Supplementary Material - Mujica et al.

1 Analyses with the Species-level database

1.1 Clean database - excluding species with any remark

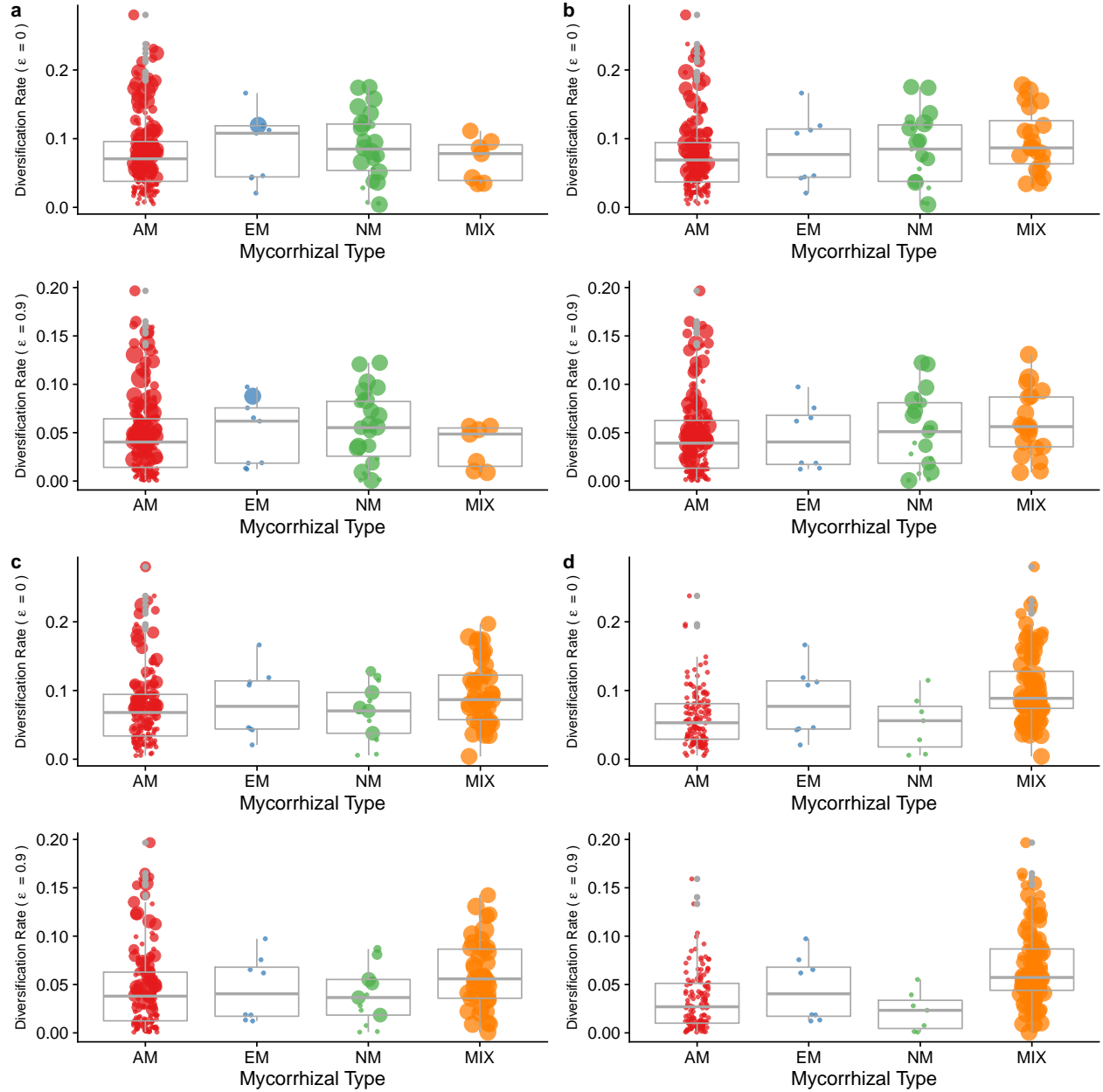### 1.1.1 Boxplots using the clean species-level database

Figure S1: Relationship between mycorrhizal type and diversification rates using the thresholds (a) 50%, (b) 60%, (c) 80% and (d) 100% for MIX state assignment. Each panel shows diversification rate estimated with epsilon = 0 (upper) and diversification rate estimated with epsilon = 0.9 (lower). AM: Arbuscular mycorrhiza, EM: Ectomycorrhiza, NM: non-mycorrhizal and MIX (families with no dominance of any specific mycorrhizal association). The size of the points indicates the Mycorrhizal Type Diversity Index value for each lineage, indicating a predominance of larger indices with higher diversification rates.

1.1.2 Summary statistics using clean species-level database

1.1.2.1 phyANOVA

Table S1: summary statistics for phyANOVA for both values of epsilon. Significant values are highlighted in bold.

Threshold	F.r0	pvalue.r0	F.r09	pvalue.r09
50	0.385	0.857	0.494	0.81
60	1.538	0.371	0.928	0.633
80	3.784	0.084	3.262	0.117
100	24.583	**0.001**	27.097	**0.001**

1.1.2.2 Standard ANOVA

Table S2: summary statistics for phyANOVA for both values of epsilon. Significant values are highlighted in bold.

Threshold	F.r0	pvalue.r0	F.r09	pvalue.r09
50	0.396	0.756	0.501	0.682
60	1.563	0.199	0.948	0.418
80	3.529	**0.015**	2.997	**0.031**
100	23.996	**0**	26.323	**0**

1.1.3 Posthoc tests using clean species-level database

1.1.3.1 phyANOVA

Table S3: Pairwise Corrected p-values for phyANOVA. Significant values are highlighted in bold.

Threshold	Mycorrhizal.Type	AM.r0	EM.r0	MIX.r0	NM.r0	AM.r09	EM.r09	MIX.r09	NM.r09
50	AM	1	1	1	1	1	1	1	1
50	EM	1	1	1	1	1	1	1	1
50	MIX	1	1	1	1	1	1	1	1
50	NM	1	1	1	1	1	1	1	1
60	AM	1	1	0.264	1	1	1	0.69	1
60	EM	1	1	1	1	1	1	1	1
60	MIX	0.264	1	1	0.995	0.69	1	1	1
60	NM	1	1	0.995	1	1	1	1	1
80	AM	1	1	**0.036**	1	1	1	0.096	1
80	EM	1	1	1	1	1	1	1	1
80	MIX	**0.036**	1	1	0.1	0.096	1	1	0.096
80	NM	1	1	0.1	1	1	1	0.096	1
100	AM	1	0.726	**0.006**	0.726	1	0.747	**0.006**	0.747
100	EM	0.726	1	0.616	0.684	0.747	1	0.376	0.747
100	MIX	**0.006**	0.616	1	**0.006**	**0.006**	0.376	1	**0.006**
100	NM	0.726	0.684	**0.006**	1	0.747	0.747	**0.006**	1

1.1.3.2 Standard ANOVA

Table S4: Pairwise Corrected p-values for standard ANOVA. Significant values are highlighted in bold.

