

# 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%

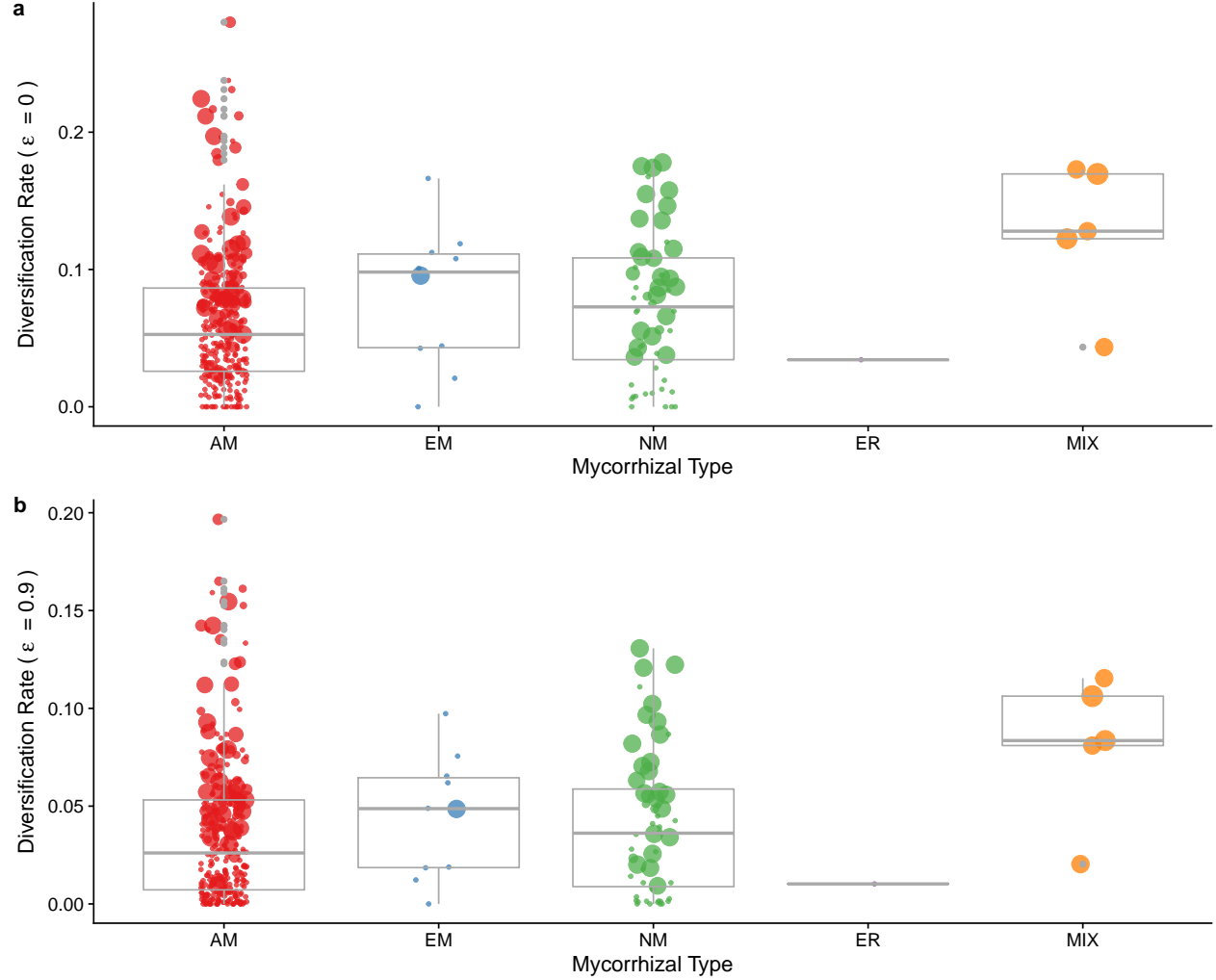


Figure 1: Relationship between mycorrhizal type and diversification rates. a) diversification rate estimated with  $\epsilon$  (relative extinction fraction) = 0 and b) diversification rate estimated with  $\epsilon$  = 0.9. AM: Arbuscular mycorrhiza, EM: Ectomycorrhiza, NM: non-mycorrhizal and MIX (families 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.

### 2.1.2 Threshold 60%

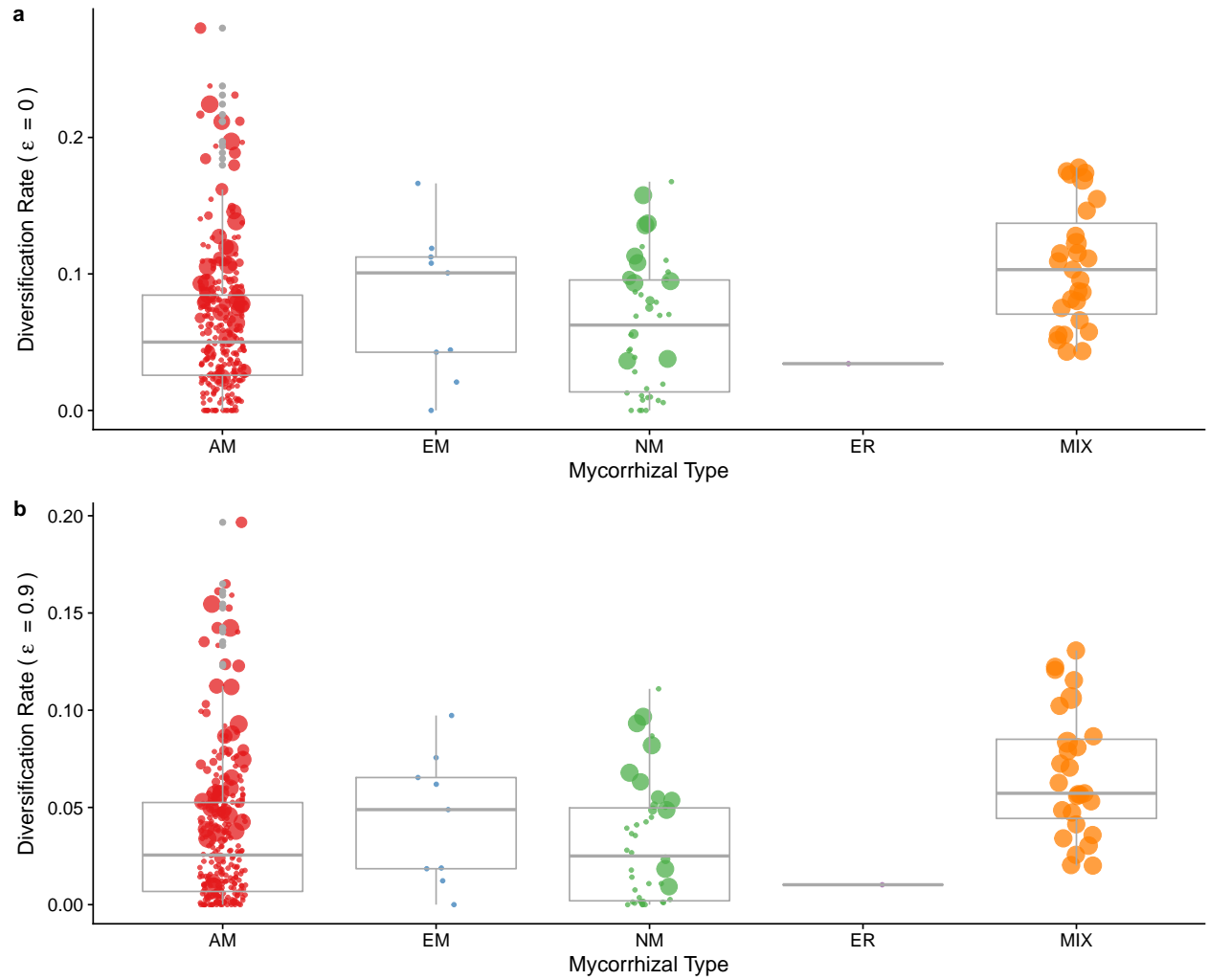


Figure 2: Relationship between mycorrhizal type and diversification rates. a) diversification rate estimated with  $(\text{relative extinction fraction}) = 0$  and b) diversification rate estimated with  $= 0.9$ . AM: Arbuscular mycorrhiza, EM: Ectomycorrhiza, NM: non-mycorrhizal and MIX (families with 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%

