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Phylogenetic impoverishment of plant communities following chronic human disturbances in the Brazilian Caatinga

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Abstract

Chronic disturbances, such as selective logging, firewood extraction and extensive grazing, may lead to the taxonomic and phylogenetic impoverishment of remaining old-growth forest communities worldwide; however, the empirical evidence on this topic is limited. We tested this hypothesis in the Caatinga vegetation – a seasonally dry tropical forest restricted to northeast Brazil. We sampled 11653 individuals (adults, saplings and seedlings) from 51 species in 29 plots distributed along a gradient of chronic disturbance. The gradient was assessed using a chronic disturbance index (CDI) based on five recognized indicators of chronic disturbances: proximity to urban center, houses and roads and the density of both people and livestock. We used linear models to test if mean effective number of lineages, mean phylogenetic distance and phylogenetic dispersion decreased with CDI and if such relationships differed among ontogenetic stages. As expected, the mean effective number of lineages and the mean phylogenetic distance were negatively related to CDI, and such diversity losses occurred irrespective of ontogeny. Yet the increase in phylogenetic clustering in more disturbed plots was only evident in seedlings and saplings, mostly because clades with more descendent taxa than expected by chance (e.g., Euphorbiaceae) thrived in more disturbed plots. This novel study indicates that chronic human disturbances are promoting the phylogenetic impoverishment of the irreplaceable woody flora of the Brazilian Caatinga forest. The highest impoverishment was observed in seedlings and saplings, indicating that if current chronic disturbances remain, they will result in increasingly poorer phylogenetically forests. This loss of evolutionary history will potentially limit the capacity of this ecosystem to respond to human disturbances (i.e., lower ecological resilience) and particularly their ability to adapt to rapid climatic changes in the region.

Key words: anthropogenic disturbance; biodiversity; community assembly; environmental filtering; forest-dependent human populations; ontogenetic response; phylogenetic diversity and structure; wood plant assemblage; seasonally dry tropical forest; semiarid ecosystem.

INTRODUCTION

Chronic human disturbances, such as the frequent and continuous removal of small portions of biomass (Singh 1998), represent a geographically-widespread and effective threat to tropical biodiversity, particularly in the socioecological context marked by the presence of dense, forest-dependent human populations (see Forest Peoples Programme 2012). The livelihoods of millions of people throughout the tropics currently depend on forest products obtained in areas considered as either biodiversity hotspots or wildernesses (Singh et al.1997, Schmidt and Ticktin 2012). This is particularly the case of seasonally dry tropical forests (SDTF), which are amongst the most endangered tropical forests (Janzen 1988, Oatham and Boodram 2006). Although large tracts of SDTF are experiencing increasing levels of habitat loss and fragmentation (i.e., acute disturbances), chronic disturbances represent a subtle but pervasive source of disturbance in this ecosystem that leads to the habitat degradation and biological impoverishment of the remaining SDTF (Mahiri and Howorth 2001, Ribeiro et al. 2015, Arroyo-Rodríguez et al. 2015).

Although the available information is still scarce and there is a lack of synthesis, research during the last decades has demonstrated some important impacts of chronic disturbances on plant assemblages (Sagar et al. 2003, Shaanker et al. 2004, Ribeiro et al. 2015). Reduced recruitment, population collapse and taxonomic impoverishment of plant assemblages have been reported, in addition to the proliferation of disturbance-adapted native and exotic species (Sagar et al. 2003, Marvier et al. 2004, Ribeiro et al. 2015). Disruptions of plant-animal interactions,

such as seed dispersal (Leal et al. 2014) and plant-protection against herbivores (Leal et al. 2015), have also been reported in sites experiencing overgrazing by livestock and firewood collection. Furthermore, forest stands experiencing intense fodder extraction and small-scale slash-and-burn agriculture usually experience soil degradation and biomass collapse as trees are replaced by shrubs and grasses (Tripathi and Singh 2012, Silvério et al. 2013). Nevertheless, to our knowledge, the impact that chronic disturbances may have on the phylogenetic dimension of plant diversity has never been investigated.

In this sense, the consequences of biodiversity loss can be predicted from evolutionary history by assessing the differences in the phylogenetic diversity and structure of plant assemblages in human-modified landscapes (Cardinale et al. 2012, Santos et al. 2014*a*, Munguía-Rosas et al. 2014). This information may be useful to guide conservation priorities for specific taxa (e.g., Pavoine et al. 2005). Also, this phylogenetic information may help to infer potential mechanisms of community assembly in these landscapes (Webb et al.2002, Cavender-Bares et al. 2009, Cavender-Bares and Reich 2012, Roeder et al. 2014) and estimate the impact that evolutionary relationships among species may have on ecological processes and ecosystem functioning (Webb et al. 2002, Cadotte et al 2008).