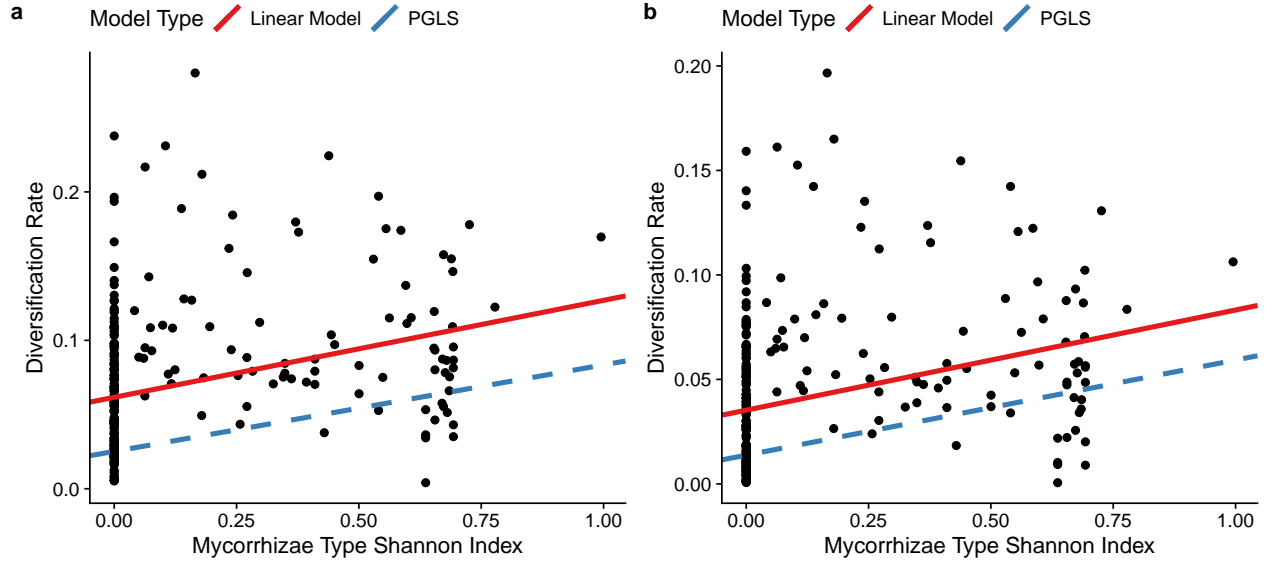| Types	50.r0	60.r0	80.r0	100.r0	50.r09	60.r09	80.r09	100.r09
EM-AM	0.964	0.992	0.985	0.613	0.993	1	1	0.78
MIX-AM	0.995	0.146	**0.012**	**0**	0.858	0.348	**0.036**	**0**
NM-AM	0.776	0.938	0.911	0.808	0.831	0.974	0.778	0.626
MIX-EM	0.954	0.769	0.704	0.237	0.866	0.768	0.622	0.106
NM-EM	1	1	0.897	0.411	0.996	0.993	0.927	0.404
NM-MIX	0.892	0.632	0.09	**0**	0.663	0.78	0.081	**0**

1.1.4 Scatterplots

Figure S2: Scatterplots showing the relationship between mycorrhizal diversity index and diversification rates. Diversification rates were estimated with epsilon = 0 (a) and with epsilon = 0.9 (b). The red and blue lines indicate the results of a linear model and a phylogenetic generalized least squares (PGLS) fit, respectively.

Table S5: Summary statistics for the phylogenetic and parametric regressions using the full genus dataset. Significant values are highlighted in bold.

epsilon	pvalue.PGLS	R2.PGLS	pvalue.LM	R2.LM
0.0	**4.063e-07**	0.08904	**1.676e-07**	0.09458
0.9	**3.483e-07**	0.09007	**2.844e-07**	0.09109

1.2 Full species-level database - including species with any remark

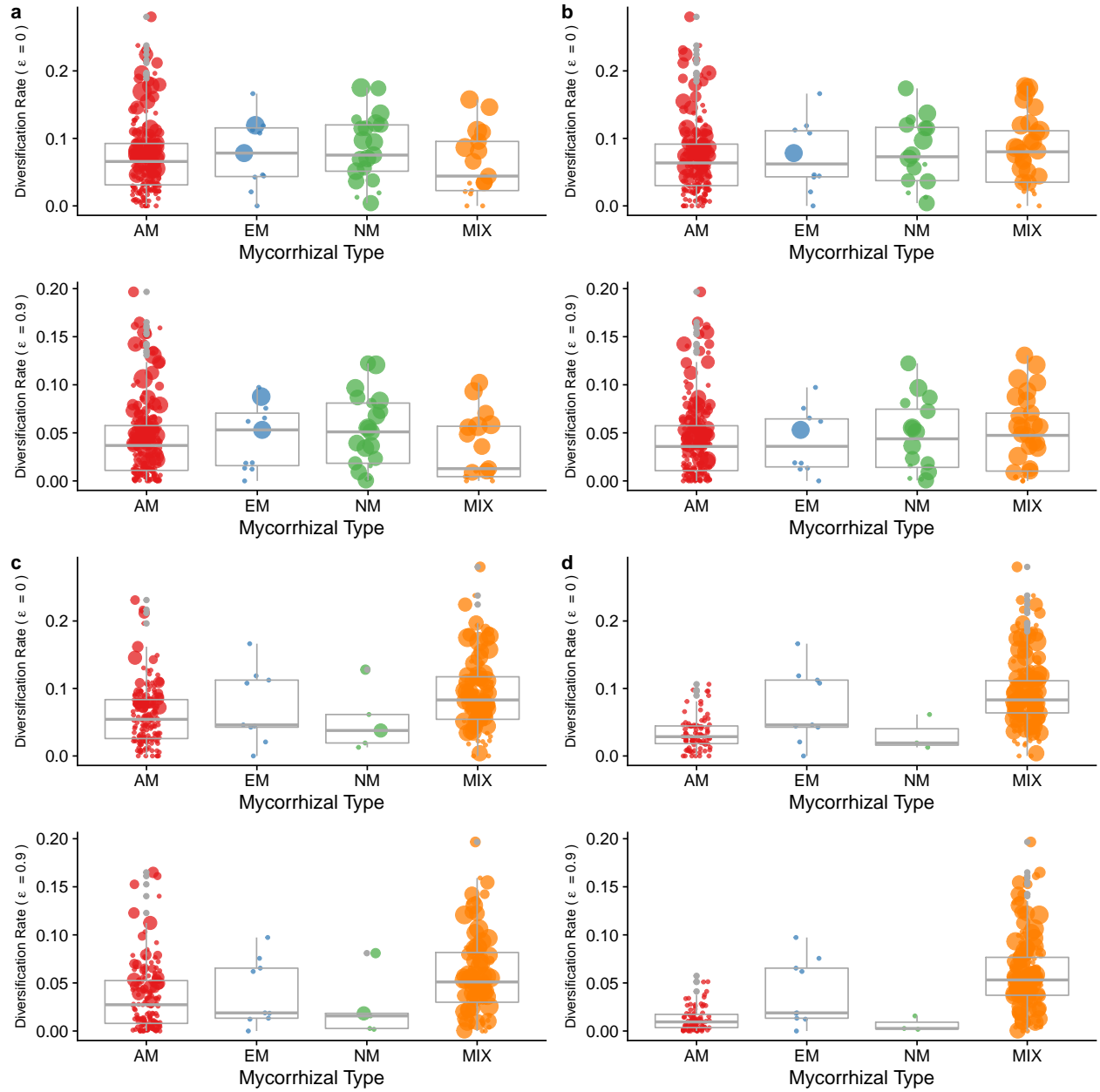### 1.2.1 Boxplots using full species-level database

Figure S3: Relationship between mycorrhizal type and diversification rates using the thresholds (a) 50%, (b) 60%, (c) 80% and (d) 100% for MIX state assignment. Each panel shows diversification rate estimated with epsilon = 0 (upper) and diversification rate estimated with epsilon = 0.9 (lower). AM: Arbuscular mycorrhiza, EM: Ectomycorrhiza, NM: non-mycorrhizal and MIX (families with no dominance of any specific mycorrhizal association). The size of the points indicates the Mycorrhizal Type Diversity Index value for each lineage, indicating a predominance of larger indices with higher diversification rates.

