Supplementary Material - Mujica et al.

1 Phylogenetic signal of Mycorrhizal types

Table 1: P-values for test of phylogenetic signal (D) of each mycorrhizal type.

Threshold	model	AM	EM	MIX	NM
50	random	0.000	0.000	0.842	0.000
50	BM	0.899	0.969	0.043	0.832
60	random	0.000	0.000	0.031	0.000
60	BM	0.880	0.949	0.215	0.852
80	random	0.000	0.000	0.000	0.000
80	BM	0.821	0.956	0.228	0.747
100	random	0.000	0.000	0.247	0.000
100	BM	0.083	0.958	0.000	0.643

2 Analysis per genera excluding 100% MIX families
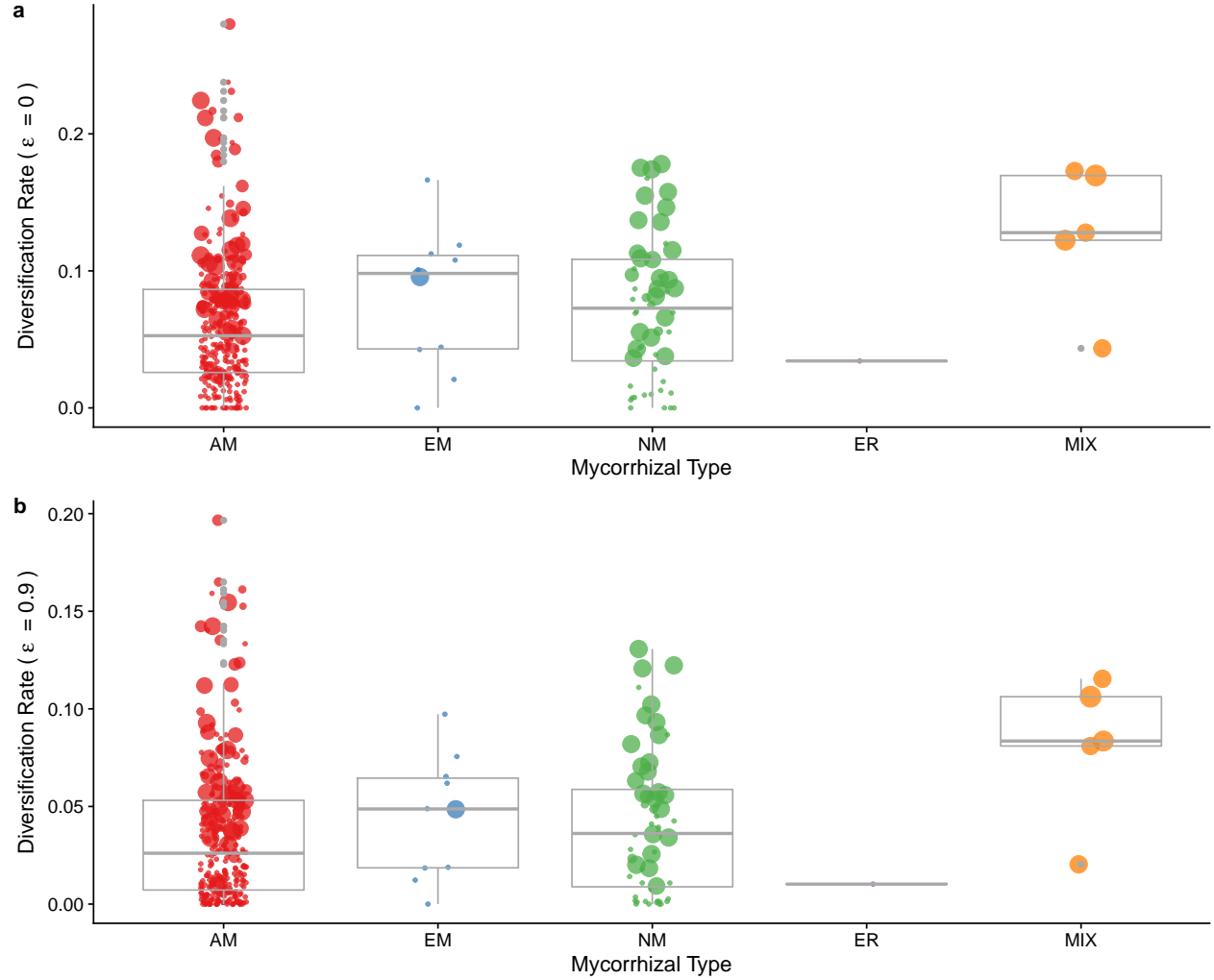
2.1 Boxplots

2.1.1 Threshold 50%

Figure 1: Relationship between mycorrhizal type and diversification rates. a) diversification rate estimated with (relative extinction fraction) = 0 and b) diversification rate estimated with = 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.
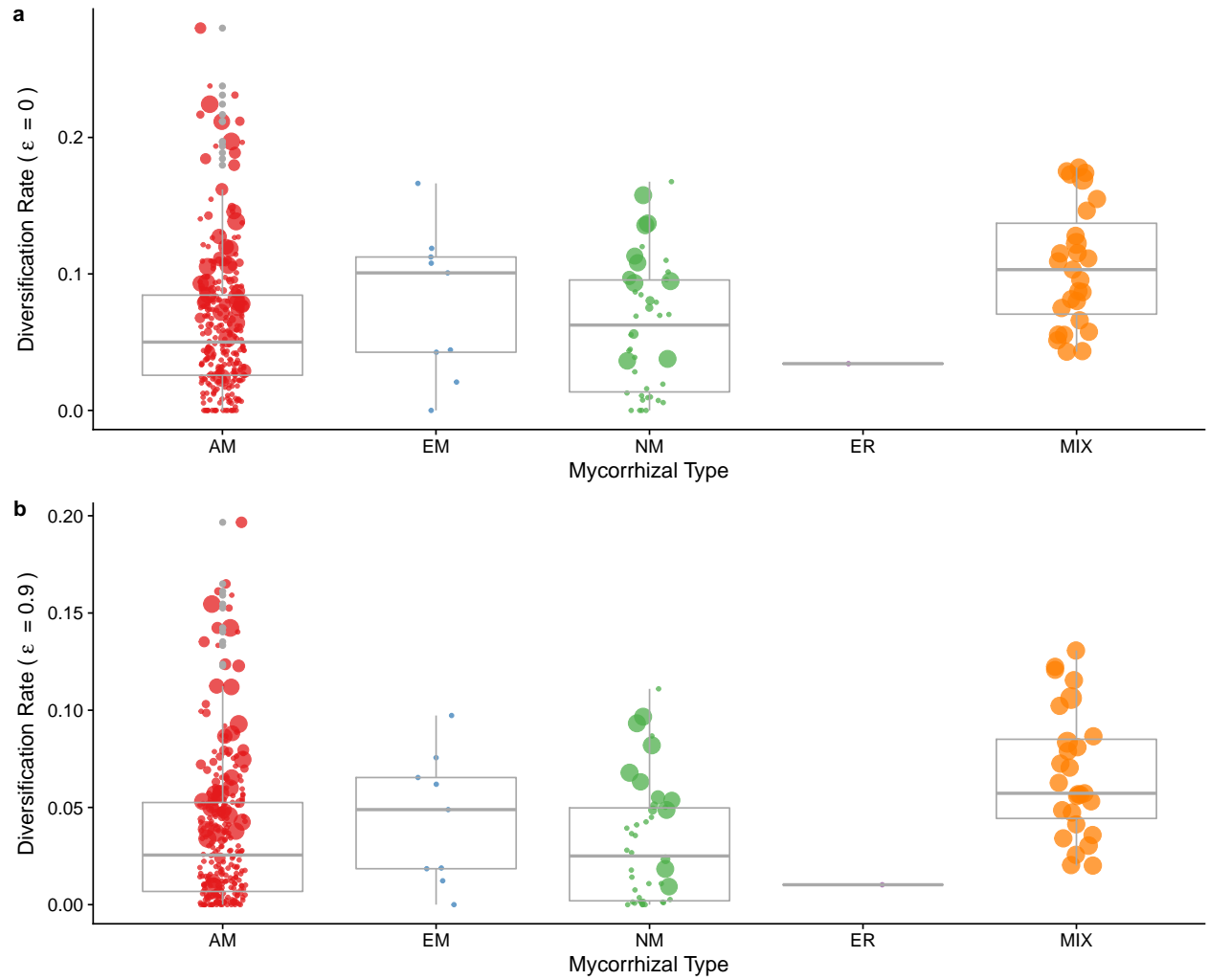
2.1.2 Threshold 60%

a

b

Figure 2: Relationship between mycorrhizal type and diversification rates. a) diversification rate estimated with (relative extinction fraction) = 0 and b) diversification rate estimated with = 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.
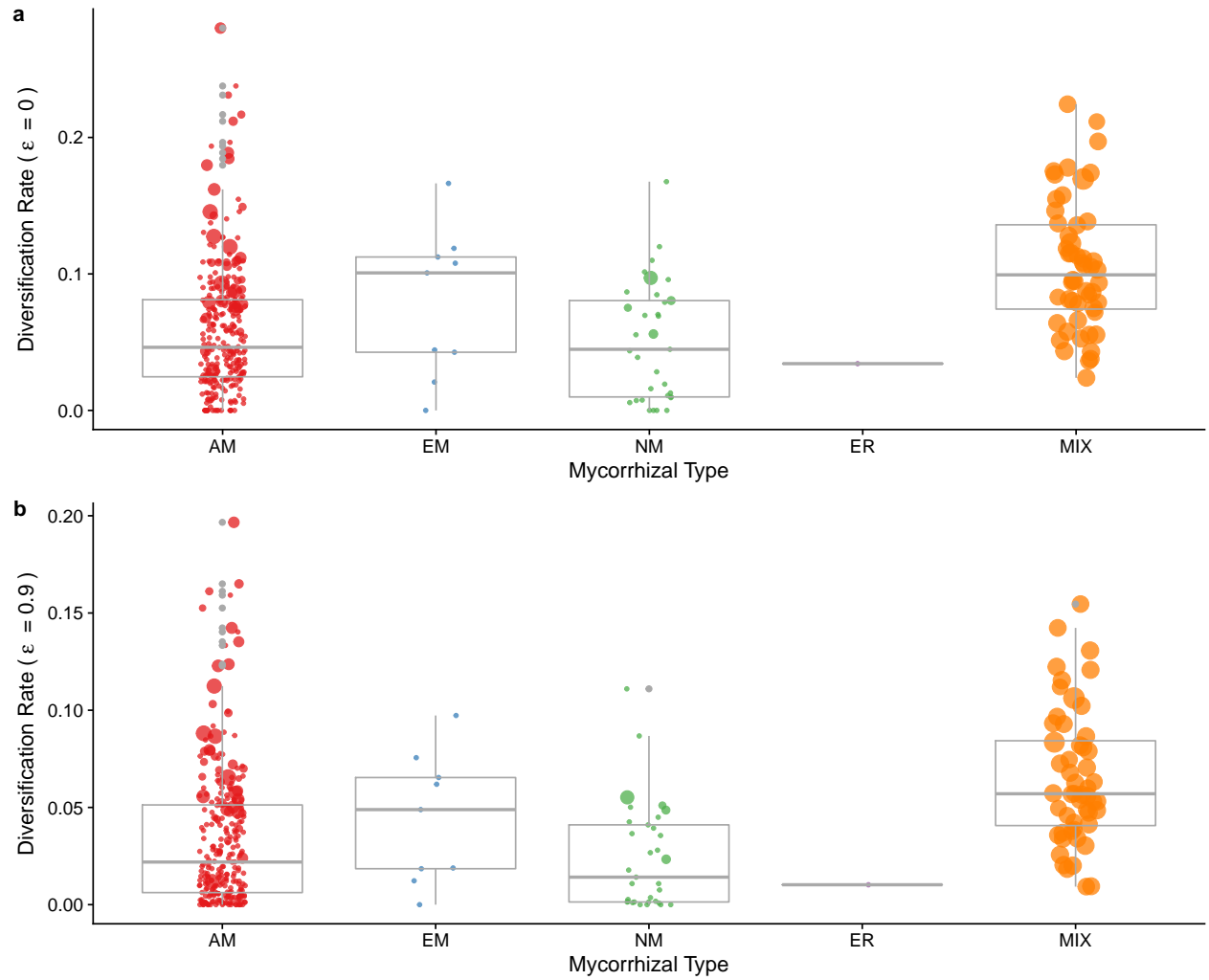
2.1.3 Threshold 80%