Human disturbances may affect the phylogenetic structure and diversity of local communities in contrasting ways, depending on the level of floristic drift following disturbance (see Arroyo-Rodríguez et al. 2012). If the balance between extirpation and proliferation of particular lineages results in the co-occurrence of more related taxa, communities in disturbed sites should be phylogenetically poorer and more clustered than those in undisturbed sites (Santos et al. 2010 and 2014*a*, Munguía-Rosas et al. 2014). On the other hand, if the outcome of the floristic reorganization results in the co-occurrence of distantly related taxa, communities

93 will be phylogenetically more diverse and disperse in disturbed sites. A third possibility is that
94 community reorganization does not result in significant changes in phylogenetic structure and
95 diversity because proliferating taxa are as disperse across the phylogeny as decreasing taxa
96 (Arroyo-Rodríguez et al. 2012, Benítez-Malvido et al. 2014). Besides limited and mixed, the
97 empirical evidence available so far relies on plant phylogenetic responses to acute anthropogenic
98 disturbances such as deforestation and forest fragmentation (Santos et al. 2010 and 2014*a*,
99 Arroyo-Rodríguez et al. 2012, Andrade et al. 2015). Also, all but one (Benítez-Malvido et al.
100 2014) evaluate tropical rainforests, and with the exception of the study by Arroyo-Rodríguez et
101 al. (2012), only assess adult trees (diameter at breast height (DBH) ≥ 10 cm), which may mask
102 long-term responses to disturbance. Thus, further studies that include seedlings and saplings are
103 needed to attain a comprehensive understanding of the impact that chronic disturbances may
104 have on the phylogenetic dimension of plant assemblages in SDTF.
105 We investigated the phylogenetic diversity and structure of woody plant assemblages in
106 distinct ontogenetic stages (adults, saplings and seedlings) in the Brazilian Caatinga vegetation.
107 This SDTF sustains over 23 million people (11.8% of the Brazilian population) and is one of the
108 most populated semi-arid regions, with 26 inhabitants km^{-1} (INSA 2012). As a consequence,
109 about 50% of the Caatinga original forest cover is composed of secondary and old-growth forests
110 (MMA and IBAMA 2011). The remaining forest experiences several chronic disturbances,
111 including fuelwood collection, fodder extraction, charcoal production, overgrazing by livestock
112 and extraction of non-timber forest products (Pereira-Filho et al. 2007, Ramos et al. 2008).
113 We tested whether chronic disturbance leads to the phylogenetic impoverishment of plant
114 assemblages using a large database of Caatinga vegetation. Because it is well known that
115 different phylogenetic indices can lead to different and even contradicting results (e.g., Roeder et

116 al. 2014), we used four complementary indices of phylogenetic diversity and structure to achieve
117 accurate and more confidence interpretations (Winter et al. 2013, Roeder et al. 2014). SDTFs
118 represent stressful environments for most drought-intolerant tropical plants (Engelbrecht et al.
119 2007, Santos et al. 2014*b*), and it is reasonable to expect that such environmental stress increases
120 with chronic disturbance (Ribeiro et al. 2015). Assuming that environmental filtering operates on
121 evolutionary conserved traits and ecological interactions (Webb et al. 2002, Gómez et al. 2010),
122 we would expect that closely related species would occur together more frequently than expected
123 by chance (phylogenetic clustering), thus reducing plant phylogenetic diversity in sites facing
124 higher disturbance pressure (Webb et al. 2002, Cavender-Bares et al. 2009, Vandelook et al.
125 2012, González-Caro et al. 2014). We also expect that such phylogenetic impoverishment would
126 occur across all ontogenetic stages, being stronger in seedling and sapling assemblages as these
127 ontogenetic stages are often more vulnerable to chronic disturbance (see Singh et al.1997, Van
128 Lent et al. 2014; Ribeiro et al. 2015).
129
130 ## METHODS
131 ### *Study area*
132 The Caatinga is a mosaic of SDTFs and scrub vegetation that encompasses 826411 km²
133 restricted to Brazil (MMA and IBAMA 2011). The study area is located in the Parnamirim
134 municipality, Pernambuco state, northeast Brazil (8°5'26''S; 39°34'41''W; see Appendix A).
135 The climate is semi-arid, with an average temperature of 26ºC and most of the 431 mm mean
136 annual rainfall is received between January and May (IBGE 1985). Soils are predominantly non-
137 calcic brown soils (clay soil), regosols and planosols (sandy soils) (IBGE 1985). Anthropogenic
138 activities since the 16th century in the Parnamirim municipality (e.g., extensive grazing and

139 temporary farming) have resulted in the loss of ca. 45% of the municipality forest cover, and the
140 remaining 55% faces gradual chronic disturbances (e.g., extraction of forest products for
141 medicinal purposes, animal and human feeding, firewood collection and extensive livestock)
142 (Ribeiro et al. 2015).

