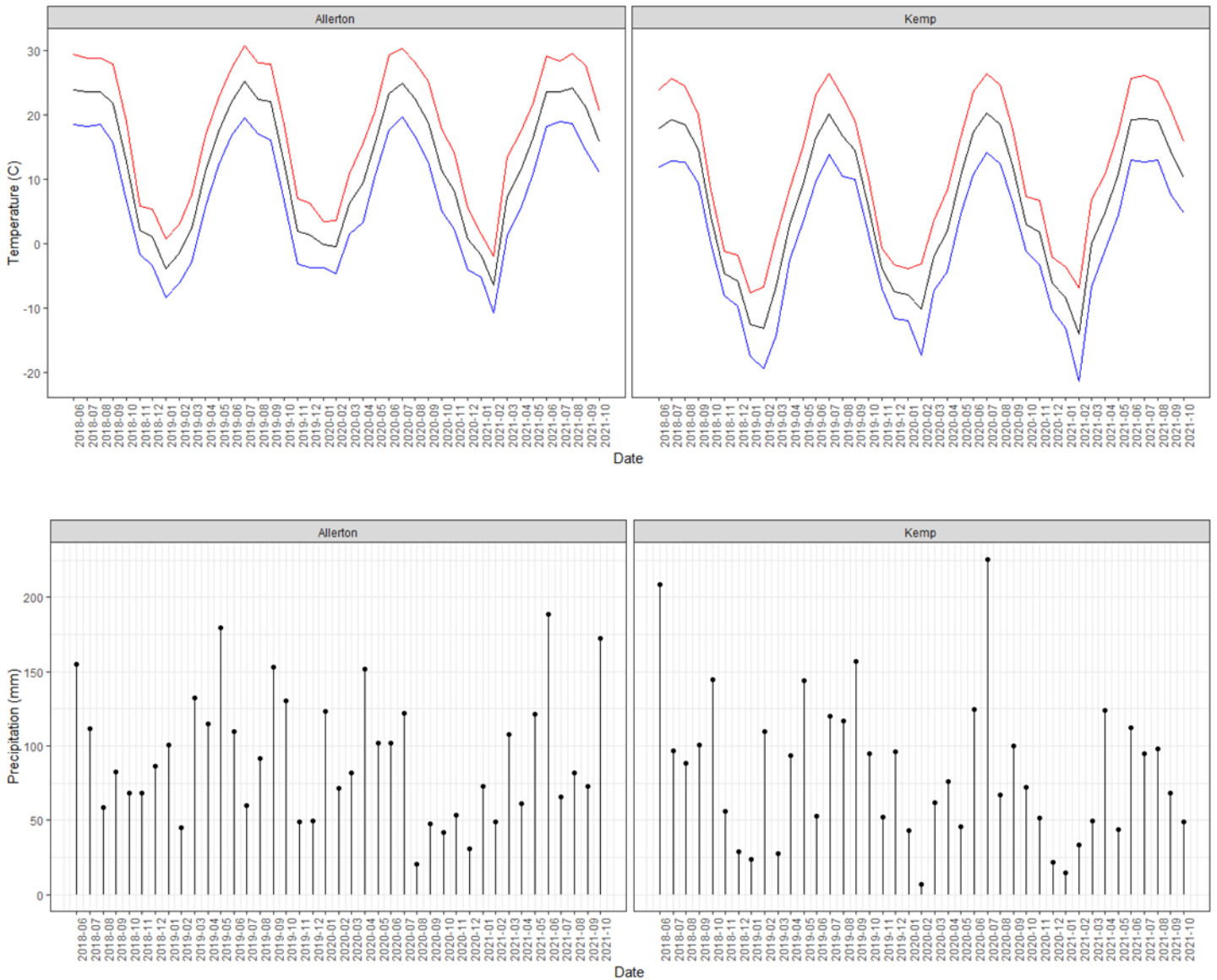


Fig. S1. Monthly weather data at the northern (Kemp Natural Resource Station) and southern (Allerton Park and Recreation Center) experimental sites. Red line = monthly maximum temperature, Black line = monthly mean temperature, Blue line = monthly minimum temperature. The first seedling cohort was planted in June 2018 and surviving seedlings harvested in October 2020. The second seedling cohort was planted in June 2019 and harvested in October 2021.
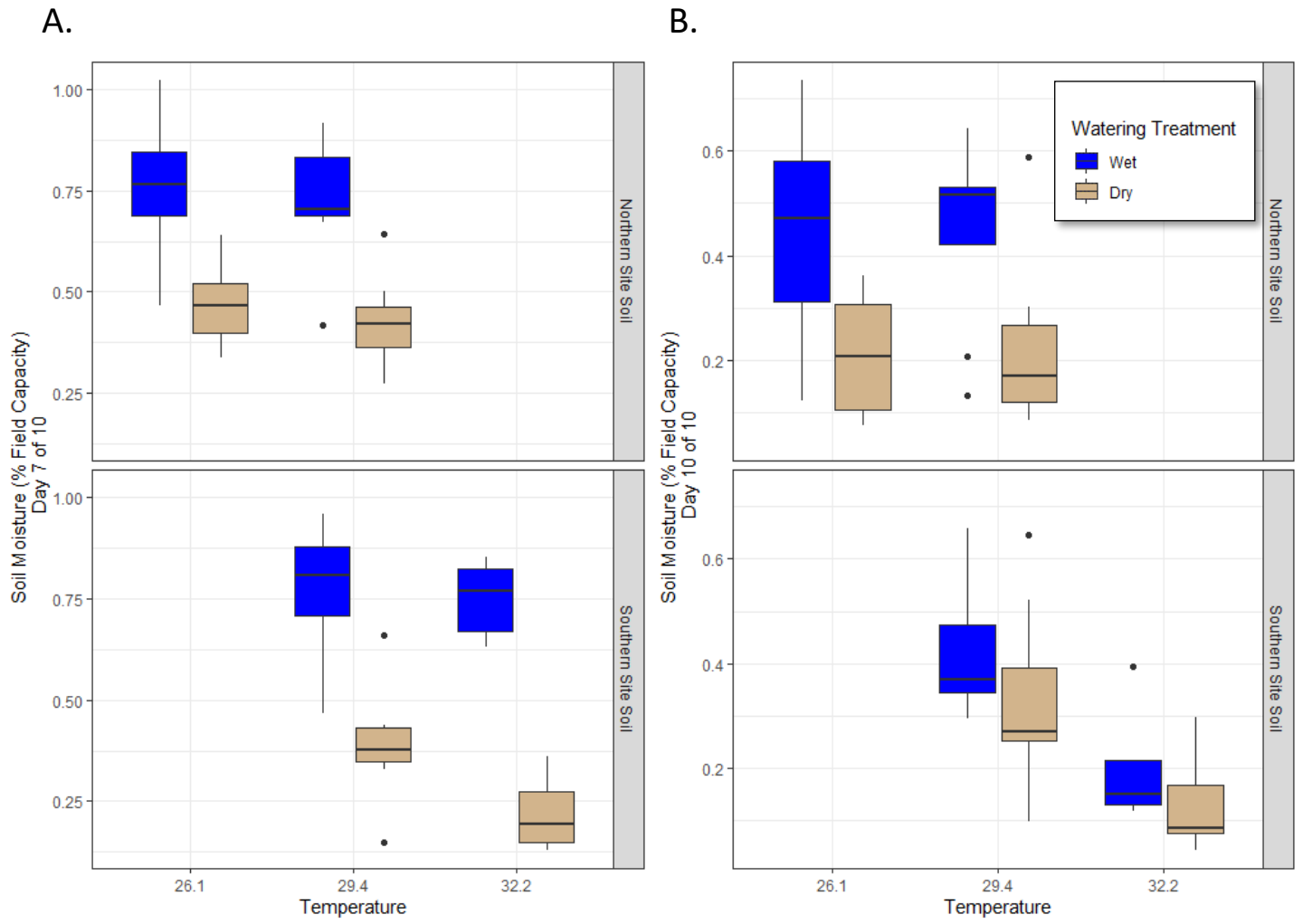
Figure S2. Soil moisture content (as % of field capacity) in experimental pots in the greenhouse experiment. A) soil moisture on day 7 of the 10 day cycle. B) soil moisture on day 10 of the 10 day cycle. For "Wet" treatments, pots were watered on Day 1 and Day 5 of the 10 day cycle. For "Dry" Treatments, pots were watered on Day 1 of the 10 day cycle.

Fig. S3
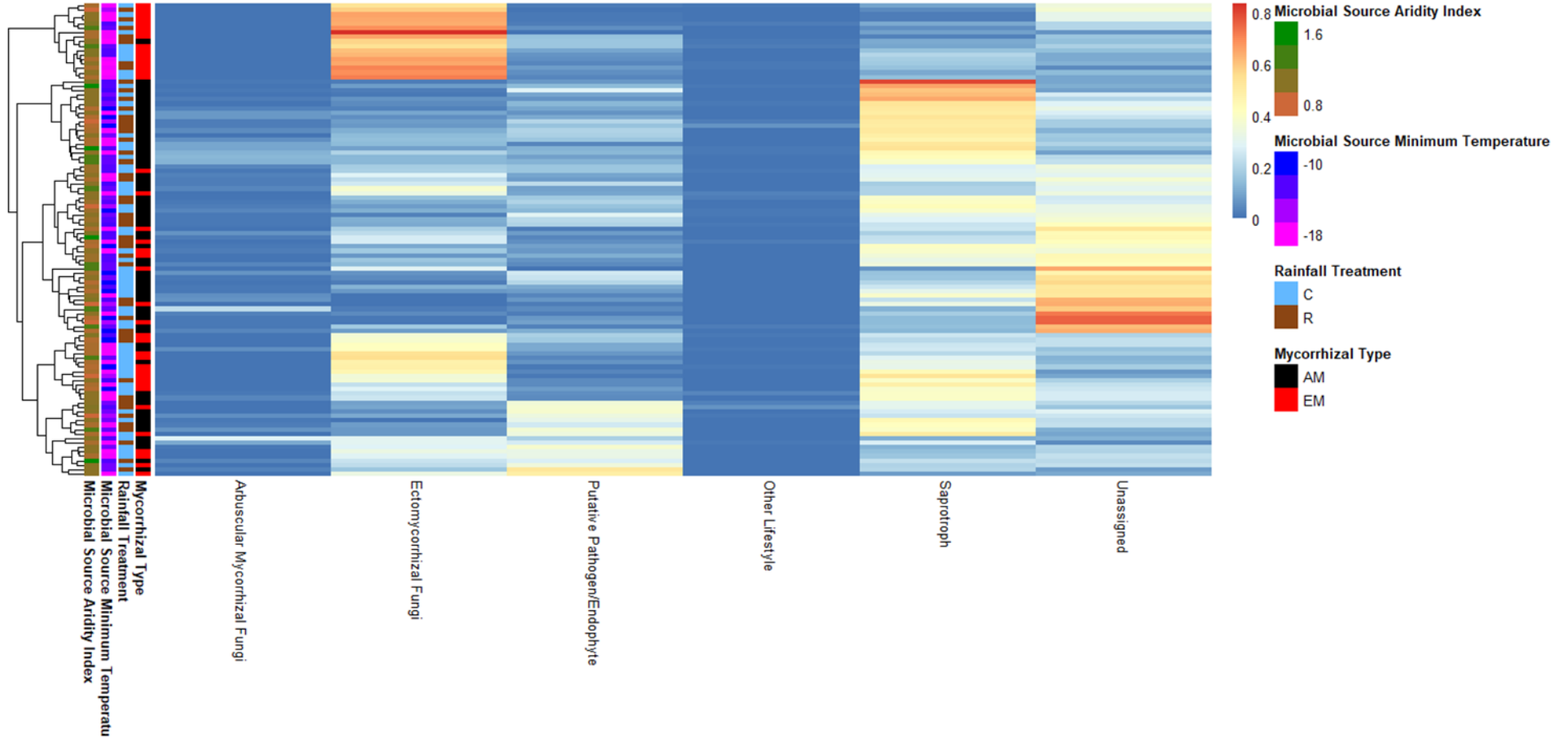
Fig. S3. Heatmap of relative abundance of fungal functional guilds in the roots of surviving seedlings at the northern experimental field site (Kemp Natural Resources Station). Relative abundance measured as the proportion of total fungal sequence reads. Each row represents the fungal community on one surviving seedling. Rows are organized by hierarchical clustering. Vertical color annotations denote microbial source site climate, experimental treatments, or seedling mycorrhizal type.

Fig. S4. Heatmap of relative abundance of the top 20 fungal species in each functional guild in the roots of surviving seedlings at the northern experimental field site (Kemp Natural Resources Station). Relative abundance measured as the proportion of total fungal sequence reads. Each row represents the fungal community on one surviving seedling. Vertical color annotations denote microbial source site climate, experimental treatments, or seedling mycorrhizal type.
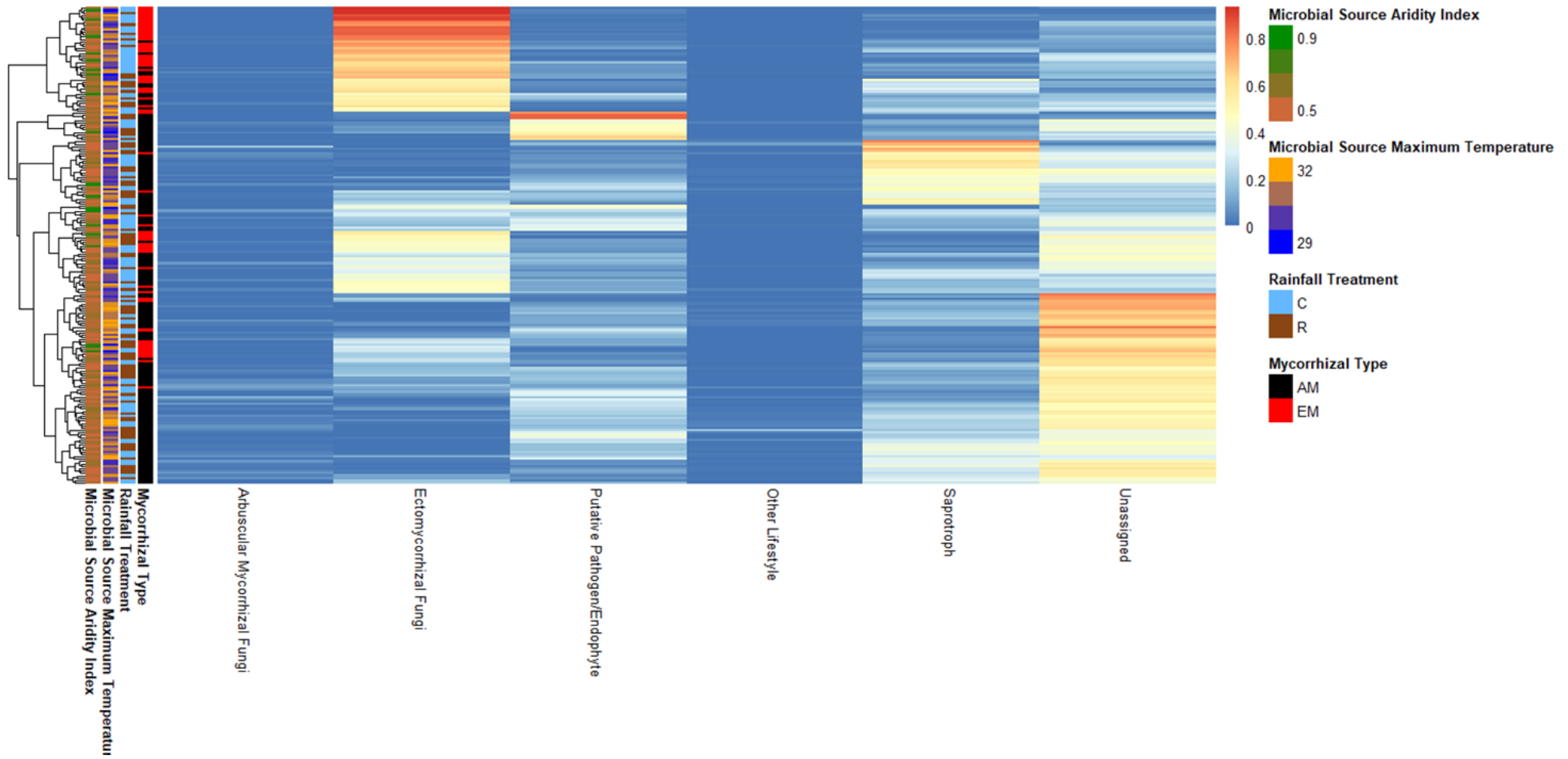
Fig S5



Fig. S5. Heatmap of relative abundance of fungal functional guilds in the roots of surviving seedlings at the southern experimental field site (Allerton Park and Recreation Center). Relative abundance measured as the proportion of total fungal sequence reads. Each row represents the fungal community on one surviving seedling. Rows are organized by hierarchical clustering. Vertical color annotations denote microbial source site climate, experimental treatments, or seedling mycorrhizal type.