1.2.2 Summary statistics using full species-level database

1.2.2.1 phyANOVA

Table S6: summary statistics for phyANOVA for both values of epsilon. Significant values are highlighted in bold.

Threshold	F.r0	pvalue.r0	F.r09	pvalue.r09
50	0.691	0.703	0.666	0.676
60	0.511	0.787	0.324	0.869
80	8.571	**0.001**	8.425	**0.001**
100	36.44	**0.001**	43.806	**0.001**

1.2.2.2 Standard ANOVA

Table S7: summary statistics for phyANOVA for both values of epsilon. Significant values are highlighted in bold.

Threshold	F.r0	pvalue.r0	F.r09	pvalue.r09
50	1.083	0.365	1.085	0.364
60	0.953	0.434	0.831	0.506
80	7.113	**0**	7.084	**0**
100	28.22	**0**	34.224	**0**

1.2.3 Posthoc tests using full species-level database

1.2.3.1 phyANOVA

Table S8: Pairwise Corrected p-values for phyANOVA. Significant values are highlighted in bold.

Threshold	Mycorrhizal.Type	AM.r0	EM.r0	MIX.r0	NM.r0	AM.r09	EM.r09	MIX.r09	NM.r09
50	AM	1	1	1	1	1	1	1	1
50	EM	1	1	1	1	1	1	1	1
50	MIX	1	1	1	0.918	1	1	1	0.924
50	NM	1	1	0.918	1	1	1	0.924	1
60	AM	1	1	1	1	1	1	1	1
60	EM	1	1	1	1	1	1	1	1
60	MIX	1	1	1	1	1	1	1	1
60	NM	1	1	1	1	1	1	1	1
80	AM	1	1	**0.006**	1	1	1	**0.006**	1
80	EM	1	1	1	1	1	1	1	1
80	MIX	**0.006**	1	1	0.255	**0.006**	1	1	0.145
80	NM	1	1	0.255	1	1	1	0.145	1
100	AM	1	0.18	**0.006**	0.922	1	0.2	**0.006**	0.742
100	EM	0.18	1	0.728	0.531	0.2	1	0.408	0.408
100	MIX	**0.006**	0.728	1	0.07	**0.006**	0.408	1	**0.015**
100	NM	0.922	0.531	0.07	1	0.742	0.408	**0.015**	1

1.2.3.2 Standard ANOVA

Table S9: Pairwise Corrected p-values for standard ANOVA. Significant values are highlighted in bold.

| Types	50.r0	60.r0	80.r0	100.r0	50.r09	60.r09	80.r09	100.r09
EM-AM	0.991	0.999	0.937	0.067	0.998	1	0.99	0.084
ER-AM	0.592	0.62	0.808	1	0.562	0.59	0.783	1
MIX-AM	0.97	0.805	**0**	**0**	0.906	0.874	**0**	**0**
NM-AM	0.763	0.958	0.996	1	0.85	0.995	0.968	0.998
ER-EM	0.561	0.663	0.649	0.527	0.593	0.723	0.735	0.601
MIX-EM	0.937	0.996	0.778	0.674	0.929	0.986	0.608	0.364
NM-EM	0.997	0.999	0.935	0.583	0.996	0.999	0.928	0.485
MIX-ER	0.838	0.407	0.12	0.05	0.87	0.413	0.113	**0.029**
NM-ER	0.352	0.501	0.979	1	0.368	0.561	0.993	0.999
NM-MIX	0.684	1	0.358	0.102	0.637	0.999	0.237	**0.03**

1.2.4 Scatterplots
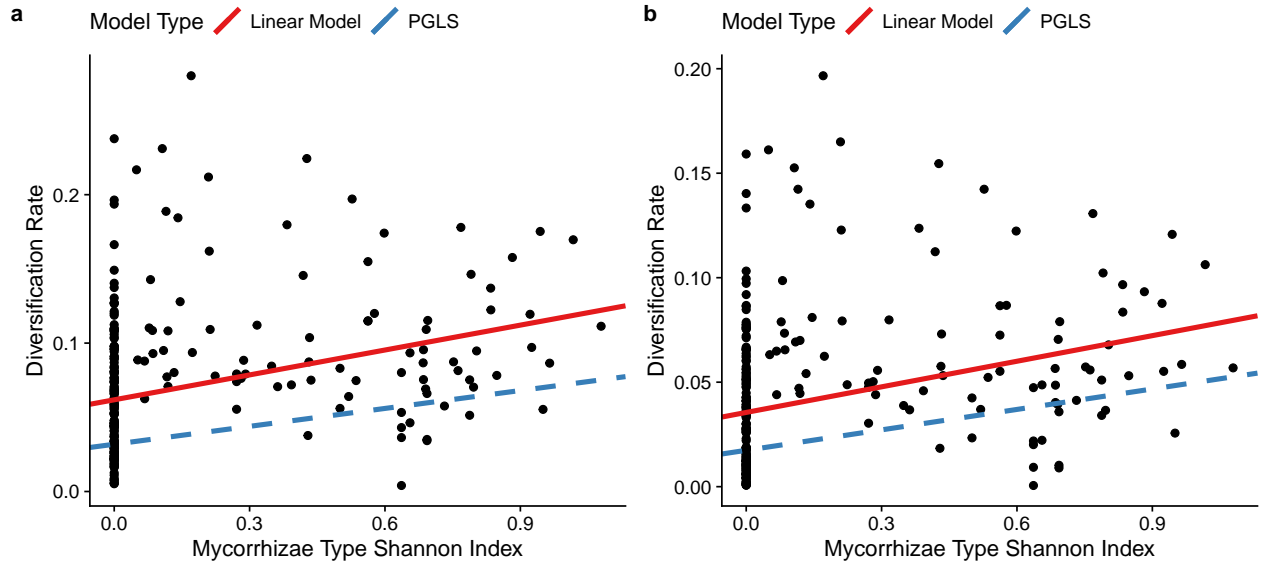
Figure S4: Scatterplots showing the relationship between mycorrhizal diversity index and diversification rates. Diversification rates were estimated with epsilon = 0 (a) and with epsilon = 0.9 (b). The red and blue lines indicate the results of a linear model and a phylogenetic generalized least squares (PGLS) fit, respectively.