143 The study was carried out in 29 50 × 20-m plots (Appendix A) established in a 220 km^2
144 landscape dominated by old-growth vegetation exposed to chronic disturbances. For each plot
145 we recorded five indicators of chronic disturbance that have been described in tropical forests
146 studies as important drivers of chronic human disturbances (Sagar et al. 2003, Martorell and
147 Peters 2005, Leal et al. 2014, Ribeiro et al. 2015): (i) proximity to the nearest house (PH); (ii)
148 proximity to the nearest road (PR); (iii) proximity to the urban center (PUC); (iv) density of
149 people living near the plot (DP); and (v) density of livestock near the plot (DL). We opted for
150 proxies instead of direct measures of logging, hunting, cutting and overgrazing because these
151 disturbances are not easily quantified and accessed at the landscape scale (Acharya and Dangi
152 2009, Arroyo-Rodríguez et al. 2015).

153 We quantified PH, PR and PUC as the reciprocal distance from the center of each plot
154 using satellite imagery from the Advanced Land Observing Satellite (ALOS). To estimate DP
155 and DL we first identified in the satellite imagery all dwellings near the plots. We identified 40
156 dwellings and we collected information on the number of people living in, and the number of
157 stock managed. This information was obtained through interviews done with each householder.
158 We then used the ALOS satellite imagery to estimate DP and DL, considering the interview data
159 in a 2-km buffer area from the center of each plot (i.e., within an area of 1256 ha). We used this
160 buffer size because local households assumed that the maximum dispersal distance of grazing
161 animals falls within two km.

Chronic disturbance index

Following Martorell and Peters (2005), all these disturbance indicators (i.e., PH, PR, PUC, DP and DL) were combined in a single Chronic Disturbance Index (CDI) through a principal component analysis (PCA) performed in R software (version 3.0.1, R Core Team 2013), using the package stats. Axis 1 of the PCA explained 41% of the variation of these indicators and was significantly correlated (mean correlation coefficients: $r = 0.66$, $P < 0.05$) with DP, DL and PH (see Appendix B and C). Thus, because DP and DL seems to be the main factors driving changes in plant communities in the region, with a stronger negative impact on seedling and sapling diversities (Ribeiro et al. 2015), this index is an accurate descriptor of important chronic human disturbances in the region. The scores of PCA axis 1 were rescaled from 0 to 100, representing the least and most disturbed sites, respectively (Martorell and Peters 2005).

Plant community sampling

In this study we surveyed trees and shrubs of plant assemblages during the rainy seasons of 2012 and 2013. We sampled adults, saplings and seedlings of these life forms in each plot to do the comparisons among ontogenetic stages. We defined adults as individuals with diameter at soil height (DSH) > 3 cm and height > 1.5 m; saplings were individuals with DSH < 3 cm and height between 1 and 1.5 m; and seedlings were individuals with height < 1 m (Rodal et al. 1992, Felfili et al. 2005). We recorded all adults found in each 50 × 20-m plot. Saplings were recorded in three 5 × 5-m subplots that were located in the center of each 50 × 20-m plot and separated by 10 m. Seedlings were sampled in 2 × 2-m subplots located in the center of each sapling subplot (see Appendix D for more information regarding the outcome of the differences in plot size on sample completeness per ontogenetic stage). All plants were identified to species level by

184 comparing the sampled species with samples from the Federal University of Pernambuco
185 herbarium. The botanical nomenclature followed APG III (Bremer et al. 2009).

186 *Phylogenetic diversity and structure*

187 For each plot we measured four complementary abundance-based phylogenetic metrics
188 (Webb et al. 2002, Webb et al. 2008, Chao et al. 2010; see Appendix E): mean phylogenetic
189 distance (MPD), net related index (NRI), and mean phylogenetic diversity of order q through T
190 years [i.e., ${}^{q}\bar{D}(T)$] considering orders 0 [${}^{0}\bar{D}(T)$] and 2 [${}^{2}\bar{D}(T)$], where ${}^{q}\bar{D}(T)$ quantifies the mean
191 effective number of lineages as a function of evolutionary time, T. The parameter q refers to the
192 value attributed to each node's relative abundance (Chao et al. 2010). When $q = 0$, only species
193 richness (presence/absence) is considered, and T represents the age of the first node (Chao et al.
194 2010).Yet when $q = 2$, only dominant or very abundant species are considered, and hence, ${}^{2}\bar{D}(T)$
195 quantifies the mean effective number of very abundant lineages as a function of evolutionary
196 time T (Chao et al. 2010). ${}^{q}\bar{D}(T)$ satisfies the replication principle, which is required in
197 biodiversity assessments as it considers the uniqueness of each species found in an assemblage
198 (Chao et al. 2010). MPD, on the other hand, measures the mean average distance (in millions of
199 years) among two random individuals in a specific sample, considering conspecifics, and the
200 NRI is a standardized metric of MPD and reflects whether taxa in a sample are more
201 phylogenetically clustered or dispersed than expected by chance (Webb et al. 2002, 2008,
202 Vamosi et al. 2009).