Figure 3: Relationship between mycorrhizal type and diversification rates. a) diversification rate estimated with (relative extinction fraction) = 0 and b) diversification rate estimated with = 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.
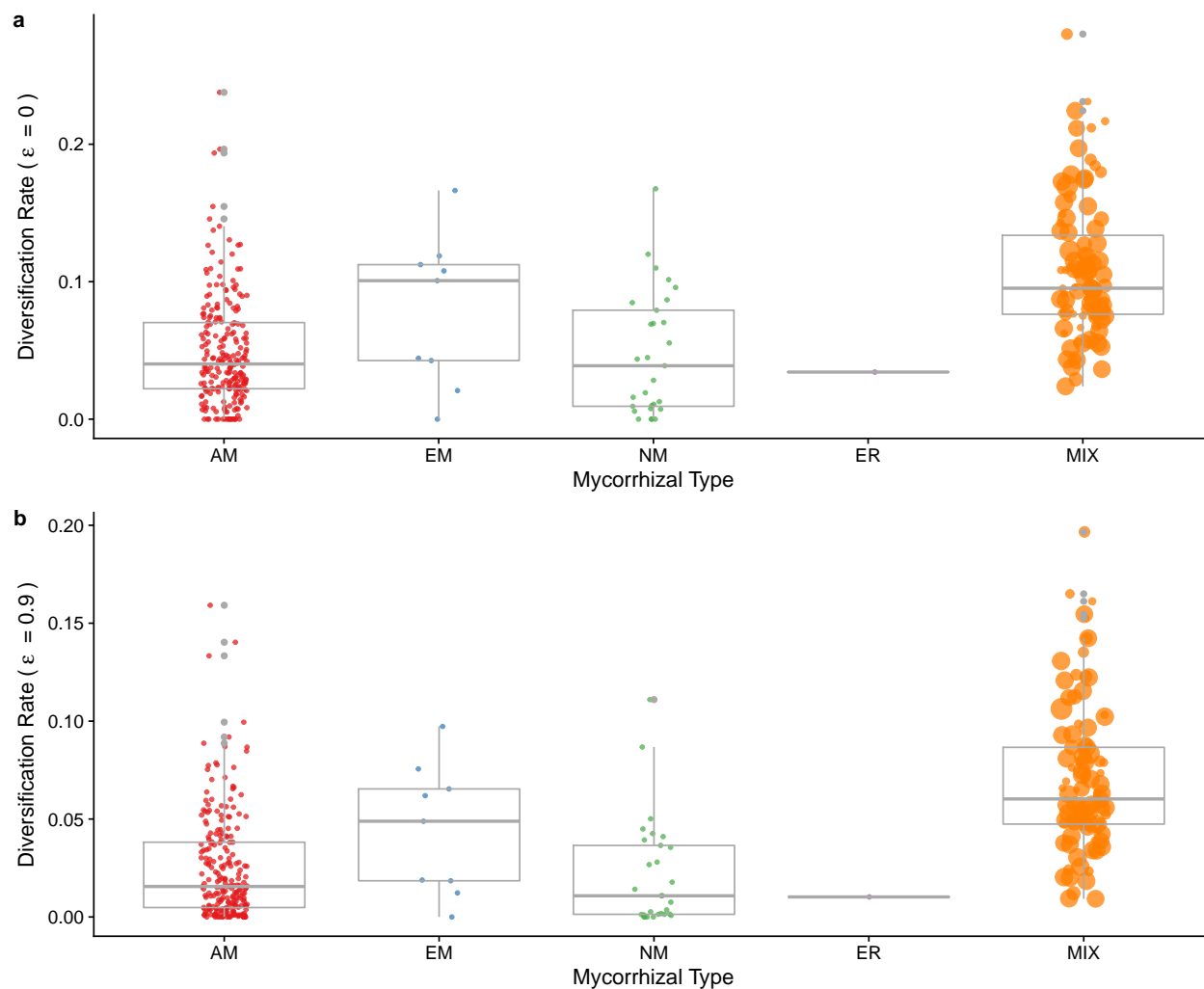
2.1.4 Threshold 100%

Figure 4: Relationship between mycorrhizal type and diversification rates. a) diversification rate estimated with (relative extinction fraction) = 0 and b) diversification rate estimated with = 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.

2.2 Summary statistics

2.2.1 phyANOVA

Table 2: Summary statistics for phyANOVA for both values of epsilon

Threshold	F_r0	pvalue_r0	F_r09	pvalue_r09
50	3.996351	0.089	3.146694	0.162
60	7.255048	0.013	7.349522	0.007
80	14.181222	0.001	13.177448	0.001
100	44.007242	0.001	52.475717	0.001

2.2.2 Standard ANOVA

Table 3: summary statistics for standard ANOVA for both values of epsilon

Threshold	F_r0	pvalue_r0	F_r09	pvalue_r09
50	3.996351	0.0080666	3.146694	0.0252019
60	7.255048	0.0000976	7.349522	0.0000859
80	14.181222	0.0000000	13.177448	0.0000000
100	44.007242	0.0000000	52.475717	0.0000000

2.3 Posthoc tests

2.3.1 phyANOVA

Table 4: Pairwise Corrected p-values for phyANOVA

Threshold	Mycorrhizal Type	AM r0	EM r0	MIX r0	NM r0	AM r09	EM r09	MIX r09	NM r09
50	AM	1.000	0.858	0.042	0.747	1.000	1.000	0.048	1.000
50	EM	0.858	1.000	0.716	0.858	1.000	1.000	0.620	1.000
50	MIX	0.042	0.716	1.000	0.042	0.048	0.620	1.000	0.048
50	NM	0.747	0.858	0.042	1.000	1.000	1.000	0.048	1.000
60	AM	1.000	1.000	0.006	1.000	1.000	1.000	0.006	1.000
60	EM	1.000	1.000	1.000	1.000	1.000	1.000	0.952	1.000
60	MIX	0.006	1.000	1.000	0.006	0.006	0.952	1.000	0.006
60	NM	1.000	1.000	0.006	1.000	1.000	1.000	0.006	1.000
80	AM	1.000	1.000	0.006	1.000	1.000	1.000	0.006	1.000
80	EM	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000
80	MIX	0.006	1.000	1.000	0.006	0.006	1.000	1.000	0.006
80	NM	1.000	1.000	0.006	1.000	1.000	1.000	0.006	1.000
100	AM	1.000	0.552	0.006	0.868	1.000	0.567	0.006	0.627
100	EM	0.552	1.000	0.552	0.552	0.567	1.000	0.468	0.567
100	MIX	0.006	0.552	1.000	0.006	0.006	0.468	1.000	0.006
100	NM	0.868	0.552	0.006	1.000	0.627	0.567	0.006	1.000

2.3.2 Standard ANOVA

Table 5: Pairwise Corrected p-values for standard ANOVA

Types	50% r0	60% r0	80% r0	100% r0	50% r09	60% r09	80% r09	100% r09
EM-AM	0.6181054	0.6863035	0.5796271	0.1543423	0.8535980	0.8658222	0.7940811	0.2458535
MIX-AM	0.0175076	0.0000419	0.0000000	0.0000000	0.0252774	0.0000466	0.0000001	0.0000000
NM-AM	0.3643504	0.9999391	0.7825962	0.9968473	0.6634857	0.9395123	0.4564819	0.9238914
MIX-EM	0.3148479	0.4924541	0.4829107	0.2510813	0.2476270	0.3299713	0.3786544	0.0744958
NM-EM	0.9703962	0.7528214	0.3740249	0.1976010	0.9934429	0.7649349	0.4085420	0.1963633
NM-MIX	0.0897398	0.0015049	0.0000048	0.0000000	0.0833662	0.0003135	0.0000020	0.0000000

2.4 Phylogenetic signal of diversification rates, age, and richness

Table 6: Phylogenetic signal of the four response variables

Variable	Lambda
r (epsilon = 0)	0.4747942
r (epsilon = 0.9)	0.3581693
Stem Age	1.0000000
Richness	0.0000010