Table S10: Summary statistics for the phylogenetic and parametric regressions using the full genus dataset. Significant values are highlighted in bold.

epsilon	pvalue.PGLS	R2.PGLS	pvalue.LM	R2.LM
0.0	**5.265e-05**	0.06444	**2.528e-07**	0.09354
0.9	**4.013e-05**	0.06653	**4.977e-07**	0.08898

2 Adding randomly 20% of misassignment of mycorrhizal type
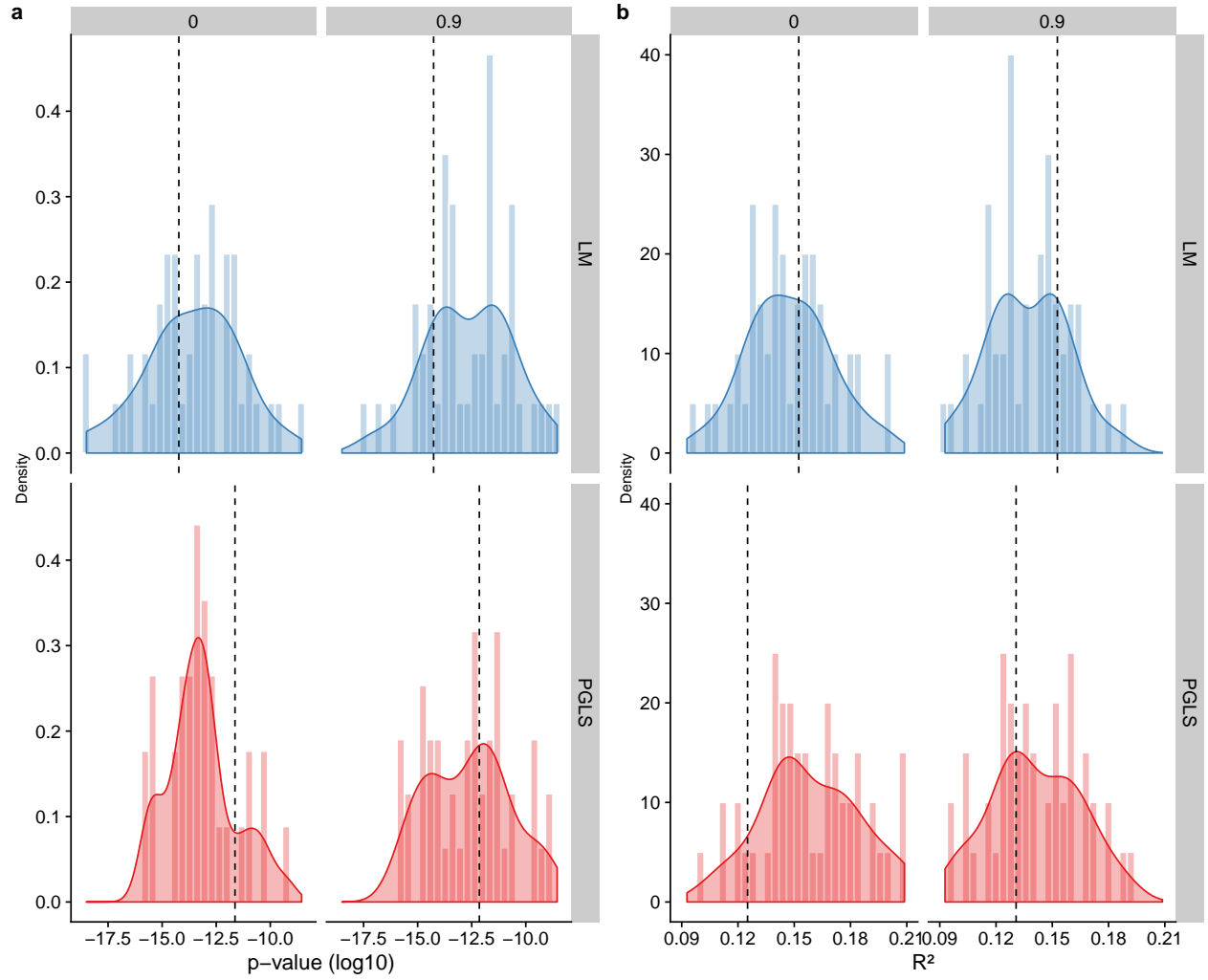
2.1 Regressions

Figure S5: Distribution of (a) p-values and (b) R^2 values for the same analyses of the main paper, but using all 50 replicate datasets with mycorrhizal types for 20% of species randomly sampled. Dashed vertical lines represent the corresponding empirical value from the main analysis.
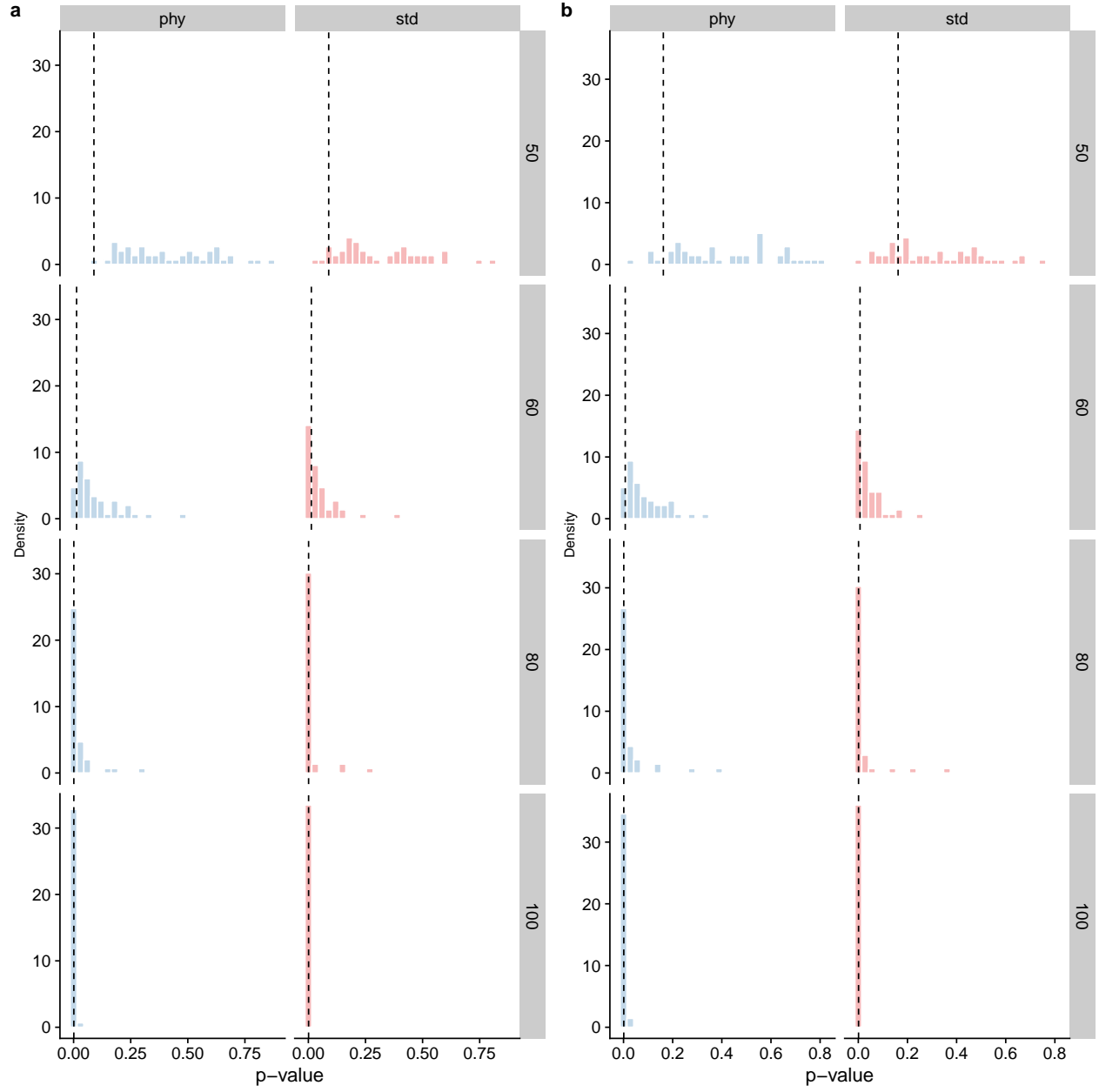
2.2 ANOVAs

Figure S6: Distribution of p-values of (a) epsilon = 0 and (b) epsilon = 0.9 for the both phylogenetic and standard ANOVA, but using all 50 replicate datasets with mycorrhizal types for 20% of species randomly sampled. Dashed vertical lines represent the corresponding empirical value from the main analysis.