203 To obtain these phylogenetic metrics, we first produced a full species list based on the
204 APG III (Bremer et al. 2009) classification, after identifying all species of adults, saplings and
205 seedlings recorded across the 29 plots. We then assembled a list of 51 species belonging to 46
206 genera and 23 families, considering the three ontogenetic stages (see Supplement 1), and

207 constructed a regional time-calibrated phylogeny by estimating the continuous phylogenetic
208 distance between the sampled species using Bayesian inference and Markov chain Monte Carlo
209 (MCMC) methods (see Appendix F and G for more details of phylogeny construction methods).
210 Based on the time-calibrated phylogeny, we obtained ${}^{q}\bar{D}(T)$ for $q = 0$ and $q = 2$ using the
211 program PhD (Chiu and Chao 2012) that runs in the software R 3.0.1 (R Core Team 2013). We
212 also used the time-calibrated phylogeny to calculate the MPD and NRI metrics using the
213 COMSTRUCT function of Phylocom 4.2 adopting the switch '-a' to weight phylogenetic metrics
214 by taxa abundances. To evaluate if the phylogenetic structure within each plot differed from the
215 phylogenetic structure expected by chance, we compared observed MPD to the expected MPD
216 for 999 randomly generated null communities (MPD.rnd) using null model 2 of Phylocom 4.2.
217 This model has the advantage of maintaining the species richness and abundance structure within
218 communities, and assumes that all species of the pool have the same chance of colonizing any
219 given plot (Arroyo-Rodríguez et al. 2012). After computing observed and expected MPD for
220 each sample, we calculated the NRI metric. NRI is defined as [-1 (MPD – PD.rnd)/MPD.sd)],
221 where MPD.sd represents the standard deviation of MPD.rnd from the 999 null communities
222 (Webb et al. 2002, 2011). Positive values of NRI indicate phylogenetic clustering, while negative
223 values represent phylogenetic overdispersion (Vamosi et al. 2009).
224 Finally, we used the NODESIG function of Phylocom 4.2 to determine which clades
225 contributed significantly to any non-random phylogenetic structure of ontogenetic stages (adults,
226 saplings and seedlings) (see Webb et al. 2011 for more details of this function). The NODESIG
227 procedure verifies the occurrence of nodes with significantly more or less descendent taxa than
228 expected by chance. Nodes that present more or fewer descendent taxa than expected by chance

are highlighted as 'sigmore' or 'sigless', respectively, and allow us to identify clades responsible for the non-random phylogenetic structure in a sample (Webb et al. 2011).

Data analyses

We used linear models to test whether ${}^{0}\bar{D}(T)$, ${}^{2}\bar{D}(T)$ and MPD decreased and NRI increased with CDI, and whether such relationships differed among ontogenetic stages. We included plot relative abundance as a covariable in the models to control for differences in abundance across plot sizes. These analyses were done in JMP 8 (SAS Institute Inc.) with the standard least squares personality and the Gaussian distributions for all response variable errors after checking that they followed a Normal distribution with Shapiro-Wilk tests (see Appendix H). We also assessed if the species declining in more disturbed plots were more distantly related than those species proliferating in such plots. To do this, we correlated the CDI with the abundance of each species. These analyses were carried out using the software R 3.0.1 (R Core Team 2013), using the package Hmisc.

RESULTS

We recorded 10634 adult plants (362 ± 92.1 stems per plot; mean ± SD) belonging to 51 species (18.5 ± 3.6) (see Appendix I). For the sapling assemblage, we recorded 717 stems (11.6 ± 6.5) from 40 species (6.7 ± 2.2) (Appendix I). In the seedling community, we recorded 302 stems (10.6 ± 3.5) from 34 species (5.1 ± 1.8) (Appendix I). The most representative families in the three ontogenetic classes were Euphorbiaceae and Fabaceae, with 10–13 species per ontogenetic class. When considering species richness, the mean effective number of distinct lineages expected to the height of the phylogenetic tree [${}^{0}\bar{D}(T)$] varied among ontogenetic stages, being significantly higher in adults (10 ± 1.5 lineages per plot), than in saplings (4.9 ± 1.4

lineages) and seedlings (4.3 ± 1.2 lineages) (Table 1). When considering the number of very abundant or dominant species [$^{2}\overline{D}(T)$], all ontogenetic stages showed a similar mean effective number of lineages: 2.3 ± 0.8 lineages per plot in adults, 2.5 ± 0.7 lineages in saplings, and 2.8 ± 0.8 lineages in seedlings (Table 1). The mean phylogenetic distance (MPD) and net relatedness index (NRI) was also similar in all ontogenetic classes. MPD averaged 106.1 ± 33.3 million years in adult assemblages, 120 ± 44.5 million years in sapling assemblages, and 126.4 ± 51.7 million years in seedling assemblages, whereas NRI averaged 2.6 ± 1.0 in adults, 1.4 ± 1.6 in saplings, and 1.8 ± 1.7 in seedlings (Table 1).

