SUPPLEMENTAL TABLES AND FIGURES

Table S1: Analysis of the relationship between species pool richness and local diversity, showing (a) the estimated parameters and 95% confidence intervals for the generalized non-linear least squares model (Michaelis-Menten) and (b) the effects of species pool richness, age, and their interaction on the standardized residuals from the Michaelis-Menten model.

a) Parameters of Michaelis-Menten model

Parameter	Estimate	LCI	UCI
α_{max} (asymptote)	22.9	19.9	25.9
α_k (half-max)	21.3	17.0	25.6

b) Analysis of model residuals

Parameter	Estimate	SE	DF	*t*	*p*
Richness	-0.126	0.049	74	-2.561	0.013
Age	-0.025	0.034	74	-0.712	0.479
Richness:Age	0.028	0.011	74	2.605	0.011

Table S2: Results of multiple-linear regression testing whether the species pool mean-pairwise combined functional and phylogenetic distance varied with species pool age, richness and site heterogeneity (age-variance).

Parameter	**Estimate**	**SE**	***t*-value**	***p*-value**	**partial-r^2**
Intercept	0.625	0.040	15.396	< 0.001	
Richness	-0.001	0.001	-0.861	0.392	0.01
Age-variance	0.014	0.005	2.997	0.004	0.11
Age	-0.037	0.008	-4.923	< 0.001	0.25

Table S3: Results of linear mixed-model testing whether the degree of functional (and phylogenetic) dispersion or clustering during community assembly changed with species pool age, accounting for species pool richness and age-variance.

Parameter	Estimate	SE	DF	*t*-value	*p*-value
Intercept	2.057	0.572	199	3.585	< 0.001
Richness	0.003	0.012	70	0.298	0.767
Age-variance	0.077	0.063	70	1.152	0.253
Age	0.440	0.105	70	-4.248	0.001

Figure S1: Estimated phylogenetic relationships of the 54 fungal isolates. The maximum likelihood tree was constructed with PhyML, using the first 740 bp of the nrDNA large ribosomal subunit. Colors indicate the age of the chronosequence site where each isolate was collected. For each isolate, the OTU id is followed by the GenBank accession number of of the associated sequence, and then the putative taxonomic assignment, based on comparison of the full nrDNA internal transcribe spacer region against the UNITE v8.2 database.