Fig. S6
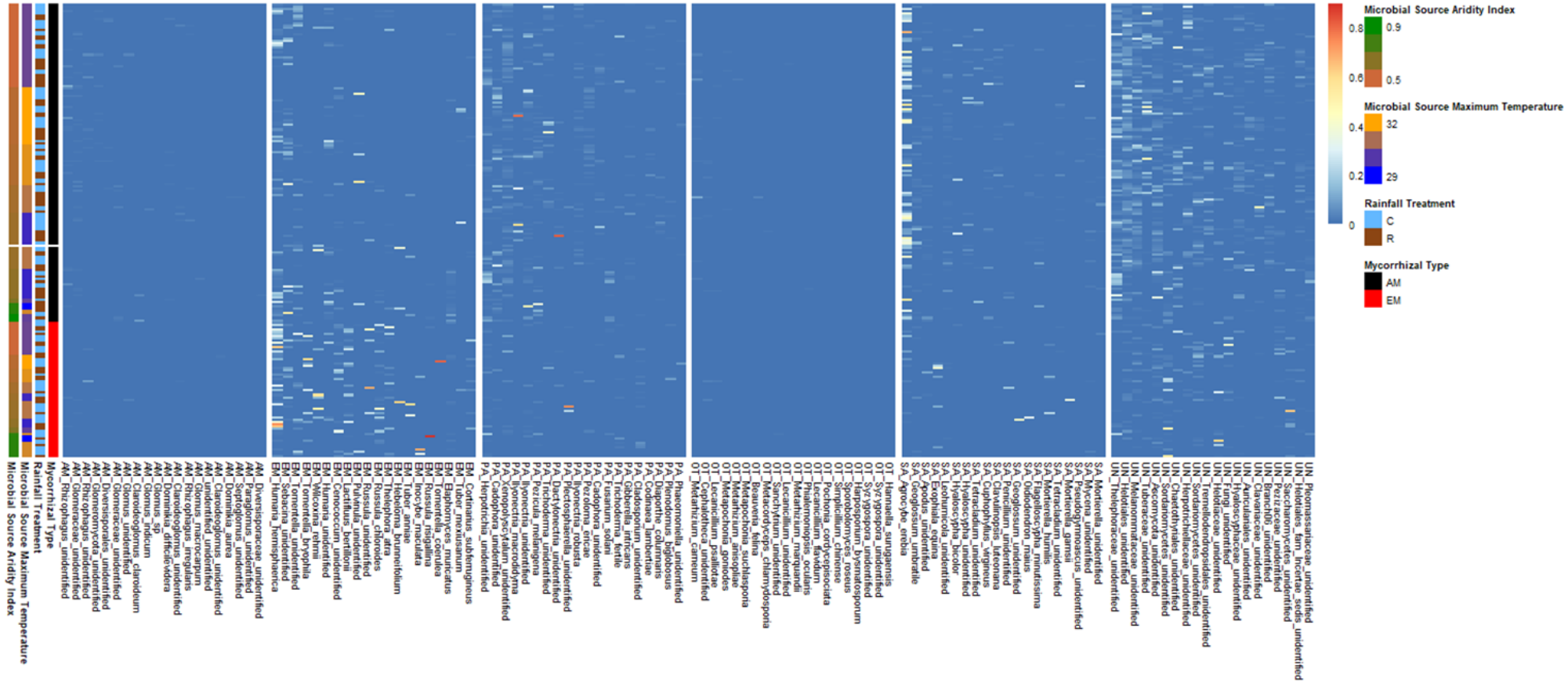


Fig. S6. Heatmap of relative abundance of the top 20 fungal species in each functional guild in the roots of surviving seedlings at the southern experimental field site (Allerton Park and Recreation Center). Relative abundance measured as the proportion of total fungal sequence reads. Each row represents the fungal community on one surviving seedling. Vertical color annotations denote microbial source site climate, experimental treatments, or seedling mycorrhizal type.

Table S1. Tree species used in field and greenhouse experiments
  A. Species range and trait values

| Species | Family | Range Center Latitude[1] | Range Center Longitude[1] | Mycorrhizal Type[2] | Drought Tolerance[3] | Cold Tolerance[4] |
|---|---|---|---|---|---|---|
| *Liquidambar styraciflua* | Altingiaceae | 33.78 | -86.54 | AM | 2.92 | -3.5 |
| *Betula alleghaniensis* | Betulaceae | 44.18 | -77.01 | EM | 3 | -18.5 |
| *Betula papyrifera* | Betulaceae | 45.90 | -84.90 | EM | 2.02 | -31.7 |
| *Carpinus carolina* | Betulaceae | 36.64 | -85.31 | EM | 2.02 | -14.9 |
| *Ostrya virginiana* | Betulaceae | 40.24 | -87.47 | EM | 3.25 | -18.5 |
| *Catalpa speciosa* | Bignoniaceae | 38.11 | -95.13 | AM | 4.22 | -4.1 |
| *Gleditsia triacanthos* | Fabaceae | 39.09 | -92.47 | AM | 4.98 | -10.7 |
| *Quercus alba* | Fagaceae | 38.30 | -86.86 | EM | 3.56 | -14.1 |
| *Quercus macrocarpa* | Fagaceae | 43.43 | -94.17 | EM | 3.85 | -21.5 |
| *Quercus rubra* | Fagaceae | 41.18 | -85.37 | EM | 2.88 | -17.6 |
| *Quercus velutina* | Fagaceae | 38.66 | -87.76 | EM | 3 | -10.7 |
| *Carya cordiformis* | Juglandaceae | 39.92 | -90.45 | EM | 4 | -15.7 |
| *Carya ovata* | Juglandaceae | 39.83 | -89.69 | EM | 3 | -12.2 |
| *Tilia americana* | Malvaceae | 43.36 | -89.43 | EM | 2.88 | -18.4 |
| *Fraxinus americana* | Oleaceae | 40.99 | -82.71 | AM | 2.38 | -15.8 |
| *Prunus serotina* | Rosaceae | 40.18 | -83.55 | AM | 3.02 | -14.8 |
| *Prunus virginiana* | Rosaceae | 44.27 | -85.92 | AM | 2.88 | NA |
| *Acer negundo* | Sapindaceae | 42.19 | -92.30 | AM | 3.03 | -23 |
| *Acer saccharinum* | Sapindaceae | 40.82 | -89.89 | AM | 2.88 | -16.9 |
| *Acer saccharum* | Sapindaceae | 41.85 | -83.27 | AM | 2.25 | -18.3 |
| *Ulmus americana* | Ulmaceae | 40.75 | -90.44 | AM | 2.92 | -22.2 |

1. USFS Climate Change Tree Atlas
2. B. Wang, Y. L. Qiu, Phylogenetic distribution and evolution of mycorrhizas in land plants. *Mycorrhiza* **16**, 299-363 (2006).
3. B. A. Hawkins, M. Rueda, T. F. Rangel, R. Field, J. A. F. Diniz-Filho, Community phylogenetics at the biogeographical scale: cold tolerance, niche conservatism and the structure of North American forests. *J. Biogeogr.* **41**, 23-38 (2014).
4. U. Niinemets, F. Valladares, Tolerance to shade, drought, and waterlogging of temperate Northern Hemisphere trees and shrubs. *Ecological Monographs* **76**, 521-547 (2006).

Table S1B. Species use across experiments

| Species | Northern Site | | | | | Southern Site | | | | |
| | Field Experiment | | Greenhouse Experiment | | | Field Experiment | | Greenhouse Experiment | | |
| | 2018 | 2019 | 2018 | 2019 | 2020 | 2018 | 2019 | 2018 | 2019 | 2020 |
|---|---|---|---|---|---|---|---|---|---|---|
| *Liquidambar styraciflua* | | | | | 24 | | | | | 23 |
| *Betula alleghaniensis* | | 15 | | | | | 7 | | | |
| *Betula papyrifera* | | | 17 | 7 | | | | 15 | | |
| *Carpinus carolina* | | | | | | | | | | 15 |
| *Ostrya virginiana* | | | 15 | | | | | 18 | | |
| *Catalpa speciosa* | | 27 | | 21 | 24 | | 21 | | 19 | 24 |
| *Gleditsia triacanthos* | | 39 | | | | | 32 | | | 23 |
| *Quercus alba* | 5 | | 4 | | 12 | 11 | | | | 16 |
| *Quercus macrocarpa* | 10 | 18 | 19 | 23 | 18 | 22 | | 21 | 24 | 16 |
| *Quercus rubra* | 70 | 36 | 10 | 19 | 21 | 100 | 15 | 21 | 21 | 22 |
| *Quercus velutina* | 6 | 25 | 16 | 23 | | 13 | | 15 | 18 | |
| *Carya cordiformis* | 9 | 20 | 16 | 15 | | 23 | | 13 | 23 | |
| *Carya ovata* | 9 | 14 | 15 | 15 | | 23 | | 19 | 17 | |
| *Tilia americana* | | 27 | | 21 | 6 | | 23 | | 17 | 11 |
| *Fraxinus americana* | | | | | 24 | | | | | 23 |
| *Prunus serotina* | | | | | 22 | | | | | |
| *Prunus virgiana* | | | 15 | | | | | 20 | | |
| *Acer negundo* | 168 | 32 | 23 | 22 | | 183 | 17 | 23 | 16 | |
| *Acer saccharinum* | | | | | 24 | | | | | |
| *Acer saccharum* | 14 | | 7 | | | 9 | | 3 | | |
| *Ulmus americana* | 16 | 24 | 22 | 22 | | 19 | 23 | 24 | 19 | |

*Values in cells indicate that the final analyzable sample size of each species in each experimental cohort (after accounting for loss due to transplant shock, etc.).

Table S2. Statistical results of phylogenetic generalized linear mixed models and mixed effect Cox regression models for seedling survival at the northern field site (Kemp Natural Resource Station, Wisconsin, USA)

| | Three Year Survival (Phylogenetic GLM) | | | | Survival Analysis (Cox Regression) | | | |
| | | | | Wald | | | | Wald |
| A. Full Experiment | Estimate | SE | z | test P | Estimate | SE | z | test P |
|---|---|---|---|---|---|---|---|---|
| Intercept | -1.518 | 0.401 | -3.787 | 0.000 | | | | |
| Rainfall Treatment | -0.043 | 0.245 | -0.175 | 0.861 | 0.083 | 0.074 | 1.130 | 0.260 |
| **Microbial Source Minimum Temperature** | **-0.495** | **0.202** | **-2.454** | **0.014** | **0.227** | **0.113** | **2.010** | **0.044** |
| Microbial Source Aridity Index | 0.090 | 0.173 | 0.519 | 0.604 | -0.021 | 0.085 | -0.250 | 0.800 |
| **Initial Seedling Height** | **-0.329** | **0.162** | **-2.035** | **0.042** | -0.071 | 0.054 | -1.310 | 0.190 |
| **Rainfall Trt*Minimum Temperature** | **0.497** | **0.225** | **2.211** | **0.027** | -0.105 | 0.074 | -1.420 | 0.160 |
| Rainfall Trt*Aridity Index | -0.172 | 0.212 | -0.836 | 0.403 | -0.022 | 0.073 | -0.300 | 0.760 |
| | | | | | | | | |
| B. Ambient Rainfall | | | | | | | | |
| Intercept | -1.540 | 0.379 | -4.065 | 0.000 | | | | |
| **Microbial Source Minimum Temperature** | **-0.456** | **0.211** | **-2.156** | **0.031** | *0.203* | *0.123* | *1.650* | *0.099* |
| Microbial Source Aridity Index | 0.092 | 0.172 | 0.535 | 0.593 | -0.018 | 0.088 | -0.200 | 0.840 |
| **Initial Seedling Height** | **-0.493** | **0.211** | **-2.337** | **0.019** | -0.025 | 0.075 | -0.340 | 0.740 |
| | | | | | | | | |
| C. Reduced Rainfall | | | | | | | | |
| Intercept | -1.527 | 0.488 | -3.128 | 0.002 | | | | |
| Microbial Source Minimum Temperature | -0.051 | 0.229 | -0.222 | 0.824 | 0.143 | 0.117 | 1.220 | 0.220 |
| Microbial Source Aridity Index | -0.070 | 0.206 | -0.341 | 0.733 | -0.054 | 0.091 | -0.600 | 0.550 |
| *Initial Seedling Height* | -0.107 | 0.239 | -0.447 | 0.655 | *-0.129* | *0.076* | *-1.690* | *0.090* |

*Bold text, P<0.05.