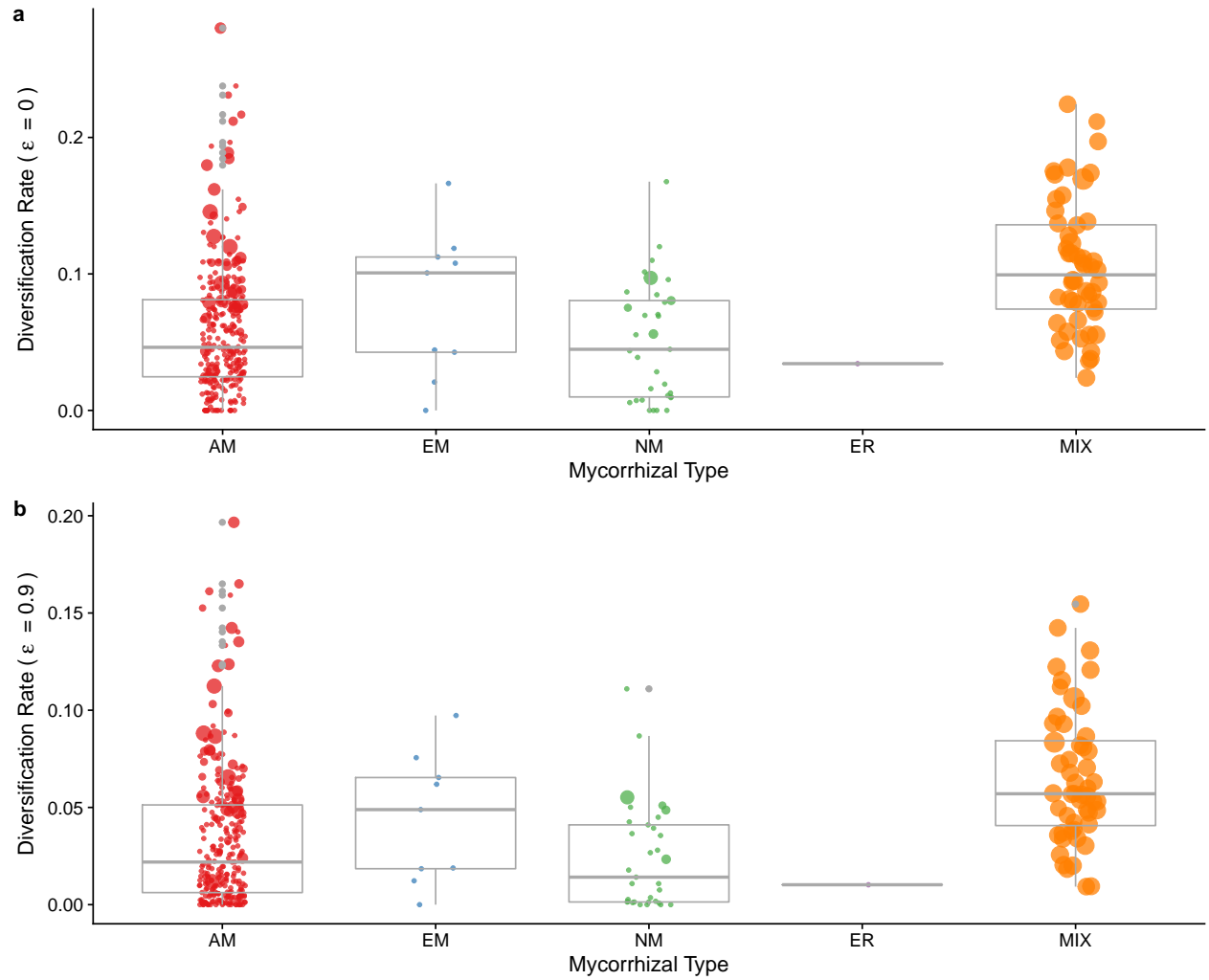


Figure 3: Relationship between mycorrhizal type and diversification rates. a) diversification rate estimated with  $(\text{relative extinction fraction}) = 0$  and b) diversification rate estimated with  $= 0.9$ . AM: Arbuscular mycorrhiza, EM: Ectomycorrhiza, NM: non-mycorrhizal and MIX (families with 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%

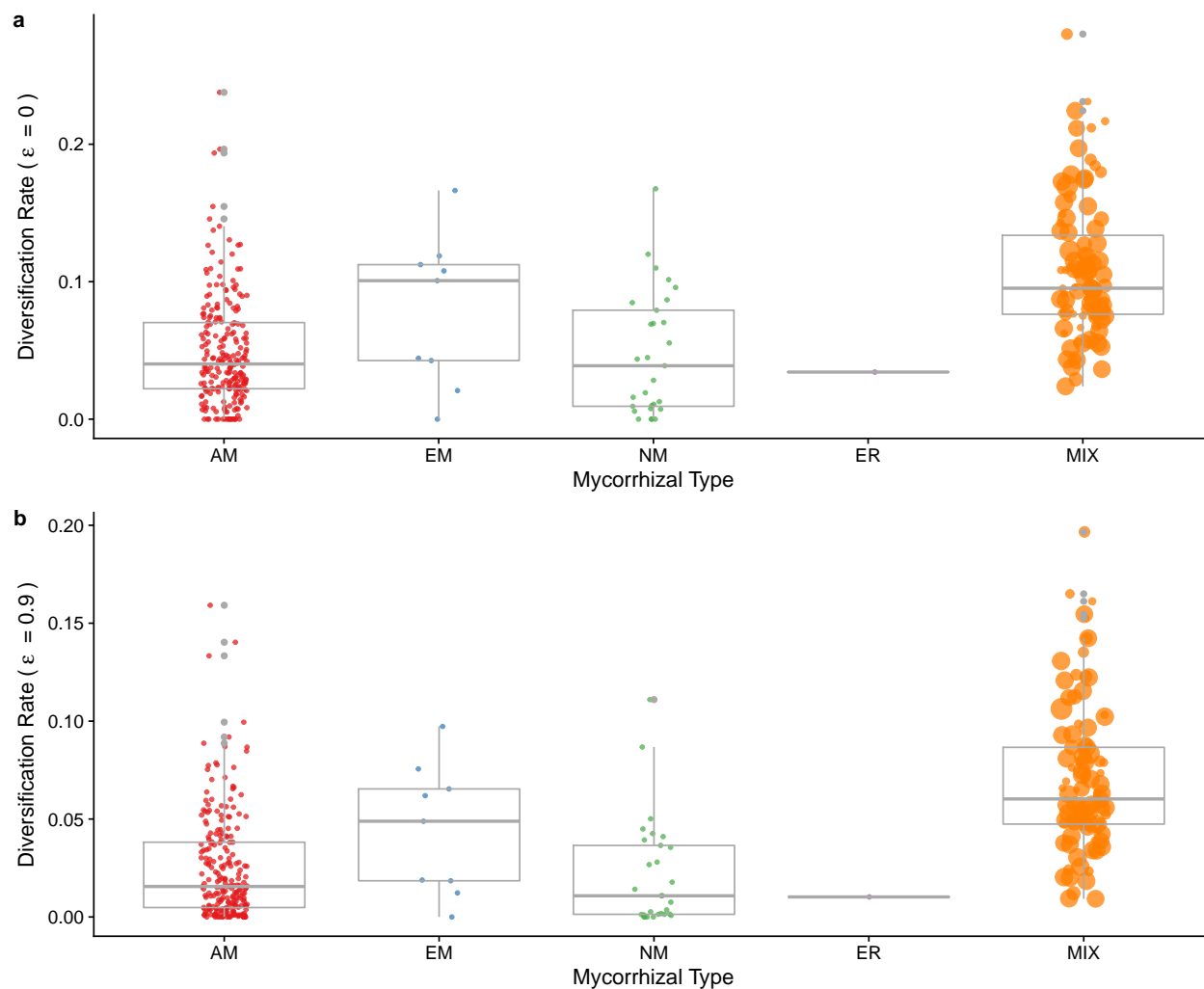


Figure 4: Relationship between mycorrhizal type and diversification rates. a) diversification rate estimated with  $(\text{relative extinction fraction}) = 0$  and b) diversification rate estimated with  $= 0.9$ . AM: Arbuscular mycorrhiza, EM: Ectomycorrhiza, NM: non-mycorrhizal and MIX (families with 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%

