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ARTICLE

Strong succession in arbuscular mycorrhizal fungal communities

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Abstract

The ecology of fungi lags behind that of plants and animals because most fungi are microscopic and hidden in their substrates. Here, we address the basic ecological process of fungal succession in nature using the microscopic, arbuscular mycorrhizal fungi (AMF) that form essential mutualisms with 70–90% of plants. We find a signal for temporal change in AMF community similarity that is 40-fold stronger than seen in the most recent studies, likely due to weekly samplings of roots, rhizosphere and soil throughout the 17 weeks from seedling to fruit maturity and the use of the fungal DNA barcode to recognize species in a simple, agricultural environment. We demonstrate the patterns of nestedness and turnover and the microbial equivalents of the processes of immigration and extinction, that is, appearance and disappearance. We also provide the first evidence that AMF species co-exist rather than simply co-occur by demonstrating negative, density-dependent population growth for multiple species. Our study shows the advantages of using fungi to test basic ecological hypotheses (e.g., nestedness v. turnover, immigration v. extinction, and coexistence theory) over periods as short as one season.

Introduction

Arbuscular mycorrhizal fungi (AMF) are among the most important fungi because they form obligate symbioses that provide phosphorus and nitrogen to 70 to 90% of plant species, including almost all agricultural crops [1, 2]. For more than two decades, the role of AMF as drivers of plant community structure, and vice versa, has been recognized [3–9]. However, owing to the resistance of AMF to cultivation, studies of their ecology have been hampered by controversies over their ability to reproduce sexually, the homogeneity of nuclei in a single individual, and the recognition of AMF species using rDNA regions of different evolutionary rate [10–16].

Detection of succession, the basic ecological process that describes the changes in community similarity over time [17], is one of the ecological investigations most sensitive to species recognition. The changes in communities over time, whether labelled succession or temporal dynamics, have been investigated extensively with modern approaches in plant communities [18–20], studied less extensively in microbial communities [21–26], and are just beginning to be examined with modern tools in AMF [reviewed by Bahram et al [27]; Table S1]. The three most thorough of these studies [reviewed by Bahram et al [27]; Table S1], include two studies that recognized fungal operational taxonomic units (OTUs) with the internal transcribed spacer (ITS) from samples taken either once in each of the four seasons [28], or three times in a single season [29], and a third that recognized AMF OTUs with small subunit (SSU or 18S) ribosomal rDNA from four sampling times from one season [30]. Using data from these three studies to analyze temporal change in fungal community composition, we found a low, albeit significant, rate of change; 0.001–0.006 units of Bray–Curtis dissimilarity per week (Fig. 1a–c).

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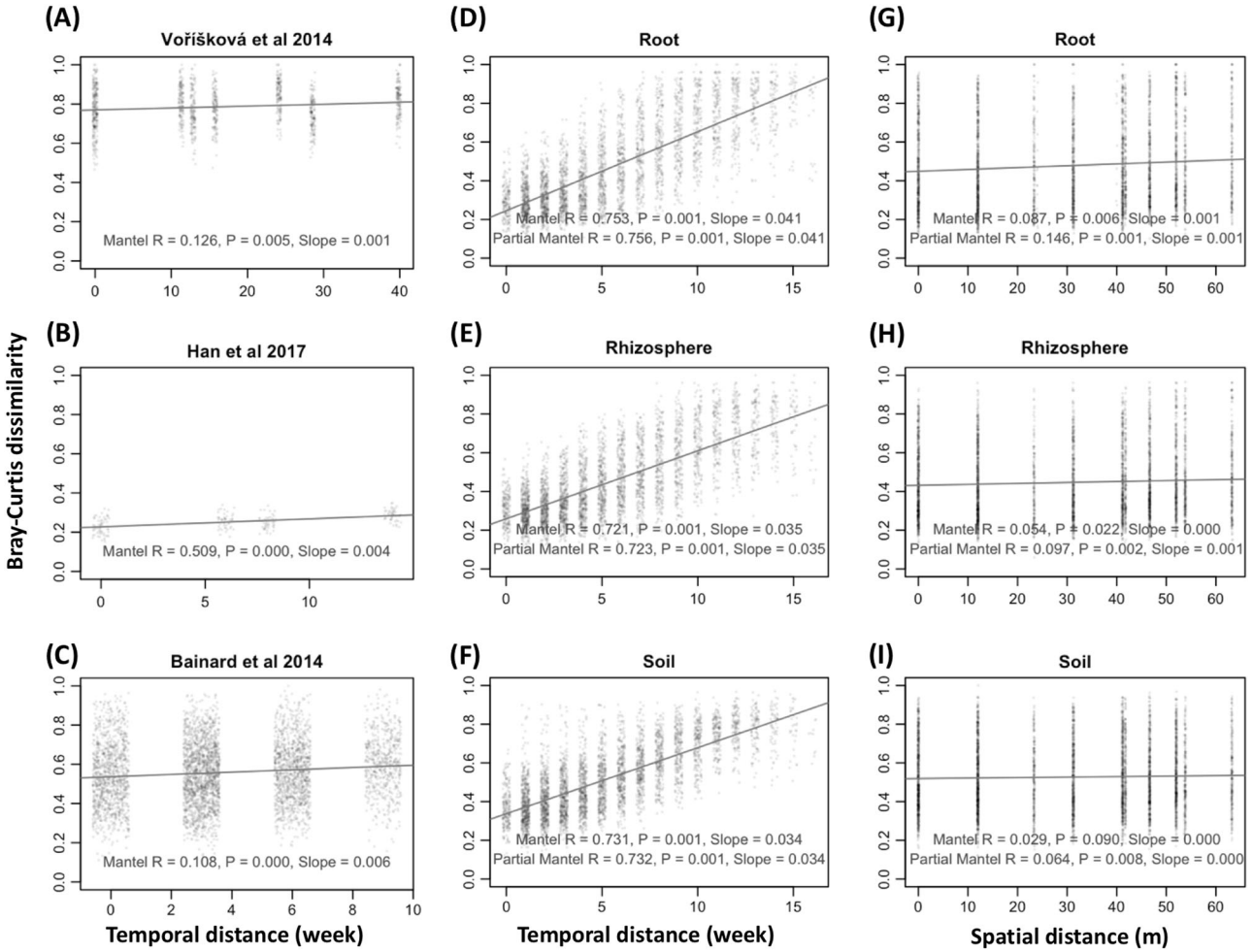

Fig. 1 Arbuscular mycorrhizal fungal community change correlated over time (temporal distance **a**–**f**) and space (spatial distance, **g**–**i**). Temporal distance (in weeks between sampling times) as correlated with Bray–Curtis community dissimilarity by Mantel testing in published data from (**a**) [28] [48 samples = 4 time points * 3 vertical layers * 4 plots (10 m^2 with c. 100 m border)], **b** [29] (21 samples = 3 time points * 7 treatments), and **c** [30] [96 samples = 4 time points * 3 crops * 2 sample type * 4 plots (6 * 2 m^2 plots with 6 m border)], and from new data presented in this study for (**d**) root (17 time points * 6 plots), **e** rhizosphere (17 time points * 6 plots) and **f** soil (18 time points*6 plots) with all plots having the dimensions 16 m * 8 m with at least a 3 m boarder. Spatial distance as correlated with Bray–Curtis community dissimilarity by Mantel testing from new data present in this study for (**g**) root, **h** rhizosphere, and **i** soil. Note the much stronger association of community dissimilarity and temporal distance reflected by *R* and slope for root, rhizosphere and soil in this study than [28, 29] and [30], and the near absence of association of community dissimilarity and spatial distance in this study. *The [29] result is based on a total fungal community dataset rather than AMF community, due to the low recovery of AMF in that study. Analyses in (**d**–**f**) treat sequence data as counts rarefied among AMF fungi and are nearly identical to analyses treating data as counts rarefied among all fungi or treating data as compositional (Fig. S5)

We hypothesized that the actual rate of change in AMF community composition should be higher than could be detected in these studies dues to two factors. First, temporal change is difficult to detect where variation in the components of the AMF system (plant symbionts, soil, hydration, and season) is large compared to the level of sampling (Table S1). Second, change in community composition is under reported when AMF species-level OTU recognition relies on the conserved SSU ribosomal rDNA [2, 10, 31, 32], rather than on the more variable ITS, which is the molecular "barcode" region used for OTU recognition in almost all other fungal studies [33–36].

Here we revisit the basic ecological process of succession by (i) using a system with low environmental heterogeneity comprising only one soil type, one irrigation scheme, two cultivars of the agricultural host plant, sorghum [*Sorghum bicolor* (L.) Moench], and weekly, triplicate sampling of soil, rhizosphere, and roots throughout the 17 weeks from seedling emergence through grain maturation, and (ii) using OTUs characterized with ITS2 by a recently published approach [37, 38] (Database S1-S2). Our data show a signal of succession in AMF communities that is more than an order of magnitude larger than previously reported. To understand the basis for this signal, we explore

patterns of the nestedness and turnover, the processes of appearance and disappearance (proxies for the processes of immigration and extinction that are appropriate for microbial, HTS datasets), and ask if the processes are deterministic or stochastic, and positively or negatively dependent on initial population size.

Methods

Sampling and sequencing

This experiment was conducted at the semiarid Kearney Agricultural Research and Extension (KARE) Center in Parlier, CA, USA (36.6008° N, 119.5109° W). Two sorghum [*Sorghum bicolor* (L.) Moench] cultivars with similar flowering times, RTx430 and BTx642, were planted in three, separate, 16×8 m^2 plots (each with ten rows) with 3 m borders between plots (Fig. S1), and were watered using drip irrigation with 80% of calculated evapotranspiration on a weekly basis [39]. The trial was planted on 27th May 2016 and plants emergence was recorded on 1st June. Weekly samples of root, rhizosphere and soil were taken in 2016 on June 8, 15, 22, 29; July 6, 13, 20, 27; August 3, 10, 17, 24, 31; and September 7, 14, 21, 28. At each sampling time, ten or more individual sorghum plants were removed from randomly chosen locations within one of the central eight rows in each plot and combined to generate one root sample and one rhizosphere sample. At the same time, ten soil cores were taken from random locations in each plot and combined to generate one soil sample. Thus, a total of 312 samples were taken, which comprise 17 weekly samples of the two cultivars, and three compartments (root, rhizosphere, and soil), all with three replicates, plus six soil samples collected prior to planting. DNAs of root, rhizosphere, and soil samples were extracted using the MoBio PowerSoil DNA kit (MoBio, Carlsbad, CA, USA). The fungal internal transcribed spacer 2 (ITS2) region was amplified using forward and reverse primers designed to contain a 29 (forward) or 25 (reverse) base linker, a 12 base barcode, a 29 (forward) or 34 (reverse) base pad, a 0–8 base heterogeneity spacer [40], and either the fungal ITS2 specific 21 base 5.8SFun primer (forward) or 27 base ITS4Fun primer (reverse) [38] (Table S2). We used Lee Taylor's ITS2 primers [38] because the 5.8SFun and ITS4Fun matched well with all Glomeromycotina lineages when we matched the primers with published SSU-ITS-LSU alignments [41] (Database S1–S2). All the raw sequences are deposited in Sequence Read Archive with the accession codes: Bioproject PRJNA412410 Biosamples SAMN07711256 - SAMN07711567. Detailed information about site description, experiment design, and molecular analysis can be found in the supplementary methods.

Bioinformatics

Overall sequencing quality was evaluated using FastQC v0.11.5 [42]. Forward and reverse reads were merged using the fastq_mergepairs command (-fastq_maxdiffpct 3) in USEARCH v8.0 [43]. Primers were removed using cutadapt v1.9.1 [44]. Quality control was carried out using the fastq_filter command (-fastq_maxee 1.0 -fastq_minlen 200) in USEARCH [43]. High quality sequences were subjected to de-replication and de-singleton, and then clustered into OTUs using the cluster_otus command in USEARCH [43]. The OTUs were searched against the raw reads using the usearch_global command (-id 0.97) in USEARCH [43]. This step generated a table of 312 samples×1293 OTUs (10,770,762 reads). The representative sequence of each OTU was identified by a BLAST search against the curated, fungal specific UNITE database [45] and the NCBI database. Fifty-two OTUs (167,749 reads) were identified as AMF (Table S3), whereas 1026 OTUs were non-AMF (10,341,780 reads) and 215 were non-fungal (261,233 reads). To use phylogenetics to equate AMF OTUs with known species, sequences representing the 52 AMF OTUs were combined with vouchered sequences downloaded from NCBI and UNITE and all sequences were aligned using MAFFT v 7.310 [46] placed in a neighbor-joining tree using MEGA v8.0 [47]. Representative sequences of AMF OTUs were deposited in GenBank with the accession codes: MG008508 - MG008559. Owing to the possibility of multiple ITS2 sequences within an individual AMF [16], we searched for OTUs with identical read abundance by analysis of variance (ANOVA). For OTUs with no difference in abundance, a series of pairwise correlations was then carried out and those OTUs with equal abundance and strong positive correlation were combined to avoid the issue of multiplicity of ITS2 sequences within individual AMF.

Statistical methods

Recent recognition that microbiome data from high-throughput sequencing (HTS) represents a random sample of the DNA molecules in an environment and not absolute counts of the molecules dictates that the data be treated as compositional [48] and not as counts, as commonly has been done. Therefore, we use one compositional and two traditional approaches to analyze our AMF data to both analyze the data as compositional and to permit comparisons with prior studies. For the first traditional approach (dataset 1), we rarefied the number of AMF sequences per sample to 100 using the rrarefy command in vegan in R [49, 50], an approach designed to eliminate the effects of different read numbers among the samples on the deduced AMF community composition. For the second traditional approach (dataset 2), we rarefied all fungal reads to 2743

and then extracted the AMF subset of this normalized fungal data, an approach designed to eliminate the effects of different fungal read numbers but retain the abundance variation of AMFs among the samples. For the compositional method (dataset 3), we imputed zeros in AMF compositional count data sets based on a Bayesian-multiplicative replacement using the cmultRepl command in zCompositions [51], and then converted these data to the centered log-ratio (CLR) using the codaSeq.clr command in CoDaSeq (https://github.com/ggloor/CoDaSeq) [48]. We present analyses of the three datasets in figure and supplemental figures to invite comparison. Direct comparison is possible with permutation tests for ANOVA (PERM ANOVA), but not for other analyses because the statistical methods for compositional datasets are different from those for traditional count datasets, e.g., Bray–Curtis dissimilarity for counts v. Aitchison distance for compositional, and principal coordinate (PCo) analysis for counts v. principal component (PC) analysis for compositional [48]. For some of our analyses, methods are not yet available for compositional datasets, e.g., partition of nestedness and turnover components of beta diversity [52].

By plotting time and AMF richness (dataset 1), we demonstrated the temporal dynamics of AMF diversity. To assess the phylogenetic relatedness of AMF OTUs within every sample, the net relatedness index (NRI) was calculated based on the above-mentioned phylogenetic trees and community composition data using the ses.mpd command ($\times -1$) in picante package [53]. Relationships between time and abundance of initially dominant and initially rare OTUs (dataset 1, 2, 3) were explored by linear mixed-effects models, including random effects of OTU identity using the lme command in the lme4 package [54]. The variance explained (conditional R^2) by the mixed effect models was calculated by the r.squaredGLMM function in MuMIn Package [55].

Bray–Curtis dissimilarities were calculated for dataset 1 and 2 to construct distance matrices of the AMF community (Hellinger transformed) using the vegdist command in vegan [49], and Aitchison distances were calculated for dataset 3 [48]. PERM ANOVA were carried out to assess the effect of compartment (soil, rhizosphere or root), time period and cultivar on the AMF community variation either detected by Bray–Curtis dissimilarities or Aitchison distances using the adonis command in vegan [49]. Euclidean dissimilarities were calculated to construct distance matrices of geographic, temporal, temperature, and solar radiation distances respectively in vegan [49]. Mantel tests were carried out to explore the correlations between these distance matrices [49]. Partial Mantel tests were carried out to explore the relationships between AMF community dissimilarity and temporal distance, after excluding the influence of geographic distance. Conversely, partial Mantel tests were carried out to explore the relationships between AMF community dissimilarity and geographic distance, after excluding the influence of temporal distance. Structural equation models (SEM) using Mantel R values as input were constructed in AMOS 25.0 [56] to explore the causal relationships among time, solar radiation, temperature, plant biomass and AMF community composition. Based on a priori and theoretical knowledge, we assumed a conceptual model in which time and solar radiation affect temperature, which in turn affects plant biomass, which further influences AMF community composition. To test the homogeneity of AMF community during succession [57], beta dispersion of AMF communities was explored by the betadisper function in vegan [49]. To graphically illustrate the AMF community composition, AMF Bray–Curtis dissimilarity matrices were ordinated by PCo analysis using the pcoa command in the Ape package [58], and AMF Aitchison distance were ordinated by PC analysis using the prcomp command in stats package [50]. The turnover and nestedness components of AMF community were calculated based on the presence/absence data using the beta.pair command (index.family = 'sorensen') in the betapart package [59], and were fitted with temporal distance using the Mantel test in vegan [49]. The nestedness of AMF community was graphically illustrated by the nestedtemp command in vegan package [49].

To test how the AMF succession might be influenced by the AMF OTU cutoff, the OTU delineation processes were repeated by changing the OTU cutoff from the defaulted 97 to 80% in increments of 1%. We calculated the AMF community Bray-Curits dissimilarity of every OTU cutoff, and fitted it with temporal distance using Mantel test, as mentioned above.

To compare the temporal dynamics of AMF communities in our study with those previously reported by Bainard et al. [30], Han et al. [29] and Voříšková et al. [28], we calculated, for the three previous studies, Bray–Curtis dissimilarities of Hellinger transformed AMF community data, and Euclidean dissimilarities of temporal distance in terms of simulated weekly sampling. Mantel tests were carried out to explore the correlations between AMF community dissimilarity and the temporal distances in vegan [49].

Results and discussion

Recognition of AMF OTUs by ITS2

To recognize AMF OTUs that approximate species more closely than SSU OTUs we use the ITS2 region of the RNA repeat [10, 32, 37, 60]. Here, using Illumina Miseq of fungal ITS2 amplified by dual-barcoded Lee Taylor's fungal specific primers [38], we successfully recognized 52

AMF OTUs with 167,749 AMF reads, belonging to *Glomus* (21 OTUs), *Rhizophagus* (13 OTUs), *Claroideoglomus* (8 OTUs), *Funneliformis* (5 OTUs), *Paraglomus* (4 OTUs), and unidentified Glomeraceae (1 OTUs) (Fig. S2). The thorough sampling (312 samples) produced a species accumulating curve that reached its plateau for the species-poor AMFs (52 OTUs) in a relative small (<5000 m^2), simple agricultural field (Fig. S3). In line with this result, of the 52 AMF OTUs, only five occurred in fewer than 10 samples, suggesting a lack of rare OTUs in our study (Fig. S4).

As described in the section on statistical methods, to both recognize the compositional nature of HTS microbiome data [48] and to permit comparisons of our results with previous studies that treat HTS data as counts, we analyzed the data both as counts and compositional. We employed two count methods: in data set 1 we rarefied to equal AMF reads and in dataset 2 we rarefied to equal fungal reads. For compositional analysis, in dataset 3 we transformed the data by the CLR method [48]. The largest difference is the detected effect of time, $R^2 = 0.438$ for dataset 1, $R^2 = 0.339$ for dataset 2 and $R^2 = 0.232$ for dataset 3 as explored by PERM ANOVA (all $P < 0.001$) (Fig. S6). Despite these differences, analyses of the three different datasets generated remarkably consistent results in all applicable analyses that similarly supported the main conclusions of our study (Fig. S5–S7).

In light of recent reports of ITS2 variation as high as 6 to 12% in AMF species-level clades [16, 61, 62], we also investigated the effect on ecological analyses of reducing, in 1% increments, the threshold of OTU recognition by ITS2. We found that the rate of AMF succession was not substantially changed until the cutoff was reduced from 97 to 85% (15% intra-OTU variation, Fig. S8), therefore, our findings are not affected by the potential intraspecific variation reported for AMF species.

The use of ITS has been questioned due to reports showing that one AMF individual can contain more than one, independently evolving rDNA repeat [10, 16, 32]. Mindful of the possibility of amplifying and sequencing more than one rDNA repeat in a single species of Glomeromycotina, we searched for possible intra-individual rDNA polymorphism by correlating read abundance for the different ITS2-OTUs over the 17 weeks of sampling. Strongly correlated ITS2 read abundance (Fig. S9) was seen for three *Rhizophagus* OTUs (118, 161, 132). Therefore, due to the possibility that they might represent a single AMF species, we treated these three *Rhizophagus* OTUs as a single species in our analysis, reducing the number of ITS2-OTUs from 52 to 50. Two other *Rhizophagus* OTUs showed similar read-abundance patterns (Fig. S9A) but the unequal abundance of reads (Fig. S9B) indicated that they represented distinct OTUs and we retained them in our analyses. To assess the effect of reducing the number of OTUs from 52 to 50, we repeated the following ecological analyses with all 52 ITS2-OTUs, finding no differences in ecological results, their significance or our subsequent conclusions (Figs. S10–S15).