Results for fixed effects shown. Models also included crossed random effects of plot (nested within seedling cohort) and phylogenetic covariance among seedling species for generalized linear models or seedling species (nested within genus) for Cox regression. DF = 585 (A), 300 (B), 285 (C)

Table S3. Statistical results of phylogenetic generalized linear mixed models for seedling survival by mycorrhizal type at the northern field site (Kemp Natural Resource Station, Wisconsin, USA)

| A. Full Experiment | Estimate | SE | z | Wald test P |
|---|---|---|---|---|
| Intercept | -1.393 | 0.534 | -2.607 | 0.009 |
| Mycorrhizal Type | -0.296 | 0.760 | -0.390 | 0.696 |
| Rainfall Treatment | 0.076 | 0.305 | 0.249 | 0.803 |
| *Microbial Source Minimum Temperature* | *-0.496* | *0.260* | *-1.911* | *0.056* |
| Microbial Source Aridity Index | 0.118 | 0.218 | 0.542 | 0.588 |
| *Initial Seedling Height* | *-0.332* | *0.170* | *-1.949* | *0.051* |
| Myc Type*Rainfall Trt | -0.289 | 0.537 | -0.537 | 0.591 |
| Myc Type*Minimum Temperature | 0.011 | 0.350 | 0.032 | 0.974 |
| Myc Type*Aridity Index | -0.060 | 0.302 | -0.199 | 0.842 |
| Rainfall Trt*Minimum Temperature | 0.255 | 0.296 | 0.863 | 0.388 |
| Rainfall Trt*Aridity Index | -0.014 | 0.264 | -0.054 | 0.957 |
| Myc Type*Rainfall Trt*Minimum Temperature | 0.673 | 0.480 | 1.400 | 0.161 |
| Myc Type*Rainfall Trt*Aridity Index | -0.701 | 0.496 | -1.412 | 0.158 |
|  |  |  |  |  |
| **B. Ambient Rainfall** |  |  |  |  |
| Intercept | -1.282 | 0.463 | -2.770 | 0.006 |
| Mycorrhizal Type | -0.680 | 0.676 | -1.007 | 0.314 |
| Microbial Source Minimum Temperature | -0.433 | 0.273 | -1.587 | 0.113 |
| Microbial Source Aridity Index | 0.066 | 0.216 | 0.308 | 0.758 |
| ***Initial Seedling Height*** | **-0.561** | **0.230** | **-2.437** | **0.015** |
| Myc Type*Minimum Temperature | -0.063 | 0.357 | -0.176 | 0.861 |
| Myc Type*Aridity Index | 0.043 | 0.290 | 0.149 | 0.882 |
|  |  |  |  |  |
| **C. Reduced Rainfall** |  |  |  |  |
| Intercept | -1.415 | 0.665 | -2.128 | 0.033 |
| Mycorrhizal Type | -0.334 | 0.942 | -0.355 | 0.723 |
| Microbial Source Minimum Temperature | -0.280 | 0.276 | -1.017 | 0.309 |

| | | | | |
|---|---|---|---|---|
| Microbial Source Aridity Index | 0.138 | 0.237 | 0.585 | 0.559 |
| *Initial Seedling Height* | -0.097 | 0.255 | -0.382 | 0.702 |
| *Myc Type\*Minimum Temperature* | *0.670* | *0.387* | *1.732* | *0.083* |
| *Myc Type\*Aridity Index* | *-0.775* | *0.421* | *-1.839* | *0.066* |
| | | | | |
| **D. Ectomycorrhizal - Ambient Rainfall** | | | | |
| Intercept | -1.664 | 0.620 | -2.686 | 0.007 |
| *Microbial Source Minimum Temperature* | *-0.519* | *0.303* | *-1.714* | *0.086* |
| Microbial Source Aridity Index | 0.091 | 0.251 | 0.361 | 0.718 |
| Initial Seedling Height | -0.305 | 0.311 | -0.981 | 0.327 |
| | | | | |
| **E. Ectomycorrhizal - Reduced Rainfall** | | | | |
| Intercept | -1.719 | 1.003 | -1.714 | 0.087 |
| Microbial Source Minimum Temperature | 0.540 | 0.332 | 1.626 | 0.104 |
| Microbial Source Aridity Index | -0.543 | 0.334 | -1.629 | 0.103 |
| *Initial Seedling Height* | -0.280 | 0.453 | -0.618 | 0.537 |
| | | | | |
| **F. Arbuscular mycorrhizal - Ambient Rainfall** | | | | |
| Intercept | -1.589 | 0.248 | -6.416 | 0.000 |
| Microbial Source Minimum Temperature | -0.358 | 0.236 | -1.518 | 0.129 |
| Microbial Source Aridity Index | 0.046 | 0.195 | 0.235 | 0.815 |
| **Initial Seedling Height** | **-0.602** | **0.263** | **-2.291** | **0.022** |
| | | | | |
| **G. Arbuscular mycorrhizal - Reduced Rainfall** | | | | |
| Intercept | -1.414 | 0.235 | -6.022 | 0.000 |
| Microbial Source Minimum Temperature | -0.295 | 0.235 | -1.256 | 0.209 |
| Microbial Source Aridity Index | 0.117 | 0.210 | 0.555 | 0.579 |
| *Initial Seedling Height* | -0.142 | 0.245 | -0.579 | 0.563 |

*Bold text, P<0.05. Italicized text, P < 0.10. Results for fixed effects shown. Models also included crossed random effects of tree seedling species (nested within genus) and plot (nested within seedling cohort). DF = 585 (A), 300 (B), 285 (C), 135 (D), 130 (E), 165 (F), 155 (G)

,

Table S4. Statistical results of phylogenetic generalized linear mixed models for seedling survival in each season at the northern field site (Kemp Natural Resource Station, Wisconsin, USA)

| | Summer 1 | | Winter 1 | | Summer 2 | | Winter 2 | | Summer 3 | |
|---|---|---|---|---|---|---|---|---|---|---|
| A. Full Experiment | N = 585 | | N = 416 | | N = 238 | | N = 150 | | N = 126 | |
| | | Wald | | Wald | | Wald | | Wald | | Wald |
| | Est | test P | Est | test P | Est | test P | Est | test P | Est | test P |
| Intercept | 1.46 | 0.000 | 0.75 | 0.036 | 0.52 | 0.134 | 1.36 | 0.009 | 2.33 | 0.000 |
| Rainfall Treatment | -0.28 | 0.217 | -0.09 | 0.705 | 0.42 | 0.182 | 0.20 | 0.692 | -0.72 | 0.250 |
| Microbial Source Minimum Temp | **0.49** | **0.023** | **-1.00** | **0.000** | -0.20 | 0.425 | -0.37 | 0.294 | -0.25 | 0.642 |
| Microbial Source Aridity Index | -0.29 | 0.101 | **0.83** | **0.011** | 0.02 | 0.920 | 0.10 | 0.724 | *-0.56* | *0.088* |
| Initial Seedling Height | 0.20 | 0.165 | 0.00 | 0.988 | **-0.49** | **0.012** | -0.46 | 0.155 | *-0.56* | *0.058* |
| Rainfall Trt*Minimum Temp | -0.06 | 0.753 | 0.16 | 0.557 | **0.66** | **0.025** | 0.44 | 0.355 | 0.12 | 0.836 |
| Rainfall Trt*Aridity Index | 0.21 | 0.202 | **-0.67** | **0.045** | -0.30 | 0.259 | -0.50 | 0.227 | *1.05* | *0.095* |
| | | | | | | | | | | |
| B. Ambient Rainfall | N = 300 | | N = 221 | | N = 128 | | N = 78 | | N = 66 | |
| Intercept | 1.45 | 0.000 | 0.54 | 0.788 | 0.45 | 0.186 | 1.92 | 0.003 | 2.08 | 0.000 |
| Microbial Source Minimum Temp | *0.44* | *0.064* | **-1.00** | **0.000** | -0.22 | 0.382 | -0.25 | 0.564 | 0.00 | 1.000 |
| Microbial Source Aridity Index | -0.26 | 0.166 | **0.72** | **0.011** | 0.05 | 0.782 | 0.00 | 1.000 | **-0.72** | **0.042** |
| Initial Seedling Height | **0.46** | **0.025** | -0.06 | 0.773 | **-0.56** | **0.029** | **-0.10** | **0.043** | *-0.90* | *0.078* |
| | | | | | | | | | | |
| C. Reduced Rainfall | N = 285 | | N = 195 | | N = 110 | | N = 72 | | N = 60 | |
| Intercept | 1.13 | 0.004 | 0.82 | 0.037 | 0.87 | 0.035 | 1.67 | 0.003 | 1.49 | 0.001 |
| Microbial Source Minimum Temp | **0.46** | **0.031** | **-0.70** | **0.019** | 0.38 | 0.236 | -0.10 | 0.825 | -0.18 | 0.580 |
| Microbial Source Aridity Index | -0.09 | 0.629 | 0.18 | 0.498 | -0.34 | 0.235 | -0.42 | 0.264 | 0.50 | 0.308 |
| Initial Seedling Height | 0.02 | 0.916 | 0.11 | 0.648 | -0.32 | 0.274 | 0.25 | 0.640 | -0.20 | 0.571 |

*Bold text, P<0.05. Italicized text, P < 0.10.
Results for fixed effects shown. Models also included crossed random effects of plot (nested within seedling cohort) and phylogenetic covariance among seedling species

Table S5. Statistical results of phylogenetic generalized linear mixed models and mixed effect Cox regression models for seedling survival at the southern field site (Allerton Park and Retreat Center, Illinois, USA)

|  | Estimate | SE | z | Wald test P | Estimate | SE | z | Wald test P |
|---|---|---|---|---|---|---|---|---|
| **A. Full Experiment** | | | | | | | | |
| Intercept | 0.181 | 0.364 | 0.498 | 0.618 | | | | |
| Rainfall Treatment | -0.206 | 0.185 | -1.110 | 0.267 | 0.134 | 0.119 | 1.120 | 0.260 |
| *Microbial Source Maximum Temperature* | *0.277* | *0.158* | *1.757* | *0.079* | -0.114 | 0.102 | -1.110 | 0.270 |
| Microbial Source Aridity Index | -0.080 | 0.163 | -0.489 | 0.625 | 0.013 | 0.100 | 0.130 | 0.890 |
| *Initial Seedling Height* | *0.234* | *0.128* | *1.835* | *0.067* | **-0.191** | **0.081** | **-2.360** | **0.018** |
| Rainfall Trt*Maximum Temperature | -0.290 | 0.190 | -1.528 | 0.126 | 0.128 | 0.119 | 1.080 | 0.280 |
| **Rainfall Trt*Aridity Index** | **-0.435** | **0.198** | **-2.192** | **-0.028** | 0.161 | 0.112 | 1.440 | 0.150 |
| | | | | | | | | |
| **B. Ambient Rainfall** | | | | | | | | |
| Intercept | -0.011 | 0.387 | -0.027 | 0.978 | | | | |
| **Microbial Source Maximum Temperature** | 0.252 | 0.150 | 1.681 | 0.093 | -0.111 | 0.100 | -1.110 | 0.270 |
| Microbial Source Aridity Index | 0.012 | 0.164 | 0.076 | 0.940 | -0.025 | 0.102 | -0.240 | 0.810 |
| Initial Seedling Height | 0.248 | 0.171 | 1.447 | 0.148 | -0.210 | 0.115 | -1.830 | 0.068 |
| | | | | | | | | |
| **C. Reduced Rainfall** | | | | | | | | |
| Intercept | 0.027 | 0.380 | 0.097 | 0.923 | | | | |
| Microbial Source Maximum Temperature | 0.010 | 0.174 | 0.060 | 0.952 | -0.047 | 0.954 | -0.460 | 0.640 |
| **Microbial Source Aridity Index** | **-0.634** | **0.202** | **-3.142** | **0.002** | 0.391 | 0.139 | 2.820 | 0.005 |
| Initial Seedling Height | 0.195 | 0.185 | 1.054 | 0.292 | -0.162 | 0.851 | -1.450 | 0.150 |

Survival Analysis (Cox Regression)

*Bold text, P<0.05. Italicized text, P < 0.10.
Results for fixed effects shown. Models also included crossed random effects of plot (nested within seedling cohort) and phylogenetic covariance among seedling species for generalized linear models or seedling species (nested within genus) for Cox regression. DF = 542 (A), 269 (B), 273 (C)

Table S6. Statistical results of phylogenetic generalized linear mixed models for seedling survival by mycorrhizal type at the southern field site (Allerton Park and Retreat Center, Illinois, USA)

| A. Full Experiment | Estimate | SE | z | Wald test P |
|---|---|---|---|---|
| Intercept | 0.499 | 0.571 | 0.874 | 0.382 |
| Mycorrhizal Type | -0.631 | 0.779 | -0.810 | 0.418 |
| Rainfall Treatment | -0.130 | 0.256 | -0.509 | 0.611 |
| **Microbial Source Maximum Temperature** | **0.485** | **0.210** | **2.316** | **0.021** |
| **Microbial Source Aridity Index** | **-0.466** | **0.230** | **-2.021** | **0.043** |
| Initial Seedling Height | 0.209 | 0.134 | 1.564 | 0.118 |
| Myc Type*Rainfall Trt | -0.271 | 0.385 | -0.703 | 0.482 |
| *Myc Type*Maximum Temperature* | *-0.553* | *0.287* | *-1.928* | *0.054* |
| **Myc Type*Aridity Index** | **0.915** | **0.312** | **2.934** | **0.003** |
| **Rainfall Trt*Maximum Temperature** | **-0.685** | **0.256** | **-2.672** | **0.008** |
| *Rainfall Trt*Aridity Index* | *-0.525* | *0.294* | *-1.784* | *0.074* |
| **Myc Type*Rainfall Trt*Maximum Temperature** | **1.013** | **0.401** | **2.527** | **0.012** |
| Myc Type*Rainfall Trt*Aridity Index | 0.175 | 0.420 | 0.416 | 0.677 |
| | | | | |
| B. Ambient Rainfall | | | | |
| Intercept | 0.239 | 0.569 | 0.420 | 0.675 |
| Mycorrhizal Type | -0.502 | 0.788 | -0.638 | 0.524 |
| **Microbial Source Maximum Temperature** | **0.449** | **0.195** | **2.305** | **0.021** |
| Microbial Source Aridity Index | -0.311 | 0.232 | -1.337 | 0.181 |
| Initial Seedling Height | 0.193 | 0.180 | 1.073 | 0.283 |
| *Myc Type*Maximum Temperature* | *-0.518* | *0.282* | *-1.837* | *0.066* |
| **Myc Type*Aridity Index** | **0.719** | **0.320** | **2.247** | **0.025** |
| | | | | |
| C. Reduced Rainfall | | | | |
| Intercept | 0.476 | 0.595 | 0.800 | 0.424 |
| Mycorrhizal Type | -0.750 | 0.802 | -0.935 | 0.350 |
| Microbial Source Maximum Temperature | -0.155 | 0.227 | -0.682 | 0.495 |
| **Microbial Source Aridity Index** | **-1.165** | **0.299** | **-3.892** | **0.000** |
| Initial Seedling Height | 0.207 | 0.195 | 1.067 | 0.286 |
| Myc Type*Maximum Temperature | 0.400 | 0.298 | 1.343 | 0.179 |
| **Myc Type*Aridity Index** | **1.193** | **0.387** | **3.081** | **0.002** |
| | | | | |
| D. Ectomycorrhizal - Ambient Rainfall | | | | |
| Intercept | -0.652 | 0.947 | -0.689 | 0.491 |
| Microbial Source Maximum Temperature | -0.110 | 0.224 | -0.491 | 0.623 |
| **Microbial Source Aridity Index** | **0.503** | **0.252** | **1.997** | **0.046** |
| Initial Seedling Height | 0.099 | 0.227 | 0.435 | 0.664 |
| | | | | |
| E. Ectomycorrhizal - Reduced Rainfall | | | | |

| | | | | |
|---|---|---|---|---|
| Intercept | -0.372 | 0.373 | -0.998 | 0.319 |
| Microbial Source Maximum Temperature | 0.242 | 0.228 | 1.060 | 0.289 |
| Microbial Source Aridity Index | -0.166 | 0.260 | -0.640 | 0.522 |
| *Initial Seedling Height* | -0.133 | 0.233 | -0.570 | 0.569 |
| | | | | |
| **F. Arbuscular mycorrhizal - Ambient Rainfall** | | | | |
| Intercept | 0.265 | 0.180 | 1.470 | 0.142 |
| **Microbial Source Maximum Temperature** | **0.499** | **0.191** | **2.619** | **0.009** |
| *Microbial Source Aridity Index* | *-0.393* | *0.208* | *-1.890* | *0.059* |
| Initial Seedling Height | 0.162 | 0.203 | 0.799 | 0.425 |
| | | | | |
| **G. Arbuscular mycorrhizal - Reduced Rainfall** | | | | |
| Intercept | 0.803 | 0.792 | 1.014 | 0.311 |
| Microbial Source Maximum Temperature | -0.223 | 0.267 | -0.833 | 0.405 |
| **Microbial Source Aridity Index** | **-1.251** | **0.347** | **-3.604** | **0.000** |
| **Initial Seedling Height** | **0.624** | **0.284** | **2.196** | **0.028** |