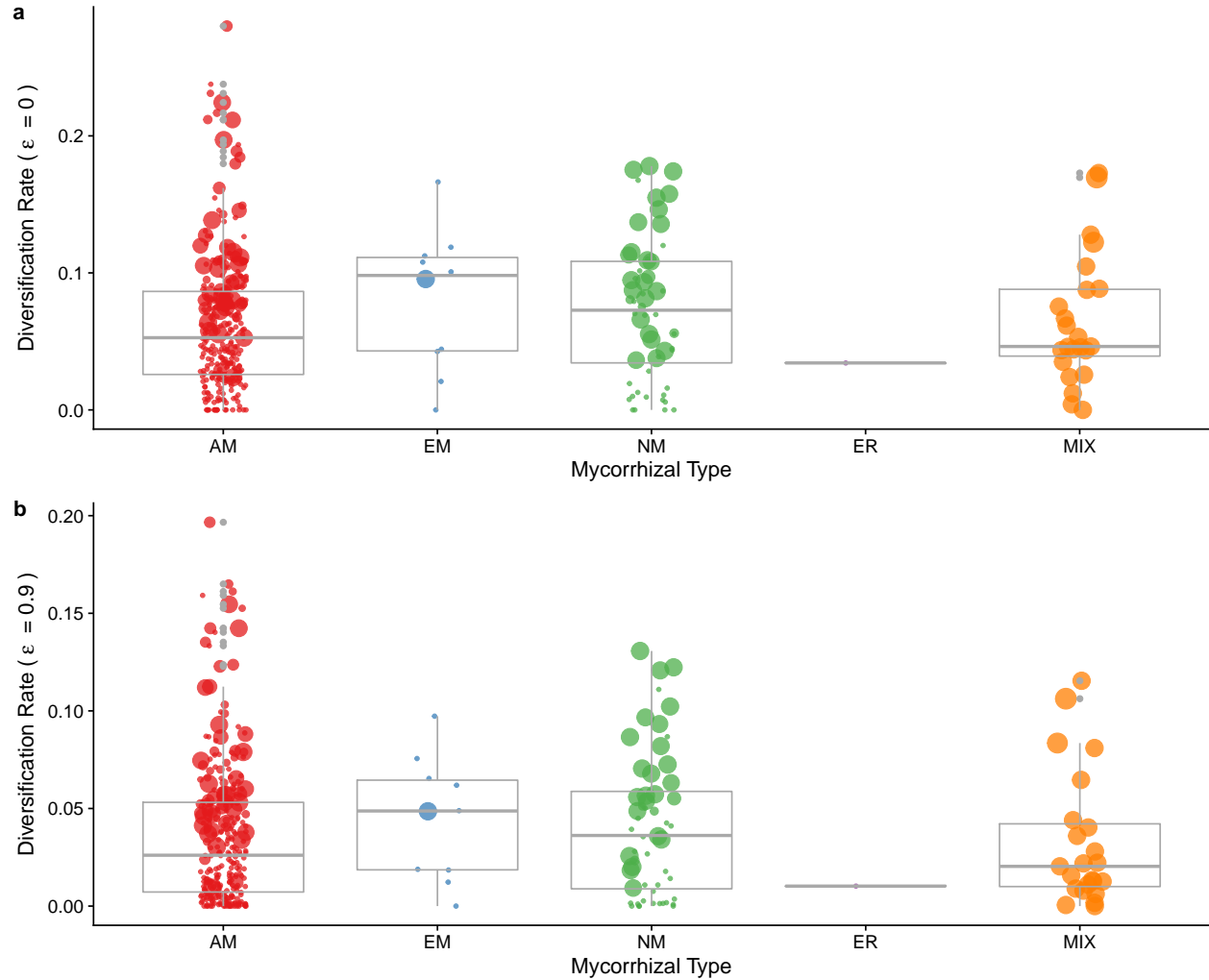


Figure 5: Relationship between mycorrhizal type and diversification rates. a) diversification rate estimated with (relative extinction fraction) = 0 and b) diversification rate estimated with = 0.9. AM: Arbuscular mycorrhiza, EM: Ectomycorrhiza, NM: non-mycorrhizal and MIX (families with no dominance 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%

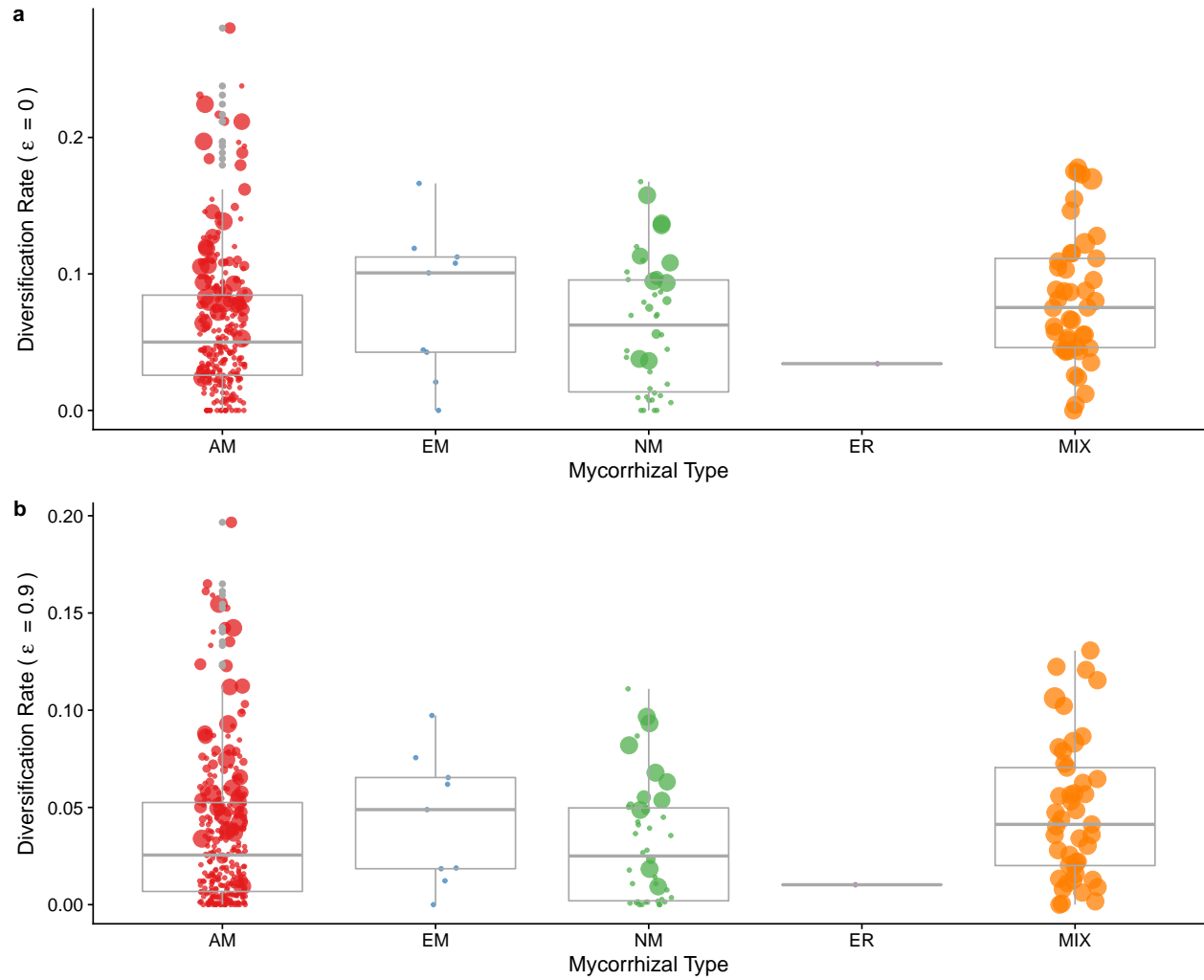


Figure 6: Relationship between mycorrhizal type and diversification rates. a) diversification rate estimated with  $(\text{relative extinction fraction}) = 0$  and b) diversification rate estimated with  $= 0.9$ . AM: Arbuscular mycorrhiza, EM: Ectomycorrhiza, NM: non-mycorrhizal and MIX (families with 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%

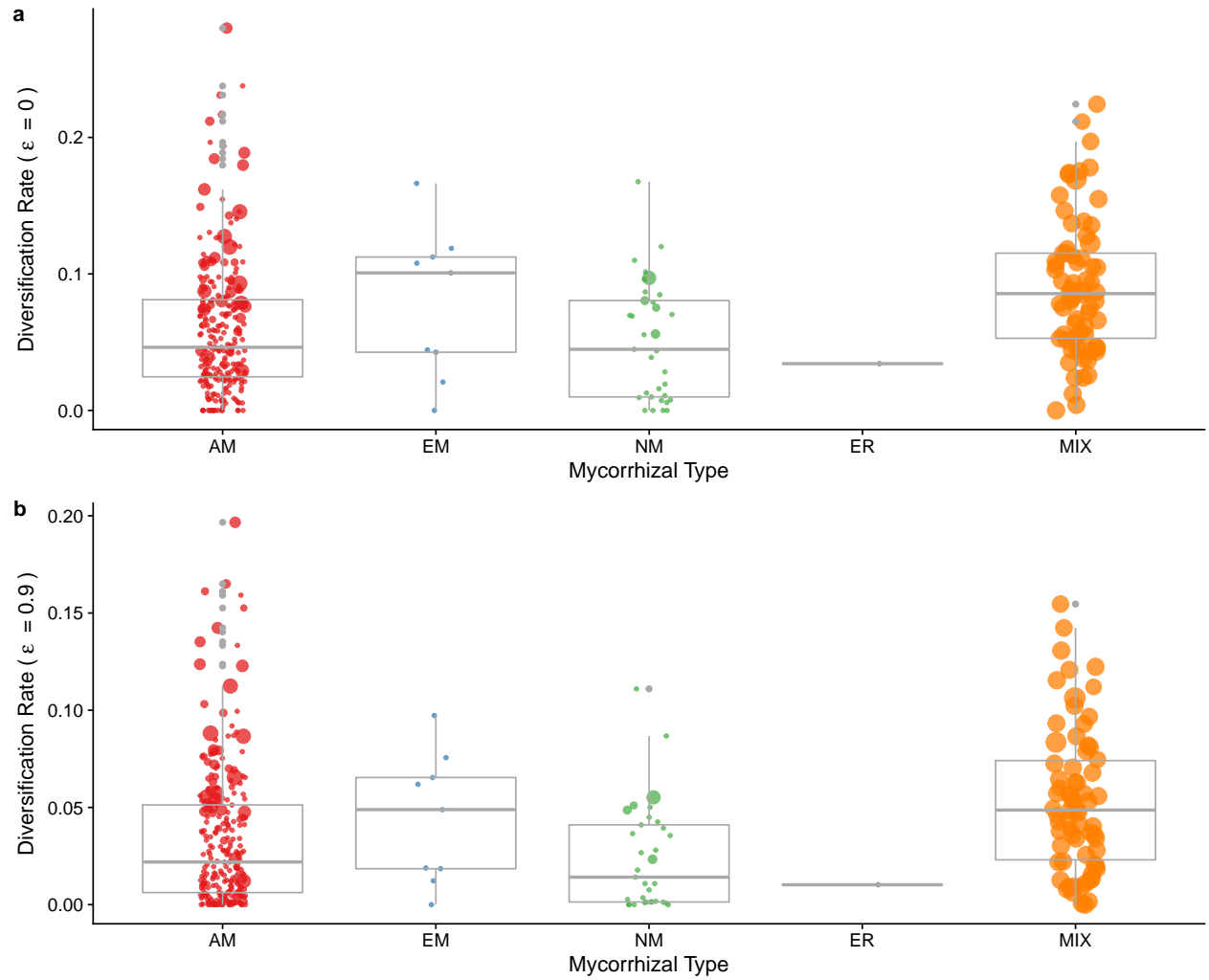


Figure 7: Relationship between mycorrhizal type and diversification rates. a) diversification rate estimated with  $(\text{relative extinction fraction}) = 0$  and b) diversification rate estimated with  $= 0.9$ . AM: Arbuscular mycorrhiza, EM: Ectomycorrhiza, NM: non-mycorrhizal and MIX (families with 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%