3   Analysis per genera including all families
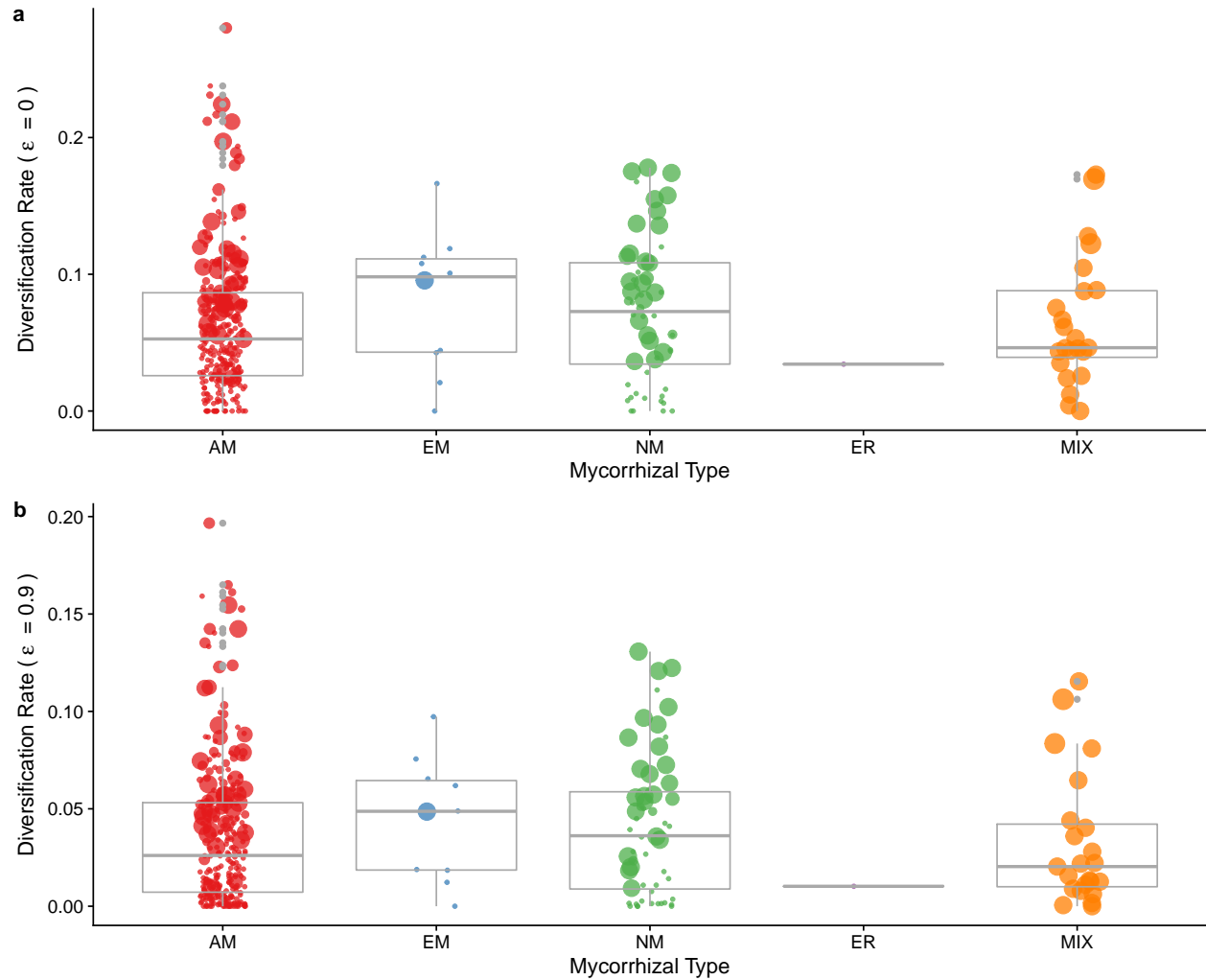
3.1   Boxplots

3.1.1   Threshold 50%

Figure 5: Relationship between mycorrhizal type and diversification rates. a) diversification rate estimated with (relative extinction fraction) = 0 and b) diversification rate estimated with = 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.
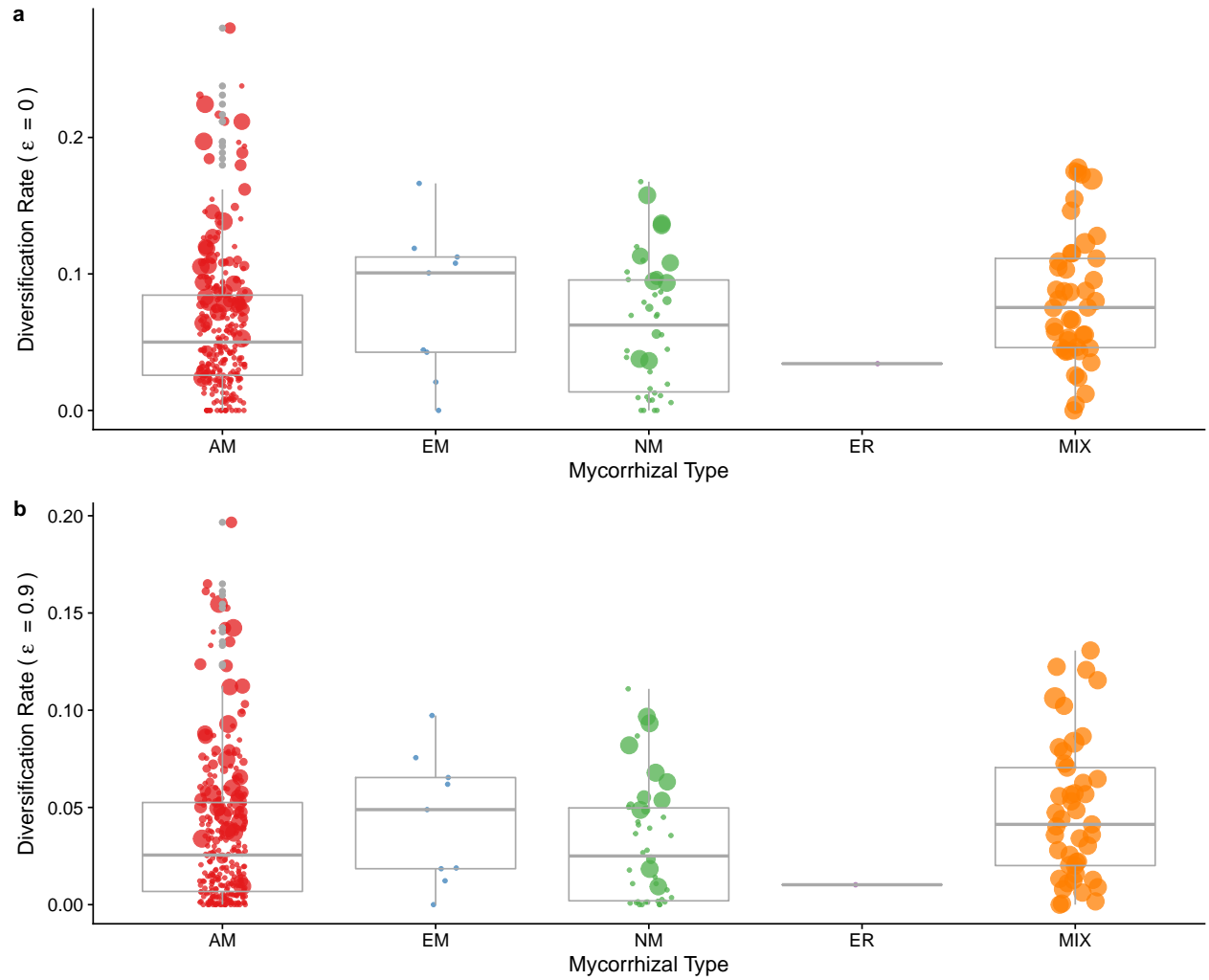
3.1.2 Threshold 60%

a

b

Figure 6: Relationship between mycorrhizal type and diversification rates. a) diversification rate estimated with (relative extinction fraction) = 0 and b) diversification rate estimated with = 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.
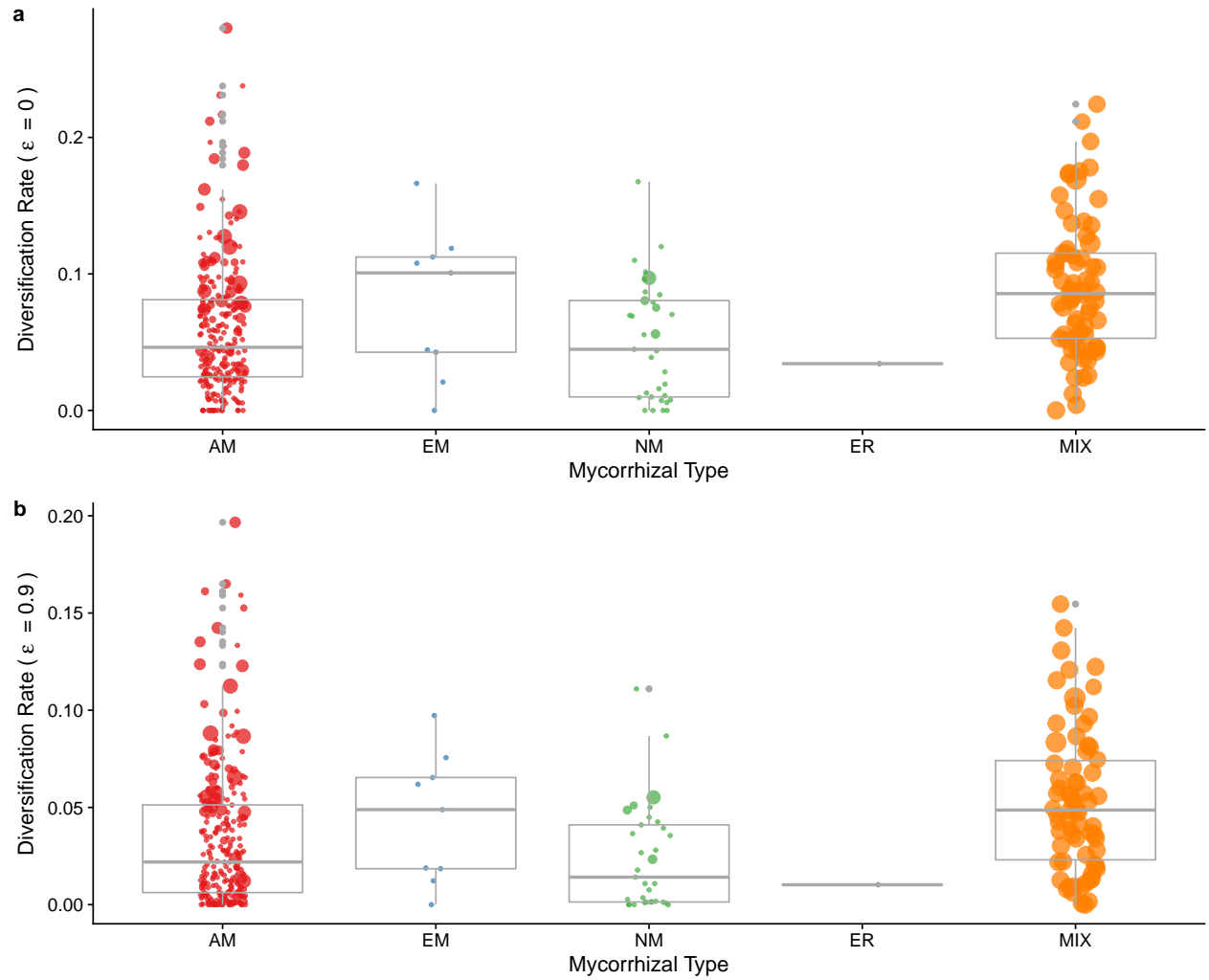
3.1.3 Threshold 80%

Figure 7: Relationship between mycorrhizal type and diversification rates. a) diversification rate estimated with (relative extinction fraction) = 0 and b) diversification rate estimated with = 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.
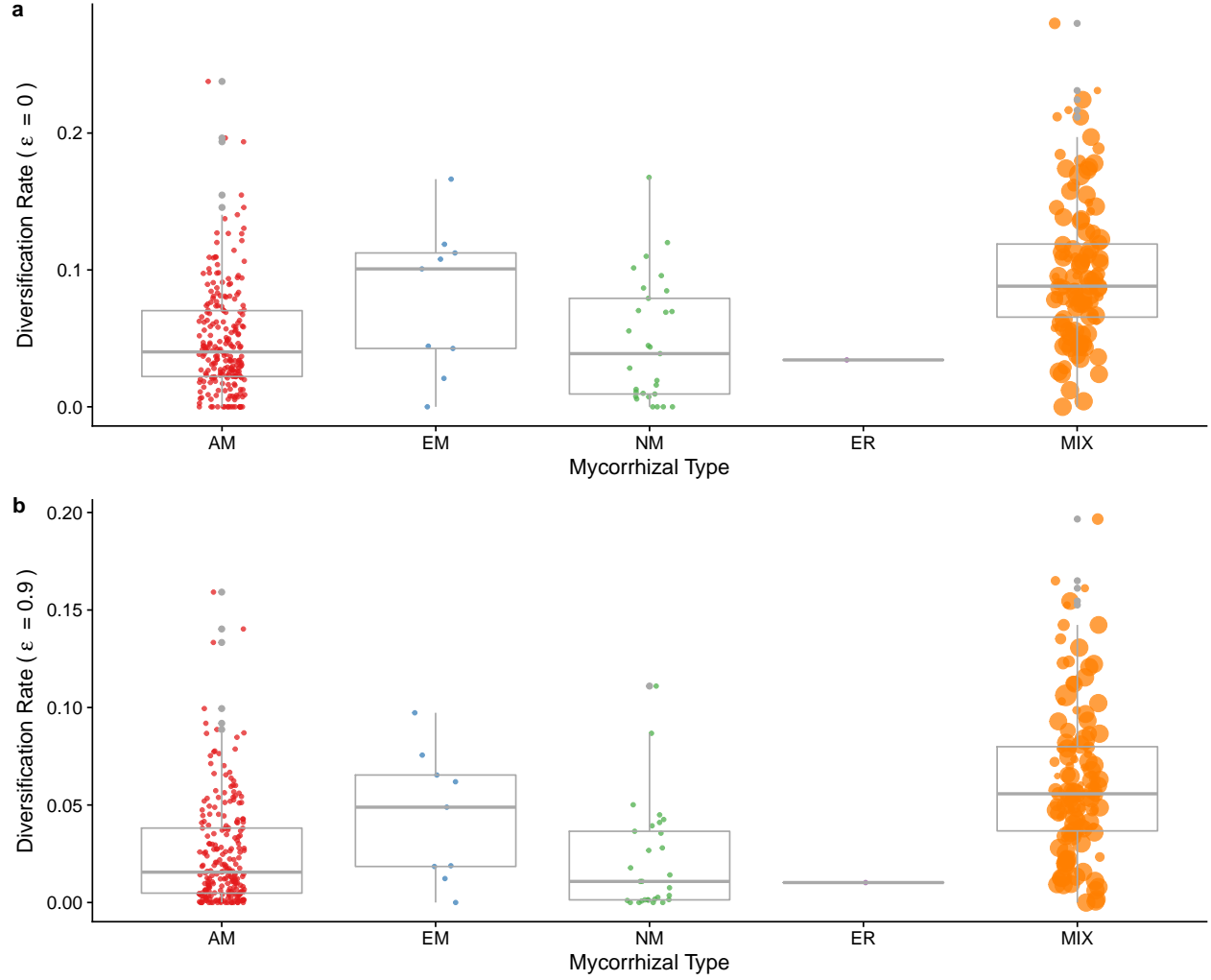
3.1.4 Threshold 100%

Figure 8: Relationship between mycorrhizal type and diversification rates. a) diversification rate estimated with (relative extinction fraction) = 0 and b) diversification rate estimated with = 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.