3 Analyses with the genus-level database

3.1 Analysis per genera excluding 100% MIX families

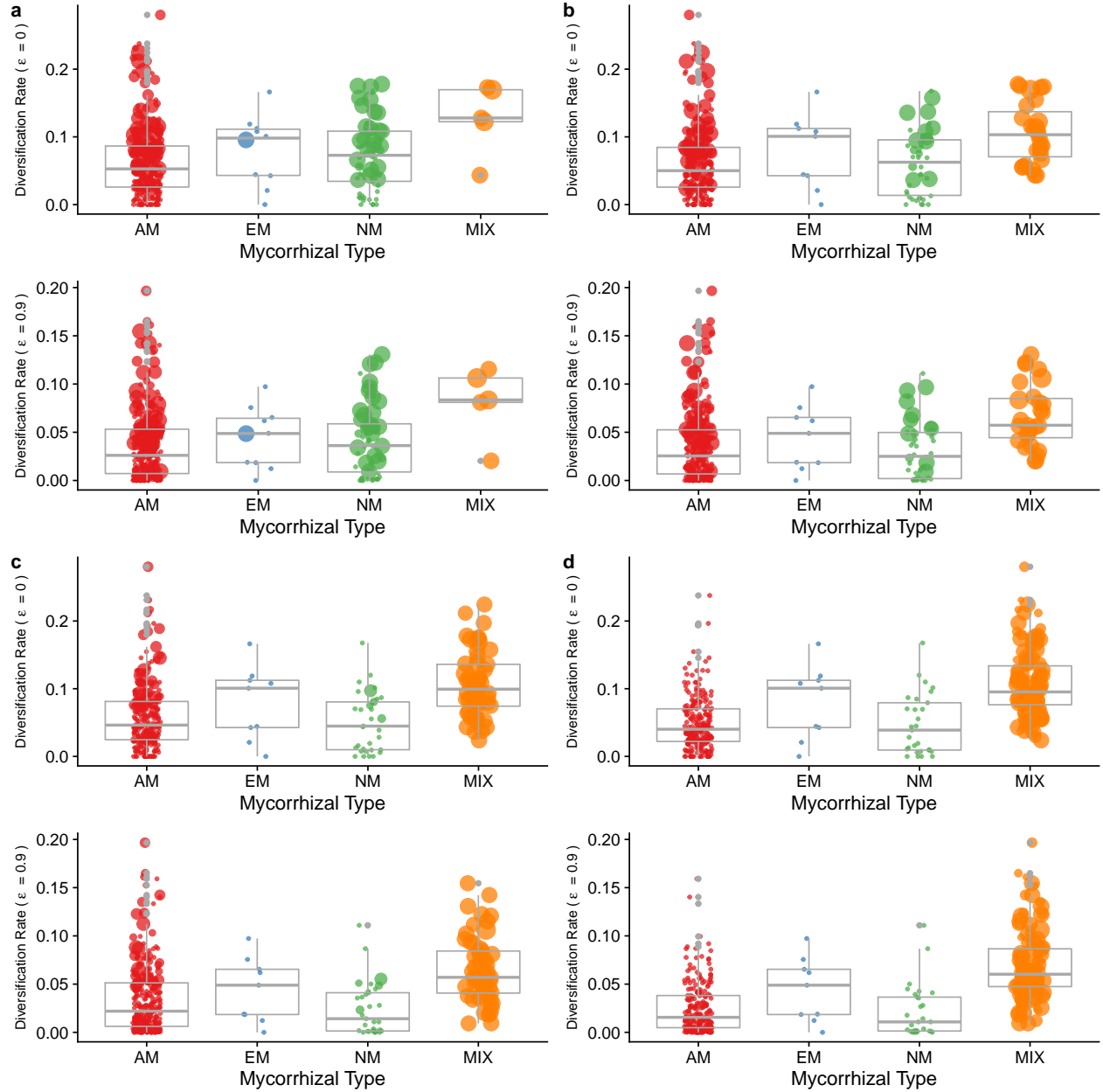### 3.1.1 Boxplots using clean genus-level database

Figure S7: Relationship between mycorrhizal type and diversification rates. a) diversification rate estimated with epsilon = 0 and b) diversification rate estimated with epsilon = 0.9. AM: Arbuscular mycorrhiza, EM: Ectomycorrhiza, NM: non-mycorrhizal and MIX (families with no dominance of any specific mycorrhizal association). The size of the points indicates the Mycorrhizal Type Diversity Index value for each lineage, indicating a predominance of larger indices with higher diversification rates.

Table S11: Mycorrhizal type assigned to each family based on 4 different percentage thresholds (50, 60, 80 and 100). Significant values are highlighted in bold.

Threshold	AM	EM	ER	MIX	NM
50	293	10	1	5	56
60	286	9	1	27	42
80	270	9	1	52	33
100	228	9	1	98	29

3.1.2 Summary statistics using clean genus-level database

3.1.2.1 phyANOVA

Table S12: Summary statistics for phyANOVA for both values of epsilon. Significant values are highlighted in bold.

Threshold	F.r0	pvalue.r0	F.r09	pvalue.r09
50	3.996	0.089	3.147	0.162
60	7.255	**0.013**	7.35	**0.007**
80	14.181	**0.001**	13.177	**0.001**
100	44.007	**0.001**	52.476	**0.001**

3.1.2.2 Standard ANOVA

Table S13: summary statistics for standard ANOVA for both values of epsilon. Significant values are highlighted in bold.

Threshold	F.r0	pvalue.r0	F.r09	pvalue.r09
50	3.996	**0.008**	3.147	**0.025**
60	7.255	**0**	7.35	**0**
80	14.181	**0**	13.177	**0**
100	44.007	**0**	52.476	**0**

3.1.3 Posthoc tests

3.1.3.1 phyANOVA

Table S14: Pairwise Corrected p-values for phyANOVA. Significant values are highlighted in bold.

Threshold	Mycorrhizal.Type	AM.r0	EM.r0	MIX.r0	NM.r0	AM.r09	EM.r09	MIX.r09	NM.r09
50	AM	1	0.858	**0.042**	0.747	1	1	**0.048**	1
50	EM	0.858	1	0.716	0.858	1	1	0.62	1
50	MIX	**0.042**	0.716	1	**0.042**	**0.048**	0.62	1	**0.048**
50	NM	0.747	0.858	**0.042**	1	1	1	**0.048**	1
60	AM	1	1	**0.006**	1	1	1	**0.006**	1
60	EM	1	1	1	1	1	1	0.952	1
60	MIX	**0.006**	1	1	**0.006**	**0.006**	0.952	1	**0.006**
60	NM	1	1	**0.006**	1	1	1	**0.006**	1
80	AM	1	1	**0.006**	1	1	1	**0.006**	1
80	EM	1	1	1	1	1	1	1	1
80	MIX	**0.006**	1	1	**0.006**	**0.006**	1	1	**0.006**
80	NM	1	1	**0.006**	1	1	1	**0.006**	1
100	AM	1	0.552	**0.006**	0.868	1	0.567	**0.006**	0.627
100	EM	0.552	1	0.552	0.552	0.567	1	0.468	0.567
100	MIX	**0.006**	0.552	1	**0.006**	**0.006**	0.468	1	**0.006**
100	NM	0.868	0.552	**0.006**	1	0.627	0.567	**0.006**	1

3.1.3.2 Standard ANOVA

Table S15: Pairwise Corrected p-values for standard ANOVA. Significant values are highlighted in bold.