As expected, MPD, $^{0}\overline{D}(T)$ and $^{2}\overline{D}(T)$ were negatively related to CDI, and such diversity losses occurred irrespective of ontogeny (Fig. 1; Table 2; Appendix J). Yet the increase in phylogenetic clustering in more disturbed plots was only evident in seedlings and saplings (Fig. 1; Table 2; Appendix J).

Adult assemblages presented significantly non-random phylogenetic structures with respect to the regional species pool in 18 out of 29 (69%) plots (see Appendix K). Within these 18 plots we identified 13 out of 104 internal nodes with more or less descendants than expected by chance (Appendix K). These nodes were composed of major clades such as Fabids, Rosids and Malvids, as well as lower clades such as order and family (e.g., Brassicales, Malvales and Fabaceae) (Appendix K). In adults, we did not find specific 'sigless' or 'sigmore' nodes exclusively related to either the most or least disturbed sites (Appendix K).

Considering sapling and seedling assemblages, we observed a significantly non-random phylogenetic structure in 14 and 15 plots, respectively (Appendix K). For these plots, saplings and seedlings had 15 and 12 out of 104 internal nodes, respectively, with more descendent taxa than expected by chance (Appendix K). In general, these nodes were evenly distributed along the

disturbance gradient, with exception of the Euphorbiaceae and its descendent taxa, which occurred frequently in the most disturbed plots (CDI > 50) (Appendix K).

Additionally, we verified that some families such as Capparaceae and Celastraceae, which are represented by a few species, did not occur in the more disturbed sites, considering all ontogenetic stages (Fig. 2). When analyzing the relationships between species abundance and disturbance, distantly related taxa such as *Fraunhofera muiltiflora* (Celastraceae), *Varronia leucocephala* (Boraginaceae), *Myracrodruon urundeuva* (Anacardiaceae) and *Bauhinia cheilantha* (Fabaceae), were negatively and significantly related to CDI, whereas closely related species such as *Croton sonderianus*, *Jatropha ribfolia* and *J. mollissima* (all within the Euphorbiaceae family) were positively and significantly related to CDI (Appendix L).

DISCUSSION

Chronic human disturbances have been increasingly considered as important drivers of habitat degradation (Singh 1998, Sagar et al. 2003, Martorell and Peters 2005, Leal et al. 2014, Arroyo-Rodríguez et al. 2015), but until now the impact that chronic disturbances might have on the phylogenetic diversity and structure of plant assemblages was unknown. As expected, our analyses indicate that the mean phylogenetic distance (MPD) and mean effective number of lineages [${}^{0}\overline{D}(T)$ and ${}^{2}\overline{D}(T)$] were negatively related to CDI, and that such a loss of evolutionary history occurred across all ontogenetic stages. This novel finding suggests that local extirpation of plant species across the disturbance gradient (see Ribeiro et al. 2015) does not occur randomly or uniformly, but in a clustered manner throughout the phylogenetic tree. This was confirmed by the metric of phylogenetic clustering (NRI), which increased in more disturbed plots especially for sapling and seedlings.

298 The decrease of phylogenetic diversity and increase of phylogenetic clustering in human-
299 modified tropical landscapes has been demonstrated in other studies, but only in response to
300 acute disturbances, such as forest loss and fragmentation (e.g., Santos et al. 2010 and 2014*a*;
301 Munguía-Rosas et al. 2014, Andrade et al. 2015). For example, Munguía-Rosas et al. (2014)
302 found that phylogenetic plant diversity (i.e., individuals with DBH > 1.6 cm) is 19% greater and
303 more overdispersed in a continuous forest when compared to an adjacent naturally fragmented
304 forest in the Yucatan Peninsula, Mexico. Santos et al. (2014*a*) also documented the loss of tree
305 phylogenetic diversity (DBH > 10 cm) and the reduction in phylogenetic evenness in a
306 fragmented tropical landscape in central Amazonia. Finally, in a hyper-fragmented landscape of
307 the Brazilian Atlantic forest, Santos et al. (2010) show that tree phylogenetic diversity (DBH >
308 10 cm) is 11% lower in forest edges than in old-growth forest interior areas. Overall, these
309 phylogenetic responses may be the result of several mechanisms. For example, higher
310 competitive exclusion between sister taxa in conserved forests may favor the co-occurrence of
311 less related taxa in these forests (see Roeder et al. 2014). Also, environmental filtering, which
312 may operate on traits with significant phylogenetic signals (see Willis et al. 2010), can allow
313 closely related species to occur together more frequently than expected by chance in disturbed
314 forests (Munguía-Rosas et al. 2014, Santos et al. 2014*a*).
315 As we have used proxies instead of direct measures of chronic disturbances, we cannot
316 test which are the main proximate and underlying mechanisms that promoted the observed shifts
317 in phylogenetic diversity and structure. However, it is well known that plant recruitment in
318 SDTF is driven mainly by abiotic filters imposed by seasonality and frequent droughts (Ceccon
319 et al. 2006), thus supporting niche conservatism and life-history convergence at the community
320 level (Pennington et al. 2009). The continuous removal of plant individuals and biomass is

expected to impose additional recruitment and dispersal limitations; first, because it can reduce population sizes (Endress et al. 2004) and seed production (Singh et al. 1997), and second, because such removal can alter vegetation structure (e.g., reduced stem density, greater canopy openness) and microclimatic conditions (e.g., increased habitat desiccation; Kumar et al. 2008). Although all these alterations can reduce the recruitment of many native plant species (Endress et al. 2004), some exotic and native disturbance-adapted species can proliferate in degraded sites (Marvier et al. 2004, Ribeiro et al. 2015).