Succession of AMF community

Our analyses showed a strong, positive, Mantel correlation ($R = 0.617$–0.753, $P < 0.001$) between temporal distance (graphed on the *x*-axis as weeks between sampling times) and AMF community Bray–Curtis (dataset 1, 2) or Aitchison (dataset 3) dissimilarity in root, rhizosphere, and soil samples (Fig. 1d–f; Fig. S5). The slope of the change in dissimilarity per week found here (0.034–0.041 units of Bray–Curtis dissimilarity per week, dataset 1), is 34–41 times greater than the first previously mentioned study (0.001 units of Bray–Curtis dissimilarity per week, Fig. 1a) [28], 8.5–10.25 times greater than the second (0.004 units of Bray–Curtis dissimilarity per week, Fig. 1b) [29], and 5.6–6.8 times greater than the third (0.006 units of Bray–Curtis dissimilarity per week, Fig. 1c) [30]. This change in AMF community composition can also be visualized by ordination (PCo for dataset 1, 2; PC for dataset 3) analysis (Fig. 2a; Fig. S6), by a proportional bar plot of AMF relative abundance (dataset 1, Fig. 2b), or by a bar plot of percentage of AMFs in total fungal reads (dataset 2, Fig. 2c), in addition to the graph of community dissimilarity and temporal distance (Fig. 1d–f; Fig. S5; Fig. S8; Fig. S10). This strong AMF succession was also seen using PERM ANOVA ($R^2 = 0.232$–0.438; $P < 0.001$, Fig. 2a; Fig. S6). This succession is not confounded by beta dispersion in root, rhizosphere, and soil (Fig. S16). We recognize that the concept of succession, which was developed for plant communities, is controversial when applied to microbial communities. Here, we adopt a recent definition of succession as, "… somewhat orderly and predictable manner by which communities change over time following the colonization of a new environment…" [22], by treating a newly emerged plant root, as well its associated rhizosphere and soil, as new environments for AMFs to colonize and initiate succession.

Geographic distance is a factor known to have a major effect on AMF community composition [12, 27, 63]. In contrast to temporal distance, our analysis of the effect of geographic distance using Mantel and partial Mantel tests showed a small effect (slope of the change in dissimilarity over distance = 0 to 0.001 per meter, R never greater than 0.15) on the variation of AMF community dissimilarity in root, rhizosphere, and soil (Fig. 1g–i). Thus, we can infer that agricultural cultivation of a single plant species (*S. bicolor*) homogenizes AMF communities over at a range of from 10 to 60 m, but we cannot rule out environmental

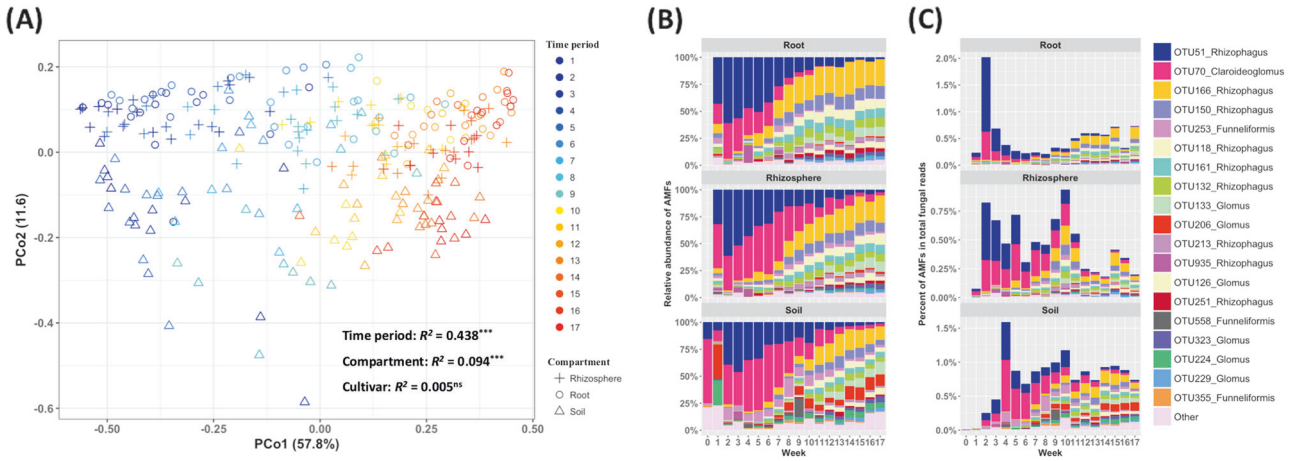

Fig. 2 Change in composition of arbuscular mycorrhizal fungal communities in three compartments (root, rhizosphere, and soil) over 17 weekly time period (TP) samplings. **a** Principal coordinate (PCo) analysis by PERM ANOVA showing significant association of community composition with time period (TP) and compartment but not cultivar (***$P < 0.001$; ns: not significant). Note that TP accounts for nearly half the variance, which is far more than is accounted for by compartment (root, rhizosphere or soil) or plant genotype (sorghum cultivar RTx430 or BTx642). **b** Bar graph of AMF operational taxonomic unit (OTU) relative abundance at each TP and **c** Bar graph of AMF OTUs percentage in total fungal reads at each TP for the three compartments, root, rhizosphere and soil. Note the strong change in AMF community composition over time. Analysis in **a** treats sequence data as counts rarefied among AMF fungi and is nearly identical to analyses treating data as counts rarefied among all fungi or treating data as compositional (Fig. S6)

heterogeneity that might occur at finer scales and that could affect AMF community composition.

AMF community ecology follows approaches developed for plants with a major difference being the immediate source of energy, insolation for plants and symbiotic partners for AMF [1], sorghum in our case. Of course, temporal variation in insolation that directly affects the plant symbiont should have an indirect effect on AMF. Our SEM results showed that AMF community was directly affected by time and plant biomass, and also indirectly by temperature and solar radiation (Fig. 3). Surprisingly, solar radiation negatively affected plant biomass. It might be that at 36°N latitude in Central California, energy from insolation is not a limiting resource for sorghum growth, but UV radiation and drought stress associated with high insolation might detrimentally affect accumulation of sorghum biomass.

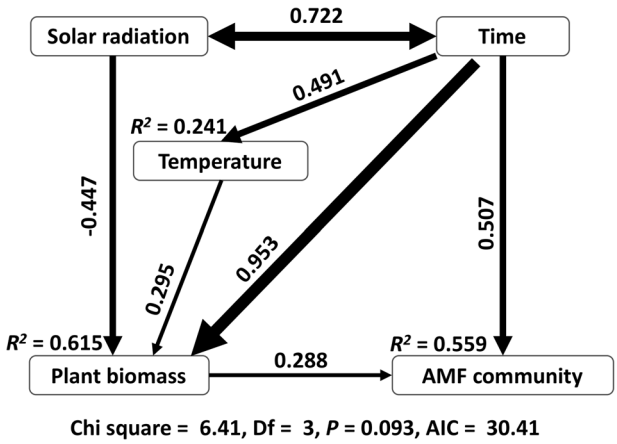

Fig. 3 Structural equation model (SEM) demonstrates that the succession of arbuscular mycorrhizal fungal (AMF) communities was directly affected by time and aboveground biomass of sorghum, in addition to indirect (via plant biomass) effects of solar radiation and temperature. The numbers above the arrows indicate the magnitude of path coefficients (λ), and this magnitude is also depicted by the width of the lines. R^2 values represent the proportion of variance explained for each variable

Nestedness and turnover during AMF community succession

There are two, divergent patterns describing the change in community composition: turnover (where some species are replaced by others over time) and nestedness (where the earlier community is a subset of the latter community, or vice versa) [52]. Our demonstration of AMF community succession (Figs. 1d–f, 2) was accompanied by an increase in richness (Fig. 4a–c) over the 17 weeks from emergence of seedlings to maturation of grain in sorghum, so we expected nestedness to predominate but questioned if replacement (turnover) also was involved. Mantel tests showed that temporal distance was significantly correlated with both the components of turnover ($R = 0.193$, $P < 0.001$) and nestedness ($R = 0.214$, $P < 0.001$) of AMF community composition variation (Fig. 5; Figs. S17–S19). The co-occurrence of these two divergent patterns of change in community composition suggested that there also would be more than a single, ecological process underlying succession in the AMF community.

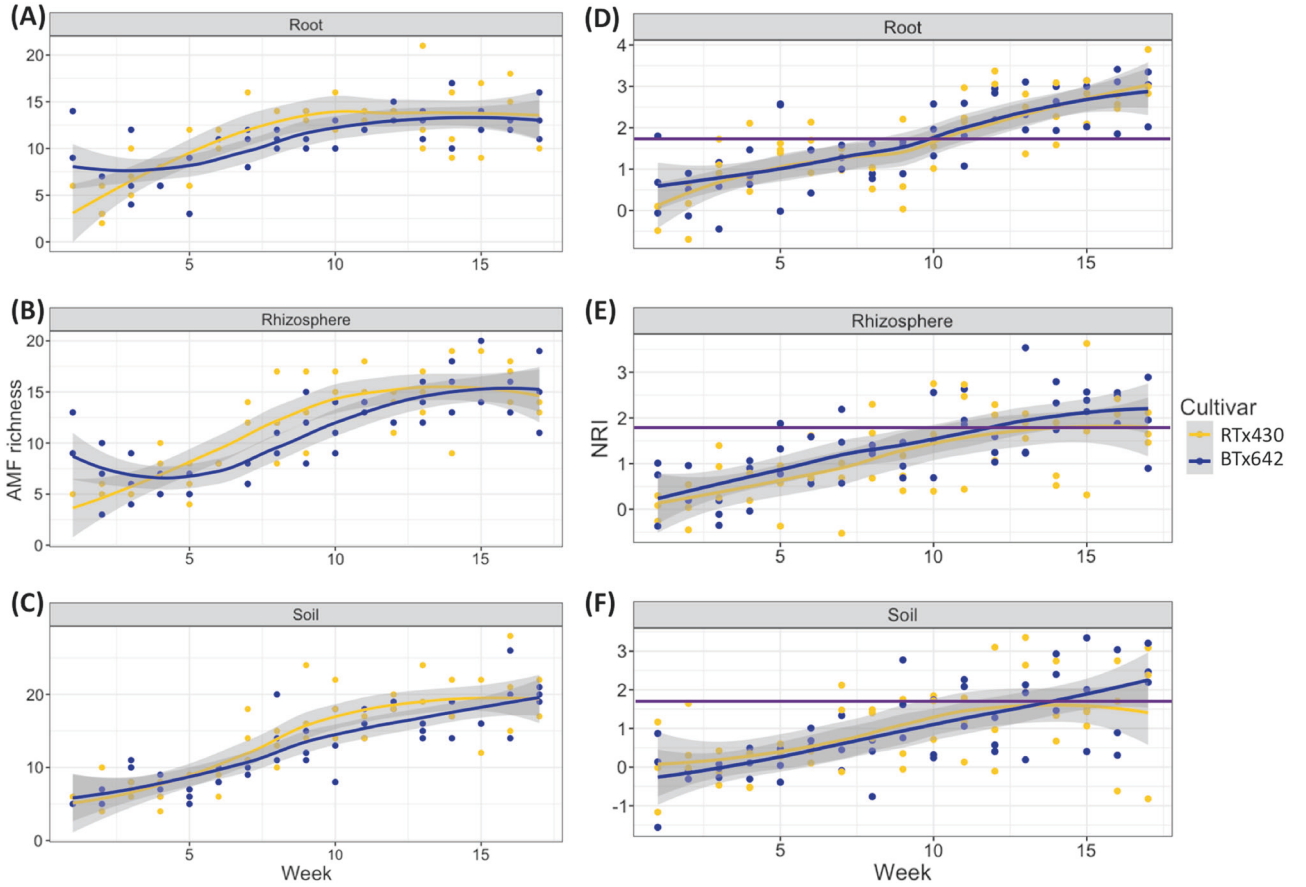

Fig. 4 Temporal dynamics of (**a**–**c**) richness and (**d**–**f**) phylogenetic relatedness of AMF communities on two sorghum cultivars. Richness shows a consistent increase over time for all three compartments (root, rhizosphere, and soil). Phylogenetic relatedness (net relatedness index, NRI) also increases over time, eventually showing significant underdispersion as it rises above the threshold of significance (horizontal, purple line). Note that the threshold is reached earlier inside roots than outside them in the rhizosphere and soil and that both cultivars (RTx430 and BTx642) behave similarly in terms of richness and NRI, consistent with the analyses in Fig. 2a

Immigration and extinction in AMF community succession

Immigration and extinction are the two fundamental processes responsible for the patterns of succession [18]. Although immigration and extinction are far more easily observed for plants than microscopic fungi, our comparison of the first week (Time Period 1, TP01) and the last week (Time Period 17, TP17) provide evidence for both processes. Two initially dominant TP01 OTUs with indicator values (*indval*) strong enough to make them significant indicators of the initial time period (OTU51_*Rhizophagus*, $indval = 0.894$, $P < 0.001$; OTU70_*Claroideoglomus*, $indval = 0.809$, $P < 0.001$) were subsequently lost and 13 initially rare OTUs (five *Rhizophagus*, $indval = 0.667$–0.811, $P < 0.001$; eight *Glomus*, $indval = 0.311$–0.816, $P < 0.05$) became significant indicators by the final sampling at TP17 (Table S4; Fig. 2b). This result was seen with abundance of AMF alone or abundance of AMF relative to all fungal, although in the later analysis, the initial dominance was delayed from TP01 to the 2nd week in root and rhizosphere and the 4th week in soil (Fig. 2c).

Again acknowledging the difficulty of asserting the absence of a microscopic fungus, the loss of the initially dominant OTUs is consistent with the action of forces causing extinction and the rise of the initially rare OTUs is consistent with the action of forces causing immigration. These two processes can be deterministic or stochastic and, in light of the expected, dramatic effect on AMF community composition of the emergence and growth of the sorghum monoculture, determinism would seem the more likely explanation. Similarly, other factors argue against chance as the dominant force, including the paucity of rare OTUs in our communities (Fig. S3–S4), which minimizes the number of OTUs most susceptible to stochastic extinction [64], and the similarity in AMF community composition throughout the sorghum field (Fig. 1g–i), which limits the local pool of potential, stochastic immigrants.

The emergence of 13 significant indicator OTUs (Table S4) by the final time period, TP17, raises the

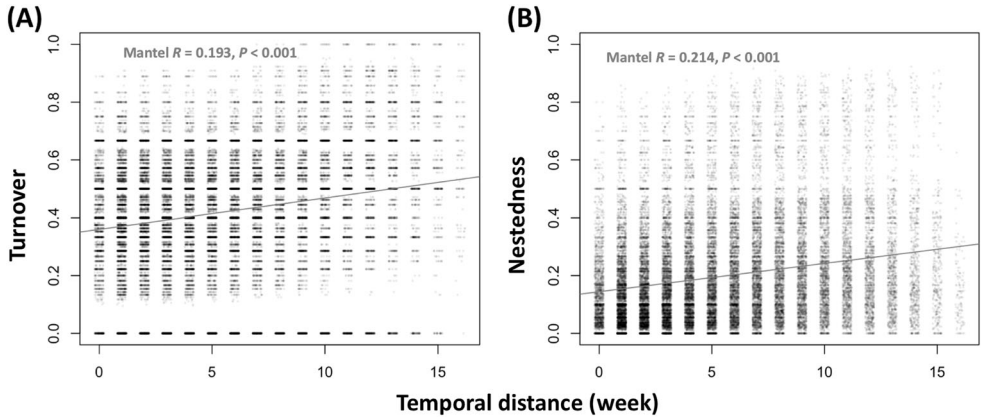

Fig. 5 Role of two patterns, (**a**) turnover and (**b**) nestedness in the change in AMF community composition over time. The compositional variance of AMF community measured by Sorenson pair-wise dissimilarity was partitioned into a turnover component (Simpson pair-wise dissimilarity) and a nestedness component (Sorenson pair-wise dissimilarity minus Simpson pair-wise dissimilarity) following Baselga [52]. Subsequently, Mantel tests were carried out to explore the correlation of temporal distance and either the turnover or nestedness components of AMF compositional variance. Both AMF turnover and nestedness showed significant and biologically meaningful associations with temporal distance. Visualization of the superimposed points was enhanced by rendering them semi-transparent and adding a small amount of noise to the temporal distances

question of coexistence of multiple species during succession. The creation of distinct niches by a developing host plant would favor coexistence of dissimilar species that could avoid competition by exploiting divergent niches (i.e., stabilizing niche differentiation, a process consistent with phylogenetic overdispersion) [65]. Conversely, the expansion of the same niche, as expected of a growing sorghum crop, would facilitate the immigration and coexistence of species adapted to the same environment. Successful immigrant taxa would be expected to show equal fitness in this expanding niche and, assuming that fitness traits are phylogenetically conserved, exhibit a phylogenetic underdispersion due to evolutionary relatedness [65]. We find a phylogenetic underdispersion of indicator AMF in the genera *Rhizophagus* and *Glomus* at TP17 (Table S4) in roots, rhizosphere, and soil (Fig. 4d–f) based calculation of the net relatedness index (NRI) from an ITS2 phylogeny (Fig. S2). The lack of significant phylogenetic underdispersion early in the season (Fig. 4d–f), indicative of stochastic community assembly, is consistent with our having planted sorghum in a fallowed field that was previously planted to oats and having no previous exposure to sorghum. Development of underdispersion, indicative of phylogenetic similarity of AMF community members, later in the season supports coexistence by equalizing fitness, likely due to the expanding niche, rather than avoiding competition by exploiting niche differences. A similar shift from initially random to significant phylogenetic relatedness has been reported for AMF communities of crop plants characterized by SSU OTUs in four soil samples taken over 9 weeks, but not for root samples, where the pattern was nonlinear over time [30]. The interpretation of phylogenetic underdisperson with equalizing fitness similarity relies on the phylogenetic conservation of traits [66], but evidence of specific, adaptive traits in AMF remains rare [67, 68].

Initial density-dependent AMF population demography

A role for population density in the decline of initially dominant OTUs and the rise of initially rare OTUs is suggested from our data, which document a decrease in relative abundance of the two OTUs dominant at TP01 (*Rhizophagus*_51, *Claroideoglomus*_70), and an increase in relative abundance of 13 OTUs rare at the same initial time period (Fig. 2b, c). In line with these observation, time is significantly negatively correlated with initial dominant OTUs and positively correlated with initial rare OTUs, as detected by linear mixed-effect modeling of all three datasets, whether rarefied for AMF reads, for all fungal reads, or not rarified and transformed by the CLR method (Fig. 6; Fig. S7). In the case of the two initially dominant OTUs whose relative abundance declined, they may have experienced a fitness disadvantage associated with high population density and their decline would be the result of competitive exclusion of species due to a disadvantage in fitness as compared to the rest of the community. Conversely, the population increases seen in the 13 initially rare OTUs may have been due to a fitness advantage at low population density, the magnitude of which would decrease as their populations grew [64]. Our results echo the only other studies to report replacement over time of dominant AMF OTUs [69, 70], in which the authors used SSU OTUs and five years of annual sampling to show that AMF OTUs dominant in newly

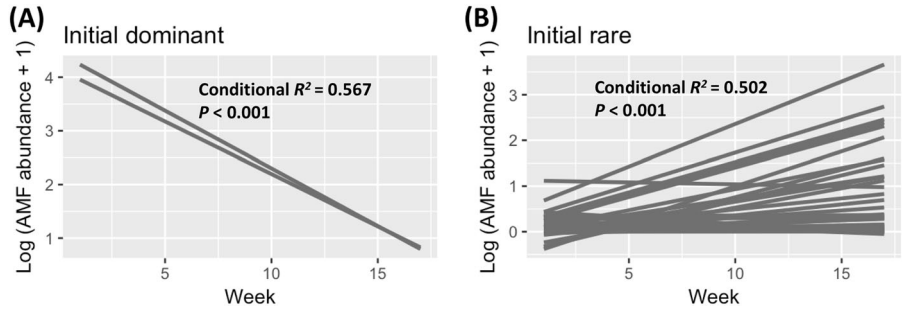

Fig. 6 Steep (**a**) decline of initially dominant OTUs and (**b**) rise of at least 13 initially rare OTUs. Relationships between time and AMF OTU abundances were explored by linear mixed-effects models, including random effects of AMF identity. The conditional R^2 calculated here can be interpreted as the variance explained by the mixed-effects models. Analyses in (**a**, **b**) treat sequence data as counts rarefied among AMF fungi and are nearly identical to analyses treating data as counts rarefied among all fungi or treating data as compositional (Fig. S7)

germinated seedlings were almost entirely replaced by previously rare types; however, with few samples and broad OTU recognition, they were unable to correlate the replacement with population density [69, 70].

The negative density-dependent population growth observed here is explained in plant communities by two mechanisms, resource partitioning and escape from natural enemies [65]. Resource partitioning posits that different species either use different resources or partition the use of shared, limited resources [71]. As a result, species with large populations should experience limited population growth due to strong intraspecific competition, whereas species with small populations should experience high population growth due to the lack of intraspecific competition. However, support for the partitioning mechanism is not seen in the case of the six, closely related *Rhizophagus* OTUs (Table S4) that were shown, above, to be similar enough in fitness to avoid competitive exclusion and, therefore, too similar to occupy different niche spaces. Neither does partition theory appear to explain the inability of *Rhizophagus* OTU 51 to maintain population size in the final time period, likely due to competitive exclusion, because this process would not be expected to occur with effective partitioning [71]. Under the mechanism of natural enemy escape, species with large populations experience limited population growth rate due to the attraction and accumulation of more specific predators and pathogens, whereas species with small population experience high population growth rates due to the escape from host-specific natural enemies [65]. Alas, we do not have any data on predators and pathogens of AMF from our study, although these organisms must exist [72, 73].

The negative, density-dependent population growth seen for at least 13, initially rare, OTUs, indicates that populations of these AMF are able to increase in size while co-occurring with stable populations of other species. This invasibilty, together with the facts that these fungi live at the same trophic level and inhabit the same roots (Figs. 2 and 6; Table S4), suggests that these representatives of two AMF genera, *Rhizophagus* and *Glomus*, not only co-occur, but also co-exist [74]. These 13 AMF OTUs represent the first microbes where negative density-population growth in support of co-existence has been demonstrated over a long period [74], but further research will be needed to determine which phenotypic trade-offs may be associated with co-existence, such as, aspects of colonization and life-history strategy, differential interaction with host plants, peers and antagonists, and variation in adaptation to features of the abiotic environmental.

