**Supporting Information of the article**

**Taxonomic, phylogenetic and functional responses of plant communities in different life-stages to forest cover loss**

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**Phylogenetic Data**

We built a regional time-calibrated molecular phylogenetic tree using the juvenile and tree assemblages recorded in the 20 forest remnants. The tree was built using all the 654 species recorded in the two ontogenetic stages and *Amborella* *trichocarpa* and *Magnolia virginiana* species as external groups to root. We excluded 33 species that were identified only to family level. We assembled DNA sequence data using two plastid [ribulose-bisphosphate carboxylase gene (*rbc*L) and maturase K (*mat*K)] and one nuclear [5.8S ribosomal RNA gene] marker available in GenBank. When the sequences were not available for the species we randomly selected species within the genus to estimate the relatedness to that genus. The effect on branch length estimation of using these substitutions is expected to be minimum due to the extent of the phylogenetic sample (Cadotte et al., 2008; Cadotte, Cavender-Bares, Tilman, & Oakley, 2009). We excluded 51 species for which sequences were not found even for the genus level. We used the Program Geneious 7.1.4 (Kearse et al., 2012) to align the sequences and combine them into a supermatrix. The Maximum Likelihood analysis was performed using FastTree 2 (Price, Dehal, & Arkin, 2010), allowing the general time reversible (GTR) + γ model to be estimated, and using the default settings. Multiple runs were performed to ensure that the resulting phylogeny was not stuck on a local optimum. Thus, we created a time-calibrated phylogeny through fossil calibration points according to Bell et al. (2010) using the software BEAST v1.8.2 (Drummond, Suchard, Xie, & Rambaut, 2012). The calibration points used were: I Gentianales (54-78 MY), II Malpighiales (88-97 MY) and Fabaceae (49-77 MY). Simultaneous divergence-time and phylogenetic analyses were conducted using MCMC methods implemented in BEAST v1.8.2, which employs a lognormal relaxed-clock model to estimate divergence times.

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**TABLE S1.** General information on the selected forest remnants, showing the percentage of forest cover (FC) at the landscape scale (500m, 1000m, 1500m buffer radius), plant species richness, density of trees, basal area of trees and percentage of canopy openness (measured at 1.5m above the ground).

|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Forest  remnants | FC 500m (%) | FC 1000m (%) | FC 1500m (%) | Species richness - adult | Species richness - juvenile | Density (trees/ha) | Total basal area (m²/ha) | Canopy openness (%) |
| 1 | 10 | 3 | 4 | 39 | 21 | 1483.3 | 27.96 | 12.2 |
| 2 | 10 | 3 | 3 | 43 | 20 | 1505.6 | 20.53 | 24.1 |
| 3 | 13 | 4 | 9 | 43 | 35 | 1480.6 | 20.55 | 11.6 |
| 4 | 28 | 11 | 7 | 38 | 31 | 1844.4 | 25.02 | 14.7 |
| 5 | 36 | 14 | 9 | 31 | 33 | 1647.2 | 28.02 | 11.9 |
| 6 | 13 | 15 | 19 | 55 | 49 | 1750 | 24.54 | 12.9 |
| 7 | 30 | 21 | 24 | 52 | 39 | 1952.8 | 25.19 | 10.7 |
| 8 | 12 | 24 | 27 | 37 | 43 | 1786.1 | 30.57 | 11.7 |
| 9 | 46 | 40 | 48 | 56 | 72 | 2091.7 | 62.6 | 6.0 |
| 10 | 72 | 46 | 41 | 63 | 89 | 2036.1 | 44.55 | 9.8 |
| 11 | 51 | 46 | 45 | 72 | 83 | 2333.3 | 44.7 | 8.0 |
| 12 | 59 | 49 | 52 | 53 | 77 | 2147.2 | 41.9 | 9.3 |
| 13 | 51 | 50 | 52 | 56 | 83 | 2322.2 | 37.3 | 8.8 |
| 14 | 73 | 52 | 39 | 57 | 80 | 2013.9 | 40.62 | 9.1 |
| 15 | 87 | 62 | 55 | 75 | 72 | 2580.6 | 59.91 | 12.0 |
| 16 | 87 | 62 | 61 | 55 | 85 | 2525 | 57.9 | 8.5 |
| 17 | 87 | 63 | 48 | 53 | 58 | 2508.3 | 35.4 | 8.3 |
| 18 | 67 | 64 | 73 | 57 | 76 | 2330.6 | 31.79 | 7.8 |
| 19 | 95 | 81 | 58 | 58 | 79 | 1958.3 | 48.9 | 8.3 |
| 20 | 98 | 93 | 86 | 81 | 106 | 2994.4 | 40.08 | 8.8 |