In this sense, it is clear from our results that the balance between extirpation and proliferation of particular lineages resulted in the co-occurrence of more related taxa in disturbed sites. For example, complete lineages such as the Capparaceae (with 2 species) and Celastraceae (with 1 species) families disappeared in sites with a higher degree of disturbance (Fig. 2). The loss of these families represents the loss of evolutionary history. The Celastraceae family, especially, is represented by just one species: *Fraunhofera multiflora*, whose genus is monotypic and endemic to the Brazilian Caatinga (Simmons et al. 2012). The abundance of several distantly related species such as *F. multiflora* (Celastraceae), *Myracrodruon urundeuva* (Anacardiaceae) and *Piptadenia stipulaceae* (Fabaceae) was also negatively and significantly related to the chronic disturbance index (Appendix L). These lineages are known to be vulnerable to chronic disturbances because they have high wood density (> 0.8 g/cm³) and are good biofuel species appreciated by local people as firewood, charcoal and fences (Ramos et al. 2008).

In contrast, many species within the species-rich Euphorbiaceae family, such as those within the *Croton* and *Jatropha* genera, incremented their frequency and abundance in more disturbed plots (also see Ribeiro et al. 2015). The abundance of *Croton sonderianus* and *Jatropha ribifolia* (Euphorbiaceae) was also positively related to the disturbance index

(Appendix L). Euphorbiaceae is the second most common family in the Caatinga flora (103 species, Moro et al. 2014), and many species within this family (e.g., *Croton sonderianus* and *Cnidoscolus quercifolius*) are recognized as aggressive colonizers of human-disturbed habitats (Carvalho et al. 2001). The mechanisms related to these species' ability to colonize disturbed habitats are poorly explored, but are probably related to their degree of relatedness that make this species more ecologically similar and able to compete more strongly than distant relatives (Cahill et al. 2008, but see Fritschie et al. 2014).

Conclusions and implications for conservation

Chronic human disturbances can negatively affect the biological diversity of tropical biotas at the population, community and ecosystem levels (Sagar et al. 2003; Shaanker et al. 2004). In fact, there is ample anecdotal evidence in the Caatinga literature establishing causal connections between overexploitation of long-lived hardwood species, intense firewood collection, overgrazing by goats, slash-and-burning agriculture and the emergence of degraded habitats, ranging from impoverished forest assemblages to desertified areas (Leal et al. 2005, MMA and IBAMA 2011). Here we document, for the first time, that chronic disturbances also promote the phylogenetic impoverishment of the irreplaceable woody flora of the Brazilian Caatinga forest. The greatest impoverishment was observed in seedlings and saplings, thus indicating that if current chronic disturbances remain, they will result not only in taxonomically poorer plant assemblages (Ribeiro et al. 2015), but also in phylogenetically impoverished forests.

Such phylogenetic impoverishment will limit the capacity of the ecosystem to respond to human disturbances (i.e., lower ecological resilience) (Willis et al. 2008). Hence, to retain the evolutionary capital of the Caatinga, we should promote strategies that include: (i) investments in research and implementation of rural programs able to promote better practices in terms of

sustainable forest resource use and livestock management; (ii) government incentives that involves programs and funds to restore disturbed sites; (iii) law enforcement with a view to move forest extractivism towards sustainable standards; and (iv) increase the coverage of strictly protected areas, considering the phylogenetic diversity, while restricted future chronic disturbances in these areas.

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LITERATURE CITED

Acharya, K. P., and R. B. Dangi. 2009. Case studies on measuring and assessing forest degradation in Nepal: review of data and methods. Forest Resources Assessment Programme, Rome.