*Bold text, P<0.05. Italicized text, P < 0.10. Results for fixed effects shown. Models also included crossed random effects of tree seedling species (nested within genus) and plot (nested within seedling cohort). DF = 542 (A), 269 (B), 273 (C), 119 (D), 119 (E), 150 (F), 154 (G)

Table S7. Statistical results of phylogenetic generalized linear mixed models for seedling survival in each season at the southern field site (Allerton Park and Retreat Center, Illinois, USA)

| | Summer 1 | | Winter 1 | | Summer 2 | | Winter 2 | | Summer 3 | |
|---|---|---|---|---|---|---|---|---|---|---|
| A. Full Experiment | N = 542 | | N = 454 | | N = 348 | | N = 314 | | N = 281 | |
| | Est | Wald test P | Est | Wald test P | Est | Wald test P | Est | Wald test P | Est | Wald test P |
| Intercept | 2.23 | 0.000 | 1.26 | 0.000 | 2.31 | 0.000 | 2.66 | 0.000 | 2.65 | 0.000 |
| Rainfall Treatment | -0.35 | 0.149 | 0.10 | 0.659 | 0.13 | 0.758 | -0.49 | 0.234 | -0.54 | 0.226 |
| Microbial Source Maximum Temp | -0.04 | 0.828 | -0.01 | 0.972 | 0.48 | 0.101 | 0.47 | 0.121 | *0.68* | *0.082* |
| Microbial Source Aridity Index | -0.30 | 0.123 | 0.21 | 0.322 | 0.17 | 0.536 | -0.34 | 0.202 | -0.06 | 0.873 |
| Initial Seedling Height | **0.33** | **0.036** | 0.17 | 0.295 | 0.29 | 0.171 | 0.14 | 0.598 | -0.08 | 0.724 |
| Rainfall Trt*Maximum Temperature | 0.04 | 0.874 | 0.09 | 0.702 | **-0.76** | **0.049** | -0.59 | 0.136 | -0.61 | 0.189 |
| Rainfall Trt*Aridity Index | 0.06 | 0.773 | -0.13 | 0.619 | **-0.84** | **0.014** | -0.13 | 0.710 | -0.29 | 0.495 |
| | | | | | | | | | | |
| B. Ambient Rainfall | N = 269 | | N = 231 | | N = 159 | | N = 175 | | N = 145 | |
| Intercept | 2.11 | 0.000 | 1.18 | 0.003 | 2.38 | 0.000 | 2.93 | 0.000 | 2.62 | 0.000 |
| Microbial Source Maximum Temp | -0.06 | 0.801 | -0.06 | 0.742 | 0.50 | 0.110 | *0.53* | *0.088* | 0.64 | 0.108 |
| Microbial Source Aridity Index | -0.21 | 0.323 | 0.24 | 0.262 | 0.20 | 0.493 | -0.45 | 0.132 | -0.07 | 0.844 |
| Initial Seedling Height | *0.39* | *0.085* | 0.10 | 0.633 | 0.41 | 0.160 | 0.21 | 0.603 | -0.06 | 0.851 |
| | | | | | | | | | | |
| C. Reduced Rainfall | N = 273 | | N = 223 | | N = 155 | | N = 168 | | N = 136 | |
| Intercept | 1.94 | 0.000 | 1.33 | 0.000 | 2.51 | 0.000 | 1.90 | 0.000 | 2.11 | 0.000 |
| Microbial Source Maximum Temp | 0.01 | 0.966 | 0.11 | 0.570 | -0.25 | 0.350 | -0.02 | 0.930 | 0.09 | 0.797 |
| Microbial Source Aridity Index | -0.28 | 0.151 | 0.02 | 0.932 | **-0.75** | **0.003** | *-0.48* | *0.074* | -0.44 | 0.198 |
| Initial Seedling Height | 0.29 | 0.172 | 0.24 | 0.316 | 0.20 | 0.560 | -0.01 | 0.965 | -0.17 | 0.566 |

*Bold text, P<0.05. Italicized text, P < 0.10.
Results for fixed effects shown. Models also included crossed random effects of plot (nested within seedling cohort) and phylogenetic covariance among seedling species

Table S8. Statistical results of phylogenetic linear mixed models for seedling biomass in greenhouse experiment using background soil from the northern field site (Kemp Natural Resource Station, Wisconsin, USA)

| A)  Full Experiment | Estimate | SE | Z | P |
|---|---|---|---|---|
| (Intercept) | 1.199 | 4.757 | 0.252 | 0.801 |
| Microbial Source Aridity Index | 0.356 | 0.188 | 1.890 | 0.059 |
| Microbial Source Minimum Temperature | -0.280 | 0.202 | -1.387 | 0.166 |
| Treatment Cool-Dry | -1.141 | 0.249 | -4.579 | <0.0001 |
| Treatment Warm-Wet | -1.417 | 0.273 | -5.193 | <0.0001 |
| Treatment Warm-Dry | -2.554 | 0.284 | -9.009 | < 0.0001 |
| Treatment Cool-Dry * MS Aridity Index | -0.446 | 0.254 | -1.758 | 0.079 |
| Treatment Warm-Wet * MS Aridity Index | -0.294 | 0.283 | -1.039 | 0.299 |
| Treatment Warm-Dry * MS Aridity Index | -0.304 | 0.283 | -1.077 | 0.281 |
| Treatment Cool-Dry * MS Minimum Temperature | 0.100 | 0.251 | 0.399 | 0.690 |
| Treatment Warm-Wet * MS Minimum Temperature | 0.287 | 0.324 | 0.886 | 0.376 |
| Treatment Warm-Dry * MS Minimum Temperature | 0.575 | 0.327 | 1.760 | 0.078 |
| | | | | |
| B)  Cool-Wet Treatment | | | | |
| (Intercept) | 0.967 | 0.456 | 2.120 | 0.034 |
| Microbial Source Aridity Index | 0.322 | 0.233 | 1.383 | 0.167 |
| Microbial Source Minimum Temperature | -0.193 | 0.274 | -0.705 | 0.481 |
| | | | | |
| C)  Cool-Dry Treatment | | | | |
| (Intercept) | -0.110 | 0.238 | -0.463 | 0.643 |
| Microbial Source Aridity Index | -0.252 | 0.160 | -1.577 | 0.115 |
| Microbial Source Minimum Temperature | 0.073 | 0.179 | 0.406 | 0.685 |
| | | | | |
| D)  Warm-Wet Treatment | | | | |
| (Intercept) | 0.024 | 0.457 | 0.052 | 0.958 |
| Microbial Source Aridity Index | 0.053 | 0.191 | 0.275 | 0.783 |
| Microbial Source Minimum Temperature | 0.032 | 0.231 | 0.137 | 0.891 |
| | | | | |
| E)  Warm-Dry | | | | |
| (Intercept) | -1.095 | 0.468 | -2.339 | 0.019 |
| Microbial Source Aridity Index | 0.149 | 0.175 | 0.851 | 0.395 |
| Microbial Source Minimum Temperature | 0.123 | 0.201 | 0.612 | 0.541 |

*Bold text, P<0.05. Italicized text, P < 0.10. Results for fixed effects shown. Results for fixed effects shown. Models also included crossed random effects of experimental year (nested within greenhouse ID) and phylogenetic covariance among seedling species. DF = 542 (A), 150 (B), 141 (C), 132 (D), 119 (E).

Table S9. Statistical results of phylogenetic linear mixed models for seedling biomass in greenhouse experiment using background soil from the southern field site (Allerton Park and Retreat Center, Illinois, USA)

| A)   Full Experiment | Estimate | SE | Z | P |
|---|---|---|---|---|
| (Intercept) | 1.592 | 1.955 | 0.814 | 0.415 |
| Microbial Source Aridity Index | 0.158 | 0.223 | 0.710 | 0.478 |
| **Microbial Source Maximum Temperature** | **0.454** | **0.194** | **2.340** | **0.019** |
| **Treatment Cool-Dry** | **-1.985** | **0.257** | **-7.725** | **0.000** |
| Treatment Warm-Wet | -1.448 | 2.764 | -0.524 | 0.600 |
| Treatment Warm-Dry | -3.166 | 2.765 | -1.145 | 0.252 |
| Treatment Cool-Dry * MS Aridity Index | -0.386 | 0.271 | -1.425 | 0.154 |
| Treatment Warm-Wet * MS Aridity Index | -0.448 | 0.310 | -1.446 | 0.148 |
| **Treatment Warm-Dry * MS Aridity Index** | **-0.771** | **0.312** | **-2.473** | **0.013** |
| **Treatment Cool-Dry * MS Maximum Temperature** | **-0.524** | **0.270** | **-1.944** | **0.052** |
| **Treatment Warm-Wet * MS Maximum Temperature** | **-0.589** | **0.270** | **-2.186** | **0.029** |
| **Treatment Warm-Dry * MS Maximum Temperature** | **-0.818** | **0.276** | **-2.966** | **0.003** |
| | | | | |
| B)   Cool-Wet Treatment | | | | |
| (Intercept) | 1.580 | 0.662 | 2.387 | 0.017 |
| Microbial Source Aridity Index | 0.196 | 0.286 | 0.686 | 0.493 |
| Microbial Source Maximum Temperature | 0.369 | 0.237 | 1.557 | 0.119 |
| | | | | |
| C)   Cool-Dry Treatment | | | | |
| (Intercept) | -0.324 | 0.407 | -0.795 | 0.427 |
| Microbial Source Aridity Index | -0.165 | 0.211 | -0.780 | 0.435 |
| Microbial Source Maximum Temperature | -0.053 | 0.180 | -0.294 | 0.769 |
| | | | | |
| D)   Warm-Wet Treatment | | | | |
| (Intercept) | 0.217 | 0.205 | 1.057 | 0.290 |
| Microbial Source Aridity Index | -0.278 | 0.179 | -1.547 | 0.122 |
| Microbial Source Maximum Temperature | -0.139 | 0.178 | -0.781 | 0.435 |
| | | | | |
| E)   Warm-Dry | | | | |
| (Intercept) | -1.533 | 0.476 | -3.223 | 0.001 |
| **Microbial Source Aridity Index** | **-0.502** | **0.140** | **-3.592** | **0.000** |
| *Microbial Source Maximum Temperature* | *-0.222* | *0.119* | *-1.860* | *0.063* |

*Bold text, P<0.05. Italicized text, P < 0.10. Results for fixed effects shown. Results for fixed effects shown. Models also included crossed random effects of experimental year (nested within greenhouse ID) and phylogenetic covariance among seedling species. DF = 544 (A), 135 (B), 136 (C), 141 (D), 132 (E).

Table S10. Statistical results of phylogenetic generalized linear mixed models for seedling biomass in greenhouse experiment using background soil from the southern field site (Allerton Park and Retreat Center, Illinois,  USA), accounting for mycorrhizal type of the seedling species.

| A)  Full Experiment | Estimate | SE | t | P |
|---|---|---|---|---|
| (Intercept) | 2.28 | 0.32 | 7.03 | <0.001 |
| Microbial Source Aridity Index | 0.05 | 0.31 | 0.18 | 0.861 |
| **Microbial Source Maximum Temperature** | **0.75** | **0.31** | **2.41** | **0.016** |
| **Treatment Cool-Dry** | **-3.11** | **0.40** | **-7.76** | **<0.001** |
| **Treatment Warm-Wet** | **-1.78** | **0.46** | **-3.88** | **<0.001** |
| **Treatment Warm-Dry** | **-4.43** | **0.46** | **-9.56** | **<0.001** |
| **Mycorrhizal Type (EM)** | **-1.07** | **0.36** | **-2.93** | **0.003** |
| Treatment Cool-Dry * Aridity Index | -0.29 | 0.43 | -0.67 | 0.501 |
| Treatment Warm-Wet * Aridity Index | -0.47 | 0.43 | -1.08 | 0.281 |
| **Treatment Warm-Dry * Aridity Index** | **-1.13** | **0.44** | **-2.59** | **0.010** |
| *Treatment Cool-Dry * Maximum Temperature* | *-0.84* | *0.45* | *-1.85* | *0.065* |
| *Treatment Warm-Wet * Maximum Temperature* | *-0.81* | *0.45* | *-1.81* | *0.070* |
| **Treatment Warm-Dry * Maximum Temperature** | **-1.13** | **0.45** | **-2.49** | **0.013** |
| Myc Type * Aridity Index | 0.32 | 0.39 | 0.84 | 0.402 |
| Myc Type * Maximum Temperature | -0.42 | 0.39 | -1.09 | 0.277 |
| **Treatment Cool-Dry * Myc Type** | **1.91** | **0.52** | **3.68** | **<0.001** |
| Treatment Warm-Wet * Myc Type | 0.50 | 0.51 | 0.97 | 0.333 |
| **Treatment Warm-Dry * Myc Type** | **2.03** | **0.52** | **3.90** | **<0.001** |
| Treatment Cool-Dry * Myc Type * Aridity Index | -0.07 | 0.55 | -0.12 | 0.904 |
| Treatment Warm-Wet * Myc Type * Aridity Index | -0.12 | 0.54 | -0.23 | 0.819 |
| Treatment Warm-Dry * Myc Type * Aridity Index | 0.46 | 0.55 | 0.84 | 0.398 |
| Treatment Cool-Dry * Myc Type * Maximum Temperature | 0.57 | 0.56 | 1.01 | 0.310 |
| Treatment Warm-Wet * Myc Type * Maximum Temperature | 0.29 | 0.55 | 0.53 | 0.593 |
| Treatment Warm-Dry * Myc Type * Maximum Temperature | 0.53 | 0.56 | 0.95 | 0.341 |
| | | | | |
| B)  Ectomycorrhizal Cool-Wet Treatment | | | | |
| (Intercept) | 1.19 | 0.28 | 4.23 | <0.001 |
| Microbial Source Aridity Index | 0.49 | 0.30 | 1.66 | 0.097 |
| Microbial Source Maximum Temperature | 0.39 | 0.30 | 1.31 | 0.189 |
| | | | | |
| C)  Ectomycorrhizal Cool-Dry Treatment | | | | |
| (Intercept) | 0.11 | 0.48 | 0.22 | 0.823 |
| Microbial Source Aridity Index | -0.23 | 0.29 | -0.79 | 0.432 |
| Microbial Source Maximum Temperature | -0.05 | 0.24 | -0.21 | 0.832 |
| | | | | |
| D)  Ectomycorrhizal Warm-Wet Treatment | | | | |
| (Intercept) | -0.04 | 0.23 | -0.17 | 0.866 |
| Microbial Source Aridity Index | -0.21 | 0.25 | -0.82 | 0.411 |
| Microbial Source Maximum Temperature | -0.20 | 0.25 | -0.79 | 0.432 |