**TABLE S2.** Plant functional traits used in the functional analysis, showing the percentage of information available for each functional trait for adult and juvenile assemblages. Categories for each attribute were shown, and in brackets the number of species in each category (adults and juveniles, respectively). For continuous traits, the range, mean, and standard deviation are shown.

|  |  |  |
| --- | --- | --- |
| **Functional Traits** | **Data Type** | **Attributes** |
| **Regeneration Strategy** | Discrete | Shade-tolerant (284/250); Shade-intolerant (167/103) |
| Adult: 98.9% |  |  |
| Juvenile: 88.25% |  |  |
| **Dispersal Mode** | Discrete | Abiotic-dispersed (78/68); Biotic-dispersed (377/372) |
| Adult: 99.8% |  |  |
| Juvenile: 98,75% |
| **Pollination Syndrome** | Discrete | Bats (13/5); Small bees (144/153); Large bees (37/26); |
| Adult: 76.32% |  | Beetles (19/11); Birds (3/2); Butterﬂies (3/6); |
| Juvenile: 74% |  | Diverse small insects (95/71); Flies (3/3); |
|  |  | Moths - excluding hawkmoth (11/9); |
|  |  | Sphingid - hawkmoth (5/4); Wasps (5/0); Wind (10/5) |
| **Fruit Diameter** | Continuous | Adult: 0.12 - 37.5 cm (Mean = 2.33 ± 3.28) |
| Adult: 77.4% |  | Juvenile: 0.11 – 18 cm (Mean 2.22 ± 2.27) |
| Juvenile: 58.5% |  |  |
| **Wood Density** | Continuous | Adult: 0.2 – 1.08 g cm-3 (Mean = 0.67 ± 0.16) |
| 99.8% of samples |  | Juvenile: 0.25 – 1.08 g cm-3 (Mean = 0.65 ± 0.14) |

**TABLE S3.** Results of the scale of effect based on Linear Models (LM) between each response variable and the percentage of forest cover, in tree spatial scales (500, 1000 and 1500m buffer radius). The radius with the highest determination coefficients (R²) for each variable is highlighted in bold. Respectively: SRa and SRj = adult and juvenile species richness; PDa and PDj = adult and juvenile phylogenetic diversity; pMPDa and pMPDj = adult and juvenile phylogenetic mean pairwise distance; SES PDa and SES PDj = adult and juvenile SES phylogenetic diversity; SES pMPDa and SES pMPDj = adult and juveline SES phylogenetic mean pairwise distance; FDa and FDj = adult and juvenile functional diversity; fMPDa and fMPDj = adult and juvenile functional mean pairwise distance; SES FDa and SES FDj = adult and juvenile SES functional diversity; SES fMPDa and SES fMPDa = adult and juvenile SES functional mean pairwise distance.

|  |  |  |  |
| --- | --- | --- | --- |
| Taxonomic, phylogenetic and functional variables | Forest Cover - 500m | Forest cover - 1000m | Forest cover - 1500m |
| R² | R² | R² |
| SRA | 0.467 | 0.561 | **0.584** |
| SRJ | 0.665 | 0.782 | **0.822** |
| PDA | 0.327 | 0.507 | **0.589** |
| PDJ | 0.663 | **0.782** | 0.780 |
| pmpda | -0.049 | **-0.043** | -0.055 |
| pmpdj | 0.025 | 0.136 | **0.261** |
| SES pda | **0.077** | 0.023 | 0.002 |
| SES pdj | -0.046 | -0.046 | **-0.017** |
| SES pmpda | **0.065** | 0.059 | 0.015 |
| SES pmpdj | -0.043 | **-0.008** | -0.015 |
| FDA | 0.182 | 0.205 | **0.227** |
| FDJ | 0.613 | 0.702 | **0.706** |
| fmpda | **-0.043** | -0.053 | -0.056 |
| fmpdj | **0.308** | 0.249 | 0.224 |
| SES fda | 0.029 | 0.051 | **0.082** |
| SES fdpj | -0.047 | -0.047 | **-0.040** |
| SES fmpda | 0.285 | **0.320** | 0.288 |
| SES fmpdj | -0.030 | -0.037 | **-0.015** |