388 Andrade, E. R., J. G. Jardim, B. A. Santos, F. P. L. Melo, D. C. Talora, D. Faria, and E. Cazetta.
389 2015. Effects of habitat loss on taxonomic and phylogenetic diversity of understory Rubiaceae
390 in Atlantic forest landscapes. Forest Ecology and Management 349:73–84.
391 Arroyo-Rodríguez, V., J. Cavender-Bares, F. Escobar, F. P. L. Melo, M. Tabarelli, and B. A.
392 Santos. 2012. Maintenance of tree phylogenetic diversity in a highly fragmented rain forest.
393 Journal of Ecology 100:702–711.
394 Arroyo-Rodríguez, V., F. P. L. Melo, M. Martínez-Ramos, F. Bongers, R. L. Chazdon, J. A.
395 Meave, N. Norden, B. A. Santos, I. R. Leal, and M. Tabarelli. 2015. Multiple successional
396 pathways in human-modified tropical landscapes: new insights from forest succession, forest
397 fragmentation and landscape ecology research. Biological Reviews, *in press*.
398 Benítez-Malvido, J., J. C. Gallardo-Vásquez, M. Y. Alvarez-Añorve, and L. D. Avila-Cabadilla.
399 2014. Influence of matrix type on tree community assemblages along tropical dry forest edges.
400 American Journal of Botany 101:820–829.
401 Bremer, B., K. Bremer, M. W. Chase, M. F. Fay, J. L. Reveal, L. H. Bailey, D. E. Soltis, P. S.
402 Soltis, and P. F. Stevens. 2009. An update of the Angiosperm Phylogeny Group classification
403 for the orders and families of flowering plants: APG III. Botanical Journal of the Linnean
404 Society 161:105–121.
405 Cadotte, M. W., B. J. Cardinale, and T. H. Oakley. 2008. Evolutionary history and the effect of
406 biodiversity on plant productivity. Proceedings of the National Academy of Sciences U.S.A.
407 105:17012–17017.
408 Cahill, J. F., S. W. Kembel, E. G. Lamb, and P. A. Keddy. 2008. Does phylogenetic relatedness
409 influence the strength of competition among vascular plants? Perspectives in Plant Ecology,
410 Evolution and Systematics 10:41–50.

411 Cardinale, B. J., J. E. Duffy, A. Gonzalez, D. U. Hooper, C. Perrings, P. Venail, A. Narwani, G. M.
412 Mace, D. Tilman, D. A.Wardle, A. P. Kinzig, G. C. Daily, M. Loreau, J. B. Grace, A.
413 Larigauderie, D. S. Srivastava, and S. Naeem. 2012. Biodiversity loss and its impact on
414 humanity. Nature 489:326–326.
415 Carvalho, F. C., J. A. Araújo-Filho, R. Garcia, J. M. Pereira-Filho, and V. M. Albuquerque. 2001.
416 Efeito do corte da parte aérea na sobrevivência do marmeleiro (*Croton Sonderianus*
417 Muell.Arg.). Revista Brasileira de Zootecnia 30:930–934.
418 Cavender-Bares, J., K. H. Kozak, P. V. A. Fine, and S. W. Kembel. 2009. The merging of
419 community ecology and phylogenetic biology. Ecology letters 12:693–715.
420 Cavender-Bares, J., and P. B. Reich. 2012. Shocks to the system: community assembly of the oak
421 savanna in a 40-year fire frequency experiment. Ecology 93:52–69.
422 Ceccon, E., P. Huante, and E. Rincón. 2006. Abiotic factors influencing tropical dry forests
423 regeneration. Brazilian Archives of Biology and Technology 49:305–312.
424 Chao, A., C. H. Chiu, and L. Jost. 2010. Phylogenetic diversity measures based on Hill numbers.
425 Philosophical transactions of the Royal Society B 365:3599–3609.
426 Chiu, C., and A. Chao. 2012. User's Guide for Program PhD (Phylogenetic Diversity). Available
427 from http://chao.stat.nthu.edu.tw/software/PhD/PhD%20user%20guide.pdf
428 Felfili, J. M., F. A. Carvalho, and R. F. Haidar. 2005. Manual para o monitoramento de parcelas
429 permanentes nos biomas cerrado e pantanal. Universidade de Brasília, Departamento de
430 Engenharia Florestal, Brasília, Brazil.
431 Forest Peoples Programme. 2012. Forest peoples: numbers across the world. Available from
432 http://http://www.forestpeoples.org/faceted_search/results/across%20numbers%20content_type
433 %3Apublication

Fritschie, K. J., B. J. Cardinale, M. A. Alexandrou, and T. H. Oakley. 2014. Evolutionary history and the strength of species interactions: testing the phylogenetic limiting similarity hypothesis. Ecology 95:1407–1417.

Endress, B., D. L. Gorchov, and R. B. Noble. 2004. Non-timber forest product extraction: effects of harvest and browsing on an understory palm. Ecological Applications 14:1139–1153.

Engelbrecht, B. M. J., L. S. Comita, R. Condit, T. A. Kursar, M. T. Tyree, B. L. Turner, and S. P. Hubbell. 2007. Drought sensitivity shapes species distribution patterns in tropical forests. Nature 447:80–82.

Gómez, J. M., M. Verdú, and F. Perfectti. 2010. Ecological interactions are evolutionarily conserved across the entire tree of life. Nature 465:918–921.