Different AMF in root, rhizosphere, and soil

AMF are obligately dependent upon carbon from the roots of plants, so we expected that the AMF communities of the rhizosphere and soil would follow those seen in the root. This pattern was evidenced by similar trends for AMF in roots, soil, and rhizosphere in terms of temporal distance and succession, geographic distance, richness, and phylogenetic relatedness, as mentioned above. For example, the lag in response to nutrients provided by sorghum from roots to soil could be seen in the percentage of total fungal reads attributable to AMF, which peaked at TP02 in root, but peaked at TP04 in soil (Fig. 2c). Our data also suggest that different AMF species display different proportions of their thalli across the compartments of root, rhizosphere, and soil. In roots, six *Rhizophagus* OTUs were more commonly detected than in other compartments and, when detected, were more abundant ($indval = 0.054$ –0.399, $P < 0.05$; Table S5; Fig. 7). In rhizosphere, one *Claroideoglomus* OTU ($indval = 0.419$, $P < 0.001$) was more common and abundant than in other compartments (Table S5; Fig. 7). In soil, five *Funneliformis* OTUs ($indval = 0.103$–0.520, $P < 0.01$), three *Claroideoglomus* ($indval = 0.051$–0.167, $P < 0.01$), two *Paraglomus* ($indval = 0.047$–0.144, $P < 0.05$)

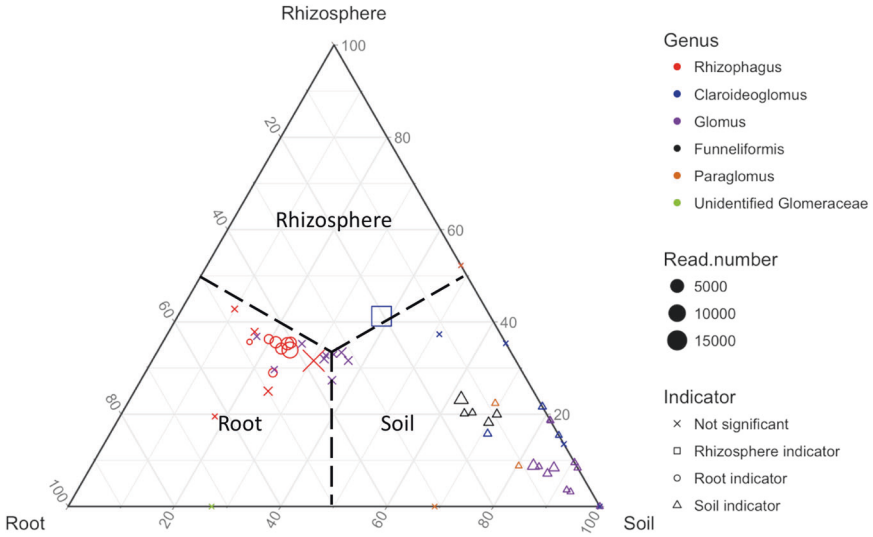

Fig. 7 Ternary plot demonstrating the distribution of arbuscular mycorrhizal fungal (AMF) operational taxonomic units (OTUs) recovered from root, rhizosphere and soil. Note a bias toward roots for *Rhizophagus* OTUs, toward rhizosphere for a Clariodeoglomus OTU, and toward soil for *Glomus, Claroideglomus, Funneliformis* and *Paraglomus* OTUs

and 11 *Glomus* (*indval* = 0.062–0.566, $P < 0.01$) were more common and abundant (Table S5; Fig. 7) than in other compartments. These results are consistent with observations that *Rhizophagus* species form abundant spores in the roots of vascular plants, whereas *Funneliformis* species form spores in the soil [75]. This variation in AMF morphology in nature also raises the possibility that AMF morphology could change over time, thereby adding variation associated with function [1] to studies of community composition.

Conclusion

Our ability to demonstrate a strong signal of succession in AMF community composition over the sorghum growing season almost certainly rests on our choice of an experimental system with fewer variables than other studies (Table S1) as well as characterization of OTUs by ITS2, which recognizes species-level taxa [2, 10, 11, 31, 32]. Treating DNA sequence data as counts or as compositional showed no loss of statistical significance of results. Our approach also found that succession in AMF communities of sorghum showed the pattern of turnover in addition to strong patterns of nestedness, as has been reported in other studies of AMF (Table S6). Unlike previous studies of AMF that reported stochastic assembly of AMF communities [76–78], we provide analyses that both immigration and extinction are deterministic in this relatively homogenous environment, based on the disappearance of initial dominant OTUs rather than rare OTUs and the homogeneity of AMF communities throughout the sorghum field, which fails to provide a pool of potential immigrants that might enter communities by chance. The increase in phylogenetic similarity (underdispersion) of the many OTUs that immigrated is consistent with equalized fitness rather than niche differentiation, as might be expected with one soil type and one host plant, although phylogenetic underdispersion of AMF has been reported for more complex systems (Table S7).

The energies supporting succession or, more broadly, temporal change in community composition, are different for the two partners of the arbuscular mycorrhizal symbiosis; the autotrophic plant community is supported by solar radiation and the heterotrophic AMF fungal community is supported by carbon fixed by the plant. For plants, the insolation inputs can be relatively consistent over the scale of plant community succession, but the energy provided to the AMF by the growing crop is clearly expanding with time. Therefore, when the abundance of specific AMF species declines during the season, the reduction can be a combination of both absolute reduction and, owing to the expanding resource provided by the plant, reduction relative to increasing abundance of other AMF species. Keeping this caveat about population density in mind, the disappearance of two initially dominant taxa suggests activity promoted by high population density, whereas the population growth of 13 immigrant OTUs suggests the opposite, activity promoted by low population density. For most of our ecological analyses, soil and rhizosphere showed the same results as our primary focus, sorghum roots. However, a difference in OTU abundance between roots on one hand and soil plus rhizosphere on the other correlates with the behavior of AMF genera, some of which live and sporulate predominately in the root and others that are known to sporulate prolifically outside the root, as has been reported in other studies of AMF (Table S8). Our study provides a foundation for more ambitious studies of AMF community ecology, where our simple experimental system would be enlarged to include diversity in hosts, soil, hydration and

fertilization, with the eventual goal of effectively studying natural systems.

Due to our inability to cultivate AMF apart from plants, many ghosts have haunted our understanding of these fungi. Just as genomics is showing that the AMF life cycle is typical of other fungi in terms of sex [79] and nuclear variation within an individual [14, 15], mycobiome ecology is showing that AMF community assembly is not a matter of chance, but a process determined by biotic and abiotic factors [80]. The several studies noted above that also found patterns of nestedness (Table S6) and genetic similarity inferred from phylogenetic underdispersion (Table S7) suggest that there may be general rules for assembly of AMF communities that await discovery. The succession of AMF fungi seen here suggests that some AMF species could be more beneficial to sorghum production than others and that these species might be added to agricultural fields along with seeds or applied later in the season. Our approach would also be useful in monitoring the persistence and effects of such additions on the AMF communities of crop plants.

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Compliance with ethical standards

Conflict of interest The authors declare that they have no conflict of interest.

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Supplementary methods

Experiment site

This experiment was conducted at the Kearney Agricultural Research and Extension (KARE) Center in Parlier, CA, USA (36.6008° N, 119.5109° W). KARE is located in the Central Valley, a semiarid zone with a mean annual temperature of 17.8°C and mean annual precipitation of 325 mm, almost all of which falls between November and April. During the course of our experiment (27th May to 28th September, 2016), no precipitation occurred; the daily minimum temperature ranged from 7.8 to 22.8°C, and the daily maximum temperature ranged from 22.8 to 40.5°C (http://ipm.ucanr.edu/WEATHER/index.html). Soils at KARE were plowed before seeding and are characterized as Hanford sandy loam with a silky substratum and pH 7.37.

Experiment design and sampling

Two sorghum [*Sorghum bicolor* (L.) Moench] cultivars with similar flowering times, RTx430 and BTx642, were planted in three, separate, 16 × 8 m^2 plots (each with ten rows) with 3 m borders between plots (Fig. S1). The seeds were sown into pre-watered fields and left unirrigated for two weeks, which is standard agricultural management practice for sorghum in the Central Valley. From the 3rd week until the final harvest, the plants were watered using drip irrigation with 80% of calculated evapotranspiration on a weekly basis.

The trial was planted on 27th May, 2016 and plants emergence was recorded on 1st June. Weekly samples of root, rhizosphere and soil were taken in 2016 on June 8, 15, 22, 29; July 6, 13, 20, 27; August 3, 10, 17, 24, 31; and September 7, 14, 21, 28. Between 10:00 and 14:00 of every sampling date, ten or more individual sorghum plants were removed from randomly chosen locations within one of the central eight rows in each plot. Both rhizosphere and root samples were taken from the pool of these ten individuals. Roots were removed from the ten plants, mixed

together, transferred to 50 ml tubes with detergent-phosphate buffer (6.33 NaH_2PO_4•H_2O and 8.5 g Na_2HPO_4•anhydrous in 1 L water, autoclaved; cooled, 200µl Silwet-77 added; pre-cooled in ice-water mixture), and vortexed at full speed for 2 min. The roots were removed from the tube, the liquid-filled tube was saved, and the roots were transferred to a 200-ml plastic cup with phosphate buffer without detergent (6.33 NaH_2PO_4•H_2O and 8.5 g Na_2HPO_4•anhydrous in 1 L water, autoclaved; pre-cooled in ice-water mixture), vortexed at full speed for 1 min twice, dried by clean paper towels, put into aluminum packet and frozen in liquid nitrogen. The saved, liquid-filled tube containing the rhizosphere was centrifuged at full speed for 3 min, the buffer discarded and the rhizosphere pellet frozen in liquid nitrogen. Simultaneously, soil at 6" depth was collected adjacent to the ten sampled plants using 6" soil collection tubes. Ten samples were mixed, transferred to a 50-ml centrifuge tube, and frozen in liquid nitrogen. Thus, a total of 312 samples were taken, which comprise 17 weekly samples of the two cultivars, and three compartments (root, rhizosphere and soil), all with three replicates, plus six soil samples collected prior to planting. The frozen root, rhizosphere and soil samples were transferred to dry ice and transported by 18:00 on the day of collection to laboratories at the University of California, Berkeley where they were stored at -80°C until grinding.

Molecular analysis

Root samples were ground, separately, with liquid nitrogen in a cryogenic grinder (6875D Freezer/Mill, SpexSamplePrep, Stanmore, UK), and root DNA was extracted from 0.2 g ground sample using the MoBio PowerSoil DNA kit (MoBio, Carlsbad, CA, USA) with all centrifugation conducted at 4°C. Rhizosphere and soil DNA was extracted from 0.2 g samples using the MoBio PowerSoil DNA kit (MoBio, Carlsbad, CA, USA) following the manufacture's protocol. DNA concentration was measured with a Qubit dsDNA HS kit (Life Technologies Inc., Gaithersburg,

MD, USA) and DNAs were adjusted to 5 ng/μl with ddH_2O. In preparation for Illumina Miseq sequencing of amplicons of the fungal internal transcribed spacer 2 (ITS2) region, PCR was performed on all samples using forward and reverse primers designed to contain a 29 (forward) or 25 (reverse) base linker, a 12 base barcode, a 29 (forward) or 34 (reverse) base pad, a 0-8 base heterogeneity spacer (Fadrosh et al 2014), and either the fungal ITS2 specific 5.8SFun primer or ITS4Fun primer (Taylor et al 2016) (Table S2). We used Lee Taylor's ITS2 primers(Taylor et al 2016) because the 5.8SFun and ITS4Fun matched well with all Glomeromycotina lineages when we matched the primers with the SSU-ITS-LSU alignment (Krüger et al 2012) (Database S1-S2). The 5.8Fun primer starts at the 2078th base of the SSU-ITS-LSU alignment (Database S1); and the ITS4Fun primer starts at the 3508th base of the reverse complementary of SSU-ITS-LSU alignment (Database S2). PCR amplification employed the one-step PCR method in the Gene Amplification PCR System (BioRad Laboratories Inc.) with initial denaturation at 96°C for 2 min, followed by 35 cycles of 94°C for 30 s, 58°C for 40 s and 72°C for 2 min, and a final extension at 72°C for 10 min. Each amplification was carried out in a 25 μl reaction mixture containing 10 μl 5PRIME HotMaster Mix (Eppendorf-5Prime, Gaithersburg, MD, USA), 2.5 μl forward primer, 2.5 μl reverse primer, 2 μl template DNA, and 8 μl nuclease-free water. Amplicon libraries were produced from a pool of three different PCRs. The yields of PCR products were measured using a Qubit dsDNA HS kit (Life Technologies Inc., Gaithersburg, MD, USA) and 200 ng of DNA from each of the 312 samples were randomly assigned to four different pools. The pooled products were purified using AMPure magnetic beads (Beckman Coulter Inc., Brea, CA, USA) following the manufacturer's instructions. Libraries were quality checked for concentration and amplicon size using the Agilent 2100 Bioanalyzer (Agilent Technologies, Santa Clara, CA, USA) at the Vincent J. Coates Genomics Sequencing Laboratory (GSL, University of California, Berkeley, CA, USA).

Pyrosequencing was performed on the Illumina Miseq PE300 sequencing platform (Illumina, Inc., CA, USA) at the GSL. All the raw sequences are deposited in Sequence Read Archive (raw data) with the accession codes: Bioproject PRJNA412410 Biosamples SAMN07711256 - SAMN07711567.

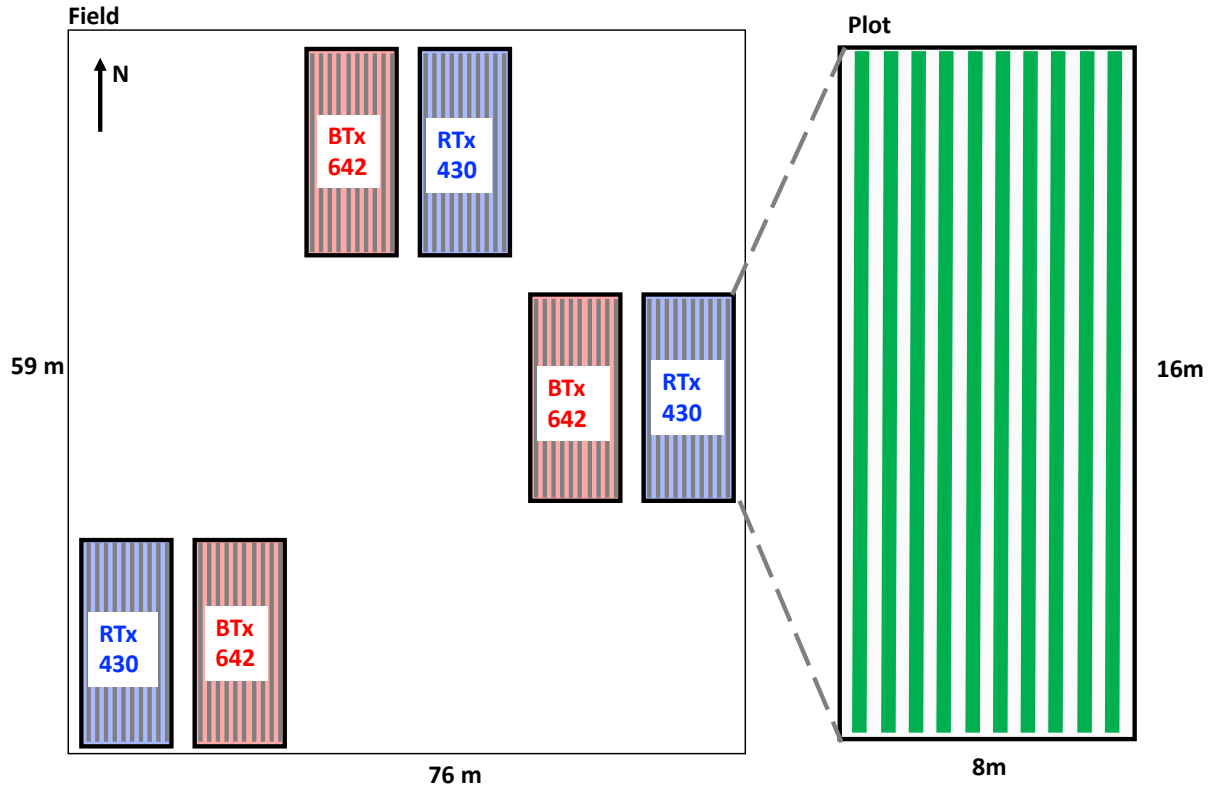


Fig. S1 Field layout of the six plots (16 x 8 m^2) of two sorghum cultivars (RTx430 and BTx642) in a field (76 x 59 m^2). Each plot consisted of ten rows of sorghum, each containing approximately 200 plants spaced 10cm apart. At each sampling time, plants were removed from randomly chosen locations within one of the central eight rows in each plot.

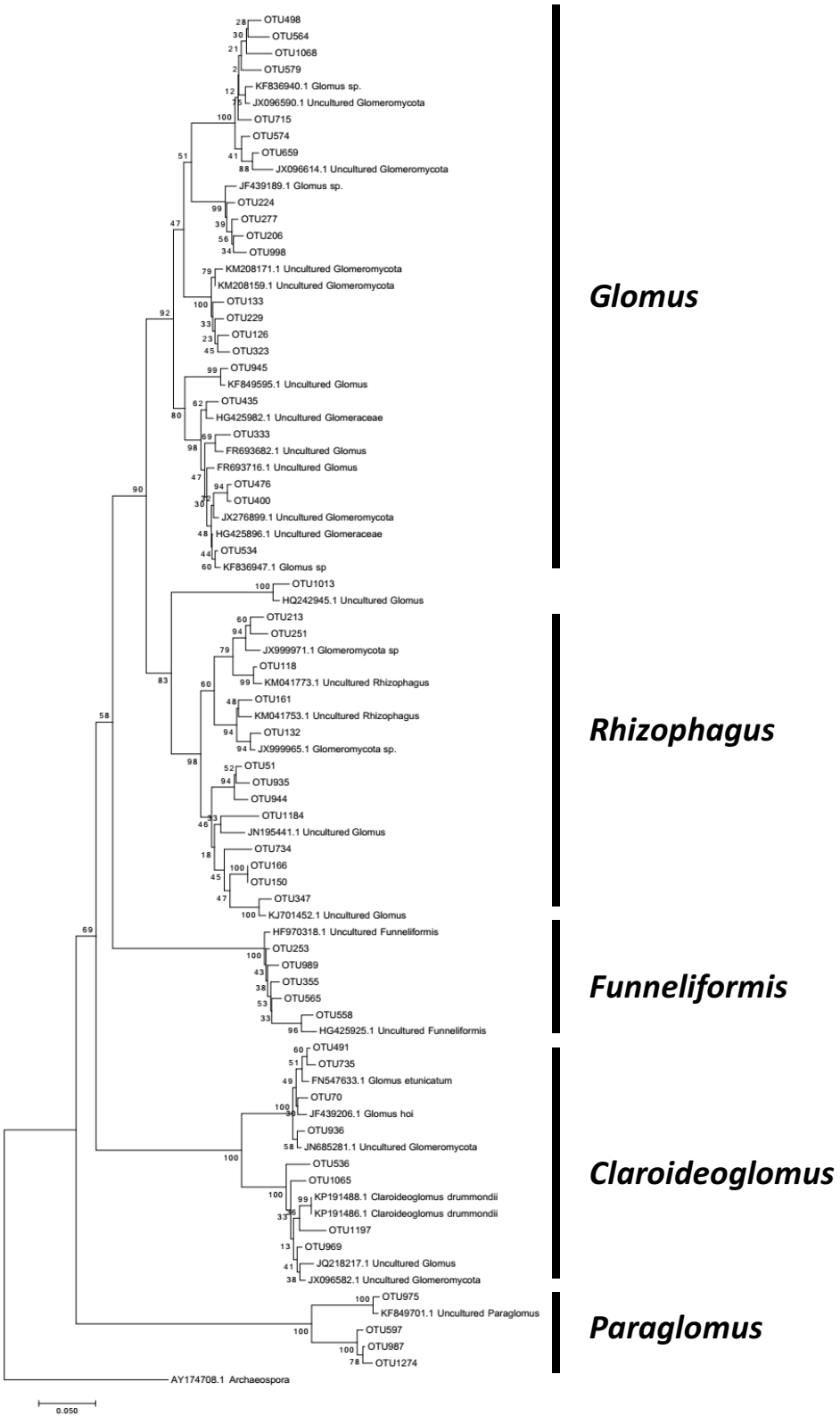

OTU498
OTU564
OTU1068
OTU579
KF836940.1 Glomus sp.
JX096590.1 Uncultured Glomeromycota
OTU715
OTU574
OTU659
JX096614.1 Uncultured Glomeromycota
JF439189.1 Glomus sp.
OTU224
OTU277
OTU206
OTU998
KM208171.1 Uncultured Glomeromycota
KM208159.1 Uncultured Glomeromycota
OTU133
OTU229
OTU126
OTU323
OTU945
KF849595.1 Uncultured Glomus
OTU435
HG425982.1 Uncultured Glomeraceae
OTU333
FR693682.1 Uncultured Glomus
FR693716.1 Uncultured Glomus
OTU476
OTU400
JX276899.1 Uncultured Glomeromycota
HG425896.1 Uncultured Glomeraceae
OTU534
KF836947.1 Glomus sp
OTU1013
HQ242945.1 Uncultured Glomus
OTU213
OTU251
JX999971.1 Glomeromycota sp
OTU118
KM041773.1 Uncultured Rhizophagus
OTU161
KM041753.1 Uncultured Rhizophagus
OTU132
JX999965.1 Glomeromycota sp.
OTU51
OTU935
OTU944
OTU1184
JN195441.1 Uncultured Glomus
OTU734
OTU166
OTU150
OTU347
KJ701452.1 Uncultured Glomus
HF970318.1 Uncultured Funneliformis
OTU253
OTU989
OTU355
OTU565
OTU558
HG425925.1 Uncultured Funneliformis
OTU491
OTU735
FN547633.1 Glomus etunicatum
OTU70
JF439206.1 Glomus hoi
OTU936
JN685281.1 Uncultured Glomeromycota
OTU536
OTU1065
KP191488.1 Claroideoglomus drummondii
KP191486.1 Claroideoglomus drummondii
OTU1197
OTU969
JQ218217.1 Uncultured Glomus
JX096582.1 Uncultured Glomeromycota
OTU975
KF849701.1 Uncultured Paraglomus
OTU597
OTU987
OTU1274
AY174708.1 Archaeospora
0.050
Glomus
Rhizophagus
Funneliformis
Claroideoglomus
Paraglomus

Fig. S2 Phylogenetic analysis of AMF ITS2 sequences of operational taxonomic units (OTUs) obtained in this study combined with named sequences from UNITE and NCBI. Generic names are applied to clades and the OTUs they contain based on named sequences that share the clade. Representative sequences of AMF OTUs were deposited in GenBank with the accession codes: MG008508 - MG008559. The phylogram is rooted with *Archaeospora* based on (BŁaszkowski et al 2006).