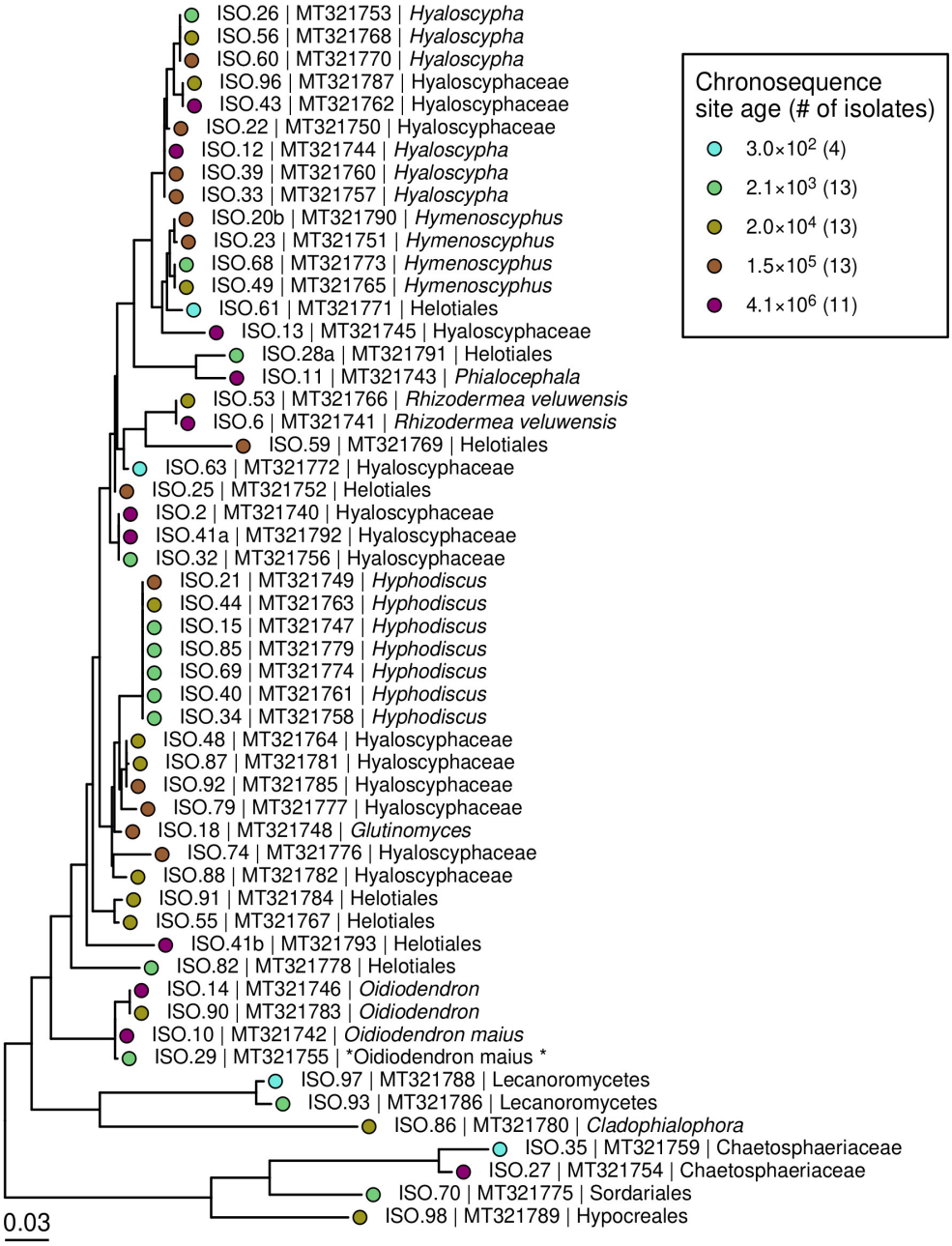
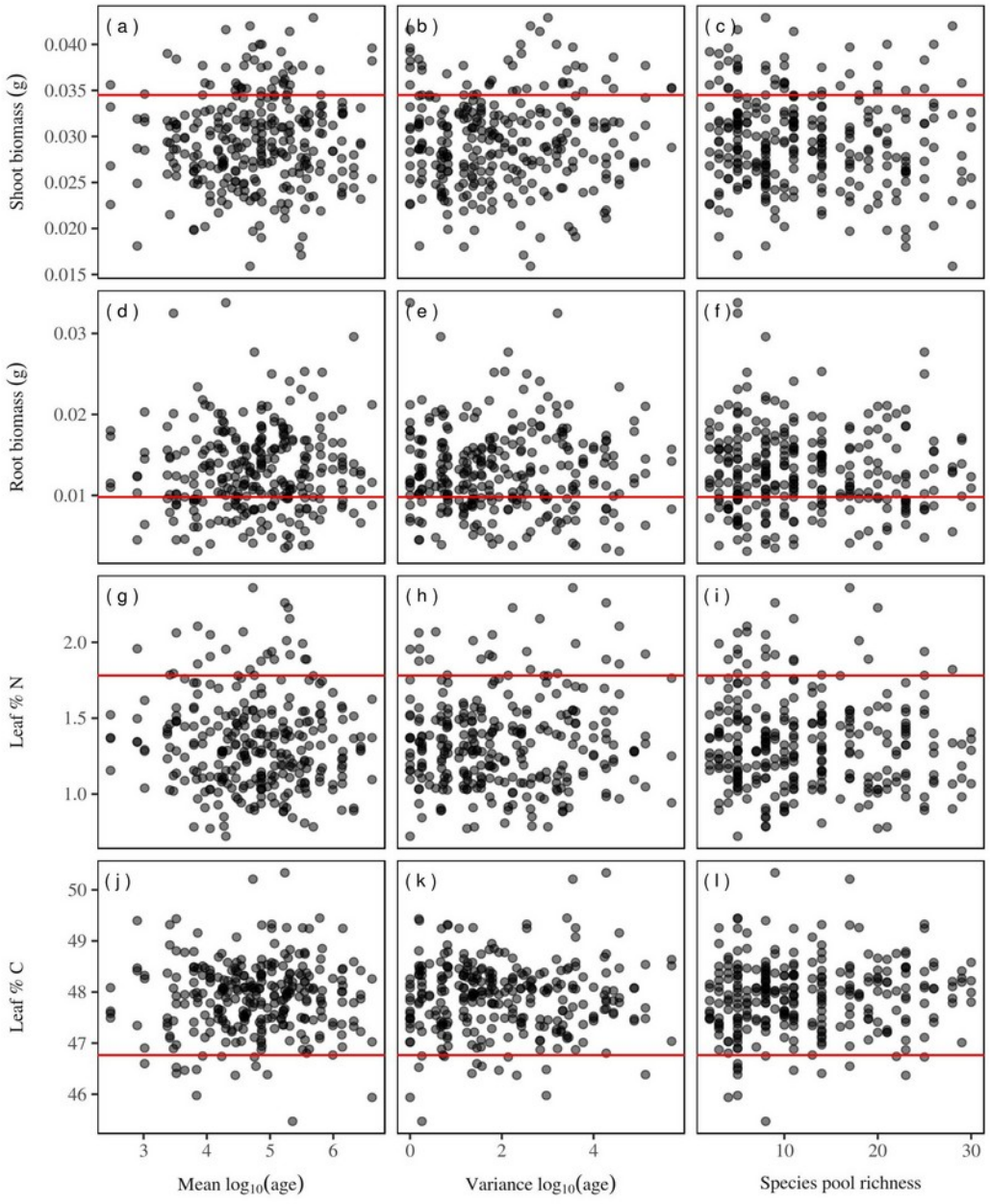