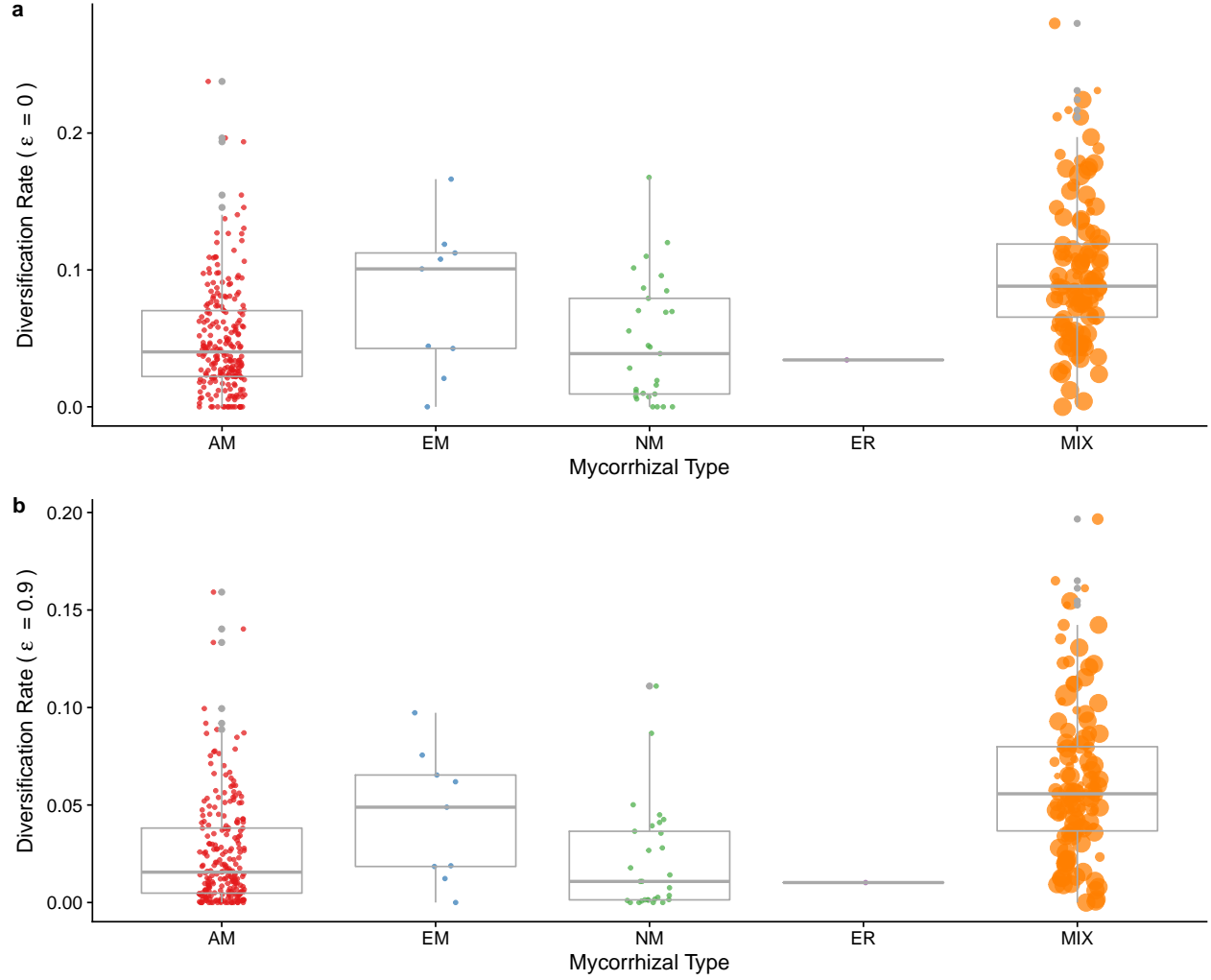


Figure 8: Relationship between mycorrhizal type and diversification rates. a) diversification rate estimated with  $(\text{relative extinction fraction}) = 0$  and b) diversification rate estimated with  $= 0.9$ . AM: Arbuscular mycorrhiza, EM: Ectomycorrhiza, NM: non-mycorrhizal and MIX (families with 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

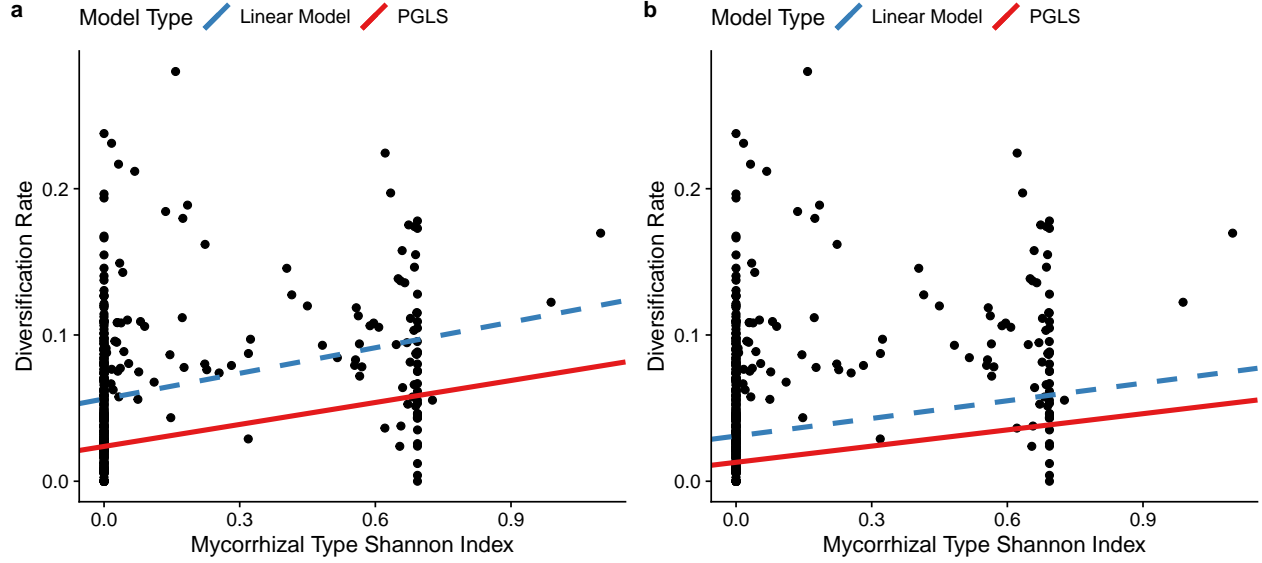


Figure 9: Scatterplots showing the relationship between mycorrhizal diversity index and diversification rates (a and c), species richness (b) and age family (d). Diversification rates were estimated with (relative extinction fraction) = 0 (a) and with = 0.9 (c). The red and blue lines indicate the results 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%