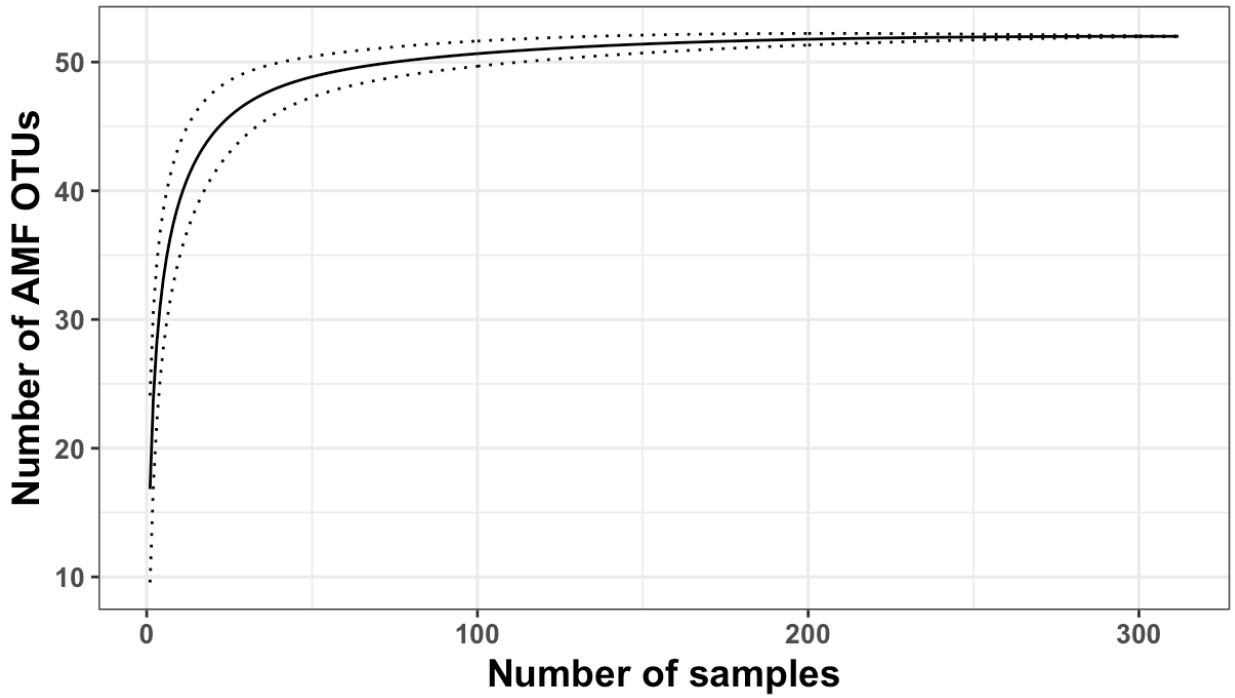


Fig. S3 The AMF species accumulation curve reaching a plateau of 48.86 ± 1.57 of 52 taxa after 50 samples.

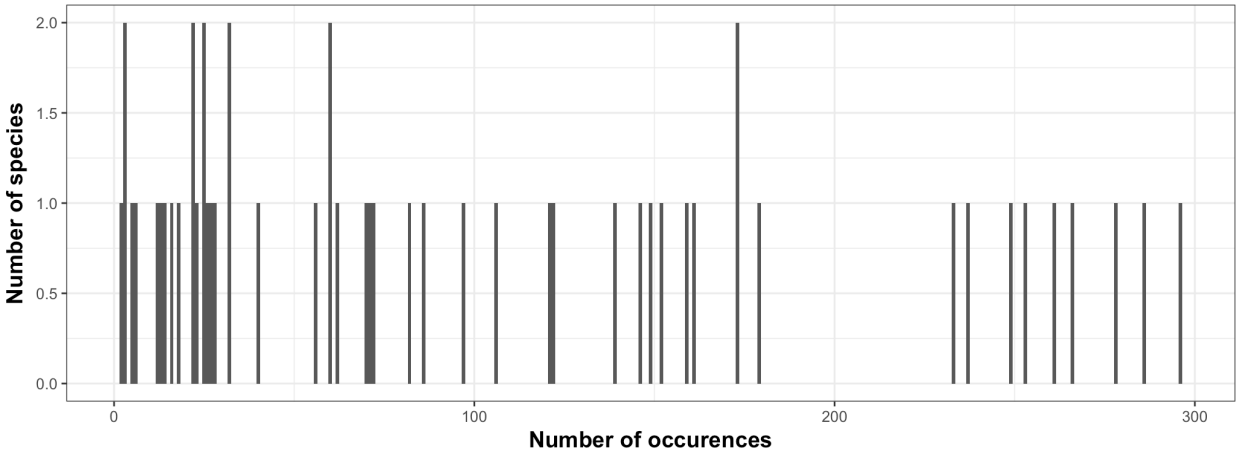


Fig. S4 The frequency of AMF OTUs found in as few as 2 to as many as 296 of all 312 communities sampled. Of the 52 AMF OTUs, only five were found in fewer than 10 samples and six were found in at least 250 samples.

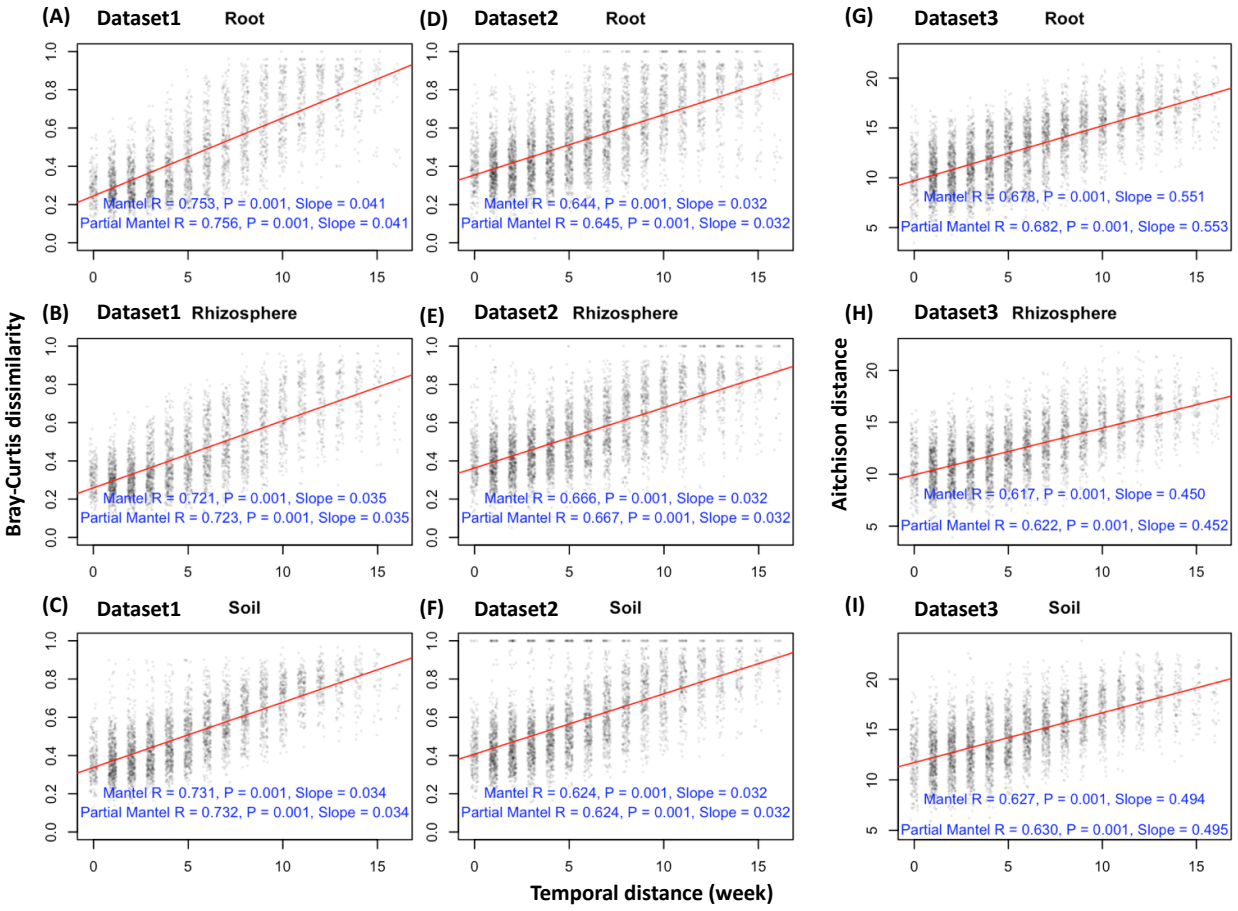
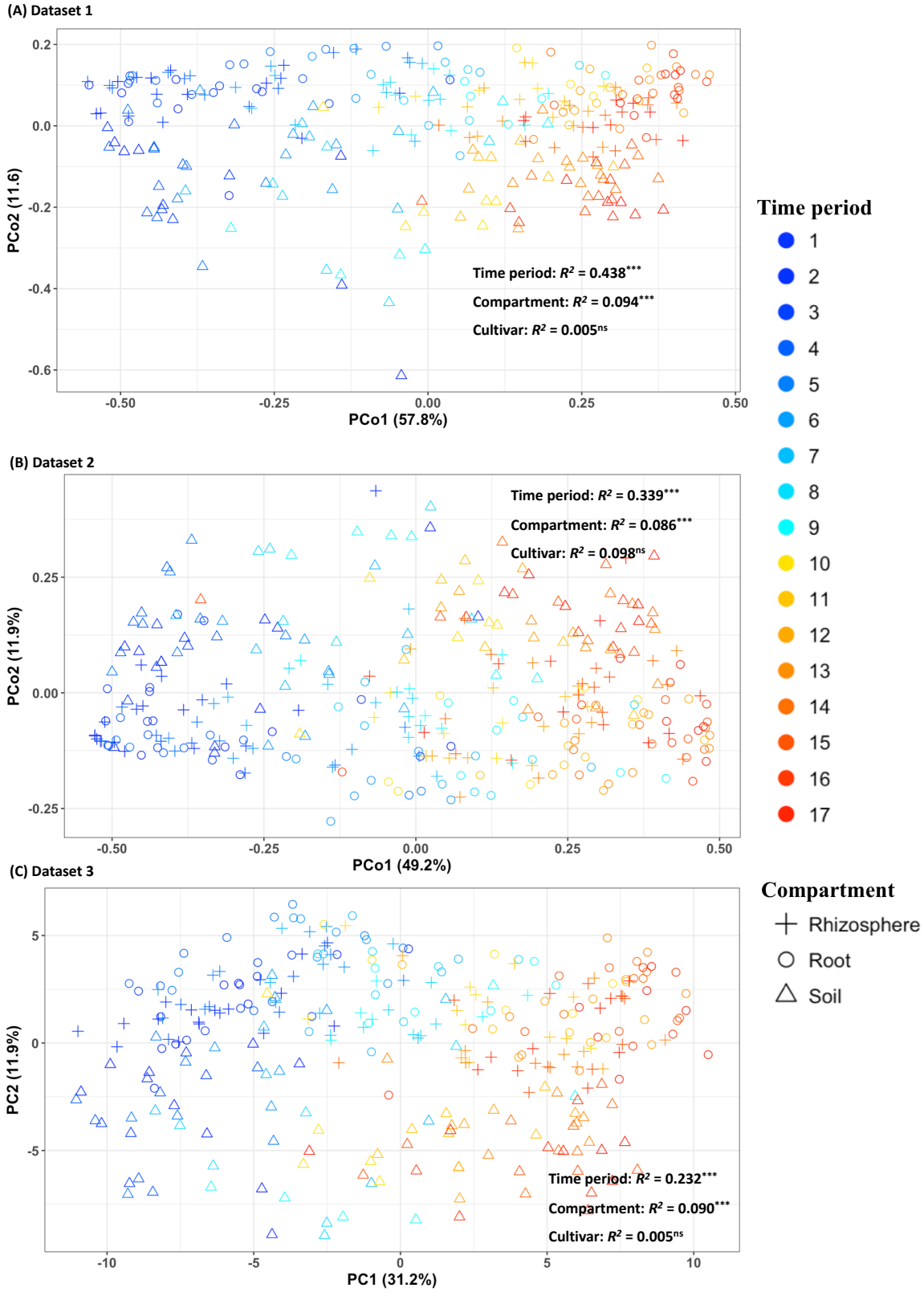


Fig. S5 Comparison of the correlation between AMF community change and temporal distance when treating the DNA sequence data as counts (A-F) or compositional (G-I) (Gloor et al 2017). Note that the result of strong succession is seen regardless of the analytical treatment. AMF datasets (A-C; See Figure 1) rarefied to equal AMF reads (dataset 1), (D-F) rarefied to equal fungal reads (dataset 2), and (G-I) transformed by the centered log-ratio method (dataset 3).


(A) Dataset 1
PCo2 (11.6)
PCo1 (57.8%)
Time period: R^2 = 0.438***
Compartment: R^2 = 0.094***
Cultivar: R^2 = 0.005ns
(B) Dataset 2
PCo2 (11.9%)
PCo1 (49.2%)
Time period: R^2 = 0.339***
Compartment: R^2 = 0.086***
Cultivar: R^2 = 0.098ns
(C) Dataset 3
PC2 (11.9%)
PC1 (31.2%)
Time period: R^2 = 0.232***
Compartment: R^2 = 0.090***
Cultivar: R^2 = 0.005ns
Time period
1
2
3
4
5
6
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8
9
10
11
12
13
14
15
16
17
Compartment
Rhizosphere
Root
Soil

Fig. S6 Comparison of change in 17 weekly samples of composition of arbuscular mycorrhizal fungal communities of soil, rhizosphere and root when treating the DNA sequence data as counts (A, B) or as compositional (C). AMF datasets (A) rarefied to equal AMF reads (dataset 1) (see Figure 2A), (B) rarefied to equal fungal reads (dataset 2), and (C) transformed by the centered log-ratio method (dataset 3). As seen in Figure 2A, the strongest correlation is between community composition and time period, a result returned by all three methods of analysis. PCo: principal coordinate; PC: principal component.

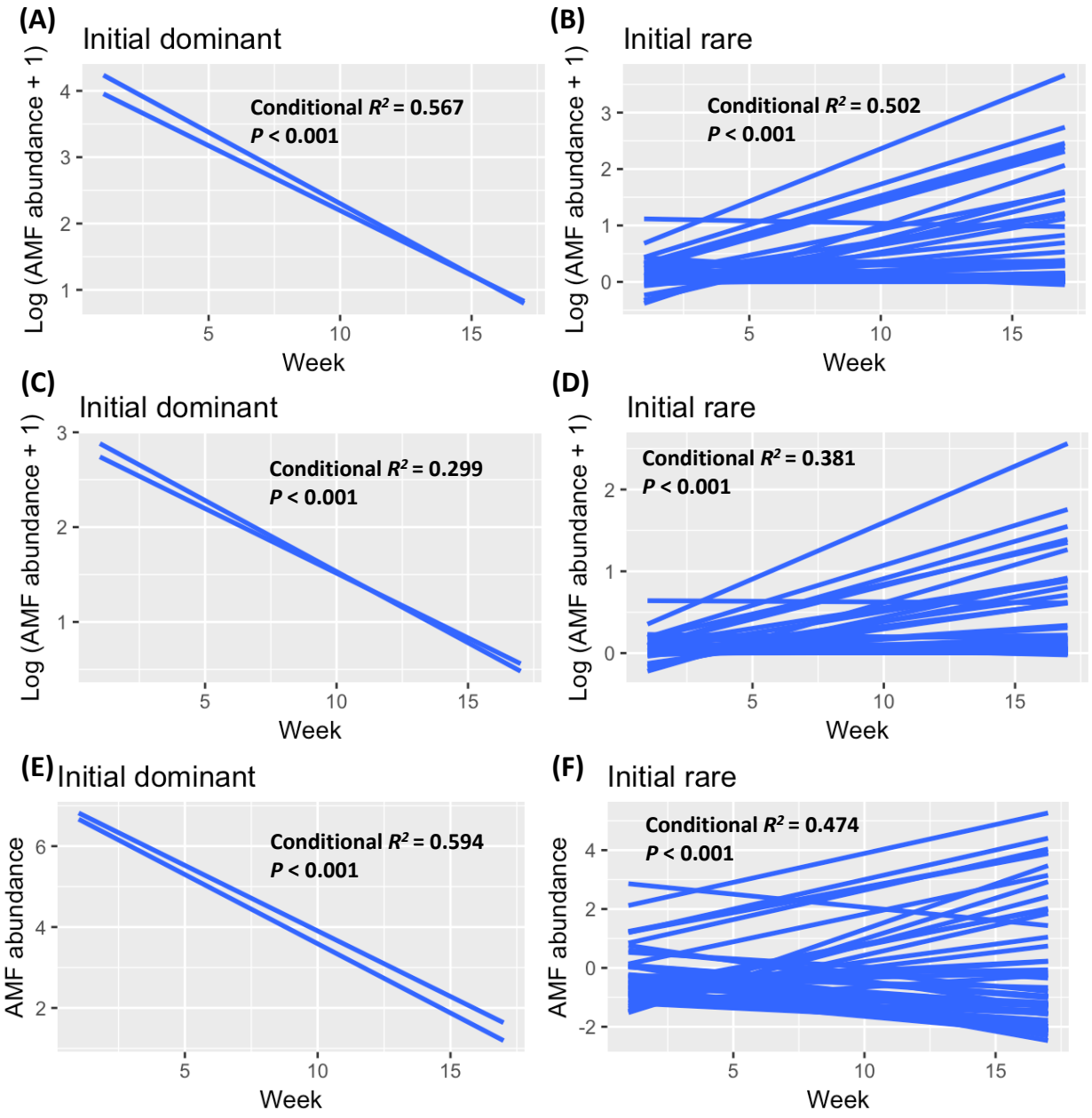


Fig. S7 Comparison of temporal change in initial dominant and initial rare arbuscular mycorrhizal fungal OTUs when treating the DNA sequence data as counts (A-D) or as compositional (E-F). AMF datasets (A-B, See Fig. 6) rarefied to equal AMF reads (dataset 1), (C-D) rarefied to equal fungal reads (dataset 2), and (E-F) transformed by the centered log-ratio method (dataset 3). Note

119 that the results are almost identical whether the data are treated as counts or considered to be
120 compositional.