Types	50.r0	60.r0	80.r0	100.r0	50.r09	60.r09	80.r09	100.r09
EM-AM	0.618	0.686	0.58	0.154	0.854	0.866	0.794	0.246
MIX-AM	**0.018**	**0**	**0**	**0**	**0.025**	**0**	**0**	**0**
NM-AM	0.364	1	0.783	0.997	0.663	0.94	0.456	0.924
MIX-EM	0.315	0.492	0.483	0.251	0.248	0.33	0.379	0.074
NM-EM	0.97	0.753	0.374	0.198	0.993	0.765	0.409	0.196
NM-MIX	0.09	**0.002**	**0**	**0**	0.083	**0**	**0**	**0**

3.2 Genus-level full database - including all families

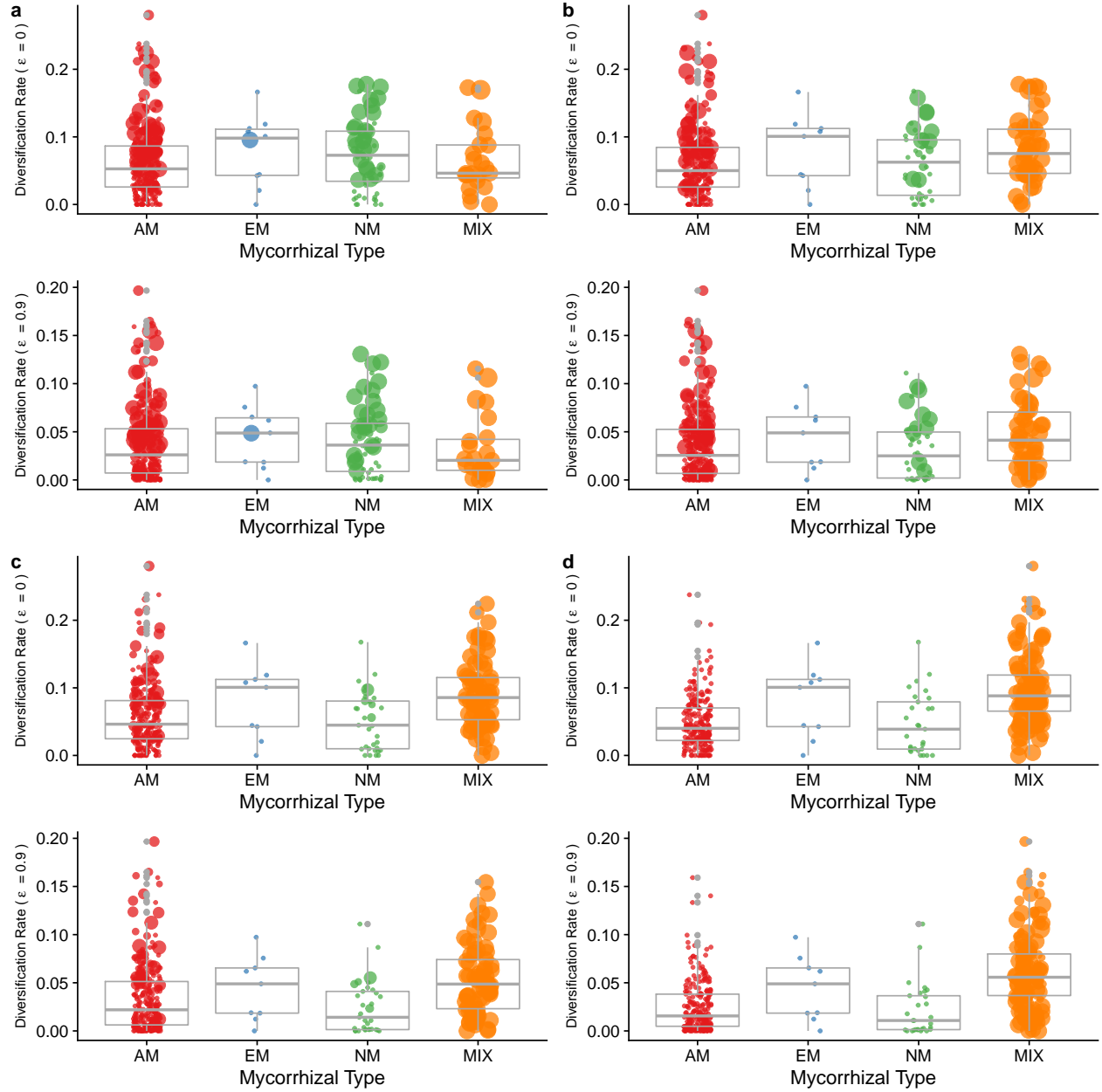### 3.2.1 Boxplots using genus-level full database

Figure S8: Relationship between mycorrhizal type and diversification rates using the thresholds (a) 50%, (b) 60%, (c) 80% and (d) 100% for MIX state assignment. Each panel shows diversification rate estimated with epsilon = 0 (upper) and diversification rate estimated with epsilon = 0.9 (lower). AM: Arbuscular mycorrhiza, EM: Ectomycorrhiza, NM: non-mycorrhizal and MIX (families with no dominance of any specific mycorrhizal association). The size of the points indicates the Mycorrhizal Type Diversity Index value for each lineage, indicating a predominance of larger indices with higher diversification rates.

3.2.2 Summary statistics

3.2.2.1 phyANOVA

Table S16: summary statistics for phyANOVA for both values of epsilon. Significant values are highlighted in bold.

Threshold	F.r0	pvalue.r0	F.r09	pvalue.r09
50	1.295	0.631	0.696	0.825
60	2.842	0.244	2.153	0.402
80	8.598	**0.005**	7.033	**0.022**
100	33.621	**0.001**	37.429	**0.001**

3.2.2.2 Standard ANOVA

Table S17: summary statistics for standard ANOVA for both values of epsilon. Significant values are highlighted in bold.

Threshold	F.r0	pvalue.r0	F.r09	pvalue.r09
50	1.295	0.276	0.696	0.555
60	2.842	**0.038**	2.153	0.093
80	8.598	**0**	7.033	**0**
100	33.621	**0**	37.429	**0**

3.2.3 Posthoc tests using genus-level full database

3.2.3.1 phyANOVA

Table S18: Pairwise Corrected p-values for phyANOVA. Significant values are highlighted in bold.

Threshold	Mycorrhizal.Type	AM.r0	EM.r0	MIX.r0	NM.r0	AM.r09	EM.r09	MIX.r09	NM.r09
50	AM	1	1	1	1	1	1	1	1
50	EM	1	1	1	1	1	1	1	1
50	MIX	1	1	1	1	1	1	1	1
50	NM	1	1	1	1	1	1	1	1
60	AM	1	1	0.355	1	1	1	0.665	1
60	EM	1	1	1	1	1	1	1	1
60	MIX	0.355	1	1	0.33	0.665	1	1	0.348
60	NM	1	1	0.33	1	1	1	0.348	1
80	AM	1	1	**0.01**	1	1	1	**0.03**	1
80	EM	1	1	1	1	1	1	1	1
80	MIX	**0.01**	1	1	**0.006**	**0.03**	1	1	**0.018**
80	NM	1	1	**0.006**	1	1	1	**0.018**	1
100	AM	1	0.64	**0.006**	0.878	1	0.796	**0.006**	0.796
100	EM	0.64	1	0.864	0.64	0.796	1	0.796	0.796
100	MIX	**0.006**	0.864	1	**0.006**	**0.006**	0.796	1	**0.006**
100	NM	0.878	0.64	**0.006**	1	0.796	0.796	**0.006**	1

3.2.3.2 Standard ANOVA

Table S19: Pairwise Corrected p-values for standard ANOVA. Significant values are highlighted in bold.