3.2 Summary statistics

3.2.1 phyANOVA

Table 7: summary statistics for phyANOVA for both values of epsilon

Threshold	F_r0	pvalue_r0	F_r09	pvalue_r09
50	1.295208	0.631	0.6957917	0.825
60	2.841724	0.244	2.1533366	0.402
80	8.598290	0.005	7.0326320	0.022
100	33.620981	0.001	37.4291814	0.001

3.2.2 Standard ANOVA

Table 8: summary statistics for phyANOVA for both values of epsilon

Threshold	F_r0	pvalue_r0	F_r09	pvalue_r09
50	1.295208	0.2757560	0.6957917	0.5550821
60	2.841724	0.0377224	2.1533366	0.0931313
80	8.598290	0.0000156	7.0326320	0.0001303
100	33.620981	0.0000000	37.4291814	0.0000000

3.3 Posthoc tests

3.3.1 phyANOVA

Table 9: Pairwise Corrected p-values for phyANOVA

Threshold	Mycorrhizal Type	AM r0	EM r0	MIX r0	NM r0	AM r09	EM r09	MIX r09	NM r09
50	AM	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000
50	EM	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000
50	MIX	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000
50	NM	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000
60	AM	1.000	1.000	0.355	1.000	1.000	1.000	0.665	1.000
60	EM	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000
60	MIX	0.355	1.000	1.000	0.330	0.665	1.000	1.000	0.348
60	NM	1.000	1.000	0.330	1.000	1.000	1.000	0.348	1.000
80	AM	1.000	1.000	0.010	1.000	1.000	1.000	0.030	1.000
80	EM	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000
80	MIX	0.010	1.000	1.000	0.006	0.030	1.000	1.000	0.018
80	NM	1.000	1.000	0.006	1.000	1.000	1.000	0.018	1.000
100	AM	1.000	0.640	0.006	0.878	1.000	0.796	0.006	0.796
100	EM	0.640	1.000	0.864	0.640	0.796	1.000	0.796	0.796
100	MIX	0.006	0.864	1.000	0.006	0.006	0.796	1.000	0.006
100	NM	0.878	0.640	0.006	1.000	0.796	0.796	0.006	1.000

3.3.2 Standard ANOVA

Table 10: Pairwise Corrected p-values for standard ANOVA

| Pairs	50% r0	60% r0	80% r0	100% r0	50% r09	60% r09	80% r09	100% r09
EM-AM	0.6162059	0.6893711	0.5870598	0.1711875	0.8524170	0.8685403	0.7997882	0.2780424
MIX-AM	0.9875513	0.0319972	0.0000212	0.0000000	0.9859562	0.1027975	0.0003794	0.0000000
NM-AM	0.3620797	0.9999399	0.7873166	0.9970677	0.6612036	0.9408275	0.4668913	0.9314088
MIX-EM	0.8330187	0.9977181	0.9370091	0.6201825	0.8153845	0.9912946	0.9091448	0.3672158
NM-EM	0.9701924	0.7554034	0.3823321	0.2164235	0.9933819	0.7692733	0.4190835	0.2261114
NM-MIX	0.9074548	0.1857903	0.0009223	0.0000003	0.7630198	0.1393994	0.0008252	0.0000000

3.4 Scatterplots
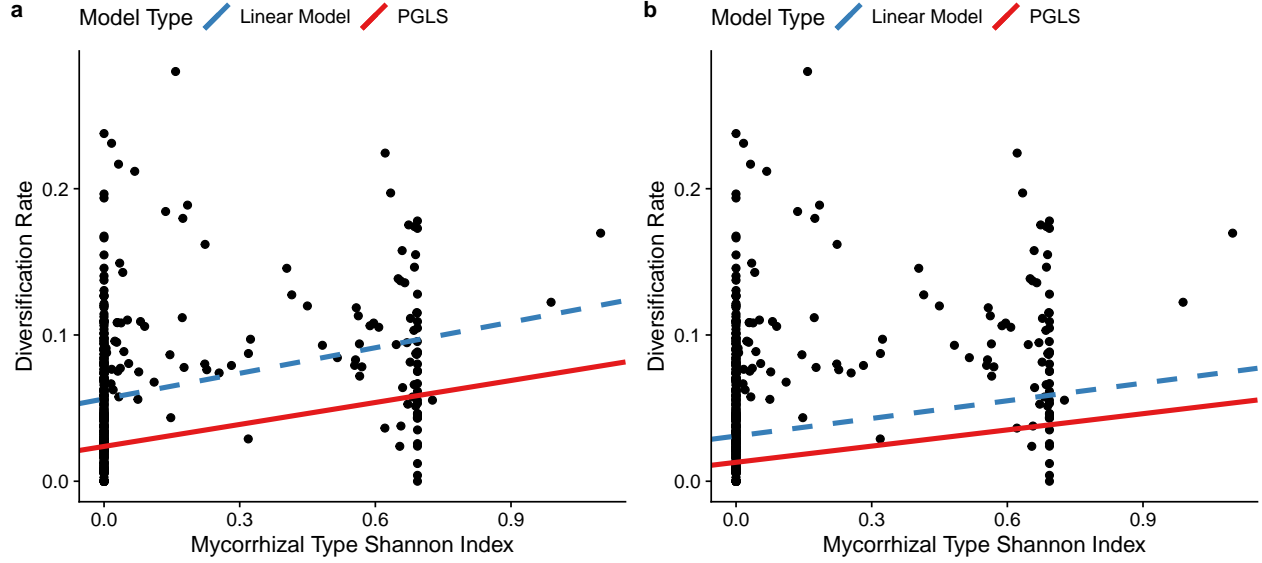
Figure 9: Scatterplots showing the relationship between mycorrhizal diversity index and diversification rates (a and c), species richness (b) and age family (d). Diversification rates were estimated with (relative extinction fraction) = 0 (a) and with = 0.9 (c). The red and blue lines indicate the results of a linear model and a phylogenetic generalized least squares (PGLS) fit, respectively.

Table 11: Summary statistics for the phylogenetic and parametric regressions using the full genus dataset.

epsilon	pvalue_PGLS	R2_PGLS	pvalue_LM	R2_LM
0.0	0e+00	0.07343	0	0.09319
0.9	1e-07	0.07157	0	0.08402

4 Family classification based on different thresholds

Table 12: Mycorrhizal type assigned to each family based on 4 different percentage thresholds (50, 60, 80 and 100)

Threshold	AM	EM	ER	MIX	NM
50%	296	10	1	23	60
60%	289	9	1	45	46
80%	273	9	1	70	37
100%	231	9	1	116	33

5 Species-level database

5.1 Clean database - excluding species with any remark

5.1.1 Boxplots

5.1.1.1 Threshold 50%
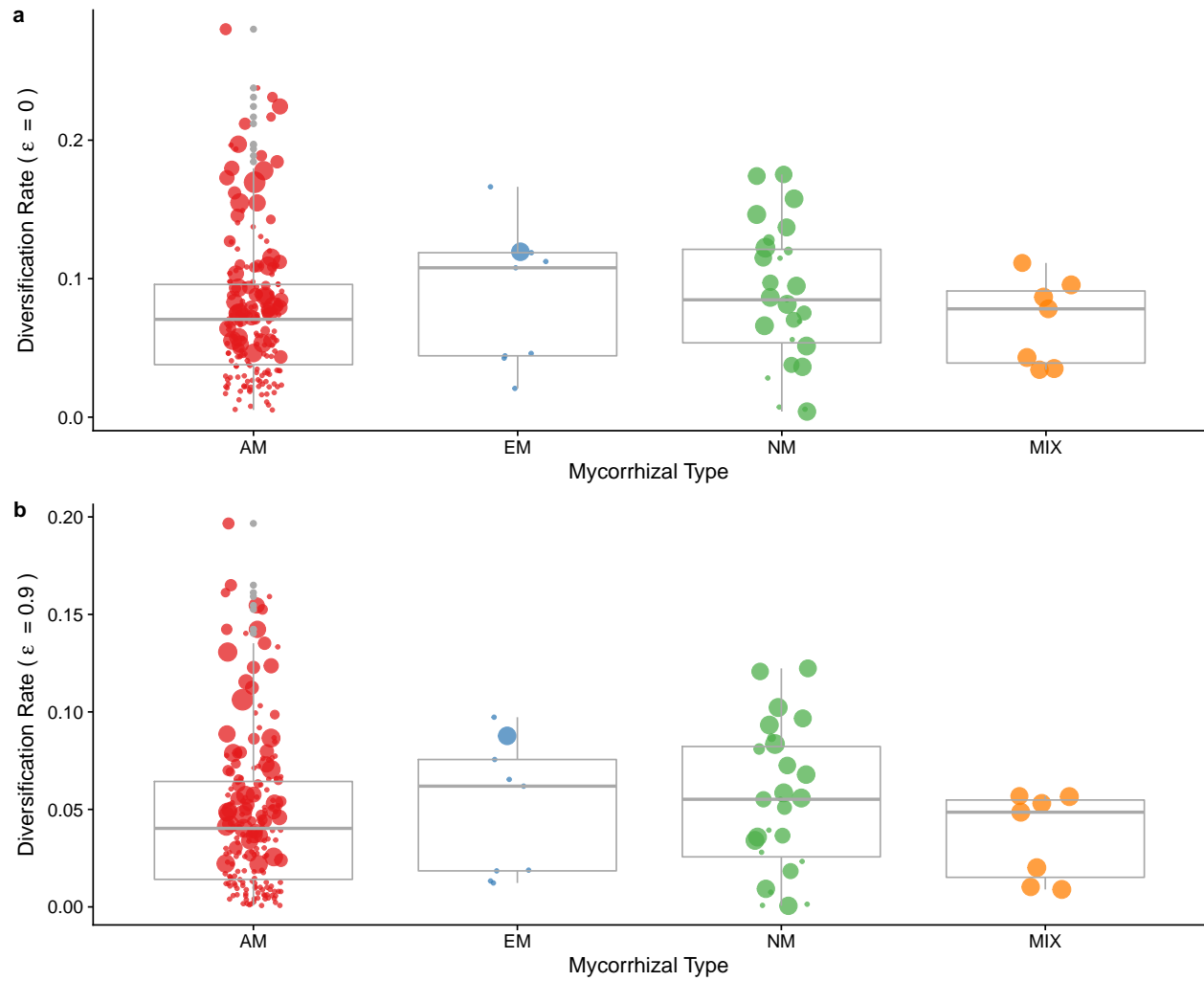
Figure 10: Relationship between mycorrhizal type and diversification rates. a) diversification rate estimated with (relative extinction fraction) = 0 and b) diversification rate estimated with = 0.9. AM: Arbuscular mycorrhiza, EM: Ectomycorrhiza, NM: non-mycorrhizal and MIX (families with no dominance 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.
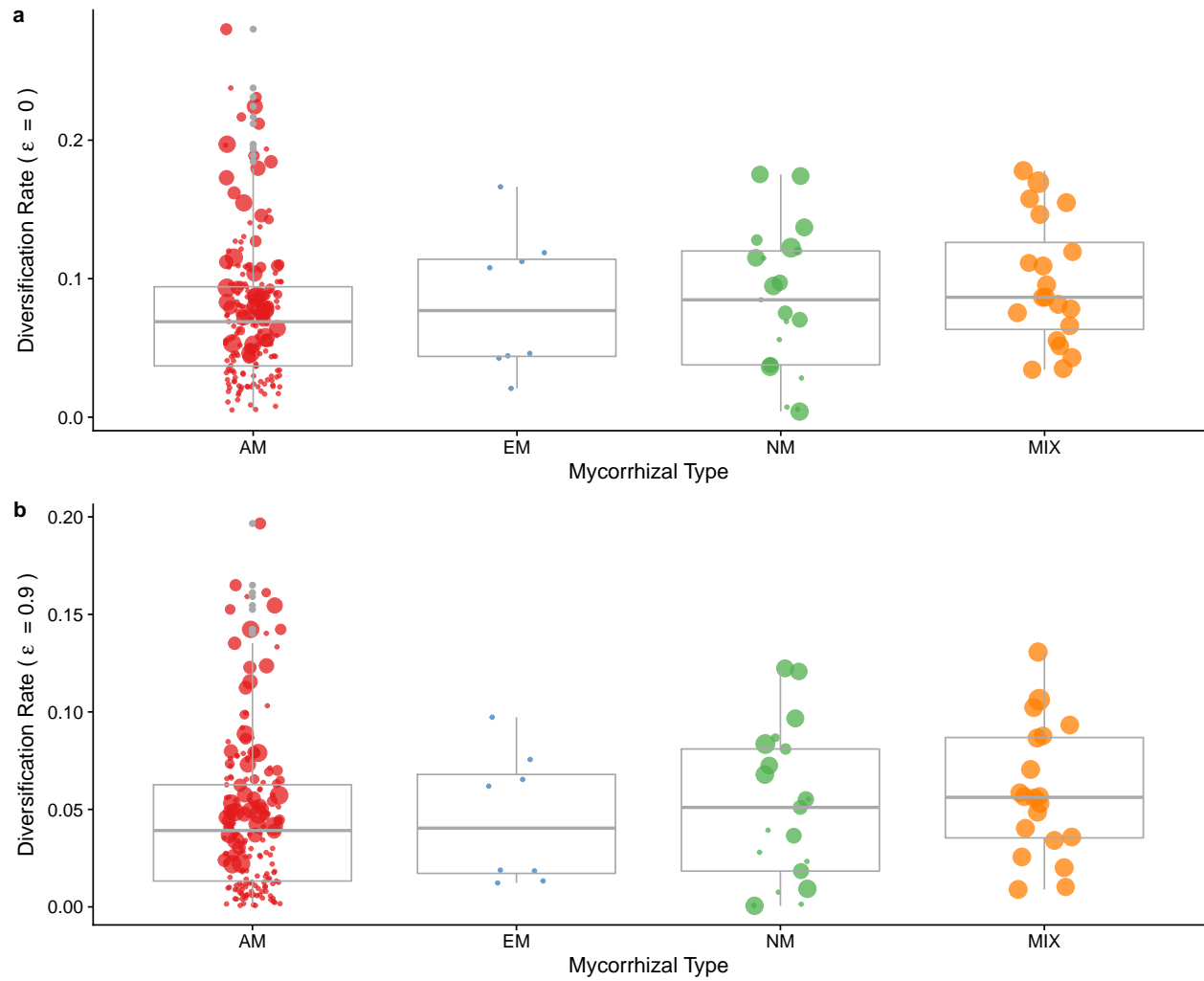
5.1.1.2 Threshold 60%