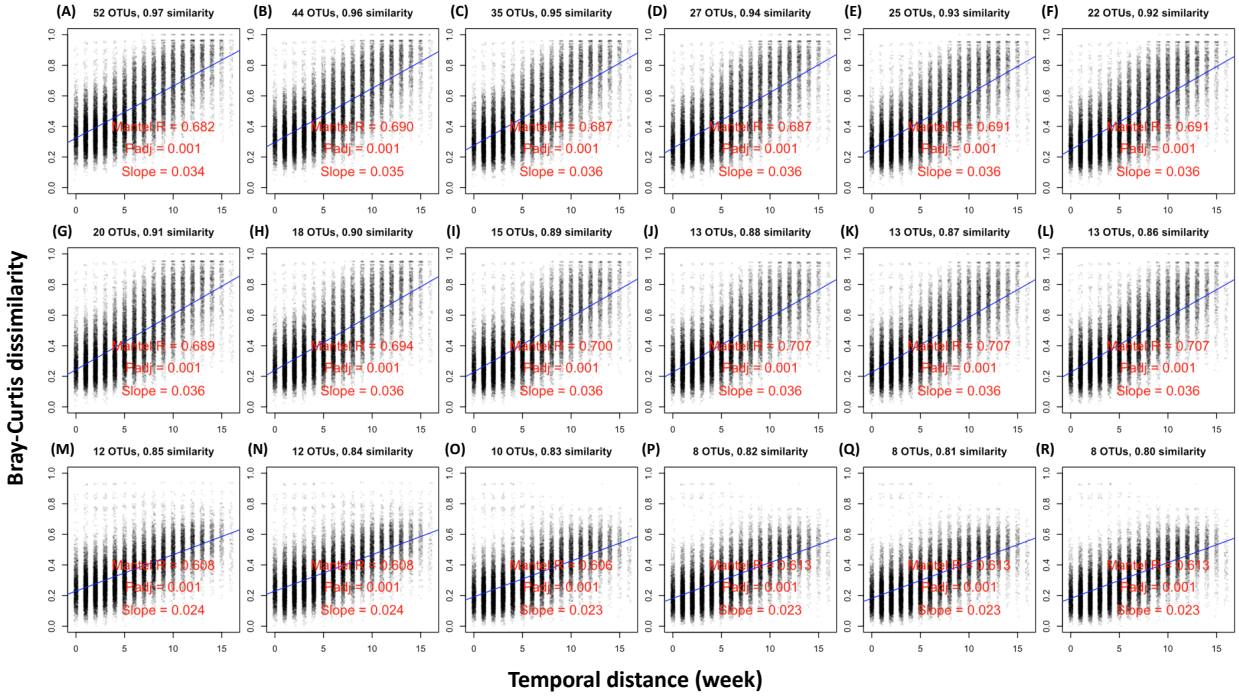


Fig. S8 Mantel correlation between temporal distance and Bray-Curtis dissimilarity of arbuscular mycorrhizal fungal (AMF) communities determined by reducing the sequence similarity used to delineate OTUs. Sequence similarities: (A) 97%, (B) 96%, (C) 95%, (D) 94%, (E) 93%, (F) 92%, (G) 91%, (H) 90%, (I) 89%, (J) 88%, (K) 87%, (L) 86%, (M) 85%, (N) 84%, (O) 83%, (P) 82%, (Q) 81% and (R) 80%. To improve visualization, we added a small amount of noise to the temporal distance and rendered the points transparent. The P value was adjusted by the Bonferroni method, to avoid the type-I error of multiple testing. **Note the sharp drop of association between community dissimilarity and temporal distance that occurred between the 86% cutoff (L) (slope = 0.036) and the 85% cutoff (M) (slope = 0.024). The slopes were stable prior to this point, 97% (A) to 86% (L), (slope = 0.034 -0.036) and after it, 85% (M) to 80% (R) (slope = 0.023 – 0.024).**

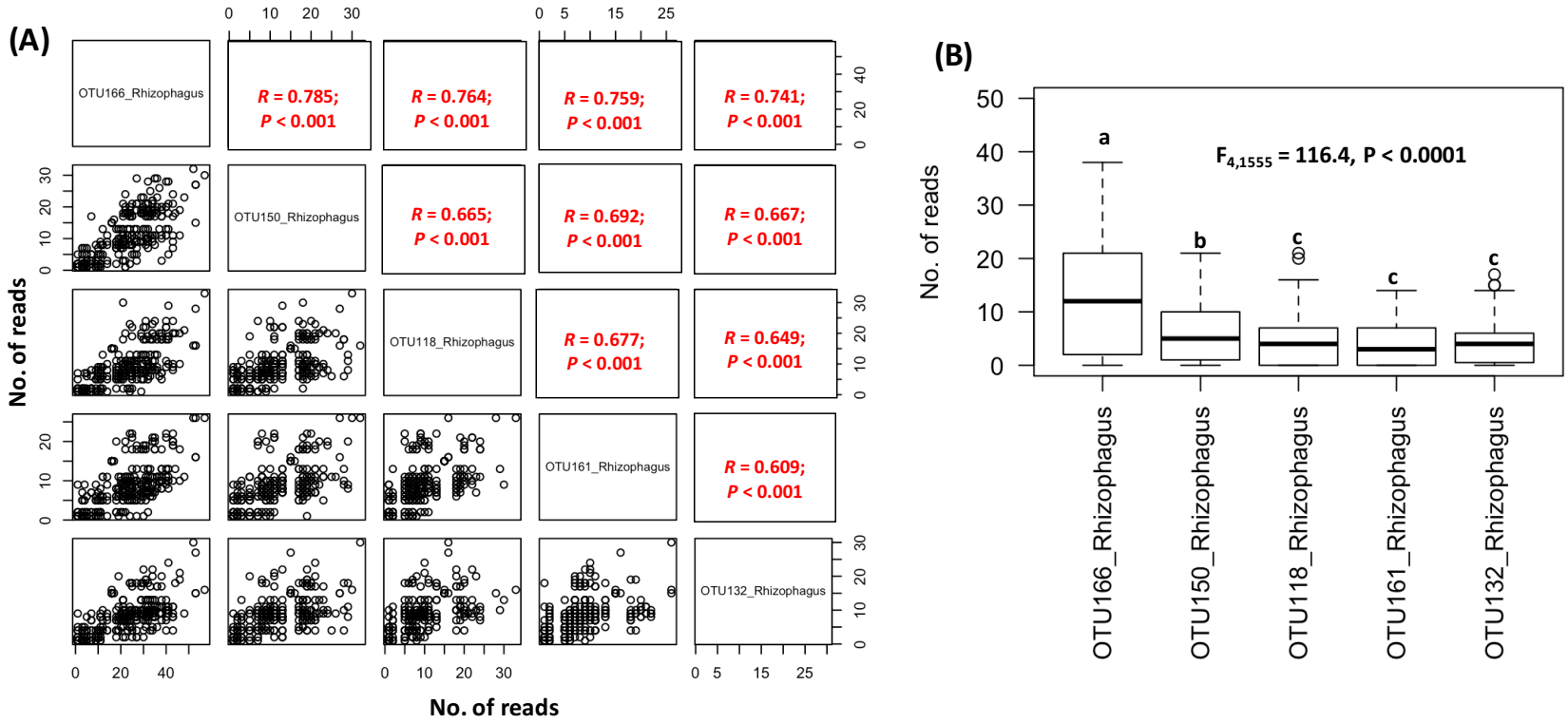
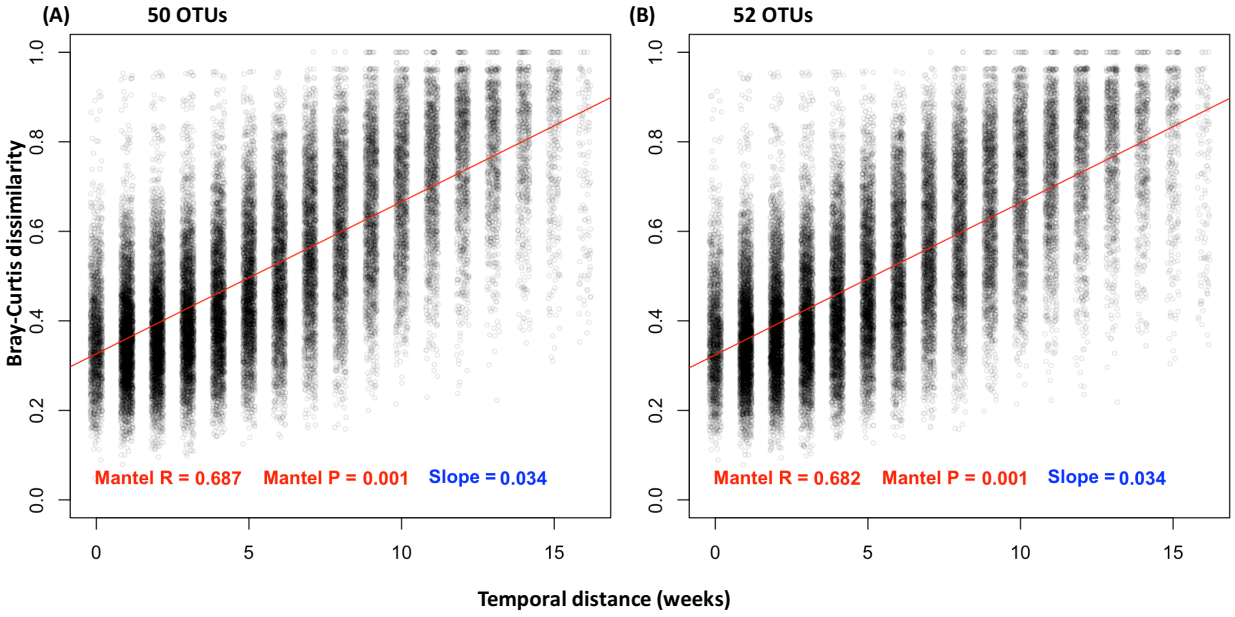


Fig. S9 Using the pattern and abundance of internal transcribed spacer 2 (ITS2) reads to identify possible cases of more than one ITS2 sequence in a single arbuscular mycorrhizal fungal (AMF) operational taxonomic unit (OTU). (A) Strong correlation (all $P < 0.001$) among abundance of five *Rhizophagus* OTUs. (B) Differences in the abundance among five *Rhizophagus* OTUs. Bars without shared letters indicate significant differences as determined by Tukey HSD. Based on their strongly correlated (A) and equalized abundance

(B), three OTUs (118, 161 and 132) were treated as a single species. Other two OTUs (166 and 150) were treated as different species because their abundances were unequal, despite their similar behavior.



142

143 **Fig. S10** Comparison of succession analyses with 50 or 52 arbuscular mycorrhizal fungal (AMF)
144 operational taxonomic units (OTUs). No substantial difference in the succession pattern of AMF
145 communities with three OTUs, i.e., 118, 161, 132 possibly belonging to one species, were (A)
146 combined (50 OTUs dataset) or (B) not (52 OTUs dataset), as demonstrated by Mantel test between
147 temporal distance and AMF Bray-Curtis dissimilarity. To improve visualization, we added a small
148 amount of noise to the temporal distance and rendered the points transparent.

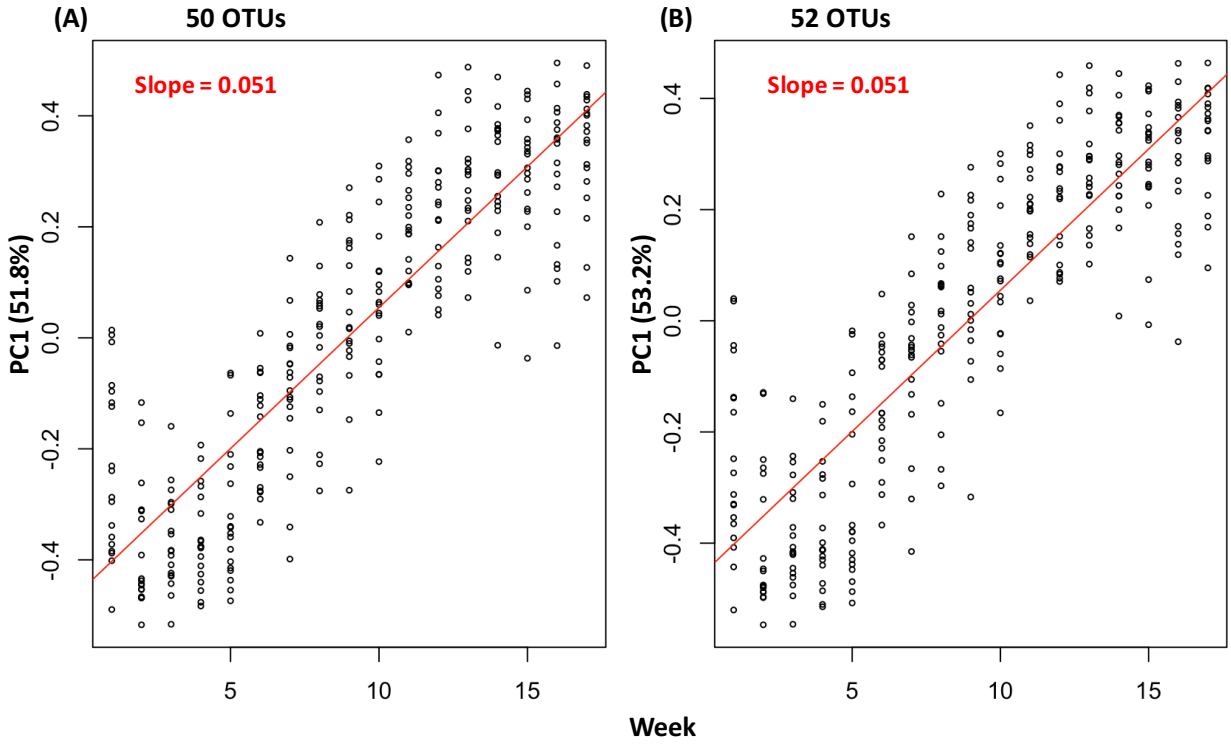
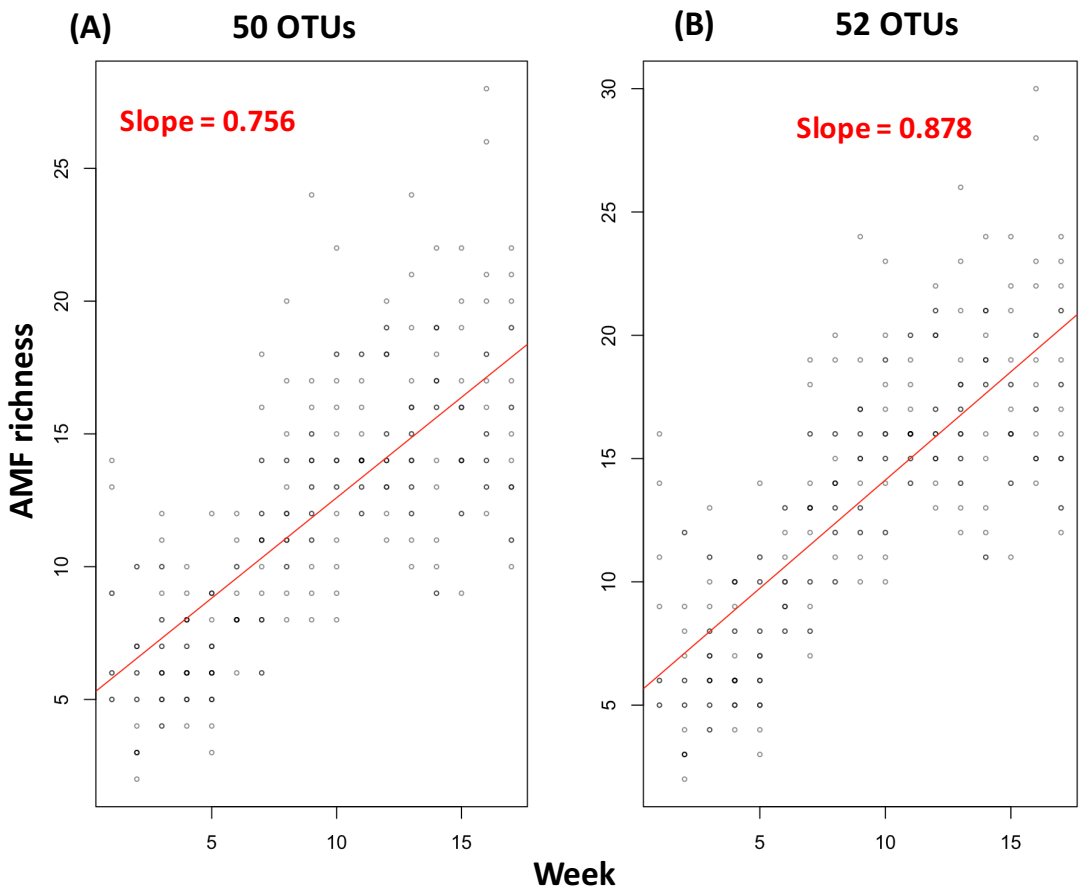


Fig. S11 Comparison of principal coordinate (PC) analyses with 50 or 52 arbuscular mycorrhizal fungal (AMF) operational taxonomic units (OTUs). No substantial difference in the temporal dynamic of AMF communities with three OTUs, i.e., 118, 161, 132 possibly belonging to one species, were (A) combined (50 OTUs dataset) or (B) not (52 OTUs dataset), as demonstrated by correlation between time and the first axis of PC analysis of AMF community



155

156 **Fig. S12** Comparison of richness with 50 or 52 arbuscular mycorrhizal fungal (AMF) operational
157 taxonomic units (OTUs). No substantial difference in the temporal dynamic of AMF richness
158 with three OTUs, i.e., 118, 161, 132 possibly belonging to one species, were (A) combined (50
159 OTUs dataset) or (B) not (52 OTUs dataset), as demonstrated by correlation between time and
160 the AMF richness.

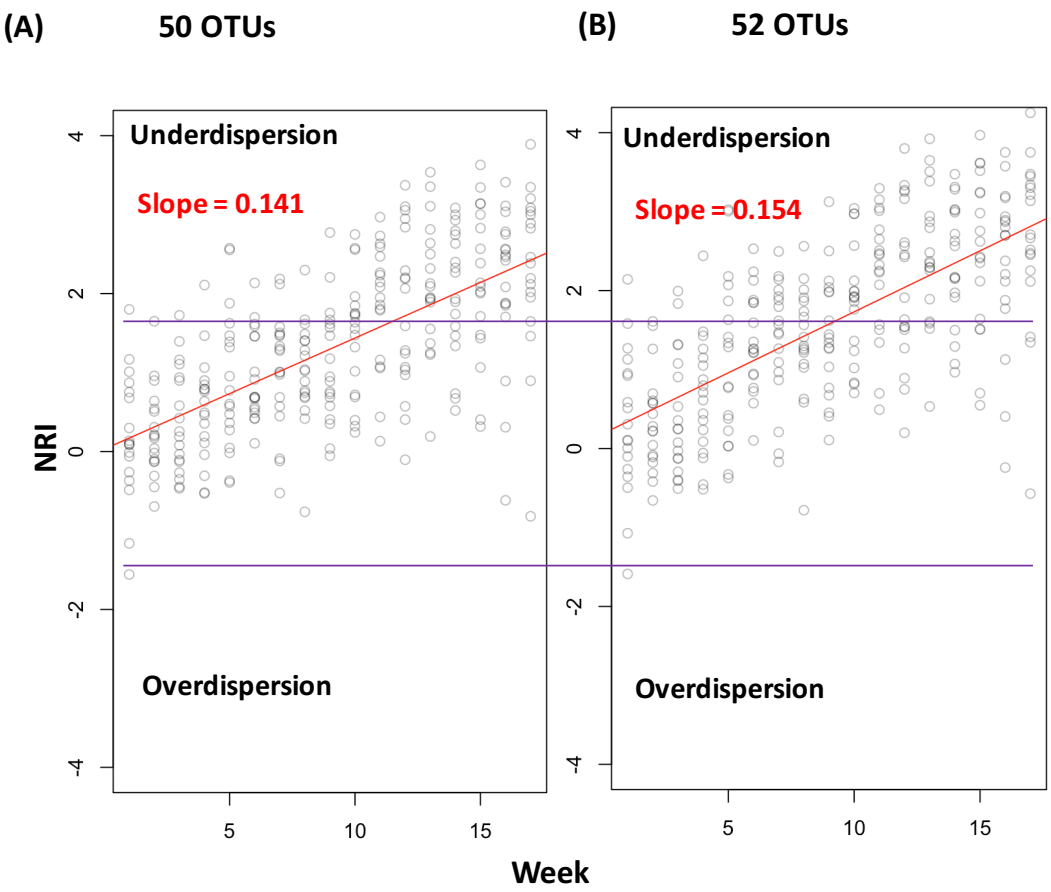
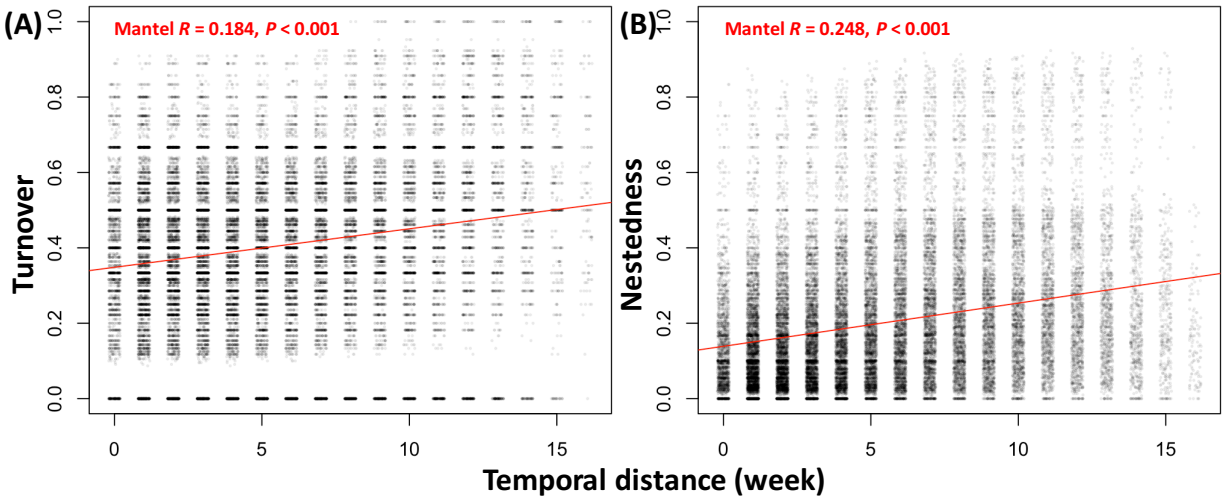
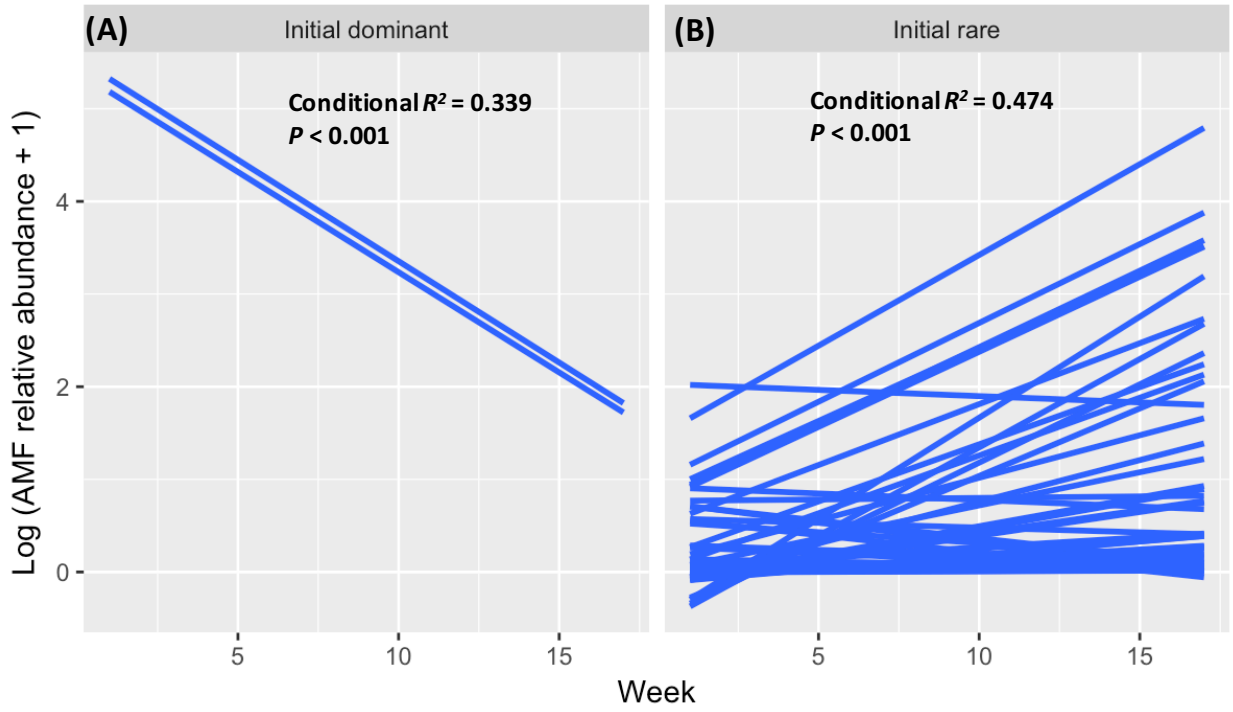


Fig. S13 Comparison of phylogenetic relatedness analyses with 50 or 52 arbuscular mycorrhizal fungal (AMF) operational taxonomic units (OTUs). No substantial difference in the temporal dynamic of net relatedness index (NRI) of AMF with three OTUs, i.e., 118, 161, 132 possibly belonging to one species, were (A) combined (50 OTUs dataset) or (B) not (52 OTUs dataset), as demonstrated by correlation between time and the AMF NRI. Note both datasets showed increases of NRI over time resulting in eventual, significant (above the upper purple horizontal line) underdispersion.