Pairs	50.r0	60.r0	80.r0	100.r0	50.r09	60.r09	80.r09	100.r09
EM-AM	0.616	0.689	0.587	0.171	0.852	0.869	0.8	0.278
MIX-AM	0.988	**0.032**	**0**	**0**	0.986	0.103	**0**	**0**
NM-AM	0.362	1	0.787	0.997	0.661	0.941	0.467	0.931
MIX-EM	0.833	0.998	0.937	0.62	0.815	0.991	0.909	0.367
NM-EM	0.97	0.755	0.382	0.216	0.993	0.769	0.419	0.226
NM-MIX	0.907	0.186	**0.001**	**0**	0.763	0.139	**0.001**	**0**

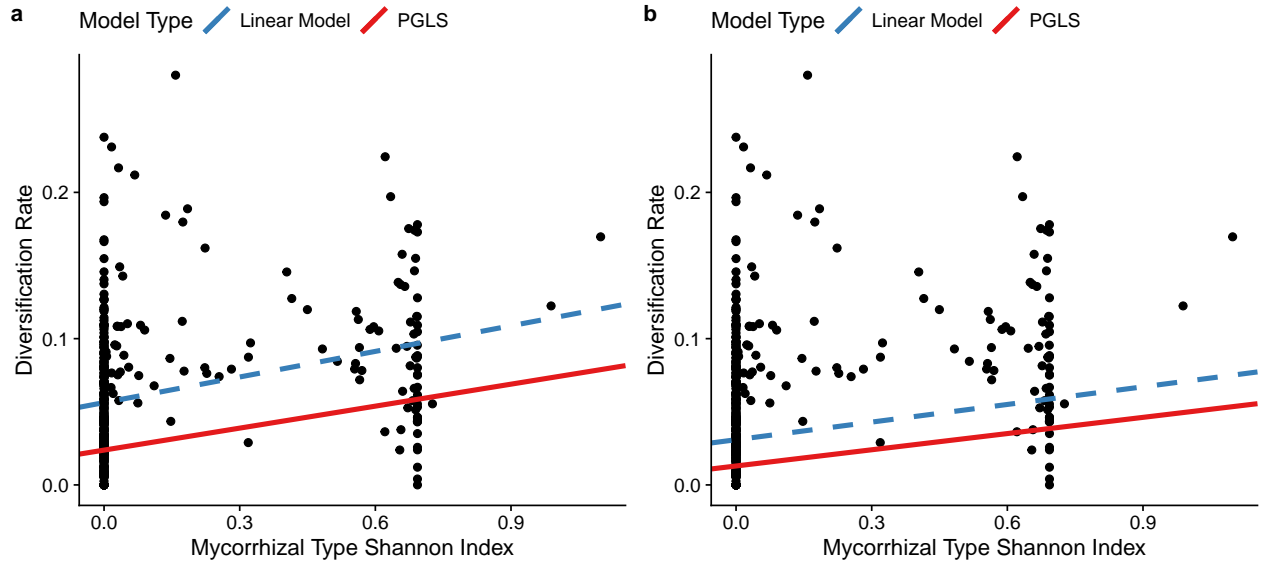### 3.2.4 Scatterplots using genus-level full database

Figure S9: Scatterplots showing the relationship between mycorrhizal diversity index and diversification rates. Diversification rates were estimated with epsilon = 0 (a) and with epsilon = 0.9 (b). The red and blue lines indicate the results of a linear model and a phylogenetic generalized least squares (PGLS) fit, respectively.

Table S20: Summary statistics for the phylogenetic and parametric regressions using the full genus dataset. Significant values are highlighted in bold.

epsilon	pvalue.PGLS	R2.PGLS	pvalue.LM	R2.LM
0.0	**4.637e-08**	0.07343	**6.325e-10**	0.09319
0.9	**6.858e-08**	0.07157	**4.512e-09**	0.08402

4 Phylogenetic signal of diversification rates, age, and richness

Table S21: P-values for test of phylogenetic signal (D) of each mycorrhizal type. Significant values are highlighted in bold.

Threshold	model	AM	EM	MIX	NM
50	random	**0**	**0**	0.842	**0**
50	BM	0.899	0.969	**0.043**	0.832
60	random	**0**	**0**	**0.031**	**0**
60	BM	0.88	0.949	0.215	0.852
80	random	**0**	**0**	**0**	**0**
80	BM	0.821	0.956	0.228	0.747
100	random	**0**	**0**	0.247	**0**
100	BM	0.083	0.958	**0**	0.643

Table S22: Phylogenetic signal of the four response variables. Significant values are highlighted in bold.

Variable	Lambda
r.e0	**0.475**
r.e09	**0.358**
Stem.Age	**1**
Richness	1e-06

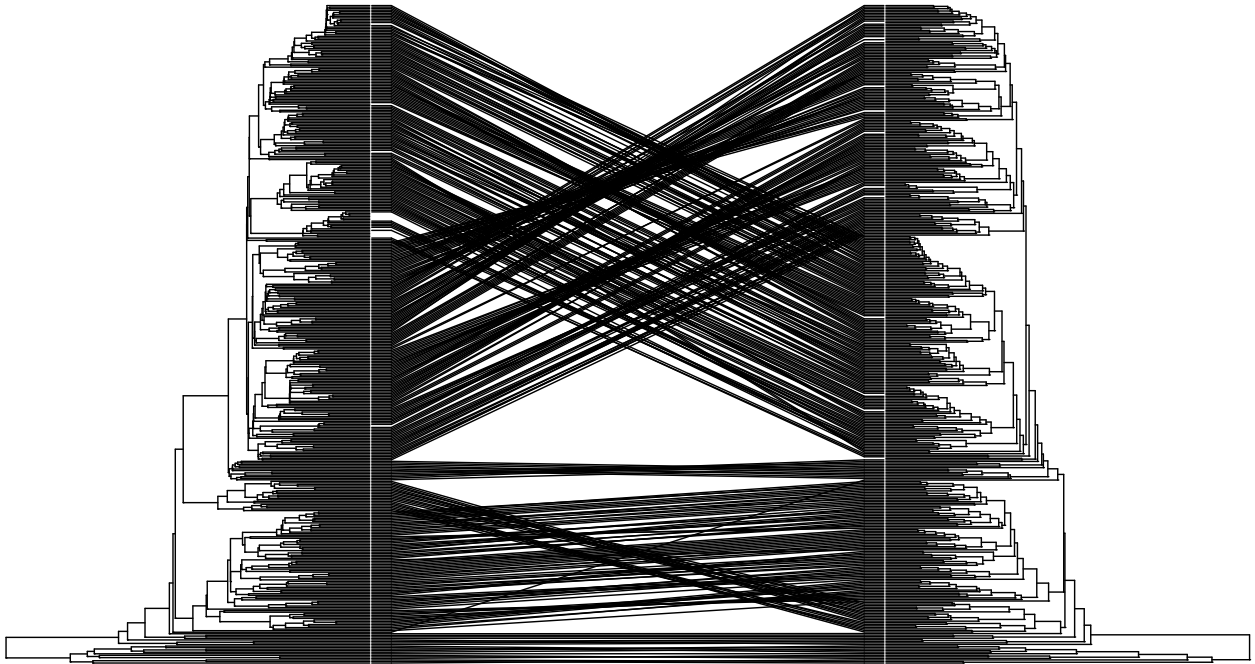# 5 Replicating main analyses with tree from Harris and Davies (2016)