Figure 11: Relationship between mycorrhizal type and diversification rates. a) diversification rate estimated with (relative extinction fraction) = 0 and b) diversification rate estimated with = 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.
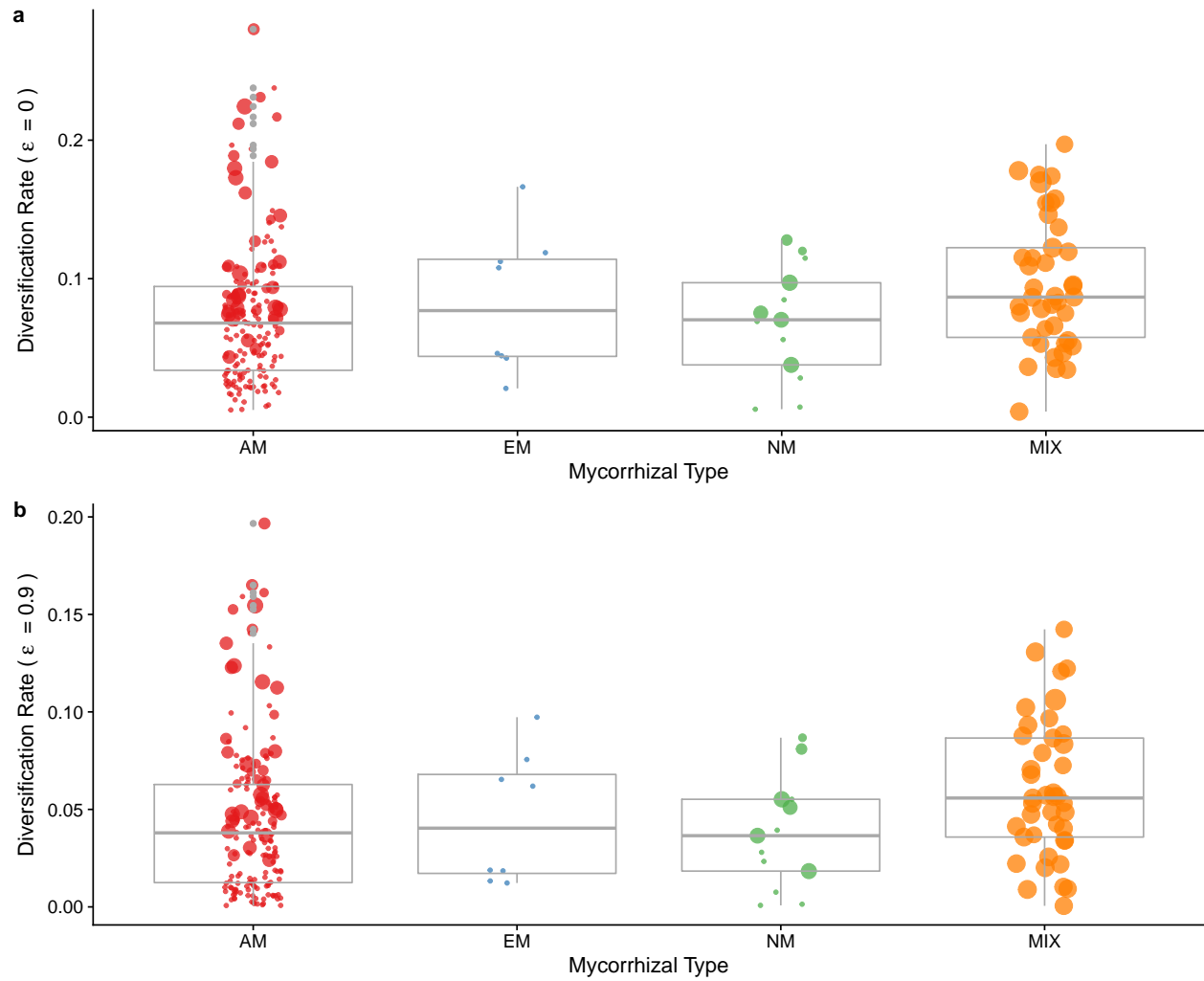
5.1.1.3 Threshold 80%

Figure 12: Relationship between mycorrhizal type and diversification rates. a) diversification rate estimated with (relative extinction fraction) = 0 and b) diversification rate estimated with = 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.
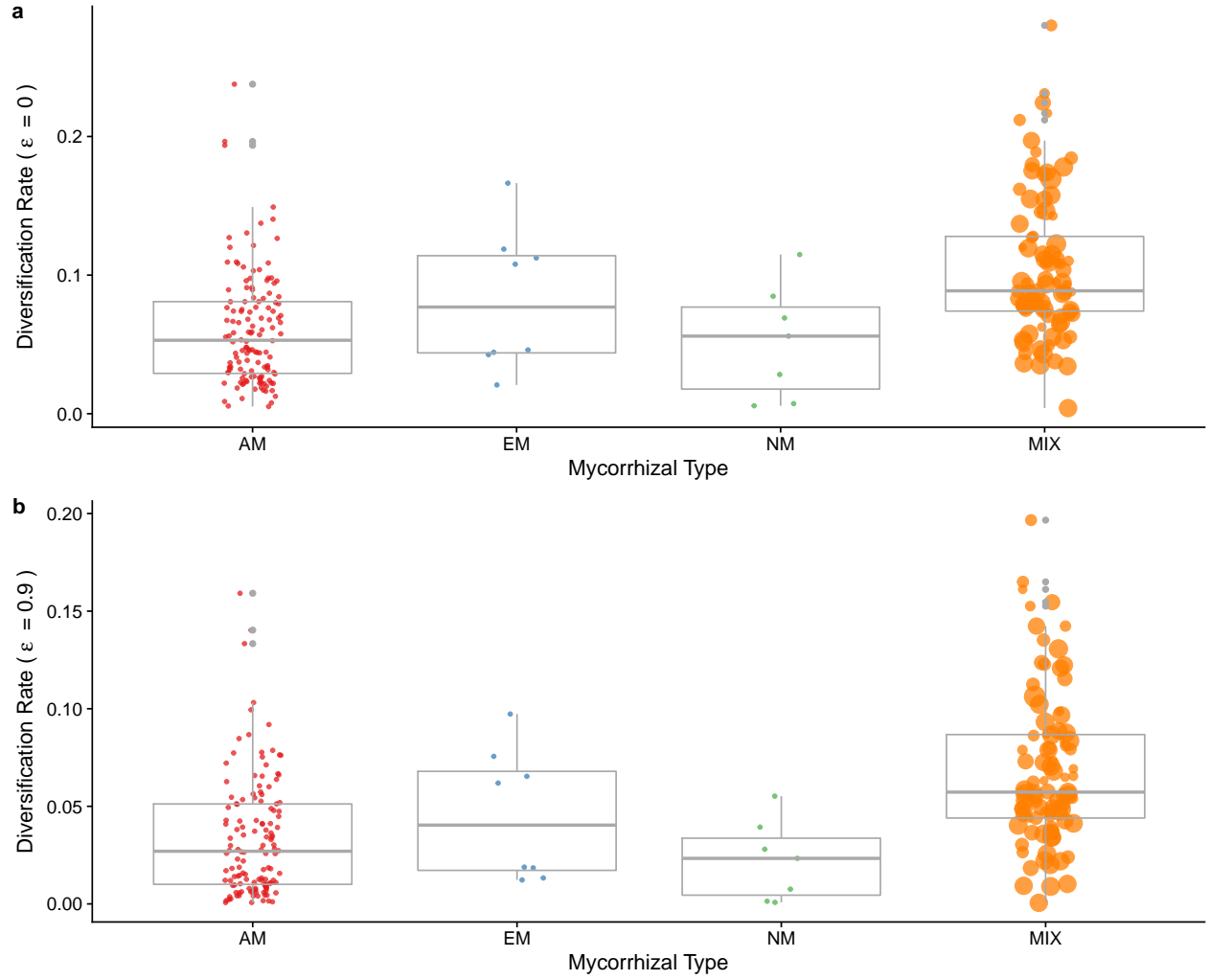
5.1.1.4 Threshold 100%

Figure 13: Relationship between mycorrhizal type and diversification rates. a) diversification rate estimated with (relative extinction fraction) = 0 and b) diversification rate estimated with = 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.