### E) Ectomycorrhizal Warm-Dry

| | | | | |
|---|---|---|---|---|
| (Intercept) | -1.05 | 0.33 | -3.17 | 0.002 |
| **Microbial Source Aridity Index** | **-0.34** | **0.16** | **-2.15** | **0.031** |
| *Microbial Source Maximum Temperature* | *-0.25* | *0.14* | *-1.76* | *0.079* |

### F) Arbuscular Mycorrhizal Cool-Wet Treatment

| | | | | |
|---|---|---|---|---|
| (Intercept) | 1.61 | 1.47 | 1.10 | 0.272 |
| Microbial Source Aridity Index | -0.13 | 0.39 | -0.33 | 0.741 |
| Microbial Source Maximum Temperature | 0.33 | 0.33 | 1.01 | 0.315 |

### G) Arbuscular Mycorrhizal Cool-Dry Treatment

| | | | | |
|---|---|---|---|---|
| (Intercept) | -0.72 | 0.36 | -2.00 | 0.045 |
| Microbial Source Aridity Index | -0.07 | 0.28 | -0.25 | 0.802 |
| Microbial Source Maximum Temperature | -0.04 | 0.27 | -0.13 | 0.893 |

### H) Arbuscular Mycorrhizal Warm-Wet Treatment

| | | | | |
|---|---|---|---|---|
| (Intercept) | 0.53 | 0.44 | 1.18 | 0.236 |
| **Microbial Source Aridity Index** | **-0.65** | **0.24** | **-2.72** | **0.006** |
| Microbial Source Maximum Temperature | -0.17 | 0.22 | -0.74 | 0.458 |

### I) Arbuscular Mycorrhizal Warm-Dry

| | | | | |
|---|---|---|---|---|
| (Intercept) | -1.64 | 1.40 | -1.18 | 0.240 |
| **Microbial Source Aridity Index** | **-0.62** | **0.20** | **-3.12** | **0.002** |
| *Microbial Source Maximum Temperature* | -0.08 | 0.16 | -0.50 | 0.615 |

*Bold text, P<0.05. Italicized text, P < 0.10. Results for fixed effects shown. Results for fixed effects shown. Models also included crossed random effects of experimental year (nested within greenhouse ID) and phylogenetic covariance among seedling species. DF = 544 (A), 80 (B), 82 (C), 85 (D), 79 (E), 55 (F), 56 (G), 53 (H), 54 (I)

Table S11. Statistical results of a permutation MANOVA testing differences in root-associate fungal community composition in survival seedlings at the northern (Kemp NRS) and southern (Allerton PRC) sites for both arbuscular (AM) and ectomycorrhizal (EM) seedlings.

| Field Site | Mycorrhizal Type | Term | Df | PsuedoF | $R^2$ | P |
|---|---|---|---|---|---|---|
| Kemp NRS | AM | **Tree Genus** | **3** | **2.626** | **0.09944** | **0.001** |
| | | Rainfall Treatment | 1 | 1.2462 | 0.01573 | 0.119 |
| | | **Microbial Inocula Source** | **11** | **1.9183** | **0.26635** | **0.001** |
| | | Residuals | 49 | | 0.61849 | |
| | | Total | 64 | | 1 | |
| Kemp NRS | EM | Tree Genus | 3 | 1.19169 | 0.08425 | 0.116 |
| | | Rainfall Treatment | 1 | 0.93773 | 0.0221 | 0.566 |
| | | **Microbial Inocula Source** | **9** | **1.21349** | **0.25737** | **0.024** |
| | | Residuals | 27 | | 0.63628 | |
| | | Total | 40 | | 1 | |
| Allerton PRC | AM | **Tree Genus** | **3** | **3.4903** | **0.0693** | **0.001** |
| | | Rainfall Treatment | 1 | 1.1618 | 0.00769 | 0.228 |
| | | **Microbial Inocula Source** | **10** | **1.4464** | **0.09573** | **0.001** |
| | | Residuals | 125 | | 0.82728 | |
| | | Total | 139 | | 1 | |
| Allerton PRC | EM | **Tree Genus** | **2** | **1.2854** | **0.04045** | **0.042** |
| | | *Rainfall Treatment* | *1* | *1.365* | *0.02148* | *0.054* |
| | | **Microbial Inocula Source** | **10** | **1.3617** | **0.21427** | **0.001** |
| | | Residuals | 46 | | 0.7238 | |
| | | Total | 59 | | 1 | |

Table S12. Linear models of fungal Shannon-Weaver diversity and richness in the bulk soils used as experimental inocula, versus the climate of the microbial source site.

A. Northern Inocula Set

| Fungal Guild | Term | Diversity | | | | Richness | | | |
|---|---|---|---|---|---|---|---|---|---|
| | | Estimate | SE | Z | P | Estimate | SE | Z | P |
| Arbuscular Mycorrhizal | Intercept | -0.17 | 1.31 | -0.13 | 0.897 | 1.19 | 5.57 | 0.21 | 0.834 |
| | Sequencing Depth | 0.00 | 0.00 | 2.82 | 0.016 | 0.00 | 0.00 | 3.12 | 0.009 |
| | Microbial Source Aridity Index | 1.38 | 1.19 | 1.16 | 0.268 | 4.83 | 5.05 | 0.96 | 0.358 |
| | Microbial Source Minimum Temperature | 0.07 | 0.05 | 1.32 | 0.212 | 0.46 | 0.23 | 1.99 | 0.070 |
| Ecto-mycorrhizal | Intercept | 1.41 | 1.03 | 1.36 | 0.198 | 23.57 | 19.27 | 1.22 | 0.245 |
| | Sequencing Depth | 0.00 | 0.00 | 1.77 | 0.103 | 0.00 | 0.00 | 0.85 | 0.410 |
| | Microbial Source Aridity Index | 1.30 | 0.94 | 1.39 | 0.190 | 0.63 | 17.46 | 0.04 | 0.972 |
| | Microbial Source Minimum Temperature | 0.07 | 0.04 | 1.57 | 0.142 | -0.15 | 0.80 | -0.19 | 0.852 |
| Pathogen/ Endophyte | Intercept | 1.96 | 1.02 | 1.92 | 0.078 | -2.55 | 21.22 | -0.12 | 0.906 |
| | Sequencing Depth | 0.00 | 0.00 | 1.16 | 0.270 | 0.00 | 0.00 | 1.48 | 0.166 |
| | Microbial Source Aridity Index | 0.81 | 0.92 | 0.88 | 0.397 | 36.98 | 19.23 | 1.92 | 0.079 |
| | Microbial Source Minimum Temperature | 0.05 | 0.04 | 1.24 | 0.239 | 1.28 | 0.88 | 1.45 | 0.172 |
| All Fungi | Intercept | 3.06 | 1.00 | 3.07 | 0.010 | 80.14 | 160.60 | 0.50 | 0.627 |
| | Sequencing Depth | 0.00 | 0.00 | 0.76 | 0.465 | 0.00 | 0.00 | 1.73 | 0.109 |
| | Microbial Source Aridity Index | 1.36 | 0.91 | 1.50 | 0.160 | 198.00 | 145.60 | 1.36 | 0.199 |
| | Microbial Source Minimum Temperature | 0.03 | 0.04 | 0.79 | 0.445 | 5.50 | 6.66 | 0.83 | 0.425 |

B. Southern Inocula Set

| Fungal Guild | Term | Diversity | | | | Richness | | | |
|---|---|---|---|---|---|---|---|---|---|
| | | Estimate | SE | Z | P | Estimate | SE | Z | P |
| Arbuscular Mycorrhizal | Intercept | 14.09 | 5.07 | 2.78 | 0.016 | 16.97 | 5.78 | 2.94 | 0.012 |
| | Sequencing Depth | 0.00 | 0.00 | -1.22 | 0.246 | 0.00 | 0.00 | -1.20 | 0.251 |
| | **Microbial Source Aridity Index** | **-3.99** | **1.00** | **-3.98** | **0.002** | **-17.45** | **7.09** | **-2.46** | **0.029** |
| | Microbial Source Maximum Temperature | -0.32 | 0.16 | -2.04 | 0.062 | -0.24 | 0.40 | -0.58 | 0.570 |
| Ecto-mycorrhizal | Intercept | 1.87 | 5.52 | 0.34 | 0.740 | 45.84 | 20.38 | 2.25 | 0.043 |
| | Sequencing Depth | 0.00 | 0.00 | 0.72 | 0.487 | 0.00 | 0.00 | 1.70 | 0.114 |
| | Microbial Source Aridity Index | -1.44 | 1.09 | -1.32 | 0.209 | -23.96 | 24.98 | -0.96 | 0.355 |
| | Microbial Source Maximum Temperature | 0.04 | 0.17 | 0.20 | 0.843 | 1.51 | 1.42 | 1.06 | 0.308 |
| Pathogen/ Endophyte | Intercept | 4.19 | 0.70 | 6.01 | 0.000 | 80.60 | 15.74 | 5.12 | 0.000 |
| | Sequencing Depth | 0.00 | 0.00 | -0.08 | 0.938 | 0.00 | 0.00 | -1.45 | 0.170 |
| | **Microbial Source Aridity Index** | **-2.33** | **0.85** | **-2.73** | **0.017** | **-68.16** | **19.30** | **-3.53** | **0.004** |
| | Microbial Source Maximum Temperature | 0.00 | 0.05 | 0.06 | 0.951 | -0.38 | 1.10 | -0.35 | 0.732 |
| All Fungi | Intercept | 6.22 | 0.88 | 7.10 | 0.000 | 635.20 | 99.15 | 6.41 | 0.000 |
| | Sequencing Depth | 0.00 | 0.00 | -0.83 | 0.422 | 0.00 | 0.00 | -0.50 | 0.624 |
| | **Microbial Source Aridity Index** | **-2.94** | **1.08** | **-2.74** | **0.017** | **-498.20** | **121.50** | **-4.10** | **0.001** |
| | Microbial Source Maximum Temperature | -0.03 | 0.06 | -0.57 | 0.577 | 0.67 | 6.92 | 0.10 | 0.924 |

DF = 12 (A) , 13 (B)

Table S13. Analysis of three fungal community aspects (Shannon-Weaver diversity, richness and relative abundance) on roots of surviving seedlings for select fungal guilds at A) the northern field site, and B) the southern field site.

A.

| Fungal Guild | Term | Diversity | | | | Richness | | | | Relative Abundance | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | | Estimate | SE | Z | P | Estimate | SE | Z | P | Estimate | SE | Z | P |
| a)Arbuscular Mycorrhizal | Intercept | 0.95 | 0.12 | 8.00 | <0.001 | 3.85 | 0.68 | 5.65 | <0.001 | 464.02 | 1.99E+06 | 0.00 | 0.998 |
| | Sequencing Depth | 0.22 | 0.05 | 4.08 | <0.001 | 1.24 | 0.23 | 5.42 | <0.001 | 471.34 | 62.60 | 7.53 | <0.001 |
| | Rainfall Treatment | 0.14 | 0.10 | 1.41 | 0.158 | *0.78* | *0.41* | *1.93* | *0.053* | 59.28 | 97.89 | 0.61 | 0.545 |
| | Microbial Source Aridity Index | -0.01 | 0.05 | -0.12 | 0.901 | -0.03 | 0.23 | -0.14 | 0.888 | 17.08 | 62.26 | 0.27 | 0.784 |
| | Microbial Source Minimum Temperature | 0.09 | 0.06 | 1.38 | 0.167 | *0.51* | *0.28* | *1.82* | *0.069* | 37.38 | 82.21 | 0.455 | 0.659 |
| b)Ecto-mycorrhizal | Intercept | 1.13 | 0.09 | 12.43 | <0.001 | 7.04 | 0.52 | 13.47 | <0.001 | 65877.00 | 1.52E+8 | 0.00 | 1.000 |
| | Sequencing Depth | 0.21 | 0.09 | 2.36 | 0.018 | 1.99 | 0.49 | 4.06 | <0.001 | 3428.40 | 531.94 | 6.45 | <0.001 |
| | Rainfall Treatment | -0.22 | 0.16 | -1.34 | 0.180 | -0.26 | 0.89 | -0.29 | 0.768 | 972.05 | 955.14 | 1.02 | 0.309 |
| | Microbial Source Aridity Index | -0.12 | 0.09 | -1.31 | 0.191 | -0.67 | 0.50 | -1.34 | 0.182 | 311.57 | 561.55 | 0.55 | 0.579 |
| | Microbial Source Minimum Temperature | **0.17** | **0.08** | **2.12** | **0.034** | **1.30** | **0.44** | **2.96** | **0.003** | 396.75 | 655.51 | 0.61 | 0.545 |
| c)Pathogen/ Endophyte | Intercept | 1.22 | 0.14 | 9.03 | <0.001 | 7.49 | 0.88 | 8.46 | <0.001 | 1071.33 | 1.56E+6 | 0.00 | 1.000 |
| | Sequencing Depth | 0.14 | 0.06 | 2.50 | 0.012 | 1.58 | 0.33 | 4.76 | 0.000 | 817.64 | 143.28 | 5.71 | 0.000 |
| | Seedling Mycorrhizal Type | 0.05 | 0.18 | 0.25 | 0.801 | -0.66 | 1.15 | -0.58 | 0.564 | -158.15 | 274.18 | -0.58 | 0.564 |
| | Rainfall Treatment | 0.07 | 0.10 | 0.67 | 0.503 | 0.42 | 0.59 | 0.72 | 0.470 | 355.47 | 250.06 | 1.42 | 0.155 |
| | Microbial Source Aridity Index | 0.04 | 0.05 | 0.74 | 0.461 | -0.19 | 0.33 | -0.57 | 0.569 | 65.82 | 164.77 | 0.40 | 0.690 |
| | Microbial Source Minimum Temperature | 0.08 | 0.06 | 1.43 | 0.154 | **0.91** | **0.35** | **2.60** | **0.009** | -160.78 | 258.31 | -0.62 | 0.534 |
| d)All Fungi | Intercept | 2.97 | 0.24 | 12.30 | <0.001 | 49.31 | 5.75 | 8.58 | <0.001 | | | | |
| | Sequencing Depth | 0.22 | 0.05 | 4.32 | <0.001 | 7.27 | 1.28 | 5.70 | <0.001 | | | | |
| | Seedling Mycorrhizal Type | *-0.50* | *0.29* | *-1.69* | *0.090* | -10.21 | 7.18 | -1.42 | 0.155 | | | | |
| | Rainfall Treatment | -0.05 | 0.09 | -0.54 | 0.589 | -0.05 | 2.19 | -0.02 | 0.981 | | | | |
| | Microbial Source Aridity Index | -0.01 | 0.05 | -0.23 | 0.817 | -0.19 | 1.21 | -0.15 | 0.877 | | | | |
| | Microbial Source Minimum Temperature | *0.11* | *0.06* | *1.89* | *0.059* | **3.16** | **1.43** | **2.21** | **0.027** | | | | |