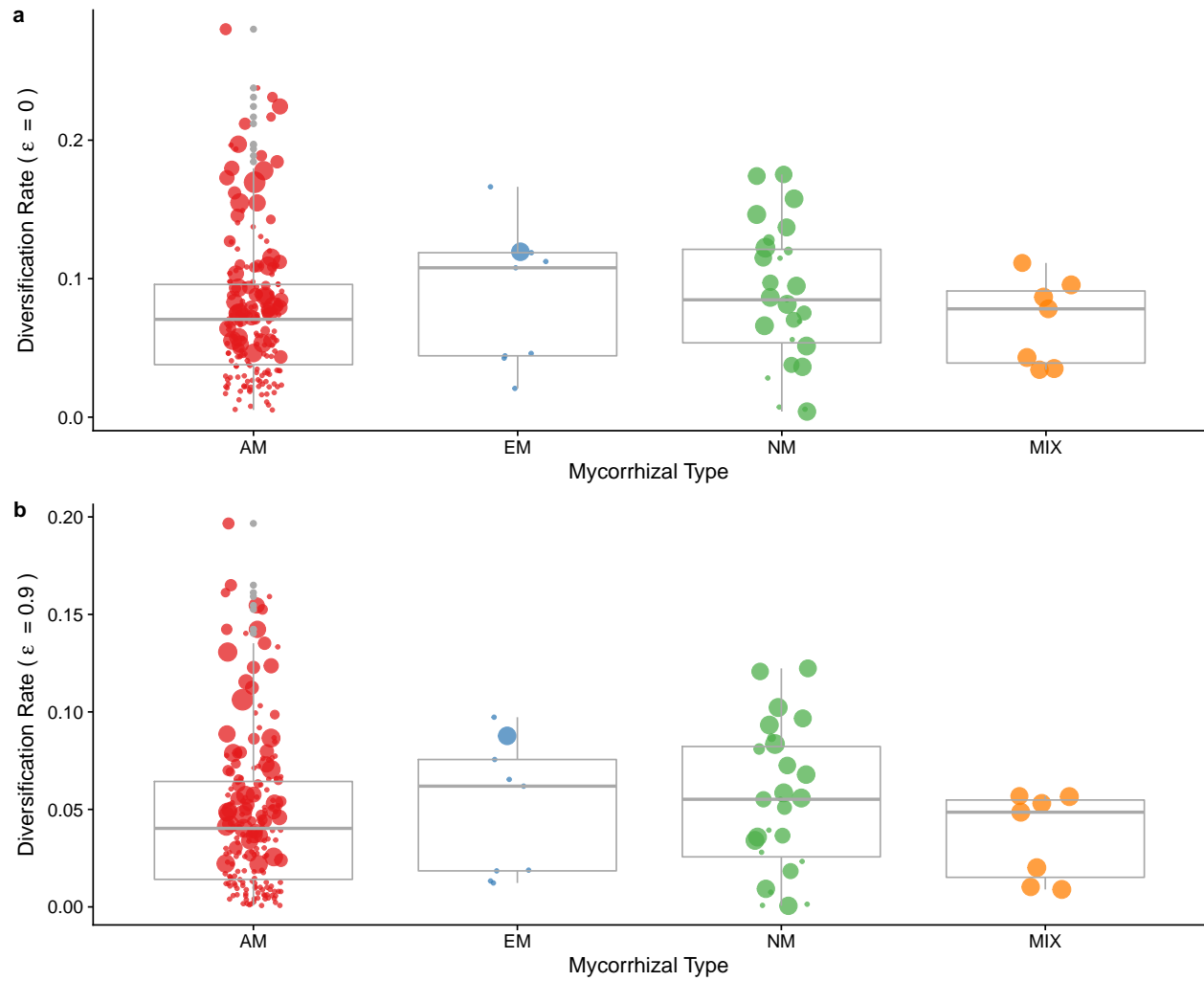


Figure 10: Relationship between mycorrhizal type and diversification rates. a) diversification rate estimated with (relative extinction fraction) = 0 and b) diversification rate estimated with = 0.9. AM: Arbuscular mycorrhiza, EM: Ectomycorrhiza, NM: non-mycorrhizal and MIX (families with no dominance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

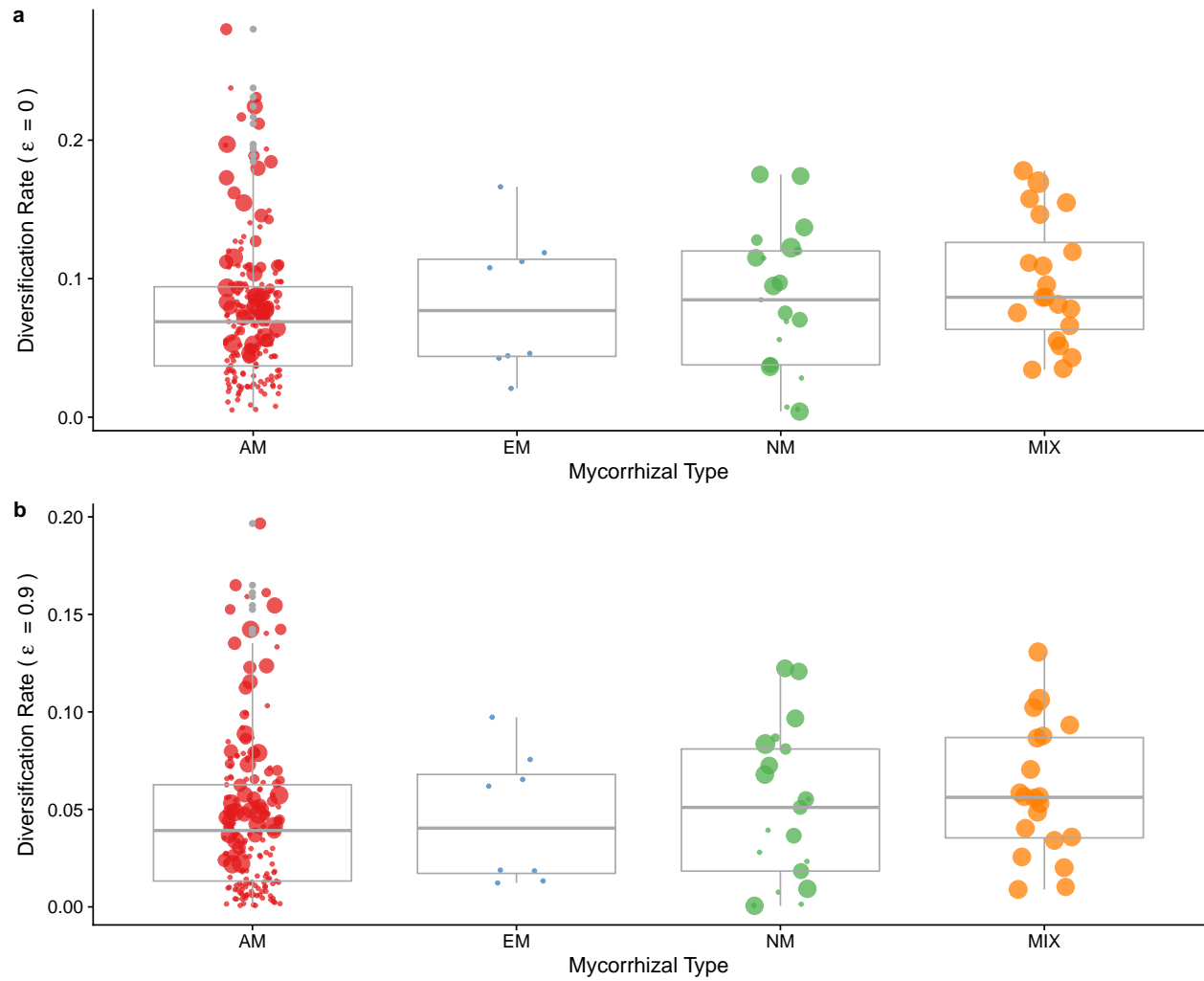


Figure 11: Relationship between mycorrhizal type and diversification rates. a) diversification rate estimated with (relative extinction fraction) = 0 and b) diversification rate estimated with = 0.9. AM: Arbuscular mycorrhiza, EM: Ectomycorrhiza, NM: non-mycorrhizal and MIX (families with no dominance 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%