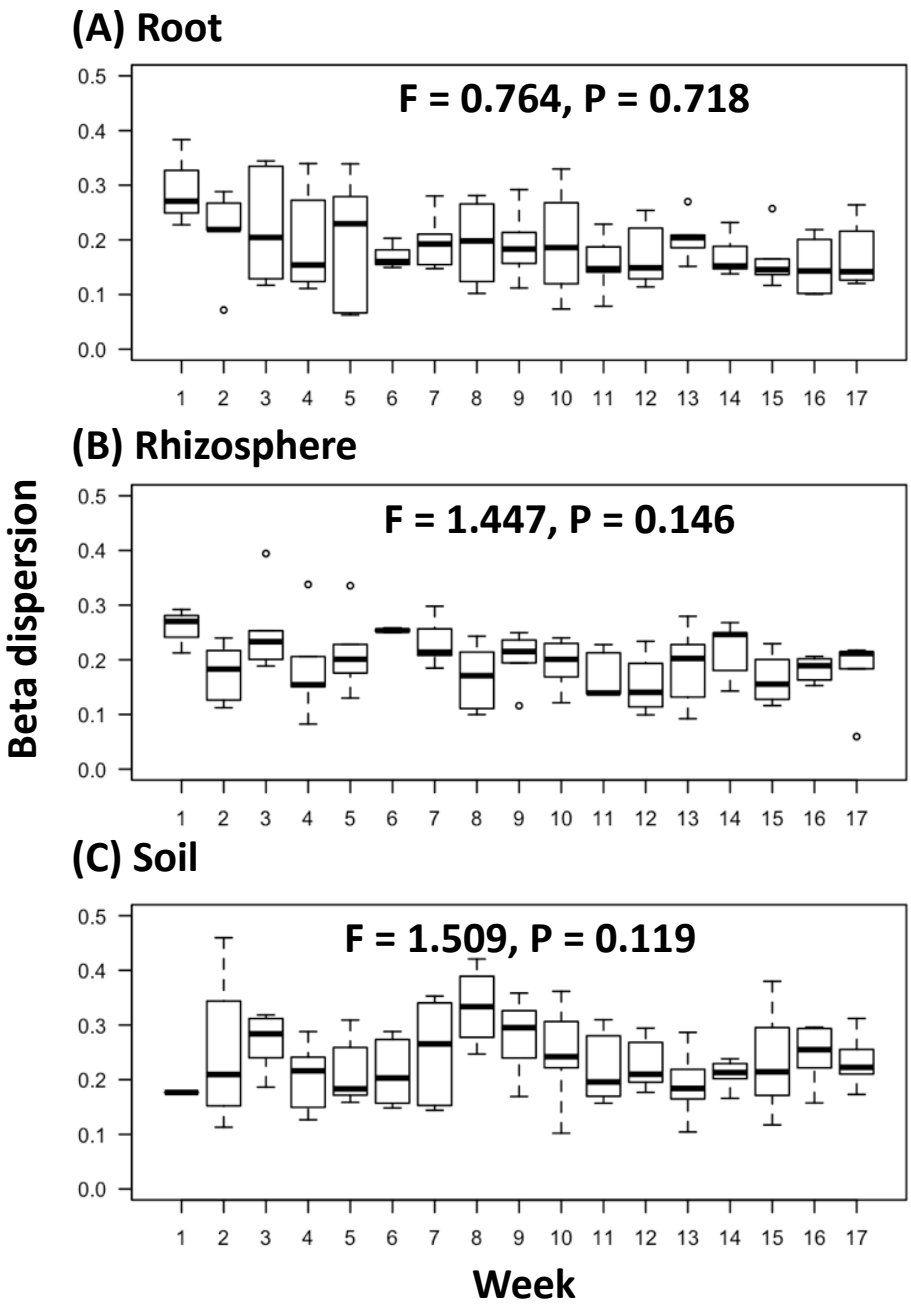
169

170 **Fig. S14** Comparison of temporal distance and turnover and nestedness with 50 (Fig. 5) or 52
171 arbuscular mycorrhizal fungal (AMF) operational taxonomic units (OTUs). Both patterns of (A)
172 turnover and (B) nestedness of AMF community over time are detected by Mantel test of the
173 correlation between temporal distance and turnover and nestedness. To improve visualization, we
174 added a small amount of noise to the temporal distance and rendered the points transparent. Note
175 three OTUs, i.e., 118, 161, 132 possibly belonging to one species, were not combined in this
176 analysis, and the results are not substantially different from those that were combined (Fig. 5).



177

178 **Fig. S15** Comparison of time and abundance analyses with 50 (Fig. 6) or 52 arbuscular mycorrhizal
179 fungal (AMF) operational taxonomic units (OTUs). Relationships between time and abundance of
180 initial dominant AMF OTUs, and initial rare AMF OTUs, as explored by linear mixed-effects
181 models, including random effects of AMF identity. The conditional R^2 that can be interpreted as
182 the variance explained by the mixed effect model was calculated. Note three OTUs, i.e. 118, 161,
183 132 possibly belonging to one species, were not combined in this analysis, and the results are not
184 substantially different from those that were combined (Fig. 6)



185

186 **Fig. S16** Permuted beta-dispersion to test the community homogeneity of the arbuscular

187 mycorrhizal fungal (AMF) communities within every sampling time period (TP) in (A) root, (B)

188 rhizosphere, and (C) soil. Note the homogeneity of AMF community variances across all TPs in

189 root, rhizosphere and soil, due to the lack of significant differences among TPs.

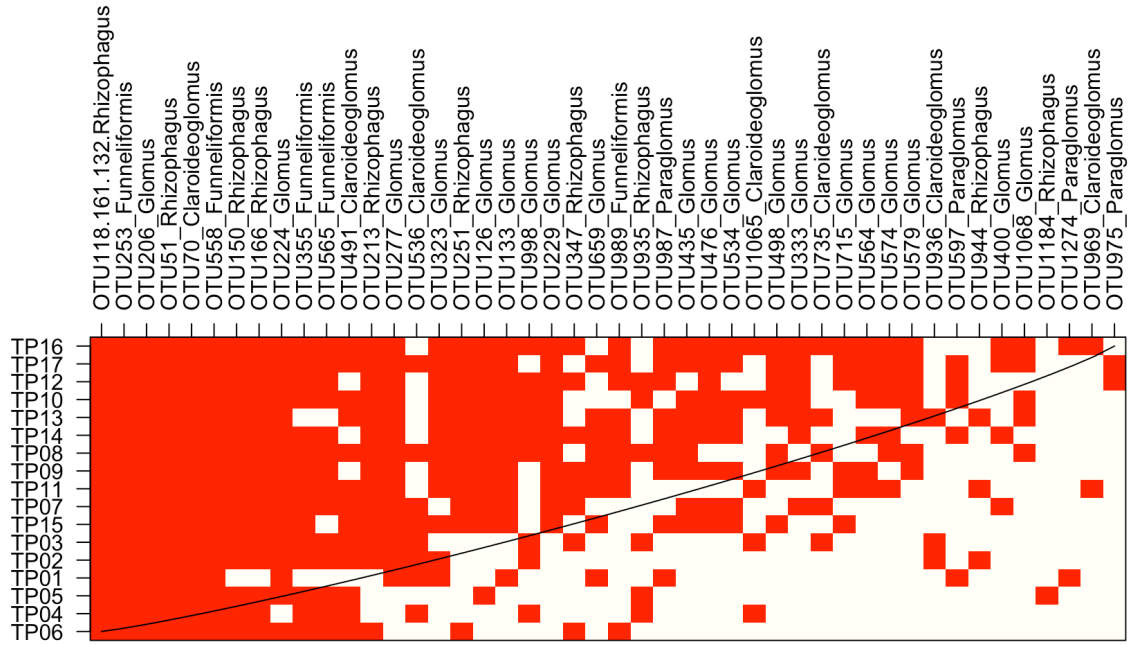


Fig. S17 Root samples showing a nested pattern of arbuscular mycorrhizal fungal (AMF) operational taxonomic units (OTUs) occurrence (in red) with time period (TP). Matrix of time × AMF is sorted to maximize nestedness by nestedtemp function in vegan package in R. The curved line shows isoclines of prefect nestedness.

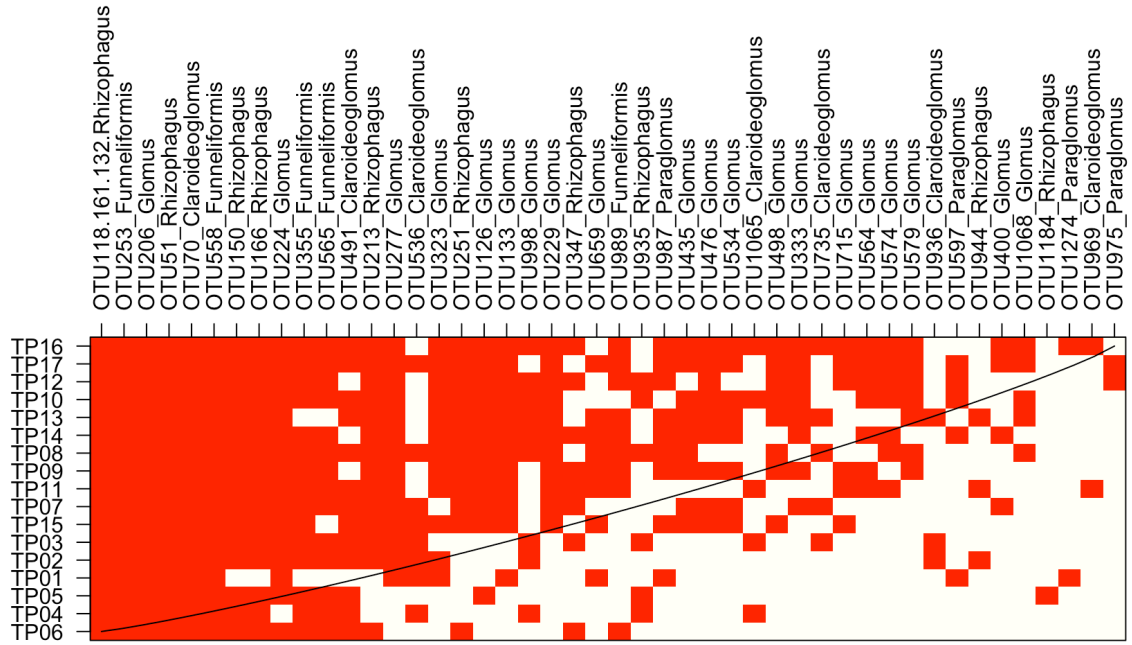


Fig. S18 Rhizosphere samples showing a nested pattern of arbuscular mycorrhizal fungal (AMF) operational taxonomic units (OTUs) occurrence (in red) with time period (TP). Matrix of time × AMF is sorted to maximize nestedness by nestedtemp function in vegan package in R. The curved line shows isoclines of prefect nestedness.

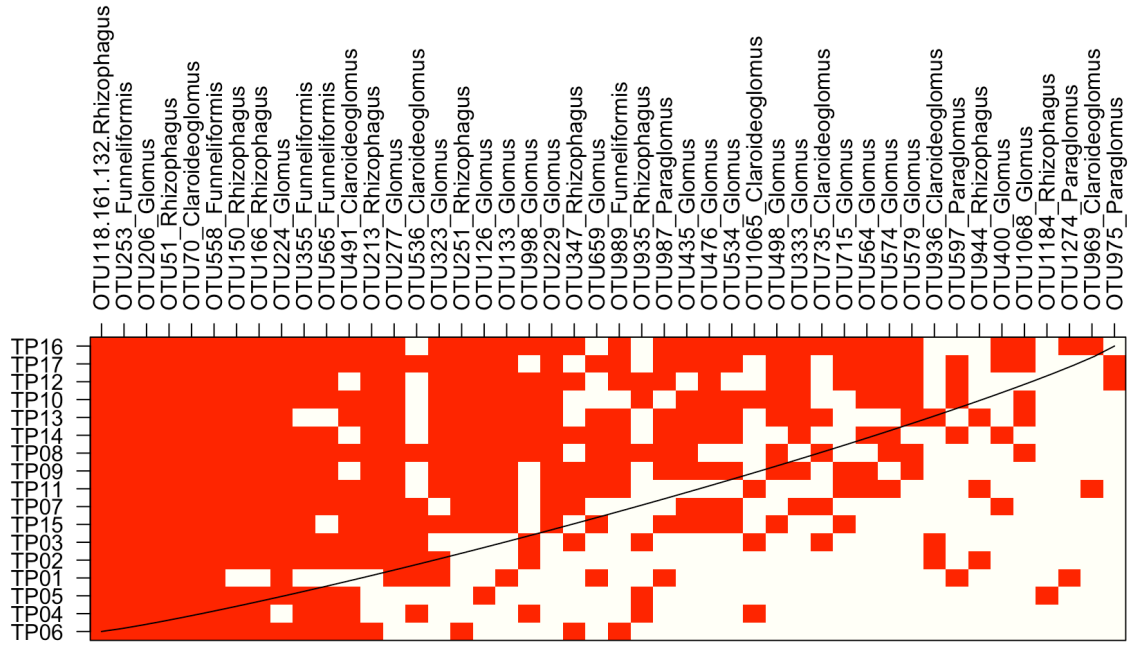


Fig. S19 Soil samples showing a nested pattern of arbuscular mycorrhizal fungal (AMF) operational taxonomic units (OTUs) occurrence (in red) with time period (TP). Matrix of time × AMF is sorted to maximize nestedness by nestedtemp function in vegan package in R. The curved line shows isoclines of prefect nestedness.

206

Table S1 A list of studies investigating the temporal dynamics of arbuscular mycorrhizal fungal (AMF) communities. Note succession of AMF communities often cannot be fully acknowledged due to (i) the lack of intensity sampling, (ii) poor AMF recognition resolution, and (iii) confounding influences by history, geography, climate and environments

Study	**Ecosystem**	**AMF recognition**	**Sampling time**	**Sample type**	**Temporal change**
(Bainard et al 2014)**	Farmed pea, lentil and wheat in temperate semiarid prairie	454 sequencing of AMF SSU	Four, tri-week samples	Root, soil	AMF richness, community composition, and net relatedness index changed by time.
(Yu et al 2012)	Pea grown in climate chamber	454 sequencing of fungal ITS	Vegetative growth, flowering, senescence	Root	Abundance of a *Glomus* AMF decreased, a *Paraglomus* AMF increased, and two *Glomus* AMF not changed with time
(Zeng et al 2014)	Maize farmed in subtropical China	tRFLP	Seedling, large ball, matured	Root, soil	AMF diversity and community composition were not influenced by sampling time
(Liu et al 2016)	Maize planted in temperate China	tRFLP	6-leaf, 13-leaf, kernel dough	Root	AMF community richness and composition changed by plant develop stage
(Bainard et al 2012)	Maize monocropped or intercropped by tree	tRFLP	Four, monthly samples (May-August)	Root	AMF community composition changed by time
(Turrini et al 2016)	Crop-maize succession	Sanger sequencing of AMF SSU	April and June	Root	AMF community composition differed between these two seasons
(Higo et al 2014, Higo et al 2015)	Soybean field with different winter rotation type in Japan	Sanger sequencing of AMF LSU	Five years (the flowering time of every year)	Root	AMF community composition differed by year
(Davison et al 2012)*	Temperate mixed forest	454 sequencing of AMF SSU	Four, monthly samples	Soil	AMF was not changed by time in ref. ; AMF community composition changed by time weakly, as demonstrated by reanalysis of ref. .

(Voříškov á et al 2014)**	Temperate oak woodland	454 sequencing of fungal ITS	Four, seasonal samples	Soil	AMF community composition changed by time, as demonstrated by reanalysis of ref. .
(Helgason et al 2014)*	Maples (eight spp.) in England garden	tRFLP	April, June, October	Root	Both AMF richness and composition affected by the three seasons
(López-García et al 2014)	Rosemary seedlings, in a mesocosm system	tRFLP	Every three months in two years	Root	AMF community composition was affected by season
(Varela-Cervero et al 2016)	Temperate forest, 5 tree species	tRFLP	Autumn, spring	Root Soil	AMF community composition was reported to be influenced by season in root, but not in soil.
(Dumbrell et al 2011)	Temperate grassland	454 sequencing of AMF SSU	11 samplings in 8 months	Root	AMF community composition differed between summer and winter; AMF beta diversity declined from Nov. to July.
(Montero Sommerfe ld et al 2013)*	Grasslands in Chile	tRFLP	August, January	Root	AMF richness and composition significantly different between winter and summer
(Hazard et al 2014)	Pasture and arable field in Ireland	tRFLP	Six samplings in two years (Mar, June, Oct, Jan, Mar, Oct)	Root	AMF richness and composition changed by season
(Barnes et al 2016b)	Short rotation coppice willow plantation in UK	tRFLP	Four times a year (Oct, June, Aug, Oct)	Root	The spatial distance-decay pattern of AMF community changed by time
(Barnes et al 2016a)	*Miscanthus giganteus* plantation in UK	tRFLP	Four times a year (Oct, June, Aug, Oct)	Root	AMF richness and community composition changed over time
(Bouffaud et al 2017)	Four long-term observatories in Europe	454 sequencing of AMF ITS2	Spring, autumn	Soil	AMF community composition is weakly affected by season

(Husband et al 2002a)	Tropical forest (seedlings of two spp. in two sites)	Sanger sequencing of AMF SSU	Two years	Root	AMF community composition changed between years
(Taylor et al 2014)*	Boreal forest	Sanger sequencing of ITS	Two years	Soil	AMF community composition not changed by time, as reanalyzed by
(Husband et al 2002b)	Tropical forest (seedling)	Sanger sequencing of AMF SSU	Four samplings (3 month, 1, 2 and 5 yr)	Root	AMF community composition changed by time
(Helgason et al 1999)	Woodland in UK	RFLP	July vs Dec.	Root	AMF community composition show difference between seasons
(Kabir et al 1997)	Corn grown in Canada	Hyphae	Apr, Jun, Aug and Oct of two years	Root Soil	The levels of intra- and extraradical fungal colonization always increased from spring to silking and decreased thereafter.
(Kivlin and Hawkes 2016)	Monoculture stands of four tree species in Costa Rica	454 sequencing of fungal LSU	Dry and wet season, two years	Soil	AMF richness and PD affected by time
(Daniell et al 2001)	Arable fields around North Yorkshire, UK	Sanger sequencing of SSU	Nine sample times in 14 months	Root	AMF composition changed by time
(Bencherif et al 2016)	Algerian steppic area	Spore	Four seasons	Soil Root	Season affect AMF spore abundance and root colonization rate, but not diversity
(Herrman n et al 2016)	Tropical rubber tree plantation	454 sequencing of AMF SSU	Chronosequence (3, 6, 16 yr)	Root	AMF community composition differed between 3 and 16 yr trees in ordination constrained by soil variables, but not in unconstrained ordination
(Krüger et al 2017)	Temperate woodland recovered from brown-coal mining	454 sequencing of AMF LSU	Spring autumn, Chronosequence (12, 20, 30, 50 yr)	Root	AMF richness and community composition not affected by the chronosequences, but community variation increased along the chronosequences