5.2 Summary statistics

5.2.1 phyANOVA

Table 13: summary statistics for phyANOVA for both values of epsilon

Threshold	F_r0	pvalue_r0	F_r09	pvalue_r09
50	0.3851399	0.857	0.4939560	0.810
60	1.5383760	0.371	0.9275641	0.633
80	3.7844578	0.084	3.2616354	0.117
100	24.5826918	0.001	27.0967625	0.001

5.2.2 Standard ANOVA

Table 14: summary statistics for phyANOVA for both values of epsilon

Threshold	F_r0	pvalue_r0	F_r09	pvalue_r09
50	0.3955297	0.7563236	0.5009815	0.6819207
60	1.5633983	0.1986397	0.9479786	0.4179219
80	3.5294456	0.0154472	2.9970343	0.0312388
100	23.9958898	0.0000000	26.3234262	0.0000000

5.3 Posthoc tests

5.3.1 phyANOVA

Table 15: Pairwise Corrected p-values for phyANOVA

Threshold	Mycorrhizal Type	AM r0	EM r0	MIX r0	NM r0	AM r09	EM r09	MIX r09	NM r09
50	AM	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000
50	EM	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000
50	MIX	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000
50	NM	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000
60	AM	1.000	1.000	0.264	1.000	1.000	1.000	0.690	1.000
60	EM	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000
60	MIX	0.264	1.000	1.000	0.995	0.690	1.000	1.000	1.000
60	NM	1.000	1.000	0.995	1.000	1.000	1.000	1.000	1.000
80	AM	1.000	1.000	0.036	1.000	1.000	1.000	0.096	1.000
80	EM	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000
80	MIX	0.036	1.000	1.000	0.100	0.096	1.000	1.000	0.096
80	NM	1.000	1.000	0.100	1.000	1.000	1.000	0.096	1.000
100	AM	1.000	0.726	0.006	0.726	1.000	0.747	0.006	0.747
100	EM	0.726	1.000	0.616	0.684	0.747	1.000	0.376	0.747
100	MIX	0.006	0.616	1.000	0.006	0.006	0.376	1.000	0.006
100	NM	0.726	0.684	0.006	1.000	0.747	0.747	0.006	1.000

5.3.2 Standard ANOVA

Table 16: Pairwise Corrected p-values for standard ANOVA

| Types	50% r0	60% r0	80% r0	100% r0	50% r09	60% r09	80% r09	100% r09
EM-AM	0.9640138	0.9924574	0.9850669	0.6125728	0.9933364	0.9999863	0.9999926	0.7802549
MIX-AM	0.9945230	0.1464660	0.0120044	0.0000000	0.8583738	0.3481935	0.0358281	0.0000000
NM-AM	0.7758750	0.9382159	0.9111597	0.8079435	0.8308462	0.9735179	0.7778657	0.6260774
MIX-EM	0.9540250	0.7689916	0.7036769	0.2367099	0.8663578	0.7681943	0.6218547	0.1059495
NM-EM	0.9997752	0.9998371	0.8968196	0.4108561	0.9964156	0.9934415	0.9273026	0.4041777
NM-MIX	0.8923413	0.6318123	0.0896241	0.0003035	0.6631972	0.7804947	0.0810474	0.0000505

5.3.3   Scatterplots
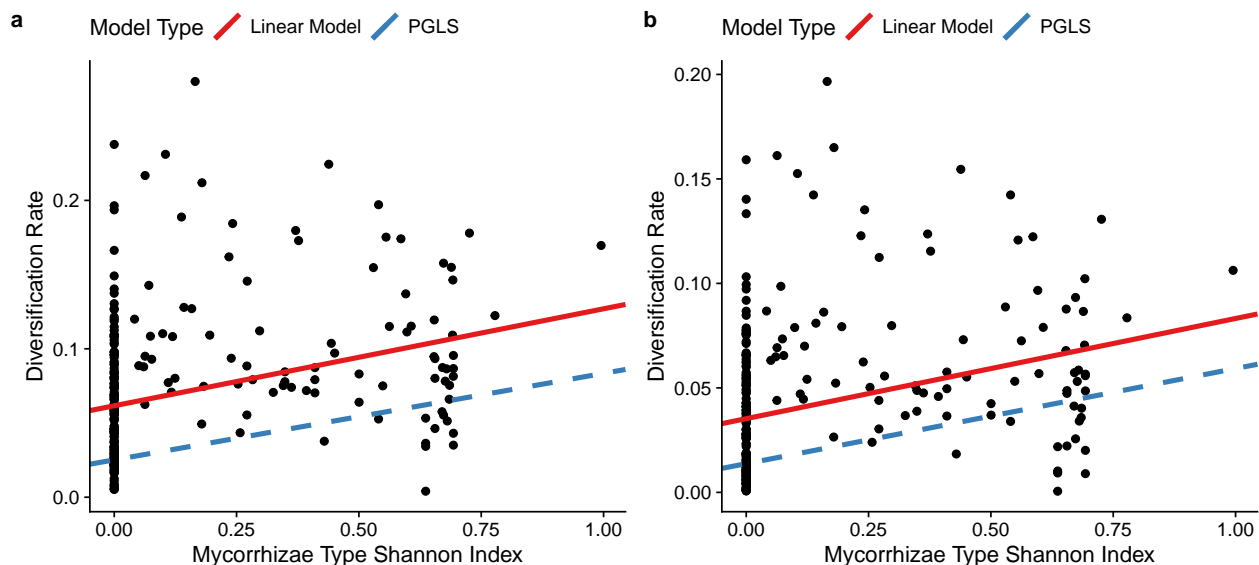
Figure 14: Scatterplots showing the relationship between mycorrhizal diversity index and diversification rates (a and c), species richness (b) and age family (d). Diversification rates were estimated with (relative extinction fraction) = 0 (a) and with = 0.9 (c). The red and blue lines indicate the results of a linear model and a phylogenetic generalized least squares (PGLS) fit, respectively.

Table 17: Summary statistics for the phylogenetic and parametric regressions using the full genus dataset.

epsilon	pvalue_PGLS	R2_PGLS	pvalue_LM	R2_LM
0.0	4e-07	0.08904	2e-07	0.09458
0.9	3e-07	0.09007	3e-07	0.09109

5.4   More inclusive database - including species with any remark
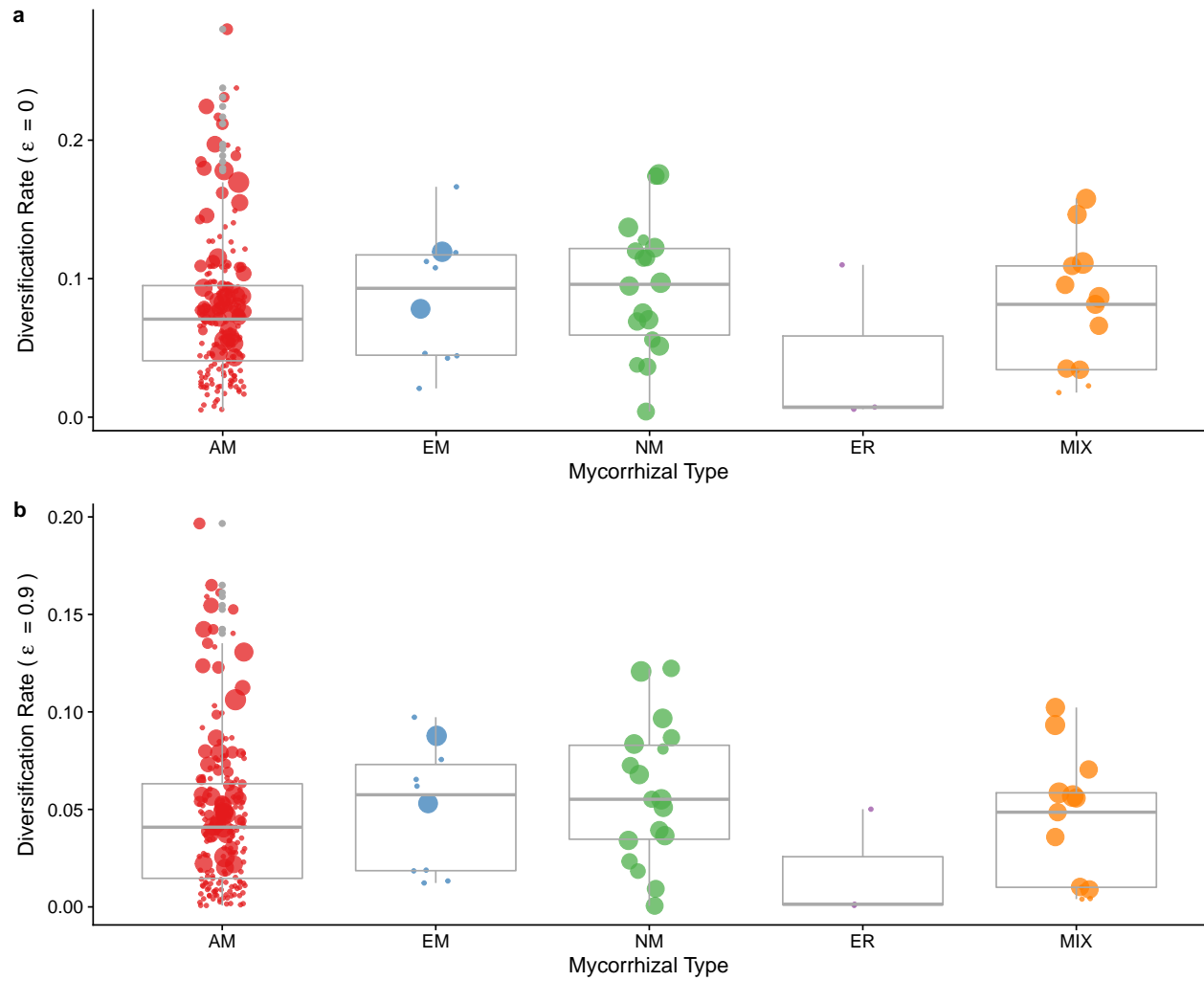
5.4.1   Boxplots

5.4.1.1   Threshold 50%

Figure 15: Relationship between mycorrhizal type and diversification rates. a) diversification rate estimated with (relative extinction fraction) = 0 and b) diversification rate estimated with = 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.
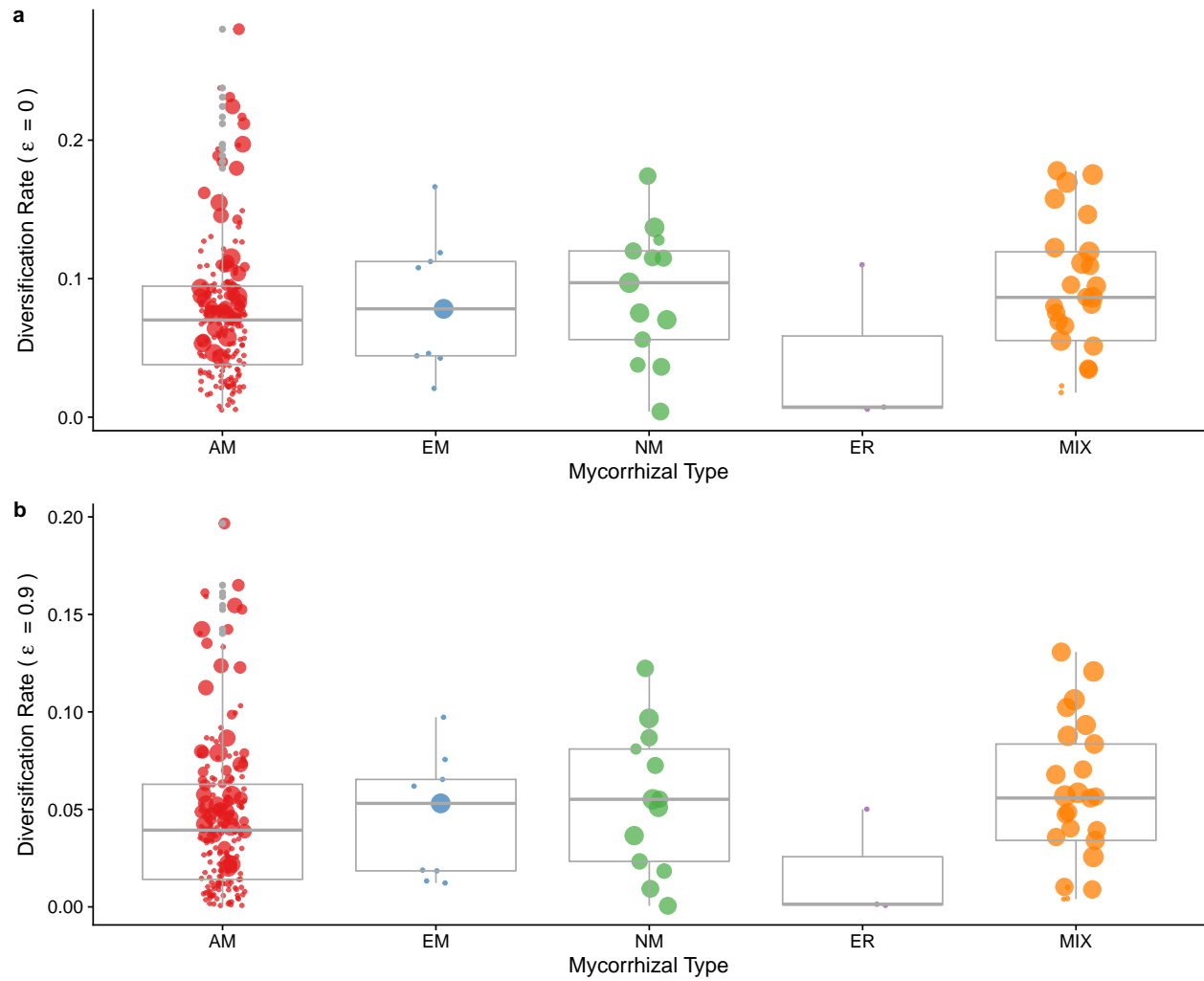
5.4.1.2 Threshold 60%