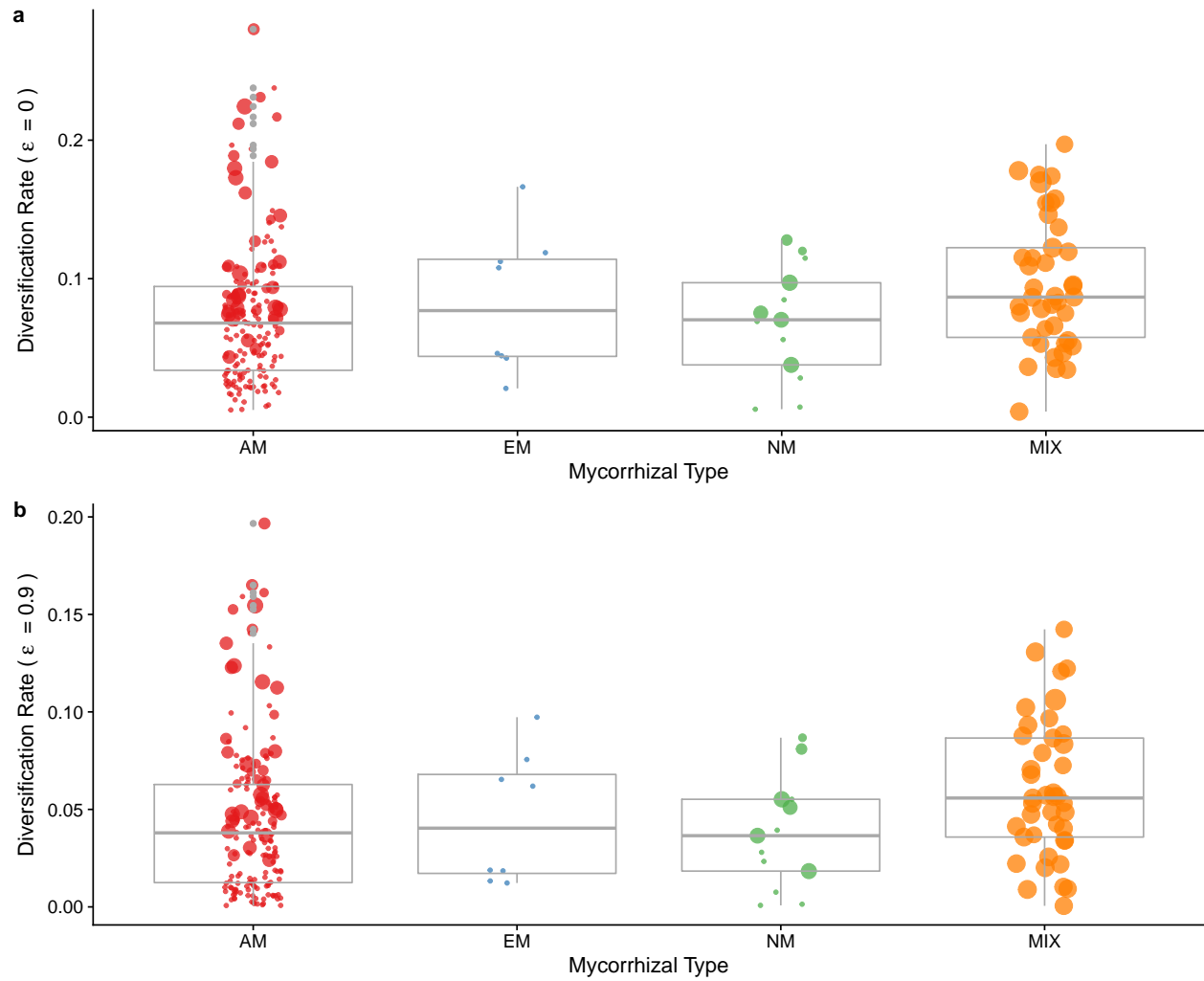


Figure 12: Relationship between mycorrhizal type and diversification rates. a) diversification rate estimated with  $(\text{relative extinction fraction}) = 0$  and b) diversification rate estimated with  $= 0.9$ . AM: Arbuscular mycorrhiza, EM: Ectomycorrhiza, NM: non-mycorrhizal and MIX (families with 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%



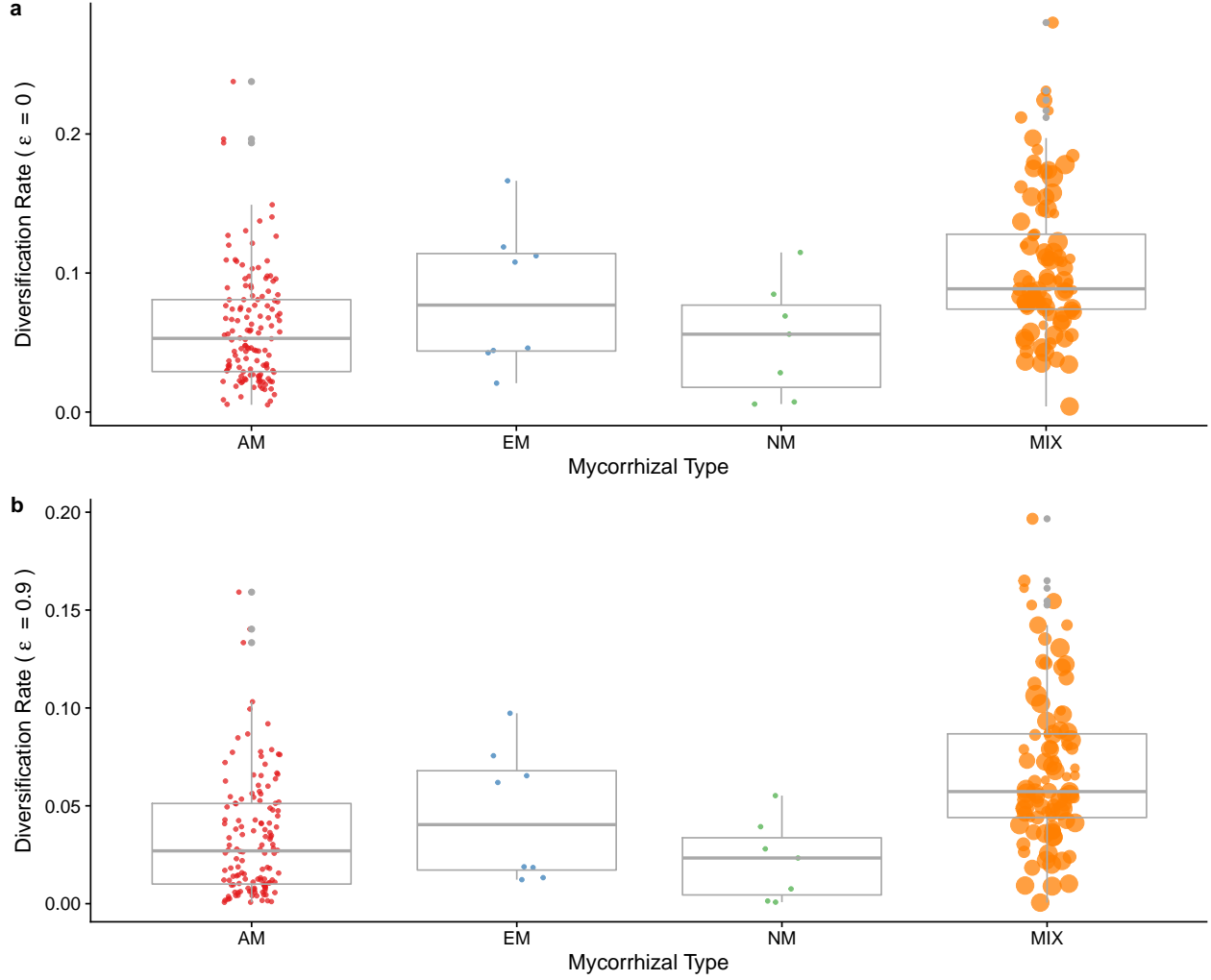


Figure 13: Relationship between mycorrhizal type and diversification rates. a) diversification rate estimated with  $(\text{relative extinction fraction}) = 0$  and b) diversification rate estimated with  $\varepsilon = 0.9$ . AM: Arbuscular mycorrhiza, EM: Ectomycorrhiza, NM: non-mycorrhizal and MIX (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

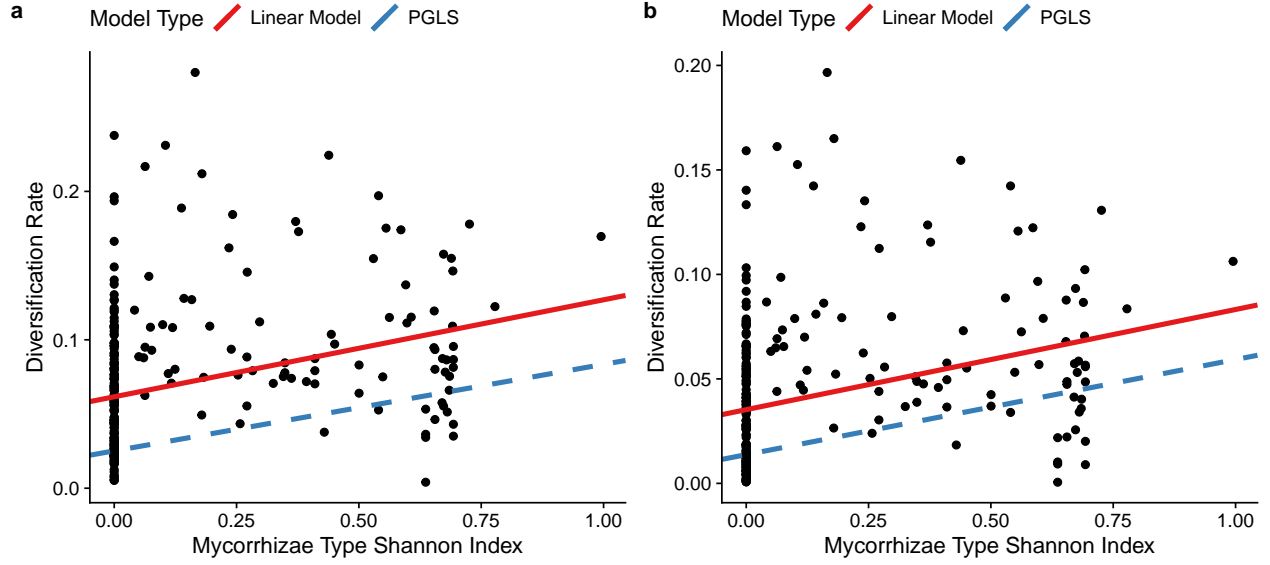


Figure 14: Scatterplots showing the relationship between mycorrhizal diversity index and diversification rates (a and c), species richness (b) and age family (d). Diversification rates were estimated with (relative extinction fraction) = 0 (a) and with = 0.9 (c). The red and blue lines indicate the results 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%