(Yu et al 2017)	Semiarid grassland and woodland in China	Spore	Chronosequence (12 yr v.s. 30yr planted Caragana microphylla)	Soil	No significant differences in community composition and diversity of AM fungi were recorded at the dunes with different revegetation duration.
(Liu et al 2009)	Temperate tree plantation in China	DGGE	Three seasons Chronosequence (5, 13, 20, 42 yrs)	Root	AMF richness was not influenced by the chronosequences, but AMF community composition was affected by season
(Sheng et al 2017)	Temperate black locust plantations in China	454 sequencing of SSU	Chronosequence (11, 23, 35, 46 yr)	Root Soil	AMF community composition changed by plant age. AMF spore density increased with plant age. AMF richness not linearly related to plant age
(Hart et al 2014)	Tropical long-lived perennial breadfruit trees	454 sequencing of AMF SSU	Chronosequence (5-6, 20-21, 42-40 yr)	Root Soil	AMF richness increased with age in root, but not in soil; AMF community composition differ between young and old trees
(Guadarrama et al 2014)	Mexican seasonal dry forests	Spore	Chronosequence (<5 yr, 11-23 yr, >30 yr) Wet vs dry season	Soil	AMF diversity was affected by season and age
(García de León et al 2016b)	Temperate alvar grasslands	454 sequencing of AMF SSU	Chronosequence (young (20 yr), intermediate (50 yr), mature)	Soil Root	AMF community composition differed between young and mature grasslands, but not between intermediate and mature grasslands.
(Honnay et al 2017)	Grassland of Belgium	454 sequencing of SSU	Chronosequence (Forested, 8-11yr, 12-20yr, ancient)	Root Soil	AMF richness and community composition were affected by successional stages
(Roy et al 2017)	Recultivation after open-cast mining in Germany	Illumina sequencing of AMF LSU	Chronosequence (2013-2015, 2011-2012, 1964-2006)	Soil	AMF community composition differed among the three phases
(Johnson et al 1991)	Abandoned fields in Minnesota	Spore	Chronosequence (12 samples of 1-60 years)	Soil	AMF richness was not influenced by the chronosequence, but AMF Shannon's diversity index increased

(Kowalchuk et al 2002)	Dunes in Netherlands	DGGE	Chronosequence (Vigorous vs degenerating stand)	Root Soil	AMF diversity is lower in the later, degraded stages
(Oba et al 2004)	Recovery from volcanic deposits in Philippines	Spore	Chronosequence (Sites with sparse or dense vegetation)	Soil	AMF diversity and composition were not significantly differed between two sites
(Pezzani et al 2006)	Two-phase mosaics in Mexican Chihuahuan Desert	Spore	Chronosequence (Pioneer vs late-successional grasses)	Soil	Spore density was higher in late than in early successional stages
(Wu et al 2007)	Primary successional volcanic desert in Japan	Spore	Chronosequence (Different altitudes)	Root Soil	AMF spore abundance, richness of morphtypes increased with decreasing altitue
(Oehl et al 2011)	Retreat of Glacier in Alps	Trap culture	Chronosequence (1875–1900, 1940–1950, 1970–1980 and 1990–2000)	Soil	AMF diversity increased with succession
(Sikes et al 2012)	Sand dune in Michigan, USA	Sanger sequencing	Chronosequence (10- 35 yr, 235- 295 yr, 450-845 yr)	Soil	AMF isolated from early succession were more phylogenetically diverse relative to intermediate and late succession while late successional fungi consistently produced more soil hyphae and arbuscules.
(Gorzelak et al 2017)	Temperate rainforests of British Columbia	454 sequencing of LSU	Chronosequence Young, mature and old)	Root Soil	No differences in richness along the host chronosequence. AMF community composition was affected by age weakly. All host age classes harboured AMF communities that were overdispersed
(Bennett et al 2013)	Re-analysis of and		Chronosequence (Young, old) June, July, October		Succession affect connectance and H2, sampling time affect link/specie of plant-AMF symbiotic network

(Krüger et al 2015)	Dunes in Australia	454 sequencing of LSU	Chronosequence (1000 yr, 120 000 yr, > 2 000 000 yr soil)	Root Soil	AMF richness peaked in the middle age. AMF community composition differed among the three stages
(Martínez-García et al 2015)	New Zealand	tRFLP, Sanger sequencing and 454 sequencing of SSU	Chronosequence (15 yr, 5000 yr, 12 000 yr, 60 000 – 120 000 yr)	Root	AMF community composition changed by successional stage
(Koziol and Bever 2016)	12 plant spp. forming a successional gradient				Mycorrhizal responsiveness change with plant successional status
(Senés-Guerrero and Schüßler 2016)	Potato Bolivia, Ecuador and Peru	454 sequencing of LSU	emergence, flowering and senescence 105 samples = 3 sites * 3 stages * 3 replicates * 4 altitudes	Root	a surprisingly conserved AMF core-species community structure in Andean potatoes, regardless of different plant stages and environmental factors

*Re-analyzed by Bahram et al (2015); **Also re-analyzed by this study in Fig. 2. SSU: small subunit; LSU, large subunit; ITS: internal transcribed spacer; DGGE: Denaturing Gradient Gel Electrophoresis; tRFLP, terminal restriction fragment length polymorphism.

209

Table S2 The forward and reverse primers that we constructed to be used for Illumina Miseq PE300 in this study. Note we constructed 24 forward and 24 reverse primers that, via a dual-indexing approach, enable us to sequence up to 576 samples in a Miseq PE 300 lane.

Primer Name	LINKER	BARCODE	PAD	SPACER	PRIMER	COMPLETE
5.8SFun_S_24_01	AATGATACGGCGACCACCGAGATCTAC	CCTAAACT	ACGG	TCTTTCCCTACACGACGCTCTTCCGATCT		AACTTTYRRCAAYGGATCWCT	AATGATACGGCGACCACCGAGATCTACACCCTAAACTACGGTCTTTCCCTACACGACGCTCTTCCGATCTAACTTTYRRCAAYGGATCWCT
5.8SFun_S_24_02	AATGATACGGCGACCACCGAGATCTAC	GTGGTATG	GGAG	TCTTTCCCTACACGACGCTCTTCCGATCT	T	AACTTTYRRCAAYGGATCWCT	AATGATACGGCGACCACCGAGATCTACACGTGGTATGGGAGTCTTTCCCTACACGACGCTCTTCCGATCTTAACTTTYRRCAAYGGATCWCT
5.8SFun_S_24_03	AATGATACGGCGACCACCGAGATCTAC	TGTTGCGT	TTCT	TCTTTCCCTACACGACGCTCTTCCGATCT	GT	AACTTTYRRCAAYGGATCWCT	AATGATACGGCGACCACCGAGATCTACACTGTTGCGTTTCTTCTTTCCCTACACGACGCTCTTCCGATCTGTAACTTTYRRCAAYGGATCWCT
5.8SFun_S_24_04	AATGATACGGCGACCACCGAGATCTAC	ACAGCCAC	CCAT	TCTTTCCCTACACGACGCTCTTCCGATCT	CGA	AACTTTYRRCAAYGGATCWCT	AATGATACGGCGACCACCGAGATCTACACACAGCCACCCATTCTTTCCCTACACGACGCTCTTCCGATCTCGAAACTTTYRRCAAYGGATCWCT
5.8SFun_S_24_05	AATGATACGGCGACCACCGAGATCTAC	GTTACGTG	GTTG	TCTTTCCCTACACGACGCTCTTCCGATCT	ATGA	AACTTTYRRCAAYGGATCWCT	AATGATACGGCGACCACCGAGATCTACACGTTACGTGGTTGTCTTTCCCTACACGACGCTCTTCCGATCTATGAAACTTTYRRCAAYGGATCWCT
5.8SFun_S_24_06	AATGATACGGCGACCACCGAGATCTAC	TACCGGCT	TGCA	TCTTTCCCTACACGACGCTCTTCCGATCT	TGCGA	AACTTTYRRCAAYGGATCWCT	AATGATACGGCGACCACCGAGATCTACACTACCGGCTTGCATCTTTCCCTACACGACGCTCTTCCGATCTTGCGAAACTTTYRRCAAYGGATCWCT
5.8SFun_S_24_07	AATGATACGGCGACCACCGAGATCTAC	TGCAGATC	CAAC	TCTTTCCCTACACGACGCTCTTCCGATCT	GAGTGG	AACTTTYRRCAAYGGATCWCT	AATGATACGGCGACCACCGAGATCTACACTGCAGATCCAACTCTTTCCCTACACGACGCTCTTCCGATCTGAGTGGAACTTTYRRCAAYGGATCWCT
5.8SFun_S_24_08	AATGATACGGCGACCACCGAGATCTAC	TTAACTGG	AAGC	TCTTTCCCTACACGACGCTCTTCCGATCT	CCTGGAG	AACTTTYRRCAAYGGATCWCT	AATGATACGGCGACCACCGAGATCTACACTTAACTGGAAGCTCTTTCCCTACACGACGCTCTTCCGATCTCCTGGAGAACTTTYRRCAAYGGATCWCT

5.8SFun_S_24_09	AATGATACGGCGACCACCGAGATCTACAC	TACCGCCTCGGA	TCTTTCCCTACACGACGCTCTTCCGATCT		AACTTTYRRCAAYGGATCWCT	AATGATACGGCGACCACCGAGATCTACACTACCGCCTCGGATCTTTCCCTACACGACGCTCTTCCGATCTAACTTTYRRCAAYGGATCWCT
5.8SFun_S_24_10	AATGATACGGCGACCACCGAGATCTACAC	ACTTTAAGGGTG	TCTTTCCCTACACGACGCTCTTCCGATCT	T	AACTTTYRRCAAYGGATCWCT	AATGATACGGCGACCACCGAGATCTACACACTTTAAGGGTGTCTTTCCCTACACGACGCTCTTCCGATCTTAACTTTYRRCAAYGGATCWCT
5.8SFun_S_24_11	AATGATACGGCGACCACCGAGATCTACAC	CCATCACATAGG	TCTTTCCCTACACGACGCTCTTCCGATCT	GT	AACTTTYRRCAAYGGATCWCT	AATGATACGGCGACCACCGAGATCTACACCCATCACATAGGTCTTTCCCTACACGACGCTCTTCCGATCTGTAACTTTYRRCAAYGGATCWCT
5.8SFun_S_24_12	AATGATACGGCGACCACCGAGATCTACAC	GAGCAACATCCT	TCTTTCCCTACACGACGCTCTTCCGATCT	CGA	AACTTTYRRCAAYGGATCWCT	AATGATACGGCGACCACCGAGATCTACACGAGCAACATCCTTCTTTCCCTACACGACGCTCTTCCGATCTCGAAACTTTYRRCAAYGGATCWCT
5.8SFun_S_24_13	AATGATACGGCGACCACCGAGATCTACAC	ATGTCCGACCAA	TCTTTCCCTACACGACGCTCTTCCGATCT	ATGA	AACTTTYRRCAAYGGATCWCT	AATGATACGGCGACCACCGAGATCTACACATGTCCGACCAATCTTTCCCTACACGACGCTCTTCCGATCTATGAAACTTTYRRCAAYGGATCWCT
5.8SFun_S_24_14	AATGATACGGCGACCACCGAGATCTACAC	TGTCTCGCAAGC	TCTTTCCCTACACGACGCTCTTCCGATCT	TGCGA	AACTTTYRRCAAYGGATCWCT	AATGATACGGCGACCACCGAGATCTACACTGTCTCGCAAGCTCTTTCCCTACACGACGCTCTTCCGATCTTGCGAAACTTTYRRCAAYGGATCWCT
5.8SFun_S_24_15	AATGATACGGCGACCACCGAGATCTACAC	CGCGGTTACTAA	TCTTTCCCTACACGACGCTCTTCCGATCT	GAGTGG	AACTTTYRRCAAYGGATCWCT	AATGATACGGCGACCACCGAGATCTACACCGCGGTTACTAATCTTTCCCTACACGACGCTCTTCCGATCTGAGTGGAACTTTYRRCAAYGGATCWCT
5.8SFun_S_24_16	AATGATACGGCGACCACCGAGATCTACAC	GAGACTATATGC	TCTTTCCCTACACGACGCTCTTCCGATCT	CCTGAG	AACTTTYRRCAAYGGATCWCT	AATGATACGGCGACCACCGAGATCTACACGAGACTATATGCTCTTTCCCTACACGACGCTCTTCCGATCTCCTGGAGAACTTTYRRCAAYGGATCWCT
5.8SFun_S_24_17	AATGATACGGCGACCACCGAGATCTACAC	AGGTACGCAATT	TCTTTCCCTACACGACGCTCTTCCGATCT		AACTTTYRRCAAYGGATCWCT	AATGATACGGCGACCACCGAGATCTACACAGGTACGCAATTTCTTTCCCTACACGACGCTCTTCCGATCTAACTTTYRRCAAYGGATCWCT
5.8SFun_S_24_18	AATGATACGGCGACCACCGAGATCTACAC	GAGGAGTAAAGC	TCTTTCCCTACACGACGCTCTTCCGATCT	T	AACTTTYRRCAAYGGATCWCT	AATGATACGGCGACCACCGAGATCTACACGAGGAGTAAAGCTCTTTCCCTACACGACGCTCTTCCGATCTTAACTTTYRRCAAYGGATCWCT

5.8SFun_S_24_19	AATGATACGGCGACCACCGAGATCTACAC	CGTAAGATGCCT	TCTTTCCCTACACGACGCTCTTCCGATCT	GT	AACTTTYRRCAAYGGATCWCT	AATGATACGGCGACCACCGAGATCTACACCGTAAGATGCCTTCTTTCCCTACACGACGCTCTTCCGATCTGTAACTTTYRRCAAYGGATCWCT
5.8SFun_S_24_20	AATGATACGGCGACCACCGAGATCTACAC	ATCTAGTGGCAA	TCTTTCCCTACACGACGCTCTTCCGATCT	CGA	AACTTTYRRCAAYGGATCWCT	AATGATACGGCGACCACCGAGATCTACACATCTAGTGGCAATCTTTCCCTACACGACGCTCTTCCGATCTCGAAACTTTYRRCAAYGGATCWCT
5.8SFun_S_24_21	AATGATACGGCGACCACCGAGATCTACAC	CCAGGGACTTCT	TCTTTCCCTACACGACGCTCTTCCGATCT	ATGA	AACTTTYRRCAAYGGATCWCT	AATGATACGGCGACCACCGAGATCTACACCCAGGGACTTCTTCTTTCCCTACACGACGCTCTTCCGATCTATGAAACTTTYRRCAAYGGATCWCT
5.8SFun_S_24_22	AATGATACGGCGACCACCGAGATCTACAC	CACCTTACCTTA	TCTTTCCCTACACGACGCTCTTCCGATCT	TGCGA	AACTTTYRRCAAYGGATCWCT	AATGATACGGCGACCACCGAGATCTACACCACCTTACCTTATCTTTCCCTACACGACGCTCTTCCGATCTTGCGAAACTTTYRRCAAYGGATCWCT
5.8SFun_S_24_23	AATGATACGGCGACCACCGAGATCTACAC	ATAGTTAGGGCT	TCTTTCCCTACACGACGCTCTTCCGATCT	GAGTGG	AACTTTYRRCAAYGGATCWCT	AATGATACGGCGACCACCGAGATCTACACATAGTTAGGGCTTCTTTCCCTACACGACGCTCTTCCGATCTGAGTGGAACTTTYRRCAAYGGATCWCT
5.8SFun_S_24_24	AATGATACGGCGACCACCGAGATCTACAC	GCACTTCATTTC	TCTTTCCCTACACGACGCTCTTCCGATCT	CCTGGAG	AACTTTYRRCAAYGGATCWCT	AATGATACGGCGACCACCGAGATCTACACGCACTTCATTTCTCTTTCCCTACACGACGCTCTTCCGATCTCCTGGAGAACTTTYRRCAAYGGATCWCT
ITS4Fun_S_24_01	CAAGCAGAAGACGGCATACGAGAT	CCTAAACTACGG	GTGACTGGAGTTCAGACGTGTGCTCTTCCGATCT		AGCCTCCGCTTATTGATATGCTTAART	CAAGCAGAAGACGGCATACGAGATCCTAAACTACGGGTGACTGGAGTTCAGACGTGTGCTCTTCCGATCTAGCCTCCGCTTATTGATATGCTTAART
ITS4Fun_S_24_02	CAAGCAGAAGACGGCATACGAGAT	GTGGTATGGGAG	GTGACTGGAGTTCAGACGTGTGCTCTTCCGATCT	G	AGCCTCCGCTTATTGATATGCTTAART	CAAGCAGAAGACGGCATACGAGATGTGGTATGGGAGGTGACTGGAGTTCAGACGTGTGCTCTTCCGATCTGAGCCTCCGCTTATTGATATGCTTAART
ITS4Fun_S_24_03	CAAGCAGAAGACGGCATACGAGAT	TGTTGCGTTTCT	GTGACTGGAGTTCAGACGTGTGCTCTTCCGATCT	TC	AGCCTCCGCTTATTGATATGCTTAART	CAAGCAGAAGACGGCATACGAGATTGTTGCGTTTCTGTGACTGGAGTTCAGACGTGTGCTCTTCCGATCTTCAGCCTCCGCTTATTGATATGCTTAART
ITS4Fun_S_24_04	CAAGCAGAAGACGGCATACGAGAT	ACAGCCACCCAT	GTGACTGGAGTTCAGACGTGTGCTCTTCCGATCT	CTA	AGCCTCCGCTTATTGATATGCTTAART	CAAGCAGAAGACGGCATACGAGATACAGCCACCCATGTGACTGGAGTTCAGACGTGTGCTCTTCCGATCTCTAAGCCTCCGCTTATTGATATGCTTAART

ITS4Fun_S_24_05	CAAGCAGAAGACGGCATACGAGAT	GTTACGTGGTTG	GTGACTGGAGTTCAGACGTGTG	GA	AGCCTCCGCTTATTGATATGCTTAART	CAAGCAGAAGACGGCATACGAGATGTTACGTGGTTGGTGACTGGAGTTCAGACGTGTGCTCTTCCGATCTGATAAGCCTCCGCTTATTGATATGCTTAART
ITS4Fun_S_24_06	CAAGCAGAAGACGGCATACGAGAT	TACCGGCTTGCA	GTGACTGGAGTTCAGACGTGTG	AC	AGCCTCCGCTTATTGATATGCTTAART	CAAGCAGAAGACGGCATACGAGATTACCGGCTTGCAGTGACTGGAGTTCAGACGTGTGCTCTTCCGATCTACTCAAGCCTCCGCTTATTGATATGCTTAART
ITS4Fun_S_24_07	CAAGCAGAAGACGGCATACGAGAT	CACCTTACCTTA	GTGACTGGAGTTCAGACGTGTG	TT	AGCCTCCGCTTATTGATATGCTTAART	CAAGCAGAAGACGGCATACGAGATCACCTTACCTTAGTGACTGGAGTTCAGACGTGTGCTCTTCCGATCTTTCTCTAGCCTCCGCTTATTGATATGCTTAART
ITS4Fun_S_24_08	CAAGCAGAAGACGGCATACGAGAT	TTAACTGGAAGC	GTGACTGGAGTTCAGACGTGTG	CA	AGCCTCCGCTTATTGATATGCTTAART	CAAGCAGAAGACGGCATACGAGATTTAACTGGAAGCGTGACTGGAGTTCAGACGTGTGCTCTTCCGATCTCACTTCTAGCCTCCGCTTATTGATATGCTTAART
ITS4Fun_S_24_09	CAAGCAGAAGACGGCATACGAGAT	TACCGCCTCGGA	GTGACTGGAGTTCAGACGTGTG		AGCCTCCGCTTATTGATATGCTTAART	CAAGCAGAAGACGGCATACGAGATTACCGCCTCGGAGTGACTGGAGTTCAGACGTGTGCTCTTCCGATCTAGCCTCCGCTTATTGATATGCTTAART
ITS4Fun_S_24_10	CAAGCAGAAGACGGCATACGAGAT	ACTTTAAGGGTG	GTGACTGGAGTTCAGACGTGTG	G	AGCCTCCGCTTATTGATATGCTTAART	CAAGCAGAAGACGGCATACGAGATACTTTAAGGGTGGTGACTGGAGTTCAGACGTGTGCTCTTCCGATCTGAGCCTCCGCTTATTGATATGCTTAART
ITS4Fun_S_24_11	CAAGCAGAAGACGGCATACGAGAT	CCATCACATAGG	GTGACTGGAGTTCAGACGTGTG	TC	AGCCTCCGCTTATTGATATGCTTAART	CAAGCAGAAGACGGCATACGAGATCCATCACATAGGGTGACTGGAGTTCAGACGTGTGCTCTTCCGATCTTCAGCCTCCGCTTATTGATATGCTTAART
ITS4Fun_S_24_12	CAAGCAGAAGACGGCATACGAGAT	GAGCAACATCCT	GTGACTGGAGTTCAGACGTGTG	CT	AGCCTCCGCTTATTGATATGCTTAART	CAAGCAGAAGACGGCATACGAGATGAGCAACATCCTGTGACTGGAGTTCAGACGTGTGCTCTTCCGATCTCTAAGCCTCCGCTTATTGATATGCTTAART
ITS4Fun_S_24_13	CAAGCAGAAGACGGCATACGAGAT	ATGTCCGACCAA	GTGACTGGAGTTCAGACGTGTG	GA	AGCCTCCGCTTATTGATATGCTTAART	CAAGCAGAAGACGGCATACGAGATATGTCCGACCAAGTGACTGGAGTTCAGACGTGTGCTCTTCCGATCTGATAAGCCTCCGCTTATTGATATGCTTAART
ITS4Fun_S_24_14	CAAGCAGAAGACGGCATACGAGAT	TGTCTCGCAAGC	GTGACTGGAGTTCAGACGTGTG	AC	AGCCTCCGCTTATTGATATGCTTAART	CAAGCAGAAGACGGCATACGAGATTGTCTCGCAAGCGTGACTGGAGTTCAGACGTGTGCTCTTCCGATCTACTCAAGCCTCCGCTTATTGATATGCTTAART