Figure S10: Association between placement of families in both Zanne's (left) and Harris and Davies' (right) phylogenies, indicating differences in the topologies.
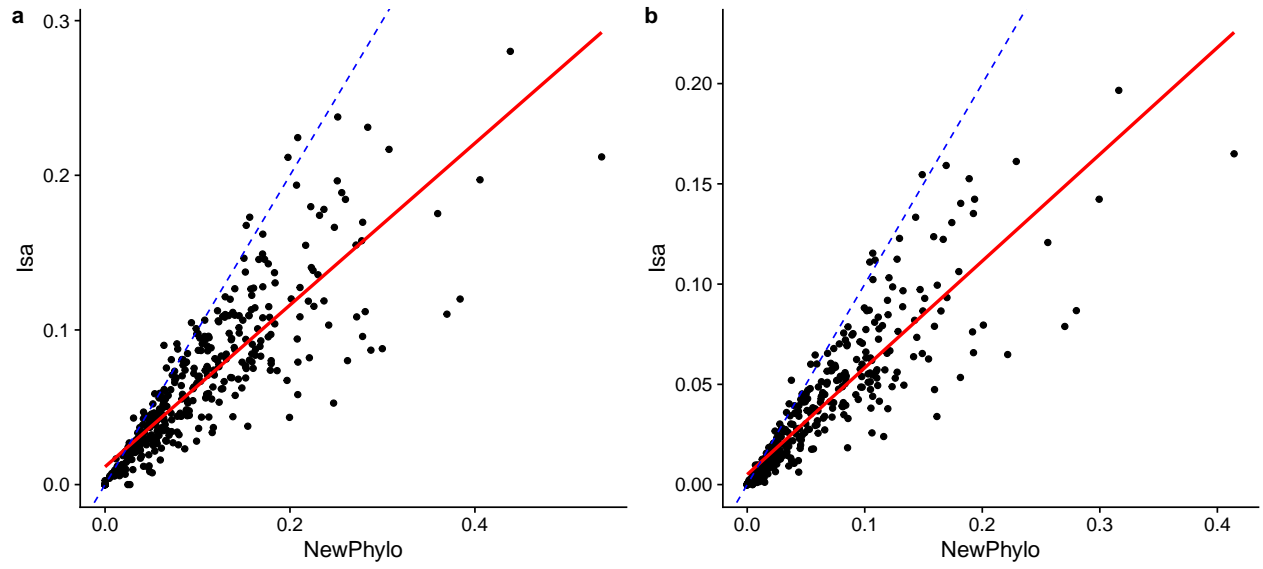
Figure S11: Relationship between net diversification calculated in our study and with the rates from Harris and Davies (2016) The rates were estimated by the authors using the same source for species richness as the main analysis, and the stem ages were obtained from their phylogeny. a: epsilon = 0; b: epsilon = 0.9. Red lines: LM fit; blue dashed lines: identity fit.
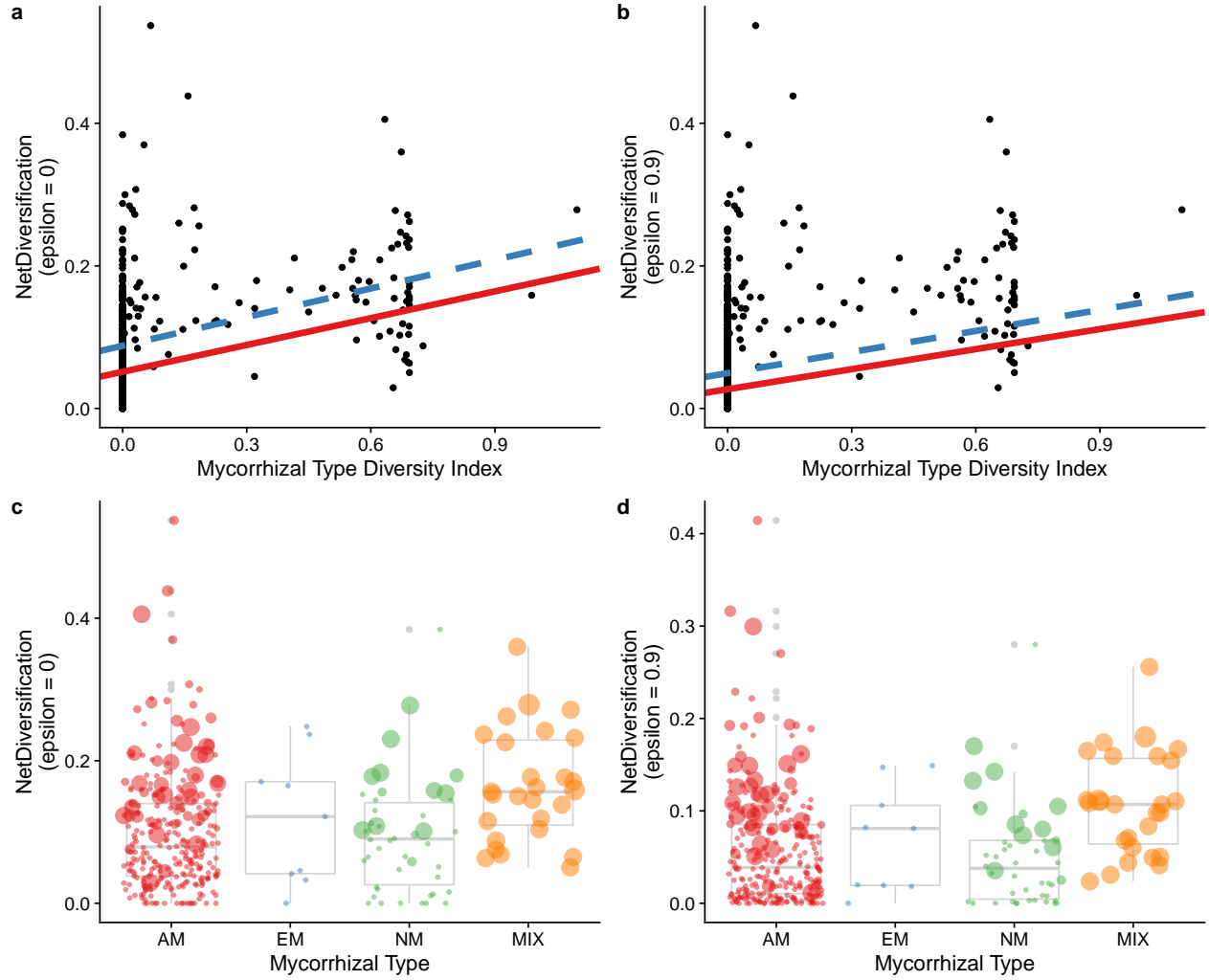
Figure S12: Main analyses replicated using Harris and Davies (2016) phylogeny. The rates were estimated by the authors using the same source for species richness as the main analysis, and the stem ages were obtained from their phylogeny. Panels a and c: epsilon = 0; panels b and d: epsilon = 0.9. Red lines: PGLS fit; blue dashed lines: LM fit.

Table S23: Summary statistics for linear models and ANOVA using Harris and Davies (2016) phylogeny.

epsilon	pvalue.PGLS	R2.PGLS	pvalue.LM	R2.LM	pvalue.stdaov	pvalue.phyaov
0.0	**2.724e-13**	0.135	**1.345e-14**	0.146	**0.019**	**0.0005**
0.9	**3.581e-13**	0.134	**1.228e-14**	0.147	**0.02**	**0.0003**