DF a) 65, b) 41  ,c) 106  ,d) 106

B.

| Fungal Guild | Term | Diversity | | | | Richness | | | | Relative Abundance | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | | Estimate | SE | Z | P | Estimate | SE | Z | P | Estimate | SE | Z | P |
| a)Arbuscular Mycorrhizal | Intercept | 1.10 | 0.27 | 4.11 | <0.001 | 3.96 | 0.90 | 4.41 | <0.001 | 275.04 | 4.16E+04 | 0.01 | 0.995 |
| | Sequencing Depth | 0.22 | 0.05 | 4.59 | <0.001 | 0.67 | 0.15 | 4.47 | <0.001 | 188.95 | 22.17 | 8.52 | <0.001 |
| | Rainfall Treatment | 0.10 | 0.09 | 1.03 | 0.304 | 0.26 | 0.29 | 0.89 | 0.374 | **-98.65** | **42.39** | **-2.33** | **0.020** |
| | Microbial Source Aridity Index | **-0.15** | **0.07** | **-2.02** | **0.043** | *-0.42* | *0.24* | *-1.77* | *0.076* | 0.02 | 35.07 | 0.00 | 0.999 |
| | Microbial Source Maximum Temperature | -0.03 | 0.07 | -0.53 | 0.599 | -0.05 | 0.21 | -0.22 | 0.823 | -1.02 | 29.91 | -0.03 | 0.973 |
| b)Ecto-mycorrhizal | Intercept | 1.14 | 0.10 | 11.34 | <0.001 | 7.48 | 1.33 | 5.62 | <0.001 | -19248.58 | NA | NA | NA |
| | Sequencing Depth | -0.05 | 0.06 | -0.88 | 0.376 | -0.32 | 0.31 | -1.02 | 0.308 | 2106.42 | 251.79 | 8.37 | <0.001 |
| | Rainfall Treatment | -0.06 | 0.13 | -0.49 | 0.625 | -0.69 | 0.65 | -1.07 | 0.283 | -481.22 | 504.25 | -0.95 | 0.340 |
| | Microbial Source Aridity Index | -0.04 | 0.07 | -0.63 | 0.527 | -0.16 | 0.60 | -0.26 | 0.792 | -699.48 | 534.68 | -1.31 | 0.191 |
| | Microbial Source Maximum Temperature | 0.10 | 0.07 | 1.33 | 0.185 | *0.76* | *0.40* | *1.89* | *0.059* | 19.08 | 308.00 | 0.06 | 0.951 |
| c)Pathogen/ Endophyte | Intercept | 1.78 | 0.06 | 29.70 | <0.001 | 11.24 | 0.68 | 16.56 | <0.001 | 994.83 | 2.54E+06 | 0.00 | 1.000 |
| | Sequencing Depth | 0.26 | 0.04 | 6.50 | <0.001 | 2.65 | 0.30 | 8.94 | <0.001 | 1118.19 | 116.47 | 9.60 | <0.001 |
| | Seedling Mycorrhizal Type | **-0.48** | **0.09** | **-5.55** | **<0.001** | **-4.28** | **0.83** | **-5.15** | **<0.001** | -537.23 | 463.71 | -1.16 | 0.247 |
| | Rainfall Treatment | -0.03 | 0.08 | -0.42 | 0.675 | -0.20 | 0.58 | -0.34 | 0.735 | 182.84 | 225.22 | 0.81 | 0.417 |
| | Microbial Source Aridity Index | **-0.08** | **0.04** | **-2.04** | **0.041** | -0.37 | 0.33 | -1.11 | 0.266 | 273.83 | 245.68 | 1.11 | 0.265 |
| | Microbial Source Maximum Temperature | -0.03 | 0.04 | -0.64 | 0.519 | -0.17 | 0.37 | -0.46 | 0.646 | -90.39 | 241.72 | -0.37 | 0.709 |
| d)All Fungi | Intercept | 2.85 | 0.07 | 38.82 | <0.001 | 50.61 | 2.18 | 23.24 | <0.001 | | | | |
| | Sequencing Depth | 0.15 | 0.04 | 3.60 | <0.001 | 7.69 | 1.02 | 7.53 | <0.001 | | | | |
| | Seedling Mycorrhizal Type | **-0.75** | **0.10** | **-7.74** | **<0.001** | **-20.67** | **2.71** | **-7.62** | **<0.001** | | | | |
| | Rainfall Treatment | 0.03 | 0.08 | 0.39 | 0.699 | -0.11 | 2.01 | -0.05 | 0.957 | | | | |
| | Microbial Source Aridity Index | -0.03 | 0.04 | -0.81 | 0.419 | 0.74 | 1.13 | 0.65 | 0.513 | | | | |
| | Microbial Source Maximum Temperature | 0.01 | 0.05 | 0.23 | 0.820 | -0.64 | 1.26 | -0.51 | 0.613 | | | | |

*Bold text, P<0.05. Italicized text, P < 0.10 (excluding the model intercept and sequencing depth terms, included for technical reasons). Results for fixed effects shown. Models also included crossed random effects seedling cohort, plot, and phylogenetic covariance among seedling species. For analysis of arbuscular mycorrhizal fungal communities, only AM associated seedling species were used. For analysis of ectomycorrhizal fungal communities, only EM associated seedling species were used. DF Northern Site: a) 65, b) 41, c) 106, d) 106 DF Southern Site: a) 140, b) 60, c) 200, d) 200

Table S14. Statistical results of generalized linear mixed models comparing survival probability for seedlings in a given microbial inocula against the average value for three aspects of community structure (Shannon-Weaver diversity, richness, and relative abundance) of various fungal guilds (and the full fungal community) in roots of surviving seedlings given that microbial inocula, at A) the northern field site and B) the southern field site.

A.

| | | | Fungal Community Aspect | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| Northern Site - Kemp Natural Resource Station | | | Diversity | | | | Richness | | | | Relative abundance | | | |
| Fungal Guild | Seedling Type | Term | Estimate | SE | z | P | Estimate | SE | z | P | Estimate | SE | z | P |
| Arbuscular Mycorrhizal | Arbuscular Mycorrhizal | (Intercept) | -1.47 | 1.06 | -1.38 | 0.167 | -1.33 | 0.87 | -1.53 | 0.126 | -1.64 | 0.76 | -2.18 | 0.030 |
| | | Rainfall Treatment | -0.85 | 1.60 | -0.53 | 0.597 | -0.76 | 1.35 | -0.56 | 0.575 | -0.28 | 1.05 | -0.26 | 0.792 |
| | | Average AMF aspect | 0.09 | 1.17 | 0.08 | 0.937 | -0.02 | 0.22 | -0.07 | 0.942 | 3.92 | 11.10 | 0.35 | 0.724 |
| | | Rainfall Trt*AMF | 0.87 | 1.65 | 0.53 | 0.599 | 0.18 | 0.31 | 0.57 | 0.572 | 5.69 | 16.12 | 0.35 | 0.724 |
| | Ambient Rainfall | (Intercept) | -1.47 | 1.06 | -1.38 | 0.167 | -1.33 | 0.87 | -1.53 | 0.126 | -1.64 | 0.76 | -2.18 | 0.030 |
| | | Average AMF aspect | 0.09 | 1.17 | 0.08 | 0.937 | -0.02 | 0.22 | -0.07 | 0.942 | 3.92 | 11.10 | 0.35 | 0.724 |
| | Reduced Rainfall | (Intercept) | -2.32 | 1.20 | -1.94 | 0.053 | -2.08 | 1.04 | -2.01 | 0.044 | -1.92 | 0.73 | -2.62 | 0.009 |
| | | Average AMF aspect | 0.96 | 1.16 | 0.83 | 0.408 | 0.16 | 0.22 | 0.73 | 0.465 | 9.61 | 11.69 | 0.82 | 0.411 |
| Ecto-mycorrhizal | Ectomycorrhizal | (Intercept) | -1.30 | 0.62 | -2.11 | 0.035 | -1.04 | 0.59 | -1.76 | 0.078 | -2.62 | 1.01 | -2.60 | 0.009 |
| | | Rainfall Treatment | -1.27 | 0.90 | -1.42 | 0.156 | -1.43 | 0.89 | -1.61 | 0.108 | 1.17 | 1.50 | 0.78 | 0.438 |
| | | Average EMF aspect | -0.04 | 0.55 | -0.07 | 0.943 | -0.05 | 0.08 | -0.55 | 0.584 | 3.15 | 2.36 | 1.33 | 0.183 |
| | | Rainfall Trt*EMF aspect | 0.99 | 0.91 | 1.09 | 0.275 | 0.14 | 0.12 | 1.17 | 0.243 | -4.00 | 3.37 | -1.19 | 0.236 |
| | Ambient Rainfall | (Intercept) | -1.30 | 0.62 | -2.11 | 0.035 | -1.04 | 0.59 | -1.76 | 0.078 | -2.62 | 1.01 | -2.60 | 0.009 |
| | | Average EMF aspect | -0.04 | 0.55 | -0.07 | 0.943 | -0.05 | 0.08 | -0.55 | 0.584 | 3.15 | 2.36 | 1.33 | 0.183 |
| | Reduced Rainfall | (Intercept) | -2.58 | 0.65 | -3.97 | 0.000 | -2.47 | 0.67 | -3.71 | 0.000 | -1.46 | 1.12 | -1.31 | 0.192 |
| | | Average EMF aspect | 0.95 | 0.72 | 1.32 | 0.186 | 0.10 | 0.09 | 1.08 | 0.280 | -0.85 | 2.40 | -0.35 | 0.723 |
| Pathogen/ Endophyte | All | (Intercept) | -0.21 | 0.84 | -0.25 | 0.801 | 0.82 | 0.72 | 1.15 | 0.251 | -1.12 | 0.34 | -3.28 | 0.001 |
| | | Rainfall Treatment | -0.84 | 1.29 | -0.65 | 0.515 | **-2.23** | **1.10** | **-2.03** | **0.043** | -0.03 | 0.59 | -0.06 | 0.954 |

| | | | Est | SE | t | p | Est | SE | t | p | Est | SE | t | p |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | | Average PEF aspect | -0.95 | 0.66 | -1.43 | 0.153 | **-0.30** | **0.10** | **-3.08** | **0.002** | -2.27 | 2.50 | -0.91 | 0.363 |
| | | Rainfall Trt*PEF aspect | 0.55 | 0.97 | 0.57 | 0.571 | **0.27** | **0.14** | **1.97** | **0.049** | -0.48 | 3.84 | -0.13 | 0.900 |
| | Ambient Rainfall | (Intercept) | -0.21 | 0.84 | -0.25 | 0.801 | 0.82 | 0.72 | 1.15 | 0.251 | -1.12 | 0.34 | -3.28 | 0.001 |
| | | Average PEF aspect | -0.95 | 0.66 | -1.43 | 0.153 | **-0.30** | **0.10** | **-3.08** | **0.002** | -2.27 | 2.50 | -0.91 | 0.363 |
| | Reduced Rainfall | (Intercept) | -1.05 | 0.98 | -1.08 | 0.282 | -1.40 | 0.83 | -1.69 | 0.092 | -1.15 | 0.49 | -2.38 | 0.017 |
| | | Average PEF aspect | -0.40 | 0.71 | -0.56 | 0.574 | -0.02 | 0.10 | -0.24 | 0.812 | -2.76 | 2.91 | -0.95 | 0.344 |
| All | All | (Intercept) | 4.45 | 2.03 | 2.19 | 0.029 | 3.57 | 1.30 | 2.75 | 0.006 | | | | |
| | | Rainfall Treatment | -4.40 | 2.91 | -1.51 | 0.131 | -3.79 | 1.88 | -2.01 | 0.044 | | | | |
| | | Average Fungal aspect | **-2.13** | **0.75** | **-2.86** | **0.004** | **-0.11** | **0.03** | **-3.78** | **0.000** | | | | |
| | | Rainfall Trt*Fungal aspect | 1.53 | 1.07 | 1.44 | 0.151 | *0.08* | *0.04* | *1.92* | *0.054* | | | | |
| | Ambient Rainfall | (Intercept) | **4.45** | **2.03** | **2.19** | **0.029** | **3.57** | **1.30** | **2.75** | **0.006** | | | | |
| | | Average Fungal aspect | **-2.13** | **0.75** | **-2.86** | **0.004** | **-0.11** | **0.03** | **-3.78** | **0.000** | | | | |
| | Reduced Rainfall | (Intercept) | 0.05 | 2.09 | 0.02 | 0.981 | -0.22 | 1.36 | -0.16 | 0.870 | | | | |
| | | Average Fungal aspect | -0.60 | 0.76 | -0.79 | 0.430 | -0.03 | 0.03 | -1.01 | 0.314 | | | | |

B.