ITS4Fun_S_24_15	CAAGCAGAAGACGGCATACGAGAT	CGCGGTTACTAA	GTGACTGGAGTTCAGACGTGTGCTCTTCCGATCT	TTCTCT	AGCCTCCGCTTATTGATATGCTTAART	CAAGCAGAAGACGGCATACGAGATCGCGGTTACTAAGTGACTGGAGTTCAGACGTGTGCTCTTCCGATCTTTCTCTAGCCTCCGCTTATTGATATGCTTAART
ITS4Fun_S_24_16	CAAGCAGAAGACGGCATACGAGAT	GAGACTATATGC	GTGACTGGAGTTCAGACGTGTGCTCTTCCGATCT	CACTTCT	AGCCTCCGCTTATTGATATGCTTAART	CAAGCAGAAGACGGCATACGAGATGAGACTATATGCGTGACTGGAGTTCAGACGTGTGCTCTTCCGATCTCACTTCTAGCCTCCGCTTATTGATATGCTTAART
ITS4Fun_S_24_17	CAAGCAGAAGACGGCATACGAGAT	AGGTACGCAATT	GTGACTGGAGTTCAGACGTGTGCTCTTCCGATCT		AGCCTCCGCTTATTGATATGCTTAART	CAAGCAGAAGACGGCATACGAGATAGGTACGCAATTGTGACTGGAGTTCAGACGTGTGCTCTTCCGATCTAGCCTCCGCTTATTGATATGCTTAART
ITS4Fun_S_24_18	CAAGCAGAAGACGGCATACGAGAT	GAGGAGTAAAGG	GTGACTGGAGTTCAGACGTGTGCTCTTCCGATCT	G	AGCCTCCGCTTATTGATATGCTTAART	CAAGCAGAAGACGGCATACGAGATGAGGAGTAAAGCGTGACTGGAGTTCAGACGTGTGCTCTTCCGATCTGAGCCTCCGCTTATTGATATGCTTAART
ITS4Fun_S_24_19	CAAGCAGAAGACGGCATACGAGAT	CGTAAGATGCCT	GTGACTGGAGTTCAGACGTGTGCTCTTCCGATCT	TC	AGCCTCCGCTTATTGATATGCTTAART	CAAGCAGAAGACGGCATACGAGATCGTAAGATGCCTGTGACTGGAGTTCAGACGTGTGCTCTTCCGATCTTCAGCCTCCGCTTATTGATATGCTTAART
ITS4Fun_S_24_20	CAAGCAGAAGACGGCATACGAGAT	ATCTAGTGGCAA	GTGACTGGAGTTCAGACGTGTGCTCTTCCGATCT	CTA	AGCCTCCGCTTATTGATATGCTTAART	CAAGCAGAAGACGGCATACGAGATATCTAGTGGCAAGTGACTGGAGTTCAGACGTGTGCTCTTCCGATCTCTAAGCCTCCGCTTATTGATATGCTTAART
ITS4Fun_S_24_21	CAAGCAGAAGACGGCATACGAGAT	CCAGGGACTTCT	GTGACTGGAGTTCAGACGTGTGCTCTTCCGATCT	GATA	AGCCTCCGCTTATTGATATGCTTAART	CAAGCAGAAGACGGCATACGAGATCCAGGGACTTCTGTGACTGGAGTTCAGACGTGTGCTCTTCCGATCTGATAAGCCTCCGCTTATTGATATGCTTAART
ITS4Fun_S_24_22	CAAGCAGAAGACGGCATACGAGAT	TGCAGATCCAAC	GTGACTGGAGTTCAGACGTGTGCTCTTCCGATCT	ACTCA	AGCCTCCGCTTATTGATATGCTTAART	CAAGCAGAAGACGGCATACGAGATTGCAGATCCAACGTGACTGGAGTTCAGACGTGTGCTCTTCCGATCTACTCAAGCCTCCGCTTATTGATATGCTTAART
ITS4Fun_S_24_23	CAAGCAGAAGACGGCATACGAGAT	ATAGTTAGGGCT	GTGACTGGAGTTCAGACGTGTGCTCTTCCGATCT	TTCTCT	AGCCTCCGCTTATTGATATGCTTAART	CAAGCAGAAGACGGCATACGAGATATAGTTAGGGCTGTGACTGGAGTTCAGACGTGTGCTCTTCCGATCTTTCTCTAGCCTCCGCTTATTGATATGCTTAART
ITS4Fun_S_24_24	CAAGCAGAAGACGGCATACGAGAT	GCACTTCATTTC	GTGACTGGAGTTCAGACGTGTGCTCTTCCGATCT	CACTTCT	AGCCTCCGCTTATTGATATGCTTAART	CAAGCAGAAGACGGCATACGAGATGCACTTCATTTCGTGACTGGAGTTCAGACGTGTGCTCTTCCGATCTCACTTCTAGCCTCCGCTTATTGATATGCTTAART

Table S3 Molecular identification of arbuscular mycorrhizal fungi in this study

OTU	Coverage	E-value	Similarity	Best NCBI hit	
OTU51_Rhizophagus	99%	2.00E-159	93%	JN195441.1	Uncultured_Glomus
OTU70_Claroideoglomus	99%	0	99%	JF439206.1	Glomus_hoi
OTU166_Rhizophagus	98%	0	98%	JN936299.1	Rhizophagus_sp.
OTU150_Rhizophagus	98%	0	97%	JN936299.1	Rhizophagus_sp.
OTU253_Funneliformis	98%	0	99%	AJ919274.1	Glomus_mosseae
OTU118_Rhizophagus*	98%	4.00E-180	98%	KM041773.1	Uncultured_Rhizophagus
OTU161_Rhizophagus*	98%	1.00E-173	97%	KM041753.1	Uncultured_Rhizophagus
OTU132_Rhizophagus*	98%	0	98%	JX999965.1	Glomeromycota_sp.
OTU133_Glomus	98%	2.00E-172	96%	KM208159.1	Uncultured_Glomeromycota
OTU206_Glomus	99%	2.00E-178	97%	GQ388297.1	Uncultured_Glomus
OTU213_Rhizophagus	98%	0	98%	JX999971.1	Glomeromycota_sp.
OTU935_Rhizophagus	98%	1.00E-156	92%	JN195441.1	Uncultured_Glomus
OTU126_Glomus	98%	5.00E-173	97%	KM208171.1	Uncultured_Glomeromycota
OTU251_Rhizophagus	98%	0	98%	GQ205073.1	Glomus_custos
OTU558_Funneliformis	99%	0	98%	HG425925.1	Uncultured_Funneliformis
OTU323_Glomus	98%	1.00E-174	97%	KM208159.1	Uncultured_Glomeromycota
OTU224_Glomus	99%	7.00E-178	98%	GQ388314.1	Uncultured_Glomus
OTU229_Glomus	98%	2.00E-179	98%	KM208159.1	Uncultured_Glomeromycota
OTU355_Funneliformis	99%	0	98%	HF970318.1	Uncultured_Funneliformis
OTU347_Rhizophagus	98%	0	98%	KJ701452.1	Uncultured_Glomus
OTU476_Glomus	99%	4.00E-180	97%	HG425896.1	Uncultured_Glomeraceae
OTU277_Glomus	99%	7.00E-178	98%	GQ388297.1	Uncultured_Glomus
OTU565_Funneliformis	99%	0	98%	U49264.1	Glomus_moessae
OTU491_Claroideoglomus	99%	0	99%	KY927389.1	Claroideoglomus_etunicatum
OTU400_Glomus	99%	7.00E-178	97%	JX276899.1	Uncultured_Glomeromycota
OTU333_Glomus	99%	0	98%	FR693682.1	Uncultured_Glomus

OTU435_Glomus	99%	0	98%	HG425982.1	Uncultured_Glomeraceae
OTU534_Glomus	98%	0	99%	KF836947.1	Glomus_sp.
OTU944_Rhizophagus	99%	1.00E-154	91%	JN195441.1	Uncultured_Glomus
OTU536_Claroideoglomus	98%	0	97%	JQ218217.1	Uncultured_Glomus
OTU989_Funneliformis	99%	0	98%	EF989113.1	Funneliformis_mosseae
OTU498_Glomus	99%	3.00E-176	98%	JX096590.1	Uncultured_Glomeromycota
OTU579_Glomus	99%	6.00E-166	96%	JX096590.1	Uncultured_Glomeromycota
OTU987_Paraglomus	99%	7.00E-159	88%	AB520480.1	Uncultured_fungus
OTU734_Rhizophagus	97%	0	98%	AF185651.1	Glomus_intraradices
OTU715_Glomus	99%	1.00E-173	97%	JX096590.1	Uncultured_Glomeromycota
OTU574_Glomus	98%	1.00E-174	97%	JX096590.1	Uncultured_Glomeromycota
OTU659_Glomus	98%	5.00E-179	98%	JX096614.1	Uncultured_Glomeromycota
OTU1068_Glomus	98%	1.00E-173	97%	HM162343.1	Uncultured_Glomeromycota
OTU564_Glomus	99%	2.00E-160	95%	GU059545.1	Glomus_indicum
OTU735_Claroideoglomus	99%	0	96%	AF004682.1	Glomus_etunicatum
OTU597_Paraglomus	98%	6.00E-166	91%	AB520480.1	Uncultured_fungus
OTU998_Glomus	99%	8.00E-177	97%	GQ388297.1	Uncultured_Glomus
OTU1184_Rhizophagus	98%	0	99%	AF185650.1	Glomus_intraradices
OTU1065_Claroideoglomus	99%	0	96%	KP191488.1	Claroideoglomus_drummondii
OTU936_Claroideoglomus	100%	0	99%	JN685281.1	Uncultured_Glomeromycota
OTU1197_Claroideoglomus	99%	0	97%	KP191486.1	Claroideoglomus_drummondii
OTU1274_Paraglomus	98%	9.00E-151	85%	AB520480.1	Uncultured_fungus
OTU969_Claroideoglomus	98%	0	97%	JX096582.1	Uncultured_Glomeromycota
OTU1013_Glomeraceae	98%	4.00E-180	96%	JN195694.1	Uncultured_Glomus
OTU975_Paraglomus	99%	0	99%	KF849701.1	Uncultured_Paraglomus
OTU945_Glomus	99%	0	99%	KF849595.1	Uncultured_Glomus

*Note: These three OTUs are combined to avoid the potential more than one rDNA repeat in a single species. However, the ecological results and conclusion are not affected (Fig. S10-S15). Representative sequences of AMF OTUs were deposited in GenBank with the accession codes: MG008508 - MG008559.

Table S4 Arbuscular mycorrhizal fungal (AMF) operational taxonomic units (OTUs) bias occurred in the first week (TP01) and the last week (TP17), as detected by indicator species analysis. Note the steep decline of two initially dominant species and the rise of 13 initially rare *Rhizophagus* and *Glomus* species

AMF OTUs	Preferred	Indicator value	*P*
OTU51_*Rhizophagus*	TP01	0.894	0.001
OTU70_*Claroideoglomus*	TP01	0.809	0.001
OTU166_*Rhizophagus*	TP17	0.855	0.001
OTU118.161.132_*Rhizophagus*	TP17	0.811	0.001
OTU150_*Rhizophagus*	TP17	0.797	0.001
OTU213_*Rhizophagus*	TP17	0.75	0.001
OTU251_*Rhizophagus*	TP17	0.667	0.001
OTU126_*Glomus*	TP17	0.816	0.001
OTU133_*Glomus*	TP17	0.788	0.001
OTU229_*Glomus*	TP17	0.762	0.001
OTU323_*Glomus*	TP17	0.711	0.001
OTU476_*Glomus*	TP17	0.474	0.007
OTU333_*Glomus*	TP17	0.415	0.01
OTU534_*Glomus*	TP17	0.318	0.05
OTU400_*Glomus*	TP17	0.311	0.035

Table S5 Arbuscular mycorrhizal fungal (AMF) operational taxonomic units (OTUs) bias occurred in the root, rhizosphere and soil, as detected by indicator species analysis. Note a number of *Rhizophagus* were more common and abundant in root, whereas *Funneliformis*, *Claroideoglomus*, *Paraglomus* and *Glomus* were more common and abundant in rhizosphere and soil

AMF OTUs	Indicator	Indicator value	*P*
OTU118.161.132_*Rhizophagus*	Root	0.399	0.001
OTU166_*Rhizophagus*	Root	0.391	0.001
OTU213_*Rhizophagus*	Root	0.37	0.001
OTU150_*Rhizophagus*	Root	0.363	0.002
OTU251_*Rhizophagus*	Root	0.236	0.009
OTU734_*Rhizophagus*	Root	0.054	0.011
OTU70_*Claroideoglomus*	Rhizosphere	0.419	0.001
OTU206_*Glomus*	Soil	0.566	0.001
OTU224_*Glomus*	Soil	0.529	0.001
OTU277_*Glomus*	Soil	0.434	0.001
OTU498_*Glomus*	Soil	0.118	0.001
OTU659_*Glomus*	Soil	0.104	0.001
OTU998_*Glomus*	Soil	0.104	0.001
OTU579_*Glomus*	Soil	0.1	0.001
OTU574_*Glomus*	Soil	0.089	0.001
OTU564_*Glomus*	Soil	0.085	0.001
OTU1068_*Glomus*	Soil	0.068	0.001
OTU715_*Glomus*	Soil	0.062	0.005
OTU253_*Funneliformis*	Soil	0.52	0.001
OTU558_*Funneliformis*	Soil	0.277	0.001
OTU355_*Funneliformis*	Soil	0.261	0.001
OTU565_*Funneliformis*	Soil	0.222	0.001
OTU989_*Funneliformis*	Soil	0.103	0.006
OTU491_*Claroideoglomus*	Soil	0.167	0.001
OTU536_*Claroideoglomus*	Soil	0.088	0.007
OTU1065_*Claroideoglomus*	Soil	0.051	0.005
OTU987_*Paraglomus*	Soil	0.144	0.001
OTU597_*Paraglomus*	Soil	0.047	0.021

Table S6 A list of studies demonstrating the nestedness of arbuscular mycorrhizal fungal (AMF) community. Note nestedness is prevailing in AMF community, but not seen in some other studies

Study	Ecosystem	AMF recognition	Conclusion
(Kawahara et al 2016)	Six locations along a pH gradient in Japan	Trap culture, Sanger sequencing of LSU	AMF communities in lower pH soils were subsets of (nested in) those in higher pH soil
(van Geel et al 2015)	Apple trees in 24 orchards in Belgium	454 sequencing of AMF SSU	Degree of nestedness of the AMF communities was related to plant-available P and N content of the soil, pointing to a progressive loss of AMF taxa with increasing fertilization.
(Vályi et al 2015)	Land use intensity gradient in Germany	454 sequencing of AMF SSU	Communities in medium and low land-use sites were subsets of high land-use communities
(Camenzind et al 2014)	Tropical montane forest in Ecuador	454 sequencing of AMF LSU	AMF community is highly nested
(Verbruggen et al 2012)	40 agricultural soils in the Netherlands	tRFLP of LSU	Communities from species-poor fields were found to be subsets of those in richer fields
(Chen et al 2017a)	Subtropical forest in China	454 sequencing of AMF SSU	Plant-AMF symbiotic network is highly nested
(Chagnon et al 2012)	Reanalysis of study in hemiboreal forest	454 sequencing of AMF SSU	Plant-AMF symbiotic network is highly nested
(Montesinos-Navarro et al 2012)	Semiarid valley	Sanger sequencing of AMF ITS	Plant-AMF symbiotic network is highly nested
(Toju et al 2014)	Temperate forest	Sequencing of fungal ITS	No significant nestedness in plant-AMF symbiotic network
(Van Geel et al 2017a)	European grasslands	454 sequencing of AMF SSU	Plant-AMF symbiotic network is highly nested
(Van Geel et al 2017b)	European vineyards	454 sequencing of AMF SSU	AMF community is highly nested

SSU: small subunit; LSU, large subunit; ITS: internal transcribed spacer; tRFLP, terminal restriction fragment length polymorphism.

225 **Table S7** List of studies investigating the phylogenetic relatedness of arbuscular mycorrhizal fungal (AMF) community. Note phylogenetic

226 underdispersion, overdisperion and stochastic are all seen, with the underdisperion most prevalent

Study	Ecosystem	AMF recognition	Conclusion
(Bainard et al 2014)	Farmed pea, lentil and wheat in temperate semiarid prairie	454 sequencing of AMF SSU	AMF communities in general are phylogenetically underdispered, with exception of the first soil and second root samplings.
(Horn et al 2014)	Temperate grassland in Germany	454 sequencing of AMF LSU	AMF communities are phylogenetically underdispersed
(Chen et al 2017b)	Temperate semiarid steppe in China	454 sequencing of AMF SSU	AMF communities are phylogenetically underdispered, regardless of precipitation and nitrogen
(Liu et al 2015a)	Alpine meadow in China	Sanger sequencing of SSU	AMF shifted from phylogenetic underdispersion to overdisersion with increasing nitrogen fertilization
(García de León et al 2016a)	Abandoned quarry in Estonia	454 sequencing of AMF SSU	Phylogenetic community composition of AMF was more clustered than global, and European taxon pools
(Davison et al 2016)	Re-analysis of global dataset of	454 sequencing of AMF SSU	Coexisting fungi were more phylogenetically clustered than the random communities defined by a variety of null models.
(Maherali and Klironomos 2012)	Meadow (50 x 50 m^2 with 2601 samples) in Canada	Spores	AMF communities are generally phylogenetically overdispersed, but a subset of AMF communities are phylogenetically underdispersed
(Maherali and Klironomos 2007)	Greenhouse controlling initial AMF phylogenetic diversity	tRFLP	Initial phylogenetic overdispersion of AMF community result in high richness
(Roger et al 2013)	Pot cultures inoculated with *Rhizophafus irregularis* isolate combinations with different phylogenetic relatedness	qPCR	When fungi were closely related, they were able to coexist in almost equal proportions

(Liu et al 2015b)	Alpine meadow in China	Sanger sequencing of SSU	AMF communities were phylogenetically clustered and random in unfertilized and fertilized plots, respectively.
(Mueller and Bohannan 2015)	Grassland in California, USA	Sanger sequencing of SSU	AMF communities were generally phylogenetically underdispered, but not significant in the nitrogen treatment
(Egan et al 2017)	Subalpine grassland, treeline and alpine tundra along an elevational gradient in Montana, USA	454 sequencing of AMF SSU	AMF communities being phylogenetically clustered at all elevations sampled
(Saks et al 2013)	Mature mixed boreonemoral forest in Estonia	454 sequencing of AMF SSU	AMF communities being frequently phylogenetically clustered compared with local and global taxon pools
(Kivlin et al 2011)	Meta-analysis of 111 published studies	14,961 public DNA sequences	AMF communities being phylogenetically clustered in the majority of sites, and only two sites had communities that were phylogenetically dispersed
(Shi et al 2017)	Alpine meadow in China	454 sequencing of AMF SSU	AMF community was phylogenetically clustered under warming, but not in control, or plots experienced clip

227 SSU: small subunit; LSU, large subunit; RFLP: restriction fragment length polymorphism.

228 **Table S8** List of studies comparing arbuscular mycorrhizal fungal (AMF) communities between root and

229 soil. Note different root and soil AMF are often seen, but not in some studies

Study	Ecosystem	AMF recognition	Conclusion
(Hempel et al 2007)	Farmed meadow in Germany	Sanger sequencing of ITS	Root is abundant in *Rhizophagus* (*Glomus* group Ab); soil is abundant in Paraglomeraceae and Archaeosporaceae
(Bainard et al 2014)	Farmed pea, lentil and wheat in temperate semiarid prairie	454 sequencing of AMF SSU	Root is abundant in *Rhizopahgus* and *Funneliformis*, soil is abundant in *Paraglomus*
(Wilde et al 2009)	Two salt marshes in Germany	Both morphological and molecular criteria	*Rhizophagus* (*Glomus*) *intraradices* is more abundant in root, *Funneliformis* (*Glomus*) *geosporum* is more abundant in soil
(Yang et al 2013)	Alpine meadow subjected to warming and grazing in China	Sanger sequencing of SSU-ITS-LSU	One Diversisporales was more abundant in soil, two Glomerales were more abundant in root
(Beauregard et al 2013)	Crop fields in Canada	DGGE	Six out of seven ribotypes show difference between root and soil
(Liu et al 2012)	Alpine Meadow subjected to fertilization in China	Soil spore isolation; Root, sanger sequencing of SSU	*Rhizophagus* was the most abundant AMF in root; *Diverspora* was the most abundant AMF in soil spores
(Hart and Reader 2002)	Pot experiment to test the colonization potential of 21 AMF isolates from three families	Percent of colonization and fungal biomass in root; Hyphal length in soil	Glomaceae isolates had high root colonization but low soil colonization, Gigasporaceae isolates showed the opposite trend whereas Acaulosporaceae isolates had low root and soil colonization.
(Verbruggen et al 2012)	40 agricultural soils in the Netherlands	tRFLP	No obvious different between root and soil AMF communities

(Wu et al 2007)	Primary successional volcanic desert in Japan	tRFLP	AMF community structures detected by spore sampling were inconsistent with those from plant roots.

SSU: small subunit; LSU, large subunit; ITS: internal transcribed spacer; tRFLP, terminal restriction fragment length polymorphism; DGGE: Denaturing Gradient Gel Electrophoresis.

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