Figure 16: Relationship between mycorrhizal type and diversification rates. a) diversification rate estimated with (relative extinction fraction) = 0 and b) diversification rate estimated with = 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.
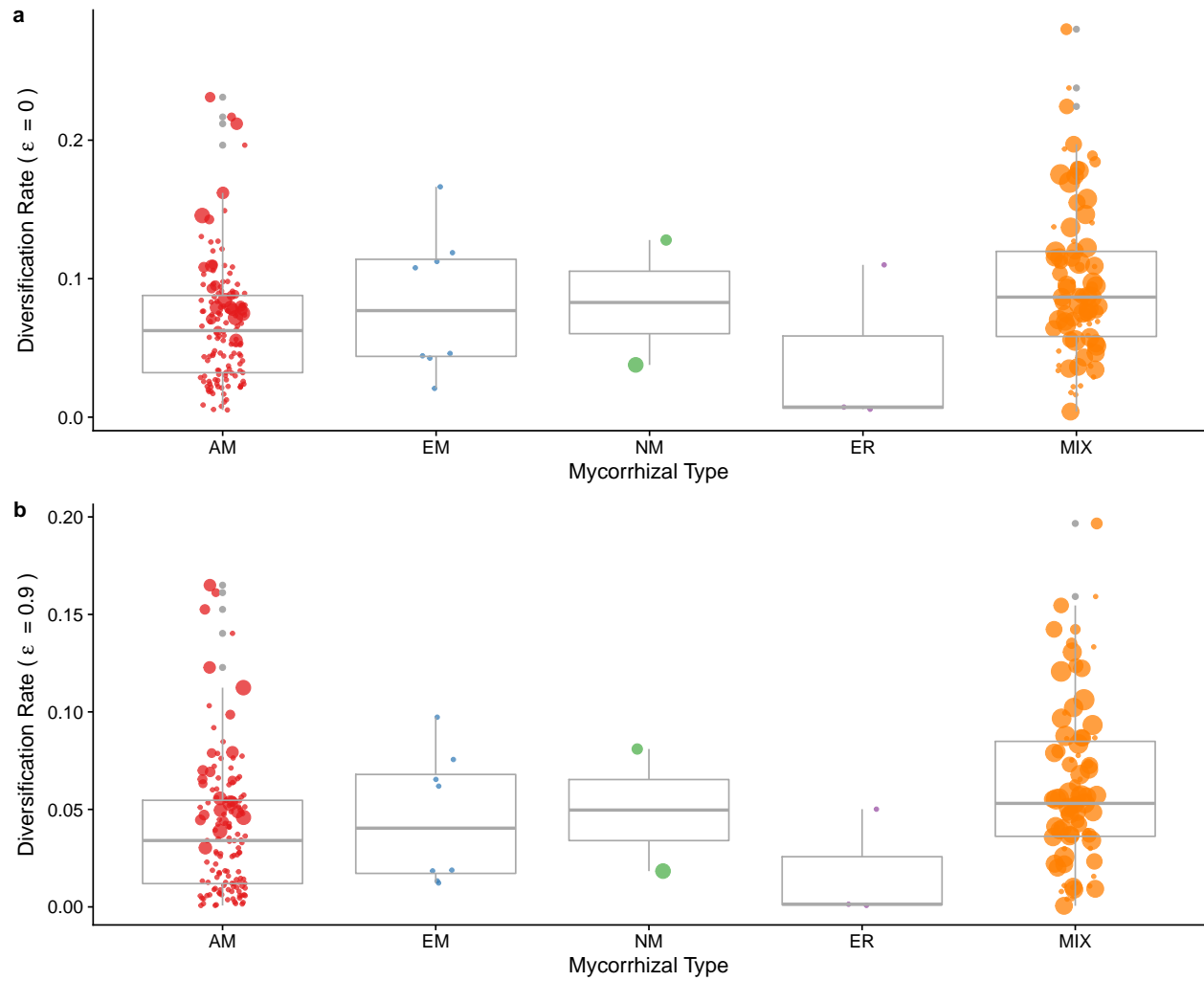
5.4.1.3 Threshold 80%

Figure 17: Relationship between mycorrhizal type and diversification rates. a) diversification rate estimated with (relative extinction fraction) = 0 and b) diversification rate estimated with = 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.
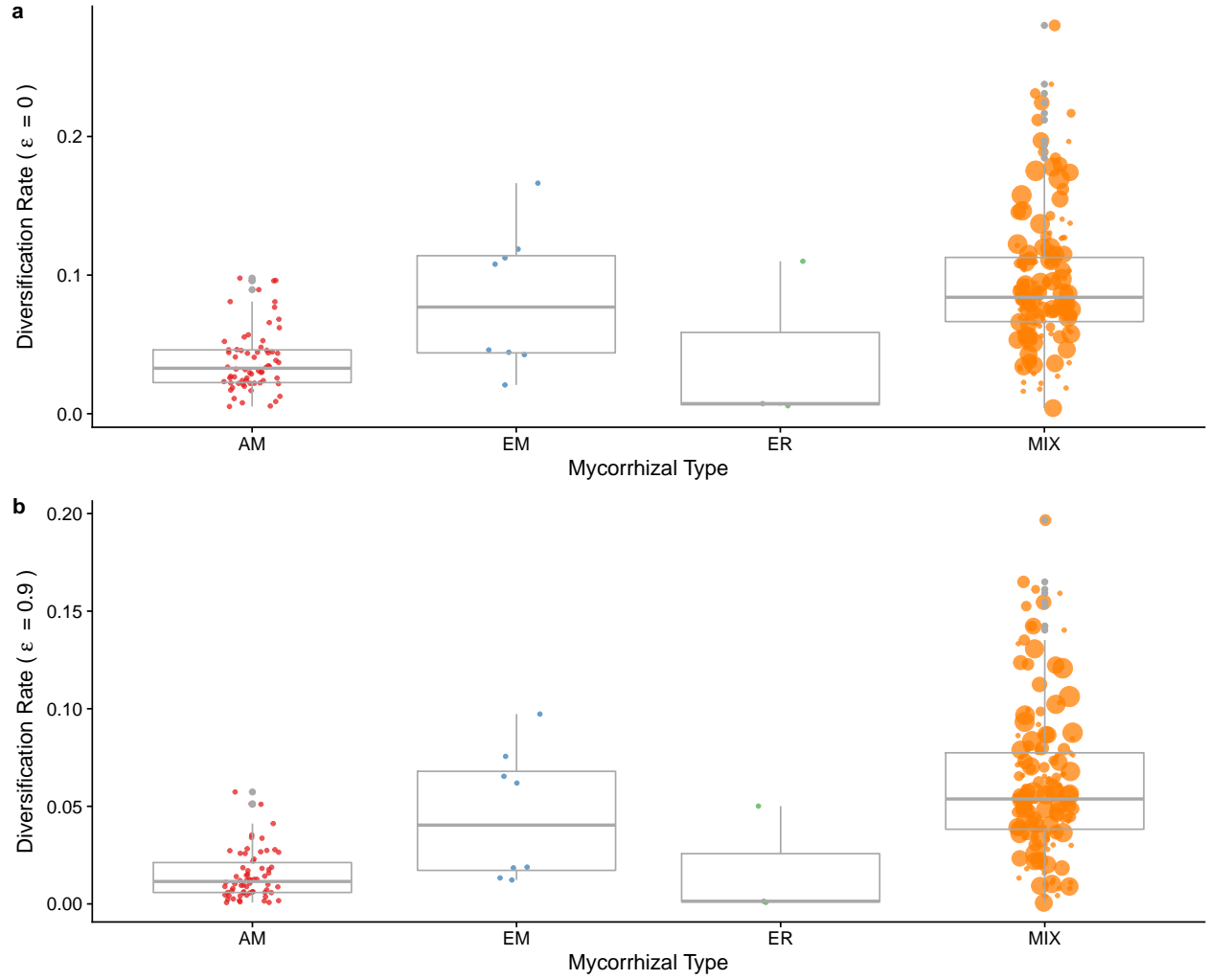
5.4.1.4 Threshold 100%

Figure 18: Relationship between mycorrhizal type and diversification rates. a) diversification rate estimated with (relative extinction fraction) = 0 and b) diversification rate estimated with = 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.

5.5 Summary statistics

5.5.1 phyANOVA

Table 18: summary statistics for phyANOVA for both values of epsilon

Threshold	F_r0	pvalue_r0	F_r09	pvalue_r09
50	0.6913713	0.703	0.6662580	0.676
60	0.5110525	0.787	0.3237887	0.869
80	8.5708941	0.001	8.4253115	0.001
100	36.4395067	0.001	43.8064306	0.001

5.5.2 Standard ANOVA

Table 19: summary statistics for phyANOVA for both values of epsilon

Threshold	F_r0	pvalue_r0	F_r09	pvalue_r09
50	1.0830611	0.3653162	1.0848972	0.3644122
60	0.9527973	0.4340430	0.8309617	0.5064990
80	7.1127102	0.0000190	7.0839219	0.0000200
100	28.2200847	0.0000000	34.2240624	0.0000000

5.6 Posthoc tests

5.6.1 phyANOVA

Table 20: Pairwise Corrected p-values for phyANOVA

Threshold	Mycorrhizal Type	AM r0	EM r0	MIX r0	NM r0	AM r09	EM r09	MIX r09	NM r09
50	AM	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000
50	EM	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000
50	MIX	1.000	1.000	1.000	0.918	1.000	1.000	1.000	0.924
50	NM	1.000	1.000	0.918	1.000	1.000	1.000	0.924	1.000
60	AM	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000
60	EM	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000
60	MIX	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000
60	NM	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000
80	AM	1.000	1.000	0.006	1.000	1.000	1.000	0.006	1.000
80	EM	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000
80	MIX	0.006	1.000	1.000	0.255	0.006	1.000	1.000	0.145
80	NM	1.000	1.000	0.255	1.000	1.000	1.000	0.145	1.000
100	AM	1.000	0.180	0.006	0.922	1.000	0.200	0.006	0.742
100	EM	0.180	1.000	0.728	0.531	0.200	1.000	0.408	0.408
100	MIX	0.006	0.728	1.000	0.070	0.006	0.408	1.000	0.015
100	NM	0.922	0.531	0.070	1.000	0.742	0.408	0.015	1.000