**TABLE S4.** Results of spatial dependency test (Moran’s index), calculated by the residuals of linear models (LM) between each diversity dimension and forest cover loss at the best scale of effect. Respectively: SRa and SRj = adult and juvenile species richness; PDa and PDj = adult and juvenile phylogenetic diversity; pMPDa and pMPDj = adult and juvenile phylogenetic mean pairwise distance; SES PDa and SES PDj = adult and juvenile SES phylogenetic diversity; SES pMPDa and SES pMPDj = adult and juveline SES phylogenetic mean pairwise distance; FDa and FDj = adult and juvenile functional diversity; fMPDa and fMPDj = adult and juvenile functional mean pairwise distance; SES FDa and SES FDj = adult and juvenile SES functional diversity; SES fMPDa and SES fMPDa = adult and juvenile SES functional mean pairwise distance.

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
|  | observed | expected | sd | P |
| SRa | -0.228 | -0.053 | 0.111 | 0.11 |
| SRj | 0.262 | -0.053 | 0.108 | **<0.01** |
| PDa | -0.068 | -0.053 | 0.110 | 0.89 |
| PDj | 0.028 | 0.053 | 0.107 | 0.45 |
| pMPDa | -0.038 | -0.053 | 0.108 | 0.89 |
| pMPDj | 0.090 | -0.053 | 0.109 | 0.19 |
| SES.PDa | -0.153 | -0.053 | 0.112 | 0.37 |
| SES.PDj | -0.166 | -0.053 | 0.112 | 0.31 |
| SES.pMPDa | -0.073 | -0.053 | -0.053 | 0.85 |
| SES.pMPDj | -0.040 | -0.053 | 0.110 | 0.91 |
| FDa | -0.056 | -0.053 | 0.110 | 0.97 |
| FDj | -0.006 | -0.053 | 0.107 | 0.67 |
| fMPDa | 0.200 | -0.053 | 0.111 | **0.02** |
| fMPDj | -0.003 | -0.053 | 0.107 | 0.64 |
| SES.FDa | 0.065 | -0.053 | 0.112 | 0.29 |
| SES.FDj | -0.051 | -0.053 | 0.109 | 0.99 |
| SES.fMPDa | 0.135 | -0.053 | 0.112 | 0.10 |
| SES.fMPDj | 0.047 | -0.053 | 0.110 | 0.36 |

Observed: observed values; Expect: expect values; sd: standard deviation; P: p-value (significative <0.05)



**FIGURE S1.** Spearman correlations between all diversity metrics evaluated for adult tree assemblage in Atlantic forest remnants, Brazil. The lower half of the matrix shows correlation scores, represented in a red (positive) to blue (negative) scale. We considered correlated variables that showed values of rs ≥ 0.7. SRa – adult species richness, PDa = Adult phylogenetic diversity, FDa = adult functional diversity, SES.PDa = SES adult phylogenetic diversity, SES.FDa = SES adult functional diversity, pMPDa = adult phylogenetic mean pairwise distance, fMPDa = adult functional mean pairwise distance, SES. pMPDa = SES adult phylogenetic mean pairwise distance and SES.fMPDa = SES adult functional mean pairwise distance.



**FIGURE S2.** Spearman correlations between all diversity metrics evaluated for juvenile assemblage in Atlantic forest remnants, Brazil. The lower half of the matrix shows correlation scores, represented in a red (positive) to blue (negative) scale. We considered correlated variables that showed values of rs ≥ 0.7. SRj – juvenile species richness, PDj = juvenile phylogenetic diversity, FDj = juvenile functional diversity, SES.PDj = SES juvenile phylogenetic diversity, SES.FDj = SES juvenile functional diversity, pMPDj = juvenile phylogenetic mean pairwise distance, fMPDj = juvenile functional mean pairwise distance, SES.pMPDj = SES juvenile phylogenetic mean pairwise distance and SES.fMPDj = SES juvenile functional mean pairwise distance.