| Southern Site - Allerton Park and Recreation Center | | | Fungal Community Aspect | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | | | Diversity | | | | Richness | | | | Relative abundance | | | |
| Fungal Guild | Seedling Type | Term | Estimate | SE | z | P | Estimate | SE | z | P | Estimate | SE | z | P |
| Arbuscular Mycorrhizal | Arbuscular Mycorrhizal | (Intercept) | -0.26 | 0.82 | -0.32 | 0.753 | -0.12 | 0.94 | -0.13 | 0.895 | -0.01 | 0.60 | -0.01 | 0.991 |
| | | Rainfall Treatment | -1.73 | 1.22 | -1.41 | 0.157 | -1.52 | 1.36 | -1.11 | 0.266 | -0.85 | 0.77 | -1.11 | 0.267 |
| | | Average AMF aspect | 0.50 | 0.73 | 0.68 | 0.494 | 0.10 | 0.23 | 0.45 | 0.653 | 9.00 | 17.31 | 0.52 | 0.603 |
| | | Rainfall Trt*AMF | 1.28 | 1.03 | 1.24 | 0.214 | 0.31 | 0.32 | 0.98 | 0.327 | 29.41 | 24.30 | 1.21 | 0.226 |
| | Ambient Rainfall | (Intercept) | -0.26 | 0.82 | -0.32 | 0.753 | -0.12 | 0.94 | -0.13 | 0.895 | -0.01 | 0.60 | -0.01 | 0.991 |
| | | Average AMF aspect | 0.50 | 0.73 | 0.68 | 0.494 | 0.10 | 0.23 | 0.45 | 0.653 | 9.00 | 17.31 | 0.52 | 0.603 |
| | Reduced Rainfall | (Intercept) | -1.99 | 0.90 | -2.19 | 0.028 | -1.64 | 0.99 | -1.66 | 0.096 | -0.86 | 0.49 | -1.77 | 0.077 |
| | | Average AMF aspect | **1.78** | **0.73** | **2.43** | **0.015** | *0.42* | *0.22* | *1.86* | *0.062* | **38.41** | **17.06** | **2.25** | **0.024** |
| Ecto-mycorrhizal | Ectomycorrhizal | (Intercept) | -0.11 | 0.84 | -0.14 | 0.892 | -2.21 | 1.03 | -2.15 | 0.032 | -2.89 | 0.99 | -2.93 | 0.003 |
| | | Rainfall Treatment | -1.81 | 1.34 | -1.35 | 0.176 | 0.63 | 1.21 | 0.52 | 0.603 | 1.63 | 1.26 | 1.30 | 0.193 |
| | | Average EMF aspect | -0.21 | 0.62 | -0.35 | 0.728 | *0.27* | *0.15* | *1.80* | *0.073* | **4.70** | **1.81** | **2.60** | **0.009** |
| | | Rainfall Trt*EMF aspect | 1.15 | 1.00 | 1.15 | 0.250 | -0.14 | 0.18 | -0.77 | 0.440 | -3.48 | 2.48 | -1.40 | 0.160 |
| | Ambient Rainfall | (Intercept) | -0.11 | 0.84 | -0.14 | 0.892 | -2.21 | 1.03 | -2.15 | 0.032 | -2.89 | 0.99 | -2.93 | 0.003 |
| | | Average EMF aspect | -0.21 | 0.62 | -0.35 | 0.728 | *0.27* | *0.15* | *1.80* | *0.073* | **4.70** | **1.81** | **2.60** | **0.009** |
| | Reduced Rainfall | (Intercept) | -1.93 | 1.05 | -1.84 | 0.066 | -1.58 | 0.63 | -2.52 | 0.012 | -1.26 | 0.78 | -1.62 | 0.105 |
| | | Average EMF aspect | 0.94 | 0.79 | 1.19 | 0.236 | 0.13 | 0.09 | 1.46 | 0.144 | 1.23 | 1.69 | 0.73 | 0.468 |
| Pathogen/ Endophyte | All | (Intercept) | 0.97 | 1.23 | 0.79 | 0.427 | 1.08 | 1.10 | 0.98 | 0.326 | 0.90 | 0.40 | 2.23 | 0.026 |
| | | Rainfall Treatment | -2.41 | 1.67 | -1.45 | 0.148 | -1.14 | 1.49 | -0.77 | 0.444 | 0.16 | 0.59 | 0.28 | 0.783 |
| | | Average PEF aspect | -0.68 | 0.81 | -0.84 | 0.402 | -0.12 | 0.12 | -1.03 | 0.301 | **-7.54** | **3.11** | **-2.42** | **0.015** |
| | | Rainfall Trt*PEF aspect | 1.46 | 1.10 | 1.33 | 0.185 | 0.10 | 0.16 | 0.63 | 0.531 | -2.98 | 4.59 | -0.65 | 0.517 |
| | Ambient Rainfall | (Intercept) | 0.97 | 1.23 | 0.79 | 0.427 | 1.08 | 1.10 | 0.98 | 0.326 | 0.90 | 0.40 | 2.23 | 0.026 |
| | | Average PEF aspect | -0.68 | 0.81 | -0.84 | 0.402 | -0.12 | 0.12 | -1.03 | 0.301 | **-7.54** | **3.11** | **-2.42** | **0.015** |
| | Reduced Rainfall | (Intercept) | -1.44 | 1.13 | -1.28 | 0.202 | -0.06 | 1.01 | -0.06 | 0.950 | 1.06 | 0.43 | 2.47 | 0.013 |

| | | | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | | Average PEF aspect | 0.78 | 0.75 | 1.05 | 0.295 | -0.02 | 0.11 | -0.20 | 0.838 | **-10.51** | **3.38** | **-3.11** | **0.002** |
| All | All | (Intercept) | 1.07 | 1.17 | 0.91 | 0.361 | 1.51 | 0.90 | 1.68 | 0.093 | | | | |
| | | Rainfall Treatment | -0.32 | 1.56 | -0.21 | 0.838 | -0.35 | 1.21 | -0.29 | 0.770 | | | | |
| | | Average Fungal aspect | -0.45 | 0.46 | -0.96 | 0.336 | *-0.04* | *0.02* | *-1.74* | *0.082* | | | | |
| | | Rainfall Trt*Fungal aspect | 0.04 | 0.62 | 0.07 | 0.947 | 0.00 | 0.03 | 0.12 | 0.903 | | | | |
| | Ambient Rainfall | (Intercept) | 1.07 | 1.17 | 0.91 | 0.361 | 1.51 | 0.90 | 1.68 | 0.093 | | | | |
| | | Average Fungal aspect | -0.45 | 0.46 | -0.96 | 0.336 | *-0.04* | *0.02* | *-1.74* | *0.082* | | | | |
| | Reduced Rainfall | (Intercept) | 0.75 | 1.04 | 0.72 | 0.474 | 1.16 | 0.80 | 1.44 | 0.149 | | | | |
| | | Average Fungal aspect | -0.40 | 0.41 | -0.98 | 0.328 | *-0.03* | *0.02* | *-1.78* | *0.075* | | | | |

*Bold text, P<0.05. Italicized text, P < 0.10. Results for fixed effects shown. Models also included random effects of plot (nested within cohort year) and phylogenetic covariance among seedling species. For analysis of arbuscular mycorrhizal fungal communities, only AM associated seedling species were used. For analysis of ectomycorrhizal fungal communities, only EM associated seedling species were used. DF = 23 for models of full experiment, 11 for models within rainfall treatments

Table S15. Mediation analysis for AM associating seedlings in the Warm-Dry treatment in the greenhouse experiment using background soil from the southern field site (Allerton Park and Retreat Center, Illinois, USA)

| Model | | Estimate | SE | Z | P |
|---|---|---|---|---|---|
| AMF diversity ~ Microbial Source Climate | (Intercept) | 14.09 | 5.07 | 2.78 | 0.016 |
| | Sequencing Depth | 0.00 | 0.00 | -1.22 | 0.246 |
| | *Microbial Source Maximum Temperature* | *-0.32* | *0.16* | *-2.04* | *0.062* |
| | **Microbial Source Aridity Index** | **-3.99** | **1.00** | **-3.98** | **0.002** |
| Seedling Biomass ~ Microbial Source Climate | (Intercept) | -0.55 | 5.66 | -0.10 | 0.923 |
| | Microbial Source Maximum Temperature | 0.04 | 0.16 | 0.23 | 0.821 |
| | **Microbial Source Aridity Index** | **-2.93** | **1.25** | **-2.34** | **0.019** |
| Seedling Biomass ~ AMF diversity | (Intercept) | -2.20 | 1.81 | -1.22 | 0.224 |
| | **Microbial Source AMF diversity** | **0.69** | **0.21** | **3.30** | **0.001** |
| Seedling Biomass ~ Microbial Source Climate + AMF diversity | (Intercept) | -2.11 | 5.62 | -0.38 | 0.708 |
| | Microbial Source Maximum Temperature | 0.03 | 0.16 | 0.16 | 0.872 |
| | Microbial Source Aridity Index | -1.00 | 1.67 | -0.60 | 0.550 |
| | *Microbial Source AMF diversity* | *0.53* | *0.31* | *1.73* | *0.083* |

Mediation analysis performed through a series of four models. Model 1: regression of AM fungal diversity in each microbial inocula source against the source climate variables. Model 2: regression of seedling biomass against the climate conditions of the microbial inocula source site. Model 3: regression of seedling biomass against the AM fungal diversity in the microbial inocula source, and Model 4: multiple regression of seedling biomass against both the climate conditions and the AM fungal diversity of the microbial inocula source. Mediation is demonstrated if 1) the independent variable (microbial source Aridity Index) is significant predictor of the dependent variable (Seedling Biomass, Model 2), 2) the independent variable is a significant predictor of the mediator (AM fungal diversity, Model 1), 3) when the dependent variable is regressed against both the mediator and the independent variable, the strength of the coefficient for the independent variable is greatly reduced (Model 4) (Baron and Kenny 1986).
Baron, R. M.; Kenny, D. A."The Moderator-Mediator Variable Distinction in Social Psychological Research: Conceptual, Strategic, and Statistical Considerations". Journal of Personality and Social Psychology. **51** (6): 1173–1182. (1986)

Table S16. Soil moisture values (% v/v) for monitored experimental plots, averaged from the dates of shelter installation (July) through shelter removal (September) for two (northern site) or three (southern site) experimental years.

| Site | Year | Plot | Ambient Soil Moisture (%) | Reduced Rainfall Soil Moisture (%) | % Difference |
|---|---|---|---|---|---|
| Kemp NRS | 2019 | A | 0.19 | 0.11 | -0.43 |
| | 2019 | B | 0.16 | 0.12 | -0.25 |
| | 2019 | C | 0.19 | 0.16 | -0.14 |
| | 2020 | A | 0.17 | 0.14 | -0.20 |
| | 2020 | B | 0.23 | 0.11 | -0.52 |
| | 2020 | C | 0.18 | 0.15 | -0.13 |
| | | | | | |
| Allerton PRC | 2019 | A | 0.21 | 0.17 | -0.22 |
| | 2019 | B | 0.25 | 0.21 | -0.15 |
| | 2019 | C | 0.28 | 0.27 | -0.04 |
| | 2020 | A | 0.22 | 0.15 | -0.31 |
| | 2020 | B | 0.18 | 0.17 | -0.07 |
| | 2020 | C | 0.16 | 0.07 | -0.59 |
| | 2021 | A | 0.24 | 0.15 | -0.36 |
| | 2021 | B | 0.33 | 0.31 | -0.05 |
| | 2021 | C | 0.21 | 0.17 | -0.20 |

**References and Notes**

1. C. Román-Palacios, J. J. Wiens, Recent responses to climate change reveal the drivers of species extinction and survival. *Proc. Natl. Acad. Sci. U.S.A.* **117**, 4211–4217 (2020). [doi:10.1073/pnas.1913007117](doi:10.1073/pnas.1913007117) [Medline](Medline)

2. M. C. Urban, Climate change. Accelerating extinction risk from climate change. *Science* **348**, 571–573 (2015). [doi:10.1126/science.aaa4984](doi:10.1126/science.aaa4984) [Medline](Medline)

3. C. D. Thomas, A. Cameron, R. E. Green, M. Bakkenes, L. J. Beaumont, Y. C. Collingham, B. F. N. Erasmus, M. F. De Siqueira, A. Grainger, L. Hannah, L. Hughes, B. Huntley, A. S. Van Jaarsveld, G. F. Midgley, L. Miles, M. A. Ortega-Huerta, A. T. Peterson, O. L. Phillips, S. E. Williams, Extinction risk from climate change. *Nature* **427**, 145–148 (2004). [doi:10.1038/nature02121](doi:10.1038/nature02121) [Medline](Medline)

4. T. Jezkova, J. J. Wiens, Rates of change in climatic niches in plant and animal populations are much slower than projected climate change. *Proc. Biol. Sci.* **283**, 20162104 (2016). [doi:10.1098/rspb.2016.2104](doi:10.1098/rspb.2016.2104) [Medline](Medline)

5. R. Berkelmans, M. J. H. van Oppen, The role of zooxanthellae in the thermal tolerance of corals: A 'nugget of hope' for coral reefs in an era of climate change. *Proc. Biol. Sci.* **273**, 2305–2312 (2006). [doi:10.1098/rspb.2006.3567](doi:10.1098/rspb.2006.3567) [Medline](Medline)

6. R. J. Rodriguez, J. Henson, E. Van Volkenburgh, M. Hoy, L. Wright, F. Beckwith, Y.-O. Kim, R. S. Redman, Stress tolerance in plants via habitat-adapted symbiosis. *ISME J.* **2**, 404–416 (2008). [doi:10.1038/ismej.2007.106](doi:10.1038/ismej.2007.106) [Medline](Medline)

7. A. A. H. A. Latef *et al*., Arbuscular mycorrhizal symbiosis and abiotic stress in plants: A review. *J. Plant Biol.* **59**, 407–426 (2016). [doi:10.1007/s12374-016-0237-7](doi:10.1007/s12374-016-0237-7)

8. S. S. Porter, R. Bantay, C. A. Friel, A. Garoutte, K. Gdanetz, K. Ibarreta, B. M. Moore, P. Shetty, E. Siler, M. L. Friesen, Beneficial microbes ameliorate abiotic and biotic sources of stress on plants. *Funct. Ecol.* **34**, 2075–2086 (2020). [doi:10.1111/1365-2435.13499](doi:10.1111/1365-2435.13499)

9. P. M. Delaux, S. Schornack, Plant evolution driven by interactions with symbiotic and pathogenic microbes. *Science* **371**, 796–807 (2021). [doi:10.1126/science.aba6605](doi:10.1126/science.aba6605) [Medline](Medline)

10. H. Lambers, C. Mougel, B. Jaillard, P. Hinsinger, Plant-microbe-soil interactions in the rhizosphere: An evolutionary perspective. *Plant Soil* **321**, 83–115 (2009). [doi:10.1007/s11104-009-0042-x](doi:10.1007/s11104-009-0042-x)

11. I. S. Acuña-Rodríguez, K. K. Newsham, P. E. Gundel, C. Torres-Díaz, M. A. Molina-Montenegro, Functional roles of microbial symbionts in plant cold tolerance. *Ecol. Lett.* **23**, 1034–1048 (2020). [doi:10.1111/ele.13502](doi:10.1111/ele.13502) [Medline](Medline)

12. L. M. Márquez, R. S. Redman, R. J. Rodriguez, M. J. Roossinck, A virus in a fungus in a plant: Three-way symbiosis required for thermal tolerance. *Science* **315**, 513–515 (2007). [doi:10.1126/science.1136237](doi:10.1126/science.1136237) [Medline](Medline)

13. T. Lehto, J. J. Zwiazek, Ectomycorrhizas and water relations of trees: A review. *Mycorrhiza* **21**, 71–90 (2011). [doi:10.1007/s00572-010-0348-9](doi:10.1007/s00572-010-0348-9) [Medline](Medline)

14. R. Lata, S. Chowdhury, S. K. Gond, J. F. White Jr., Induction of abiotic stress tolerance in plants by endophytic microbes. *Lett. Appl. Microbiol.* **66**, 268–276 (2018). [doi:10.1111/lam.12855](doi:10.1111/lam.12855) [Medline](Medline)

15. D. Naylor, D. Coleman-Derr, Drought Stress and Root-Associated Bacterial Communities. *Front. Plant Sci.* **8**, 2223 (2018). [doi:10.3389/fpls.2017.02223](doi:10.3389/fpls.2017.02223) [Medline](Medline)