5.6.2 Standard ANOVA

Table 21: Pairwise Corrected p-values for standard ANOVA

| Types	50% r0	60% r0	80% r0	100% r0	50% r09	60% r09	80% r09	100% r09
EM-AM	0.9906335	0.9990669	0.9368687	0.0668031	0.9983351	1.0000000	0.9904882	0.0842606
ER-AM	0.5916780	0.6201287	0.8078099	0.9999999	0.5624390	0.5898204	0.7833300	0.9999988
MIX-AM	0.9704447	0.8049968	0.0000096	0.0000000	0.9059429	0.8737008	0.0000137	0.0000000
NM-AM	0.7632734	0.9580943	0.9956277	0.9999797	0.8497626	0.9945419	0.9679774	0.9975875
ER-EM	0.5610997	0.6633256	0.6486835	0.5266515	0.5930503	0.7234958	0.7353815	0.6014505
MIX-EM	0.9367430	0.9959145	0.7784792	0.6740605	0.9285976	0.9858115	0.6084119	0.3636180
NM-EM	0.9970556	0.9992511	0.9345381	0.5826348	0.9956920	0.9990614	0.9281444	0.4845935
MIX-ER	0.8375240	0.4068625	0.1195281	0.0500780	0.8698165	0.4126943	0.1127114	0.0289095
NM-ER	0.3516110	0.5005647	0.9790229	0.9999973	0.3678683	0.5607224	0.9929672	0.9986134
NM-MIX	0.6835889	0.9999432	0.3583498	0.1024529	0.6372211	0.9987179	0.2368834	0.0303829

5.6.3 Scatterplots
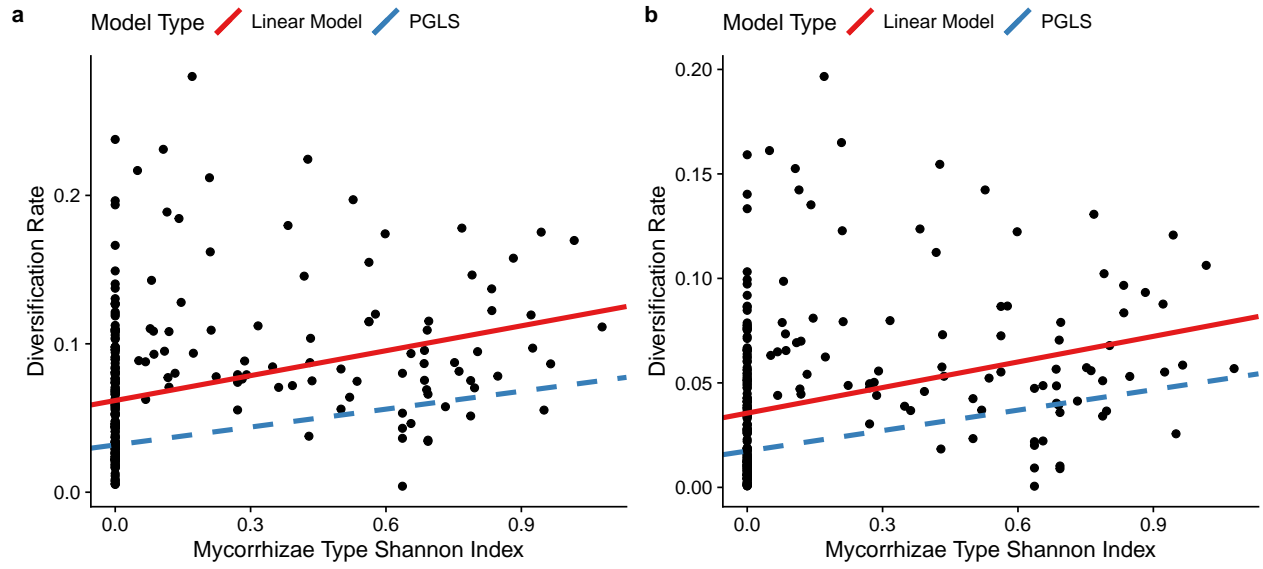
Figure 19: Scatterplots showing the relationship between mycorrhizal diversity index and diversification rates (a and c), species richness (b) and age family (d). Diversification rates were estimated with (relative extinction fraction) = 0 (a) and with = 0.9 (c). The red and blue lines indicate the results of a linear model and a phylogenetic generalized least squares (PGLS) fit, respectively.

Table 22: Summary statistics for the phylogenetic and parametric regressions using the full genus dataset.

epsilon	pvalue_PGLS	R2_PGLS	pvalue_LM	R2_LM
0.0	5.26e-05	0.06444	3e-07	0.09354
0.9	4.01e-05	0.06653	5e-07	0.08898

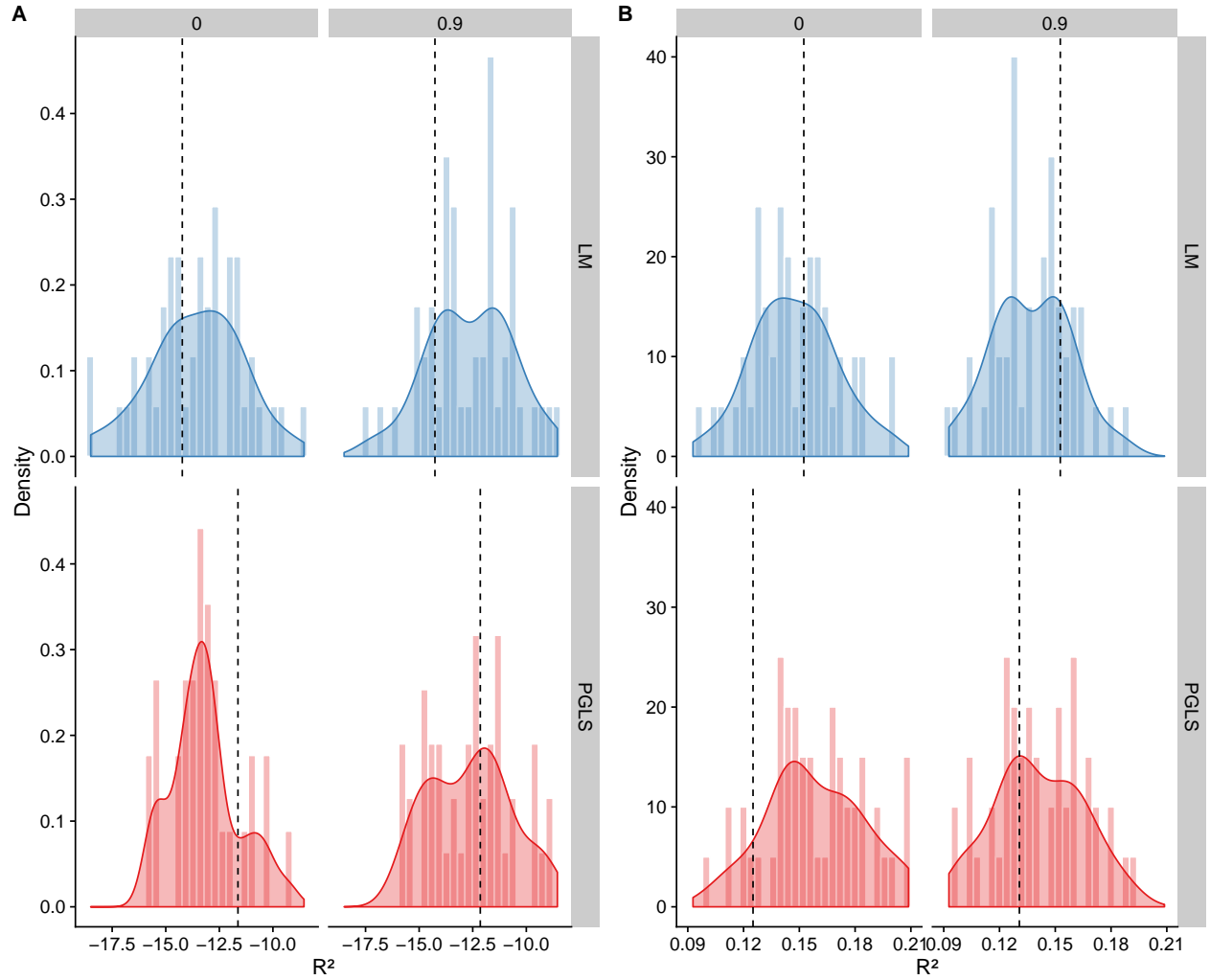# 6 Adding randomly 20% of misassignment of mycorrhizal type

6.1 Regressions

Figure 20: Distribution of (A) p-values and (B) R² 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.
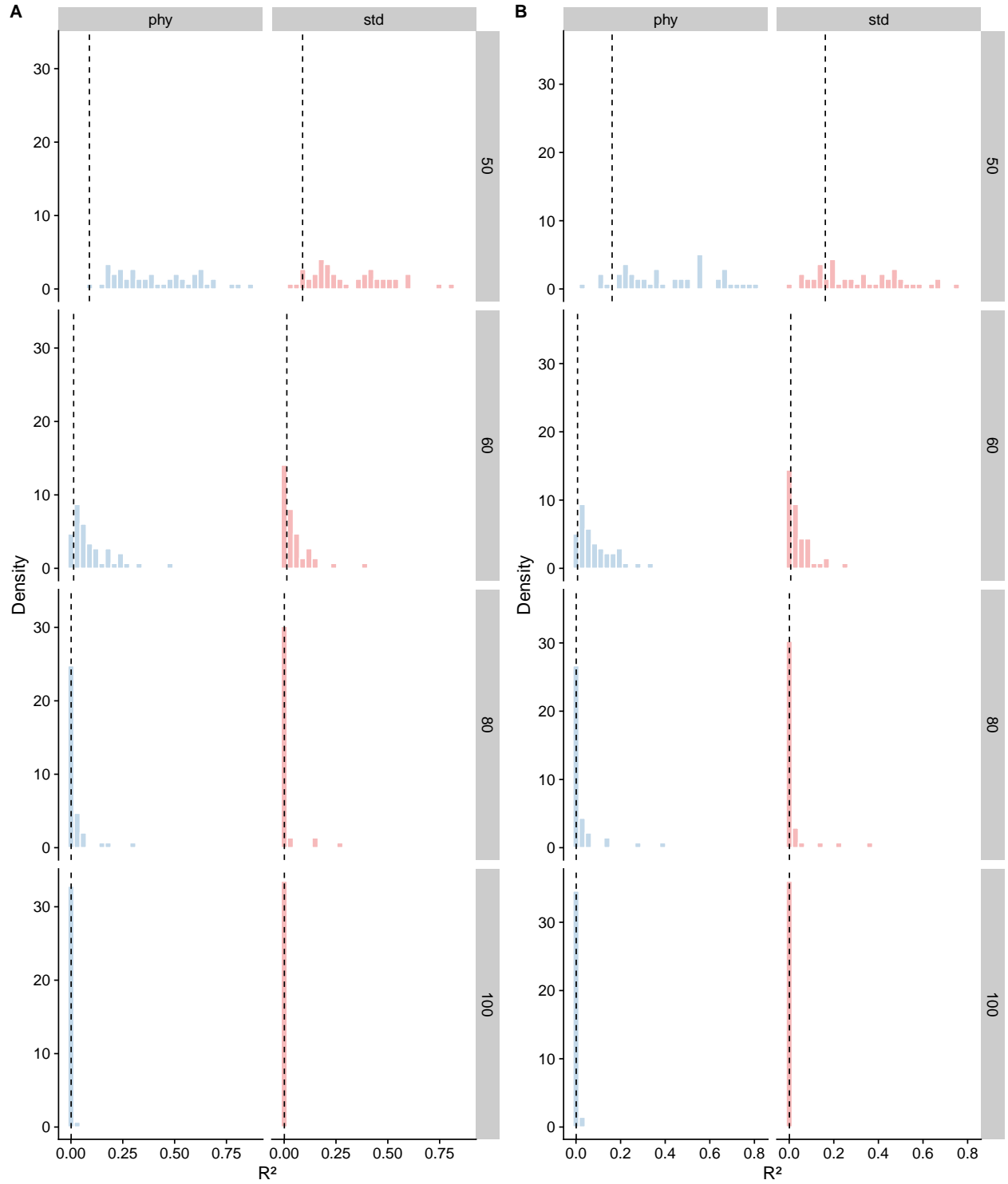
6.2 ANOVAs

Figure 21: 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.