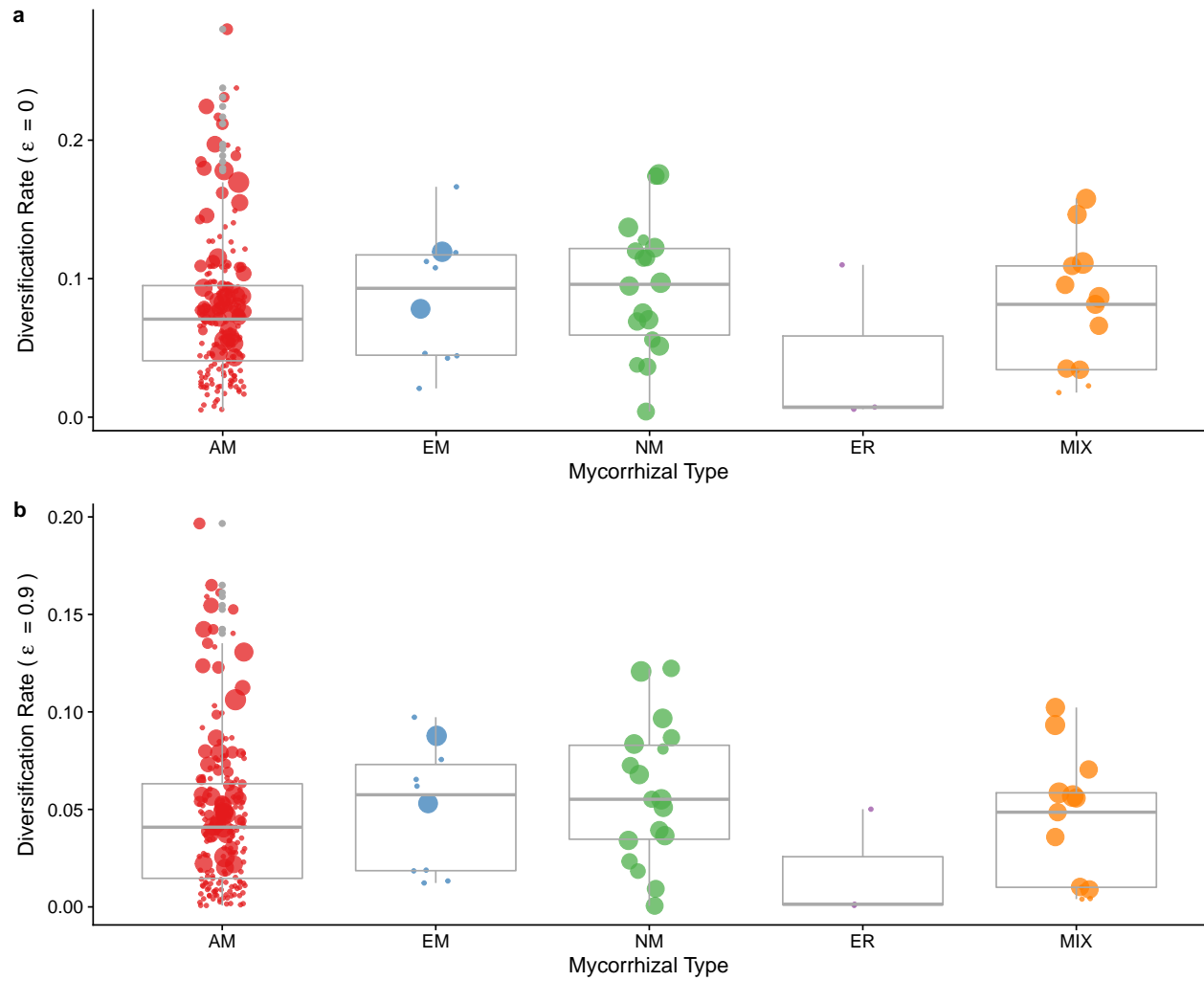


Figure 15: Relationship between mycorrhizal type and diversification rates. a) diversification rate estimated with  $(\text{relative extinction fraction}) = 0$  and b) diversification rate estimated with  $= 0.9$ . AM: Arbuscular mycorrhiza, EM: Ectomycorrhiza, NM: non-mycorrhizal and MIX (families with 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%

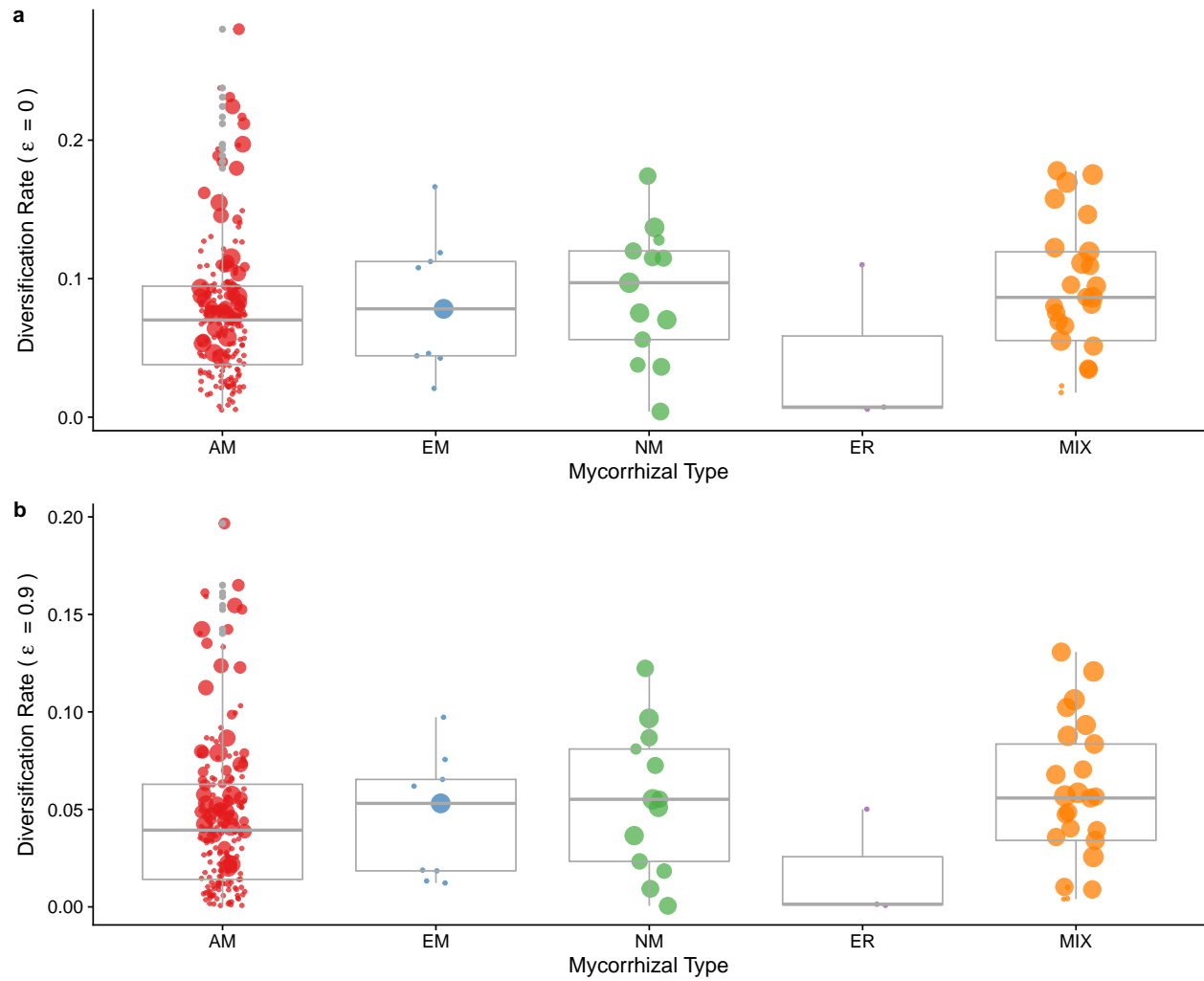


Figure 16: Relationship between mycorrhizal type and diversification rates. a) diversification rate estimated with  $(\text{relative extinction fraction}) = 0$  and b) diversification rate estimated with  $\varepsilon = 0.9$ . AM: Arbuscular mycorrhiza, EM: Ectomycorrhiza, NM: non-mycorrhizal and MIX (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%