Figure S2: Relationships between experimental manipulations of species pool composition and seedling (a-c) shoot and (d-f) root biomass and leaf tissue (g-i) nitrogen and (j-l) carbon concentrations. Horizontal lines indicate the median values for the four control seedling that were grown without fungi.



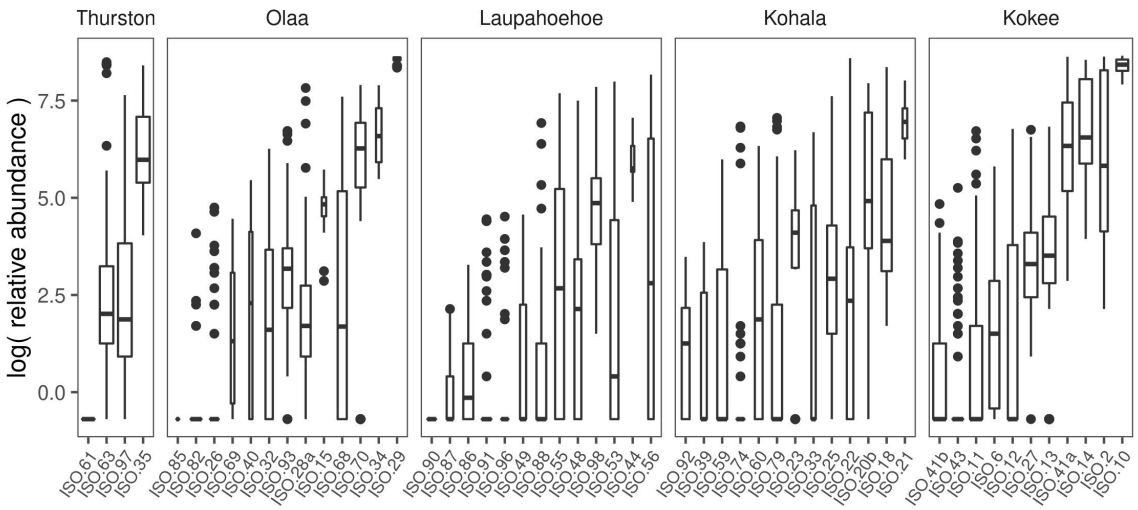


Figure S3: Fungal isolates included in species pool treatments varied in their mean relative abundance in realized local communities. However, there was no significant difference among the isolates originating from different chronosequence sites in either their relative abundance (Kruskal-Wallis $\chi^2_{(4)} = 1.48$, $P = 0.83$) or their prevalence (i.e., probability of being observed; Kruskal-Wallis $\chi^2_{(4)} = 2.95$, $P = 0.57$) at the conclusion of the experiment. Sequence counts were normalized by rarefaction and a pseudo-count of 0.1 was added to facilitate log transformation. The width of each box is proportional to the square-root of the number of isolates from each site used in the experiment and sites are arranged from youngest to oldest, left to right.