16. M. E. Afkhami, P. J. McIntyre, S. Y. Strauss, Mutualist-mediated effects on species' range limits across large geographic scales. *Ecol. Lett.* **17**, 1265–1273 (2014). [doi:10.1111/ele.12332](doi:10.1111/ele.12332) [Medline](Medline)

17. P. D. Stahl, W. K. Smith, Effects of different geographic isolates of Glomus on the water relations of *Agropyron smithii*. *Mycologia* **76**, 261–267 (1984). [doi:10.1080/00275514.1984.12023835](doi:10.1080/00275514.1984.12023835)

18. I. M. Ware, M. E. Van Nuland, Z. K. Yang, C. W. Schadt, J. A. Schweitzer, J. K. Bailey, Climate-driven divergence in plant-microbiome interactions generates range-wide variation in bud break phenology. *Commun. Biol.* **4**, 748 (2021). doi:10.1038/s42003-021-02244-5 Medline

19. C. Allsup, R. Lankau, Migration of soil microbes may promote tree seedling tolerance to drying conditions. *Ecology* **100**, e02729 (2019). doi:10.1002/ecy.2729 Medline

20. J. A. Lau, J. T. Lennon, Rapid responses of soil microorganisms improve plant fitness in novel environments. *Proc. Natl. Acad. Sci. U.S.A.* **109**, 14058–14062 (2012). doi:10.1073/pnas.1202319109 Medline

21. S. E. Smith, D. J. Read, *Mycorrhizal Symbiosis* (Academic Press, 2008).

22. M. A. Bingham, S. Simard, Ectomycorrhizal Networks of Pseudotsuga menziesii var. glauca Trees Facilitate Establishment of Conspecific Seedlings Under Drought. *Ecosystems* **15**, 188–199 (2012). doi:10.1007/s10021-011-9502-2

23. C. P. terHorst, P. C. Zee, Eco-evolutionary dynamics in plant–soil feedbacks. *Funct. Ecol.* **30**, 1062–1072 (2016). doi:10.1111/1365-2435.12671

24. S. A. Smith, M. J. Donoghue, Rates of molecular evolution are linked to life history in flowering plants. *Science* **322**, 86–89 (2008). doi:10.1126/science.1163197 Medline

25. R. R. Junker, X. He, J. C. Otto, V. Ruiz-Hernández, M. Hanusch, Divergent assembly processes? A comparison of the plant and soil microbiome with plant communities in a glacier forefield. *FEMS Microbiol. Ecol.* **97**, fiab135 (2021). doi:10.1093/femsec/fiab135 Medline

26. M. J. Choudoir, A. Barberán, H. L. Menninger, R. R. Dunn, N. Fierer, Variation in range size and dispersal capabilities of microbial taxa. *Ecology* **99**, 322–334 (2018). doi:10.1002/ecy.2094 Medline

27. P. B. Reich, R. Bermudez, R. A. Montgomery, R. L. Rich, K. E. Rice, S. E. Hobbie, A. Stefanski, Even modest climate change may lead to major transitions in boreal forests. *Nature* **608**, 540–545 (2022). doi:10.1038/s41586-022-05076-3 Medline

28. L. R. Iverson, A. M. Prasad, S. N. Matthews, M. P. Peters, Lessons Learned While Integrating Habitat, Dispersal, Disturbance, and Life-History Traits into Species Habitat Models Under Climate Change. *Ecosystems* **14**, 1005–1020 (2011). doi:10.1007/s10021-011-9456-4

29. R. J. Dial, C. T. Maher, R. E. Hewitt, P. F. Sullivan, Sufficient conditions for rapid range expansion of a boreal conifer. *Nature* **608**, 546–551 (2022). doi:10.1038/s41586-022-05093-2 Medline

30. C. C. F. Boonman, M. A. J. Huijbregts, A. Benítez-López, A. M. Schipper, W. Thuiller, L. Santini, Trait-based projections of climate change effects on global biome distributions. *Divers. Distrib.* **28**, 25–37 (2022). doi:10.1111/ddi.13431

31. G. Forzieri, V. Dakos, N. G. McDowell, A. Ramdane, A. Cescatti, Emerging signals of declining forest resilience under climate change. *Nature* **608**, 534–539 (2022). doi:10.1038/s41586-022-04959-9 Medline

32. G. B. Bonan, Forests and climate change: Forcings, feedbacks, and the climate benefits of forests. *Science* **320**, 1444–1449 (2008). doi:10.1126/science.1155121 Medline

33. Materials and methods are available as supplementary materials.

34. N. C. Johnson, G. W. T. Wilson, M. A. Bowker, J. A. Wilson, R. M. Miller, Resource limitation is a driver of local adaptation in mycorrhizal symbioses. *Proc. Natl. Acad. Sci. U.S.A.* **107**, 2093–2098 (2010). doi:10.1073/pnas.0906710107 Medline

35. P. G. Kennedy, K. G. Peay, T. D. Bruns, Root tip competition among ectomycorrhizal fungi: Are priority effects a rule or an exception? *Ecology* **90**, 2098–2107 (2009). doi:10.1890/08-1291.1 Medline

36. G. D. A. Werner, E. T. Kiers, Order of arrival structures arbuscular mycorrhizal colonization of plants. *New Phytol.* **205**, 1515–1524 (2015). [doi:10.1111/nph.13092](doi:10.1111/nph.13092) [Medline](Medline)

37. K. M. DeAngelis, G. Pold, B. D. Topçuoğlu, L. T. van Diepen, R. M. Varney, J. L. Blanchard, J. Melillo, S. D. Frey, Long-term forest soil warming alters microbial communities in temperate forest soils. *Front. Microbiol.* **6**, 104 (2015). [doi:10.3389/fmicb.2015.00104](doi:10.3389/fmicb.2015.00104) [Medline](Medline)

38. M. E. Van Nuland, D. P. Smith, J. M. Bhatnagar, A. Stefanski, S. E. Hobbie, P. B. Reich, K. G. Peay, Warming and disturbance alter soil microbiome diversity and function in a northern forest ecotone. *FEMS Microbiol. Ecol.* **96**, fiaa108 (2020). [doi:10.1093/femsec/fiaa108](doi:10.1093/femsec/fiaa108) [Medline](Medline)

39. A. Canarini, H. Schmidt, L. Fuchslueger, V. Martin, C. W. Herbold, D. Zezula, P. Gündler, R. Hasibeder, M. Jecmenica, M. Bahn, A. Richter, Ecological memory of recurrent drought modifies soil processes via changes in soil microbial community. *Nat. Commun.* **12**, 5308 (2021). [doi:10.1038/s41467-021-25675-4](doi:10.1038/s41467-021-25675-4) [Medline](Medline)

40. S. D. Frey, R. Drijber, H. Smith, J. Melillo, Microbial biomass, functional capacity, and community structure after 12 years of soil warming. *Soil Biol. Biochem.* **40**, 2904–2907 (2008). [doi:10.1016/j.soilbio.2008.07.020](doi:10.1016/j.soilbio.2008.07.020)

41. J. Fargione, D. L. Haase, O. T. Burney, O. A. Kildisheva, G. Edge, S. C. Cook-Patton, T. Chapman, A. Rempel, M. D. Hurteau, K. T. Davis, S. Dobrowski, S. Enebak, R. De La Torre, A. A. R. Bhuta, F. Cubbage, B. Kittler, D. Zhang, R. W. Guldin, Challenges to the Reforestation Pipeline in the United States. *Front. For. Glob. Change* **4**, 629198 (2021). [doi:10.3389/ffgc.2021.629198](doi:10.3389/ffgc.2021.629198)

42. D. Marčiulynienė, A. Marčiulynas, J. Lynikienė, M. Vaičiukynė, A. Gedminas, A. Menkis, DNA-Metabarcoding of Belowground Fungal Communities in Bare-Root Forest Nurseries: Focus on Different Tree Species. *Microorganisms* **9**, 150 (2021). [doi:10.3390/microorganisms9010150](doi:10.3390/microorganisms9010150) [Medline](Medline)

43. R. A. Lankau, Data from: Enhanced climate tolerance for trees derived from microbial communities, Dryad (2023); [https://doi.org/10.5061/dryad.k98sf7mb6](https://doi.org/10.5061/dryad.k98sf7mb6)

44. S. Begueria, S. M. Vicente-Serrano, SPEI: Calculation of the standardized precipitation-evapotranspiration index, R package version 1.7 (2017). https://cran.r-project.org/web/packages/SPEI/SPEI.pdf/

45. PRISM Climate Group, PRISM Climate Data, Oregon State University, (data created Jan. 2015 to Dec. 2021), accessed 16 June 2022; https://prism.oregonstate.edu/

46. A. R. Ives, R. Dinnage, L. A. Nell, M. Helmus, D. Li, Package 'phyr': model based phylogenetic analysis, R package version 1.1.0 (2020); [https://CRAN.R-project.org/package=phyr](https://CRAN.R-project.org/package=phyr)

47. Y. Jin, H. Qian, V.PhyloMaker: An R package that can generate very large phylogenies for vascular plants. *Ecography* **42**, 1353–1359 (2019). [doi:10.1111/ecog.04434](doi:10.1111/ecog.04434)

48. S. A. Smith, J. W. Brown, Constructing a broadly inclusive seed plant phylogeny. *Am. J. Bot.* **105**, 302–314 (2018). [doi:10.1002/ajb2.1019](doi:10.1002/ajb2.1019) [Medline](Medline)

49. 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](doi:10.1038/nature12872) [Medline](Medline)

50. B. Wang, Y. L. Qiu, Phylogenetic distribution and evolution of mycorrhizas in land plants. *Mycorrhiza* **16**, 299–363 (2006). [doi:10.1007/s00572-005-0033-6](doi:10.1007/s00572-005-0033-6) [Medline](Medline)

51. T. M. Therneau, coxme: Mixed Effects Cox Models, R package version 2.2-18.1 (2022); [https://CRAN.R-project.org/package=coxme](https://CRAN.R-project.org/package=coxme)

52. D. R. Cox, Regression Models and Life-Tables. *J R Stat Soc Series B Stat Methodol* **34**, 187–202 (1972).

53. R. A. Lankau, D. P. Keymer, Ectomycorrhizal fungal richness declines towards the host species' range edge. *Mol. Ecol.* **25**, 3224–3241 (2016). [doi:10.1111/mec.13628](doi:10.1111/mec.13628) [Medline](Medline)

54. H. Toju, A. S. Tanabe, S. Yamamoto, H. Sato, High-coverage ITS primers for the DNA-based identification of ascomycetes and basidiomycetes in environmental samples. *PLOS ONE* **7**, e40863 (2012). [doi:10.1371/journal.pone.0040863](doi:10.1371/journal.pone.0040863) [Medline](Medline)

55. T. J. White, T. Bruns, S. Lee, J. W. Taylor, in *PCR Protocols: A Guide to Methods and Applications,* M. A. Innis, D. H. Gelfand, J. J. Snisky, T. J. White, Eds. (Academic Press, Inc., 1990), pp. 315–325.

56. B. J. Callahan, P. J. McMurdie, M. J. Rosen, A. W. Han, A. J. A. Johnson, S. P. Holmes, DADA2: High-resolution sample inference from Illumina amplicon data. *Nat. Methods* **13**, 581–583 (2016). [doi:10.1038/nmeth.3869](doi:10.1038/nmeth.3869) [Medline](Medline)

57. R. H. Nilsson, K.-H. Larsson, A. F. S. Taylor, J. Bengtsson-Palme, T. S. Jeppesen, D. Schigel, P. Kennedy, K. Picard, F. O. Glöckner, L. Tedersoo, I. Saar, U. Kõljalg, K. Abarenkov, The UNITE database for molecular identification of fungi: Handling dark taxa and parallel taxonomic classifications. *Nucleic Acids Res.* **47**, D259–D264 (2019). [doi:10.1093/nar/gky1022](doi:10.1093/nar/gky1022) [Medline](Medline)

58. L. Tedersoo, M. Bahram, L. Zinger, R. H. Nilsson, P. G. Kennedy, T. Yang, S. Anslan, V. Mikryukov, Best practices in metabarcoding of fungi: From experimental design to results. *Mol. Ecol.* **31**, 2769–2795 (2022). [doi:10.1111/mec.16460](doi:10.1111/mec.16460) [Medline](Medline)

59. S. Polme, K. Abarenkov, R. Henrik Nilsson, B. D. Lindahl, K. E. Clemmensen, H. Kauserud, N. Nguyen, R. Kjøller, S. T. Bates, P. Baldrian, T. G. Frøslev, K. Adojaan, A. Vizzini, A. Suija, D. Pfister, H.-O. Baral, H. Järv, H. Madrid, J. Nordén, J.-K. Liu, J. Pawlowska, K. Põldmaa, K. Pärtel, K. Runnel, K. Hansen, K.-H. Larsson, K. D. Hyde, M. Sandoval-Denis, M. E. Smith, M. Toome-Heller, N. N. Wijayawardene, N. Menolli Jr., N. K. Reynolds, R. Drenkhan, S. S. N. Maharachchikumbura, T. B. Gibertoni, T. Læssøe, W. Davis, Y. Tokarev, A. Corrales, A. M. Soares, A. Agan, A. R. Machado, A. Argüelles-Moyao, A. Detheridge, A. de Meiras-Ottoni, A. Verbeken, A. K. Dutta, B.-K. Cui, C. K. Pradeep, C. Marín, D. Stanton, D. Gohar, D. N. Wanasinghe, E. Otsing, F. Aslani, G. W. Griffith, T. H. Lumbsch, H.-P. Grossart, H. Masigol, I. Timling, I. Hiiesalu, J. Oja, J. Y. Kupagme, J. Geml, J. Alvarez-Manjarrez, K. Ilves, K. Loit, K. Adamson, K. Nara, K. Küngas, K. Rojas-Jimenez, K. Bitenieks, L. Irinyi, L. G. Nagy, L. Soonvald, L.-W. Zhou, L. Wagner, M. C. Aime, M. Öpik, M. I. Mujica, M. Metsoja, M. Ryberg, M. Vasar, M. Murata, M. P. Nelsen, M. Cleary, M. C. Samarakoon, M. Doilom, M. Bahram, N. Hagh-Doust, O. Dulya, P. Johnston, P. Kohout, Q. Chen, Q. Tian, R. Nandi, R. Amiri, R. H. Perera, R. dos Santos Chikowski, R. L. Mendes-Alvarenga, R. Garibay-Orijel, R. Gielen, R. Phookamsak, R. S. Jayawardena, S. Rahimlou, S. C. Karunarathna, S. Tibpromma, S. P. Brown, S.-K. Sepp, S. Mundra, Z.-H. Luo, T. Bose, T. Vahter, T. Netherway, T. Yang, T. May, T. Varga, W. Li, V. R. M. Coimbra, V. R. T. de Oliveira, V. X. de Lima, V. S. Mikryukov, Y. Lu, Y. Matsuda, Y. Miyamoto, U. Kõljalg, L. Tedersoo, FungalTraits: A user-friendly traits database of fungi and fungus-like stramenopiles. *Fungal Divers.* **105**, 1–16 (2020). [doi:10.1007/s13225-020-00466-2](doi:10.1007/s13225-020-00466-2)