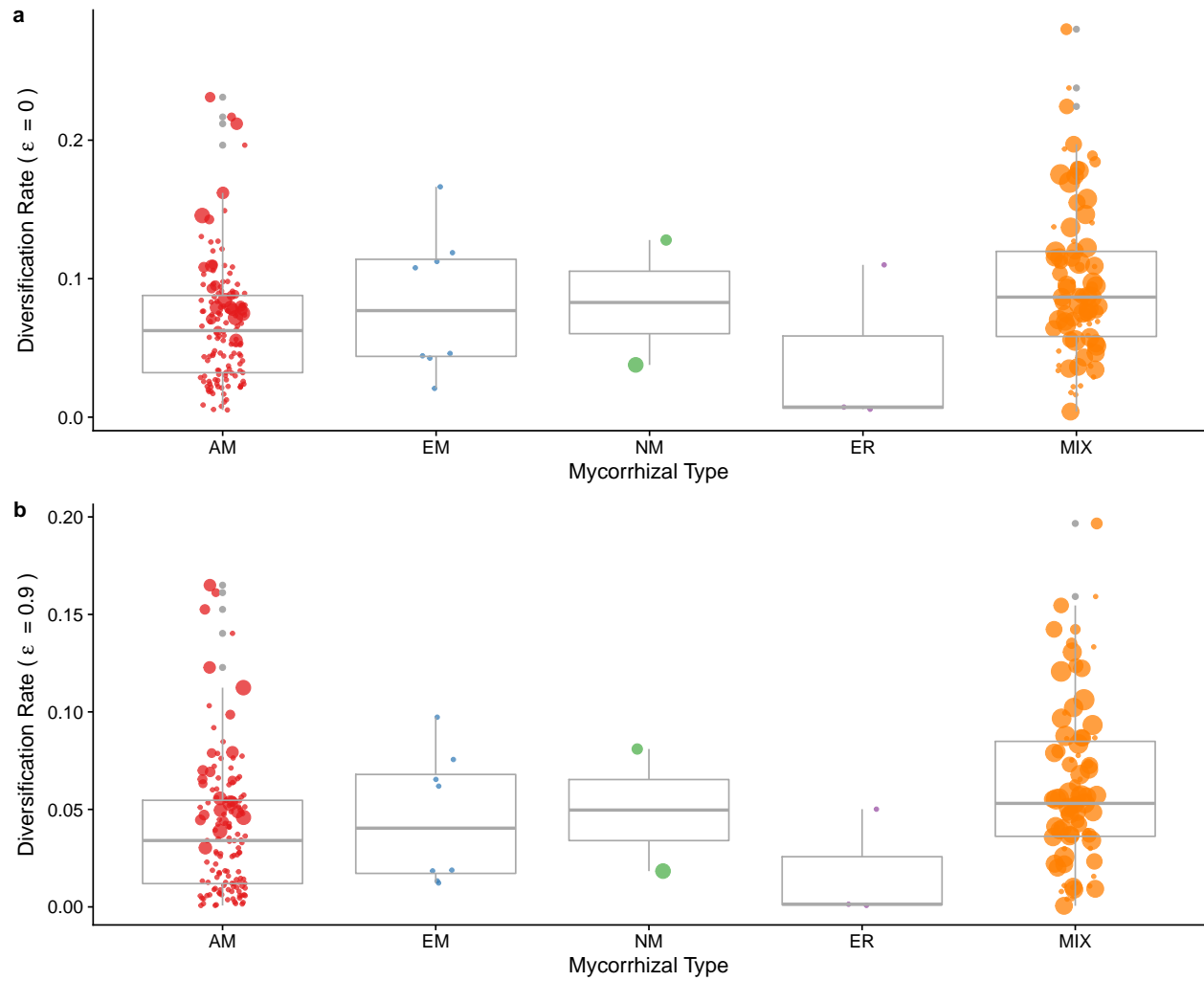


Figure 17: Relationship between mycorrhizal type and diversification rates. a) diversification rate estimated with  $(\text{relative extinction fraction}) = 0$  and b) diversification rate estimated with  $= 0.9$ . AM: Arbuscular mycorrhiza, EM: Ectomycorrhiza, NM: non-mycorrhizal and MIX (families with 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%

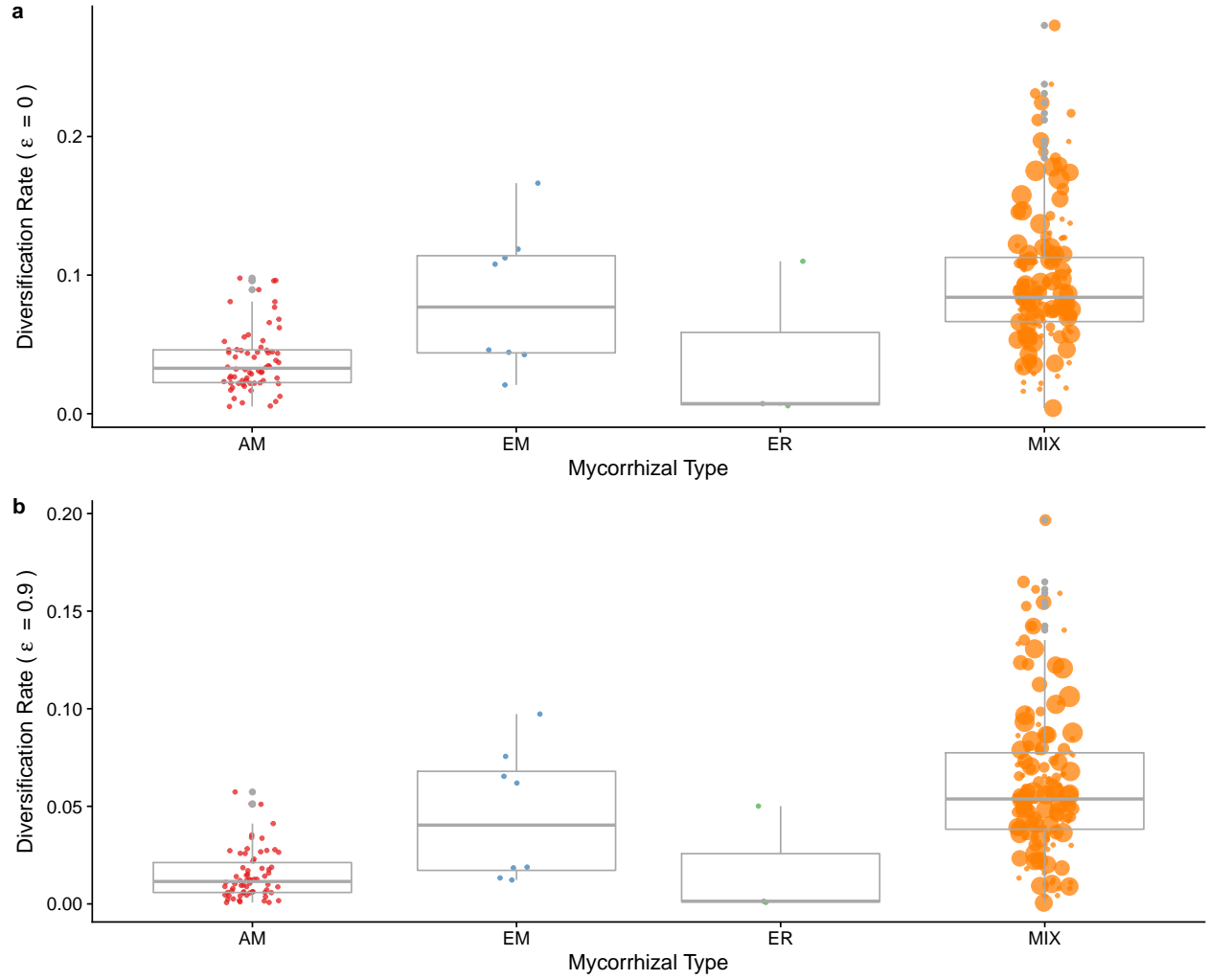


Figure 18: Relationship between mycorrhizal type and diversification rates. a) diversification rate estimated with  $(\text{relative extinction fraction}) = 0$  and b) diversification rate estimated with  $= 0.9$ . AM: Arbuscular mycorrhiza, EM: Ectomycorrhiza, NM: non-mycorrhizal and MIX (families with 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

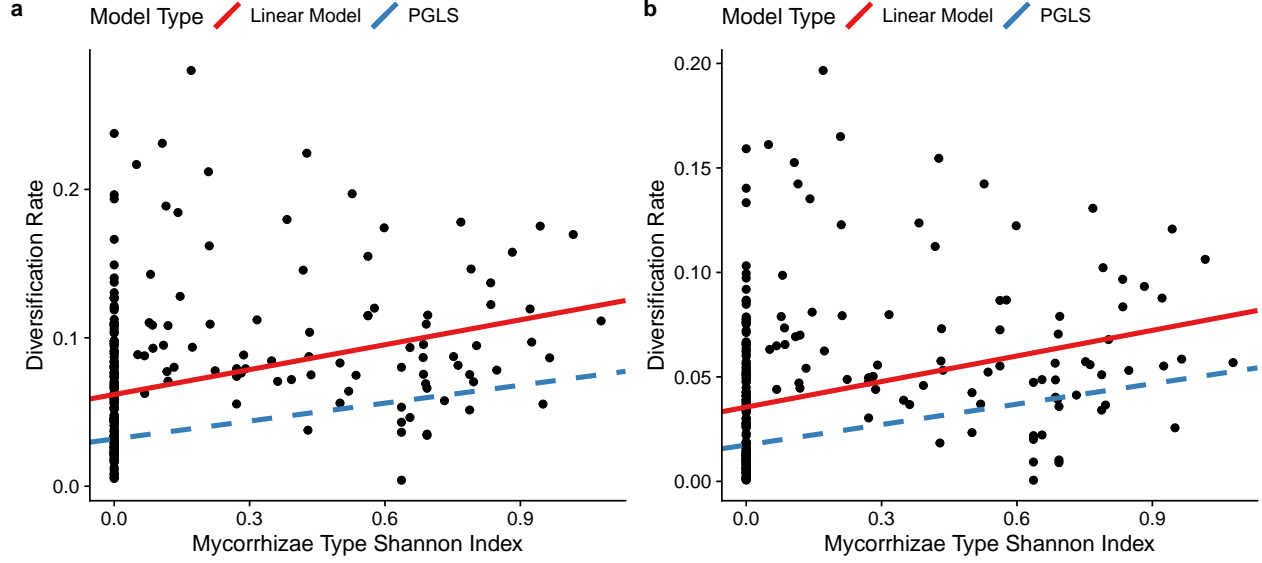


Figure 19: Scatterplots showing the relationship between mycorrhizal diversity index and diversification rates (a and c), species richness (b) and age family (d). Diversification rates were estimated with (relative extinction fraction) = 0 (a) and with = 0.9 (c). The red and blue lines indicate the results 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