González-Caro, S., M. N. Umaña, E. Álvarez, P. R. Stevenson, and N. G. Swenson. 2014. Phylogenetic alpha and beta diversity in tropical tree assemblages along regional-scale environmental gradients in northwest South America. Journal of Plant Ecology 7:145–153.

IBGE. 1985. Atlas Nacional do Brasil: Região Nordeste. IBGE, Rio de Janeiro, Brazil.

INSA. 2012. Sinopse do Censo Demográfico para o Semi-arido Brasileiro. INSA, Campina Grande, Brazil.

Janzen, D.H. 1988. Tropical Dry Forests. Pages 130-137 *in* E.O. Wilson, editor. Biodiversity. National Academy Press, Washington.

JMP®. 2008. Version 8. SAS Institute Inc., Cary, NC.

Kumar, R., and G. Shahabuddin. 2005. Effects of biomass extraction on vegetation structure, diversity and composition of forests in Sariska Tiger Reserve, India. Environmental Conservation 32:248–259.

456 Leal, I. R., J. M. C. Silva, M. Tabarelli, and T. E. Lacher. 2005. Changing the course of
457 biodiversity conservation in the Caatinga of Northeastern Brazil. Conservation Biology 19:701–
458 706
459 Leal, L. C., A. N. Andersen, and I. R. Leal. 2014. Anthropogenic disturbance reduces seed-
460 dispersal services for myrmecochorous plants in the Brazilian Caatinga. Oecologia 174:173–
461 181.
462 Leal, L. C., A. N. Andersen, and I. R. Leal. 2015. Disturbance winners or losers? Plants bearing
463 extrafloral nectaries in Brazilian Caatinga. Biotropica 47:468–474.
464 Mahiri, I., and C. Howorth. 2001 Twenty years of resolving the irresolvable: Approaches to the
465 fuelwood problem in Kenya. Land Degradation & Development 12:205–215.
466 Marvier, M., P. Kareiva, and M. G. Neubert. 2004. Habitat destruction, fragmentation and
467 disturbance promote invasion by habitat generalists in a multispecies metapopulation. Risk
468 Analysis 24:869–879.
469 Martorell, C., and E.M. Peters. 2005. The measurement of chronic disturbance and its effects on
470 the threatened cactus *Mammillaria pectinifera*. Biological Conservation 124:199–207.
471 Mehta, V. K., P. J. Sullivan, M. T. Walter, J. Krishnaswamy, and S. D. DeGloria. 2008. Ecosystem
472 impacts of disturbance in a dry tropical forest in southern India. Ecohydrology 1:149–160
473 MMA and IBAMA. 2011. Monitoramento do desmatamento nos biomas brasileiros por satélite
474 Acordo de Cooperação Técnica MMA / IBAMA: Monitoramento do Bioma Caatinga 2008 a
475 2009. IBAMA/ MMA, Brasília. Brazil.
476 Moro, M. F., E. N. Lughadha, D. L. Filer, F. S. De Araújo, and F. R. Martins. 2014. A catalogue of
477 the vascular plants of the Caatinga Phytogeographical Domain: A synthesis of floristic and
478 phytosociological surveys. Phytotaxa 160:1-30.

479 Munguía-Rosas, M. A., S. G. Jurado-Dzib, C. R. Mezeta-Cob, S. Montiel, A. Rojas, and J. M.
480 Pech-Canché. 2014. Continuous forest has greater taxonomic, functional and phylogenetic plant
481 diversity than an adjacent naturally fragmented forest. Journal of Tropical Ecology 30:1–11.
482 Oatham, M., and N. Boodram. 2006. Gap analysis of neotropical dry forests in protected areas
483 using geographical information systems and global datasets. Tropical Ecology 47: 271–278.
484 Pavoine, S., S. Ollier, and A. B. Dufour. 2005. Is the originality of a species measurable? Ecology
485 Letters 8:579–586.
486 Pennington, R. T., M. Lavin, and A. Oliveira-Filho. 2009. Woody plant diversity, evolution, and
487 ecology in the tropics: perspectives from seasonally dry tropical forests. Annual Review of
488 Ecology, Evolution, and Systematics 40:437–457.
489 Pereira-Filho, J. M., J. A. Araújo-Filho, F. C. Carvalho, and M. C. Rego. 2007. Disponibilidade de
490 fitomassa do estrato herbáceo de uma Caatinga raleada submetida ao pastejo alternado ovino-
491 caprino. Livestock Research for Rural Development 19: 1–14.
492 R Core Team. 2013. *R:* A Language and Environment for Statistical Computing, Version 3.0.1.
493 Foundation for Statistical Computing, Vienna, Austria.
494 Ramos, M. A., P. M. Medeiros, A. L. S. Almeida, A. L. P. Feliciano, and U. P. Albuquerque. 2008.
495 Use and knowledge of fuelwood in an area of Caatinga vegetation in NE Brazil. Biomass and
496 Bioenergy 32:510–517.
497 Ribeiro, E. M. S., V. Arroyo-Rodríguez, B. A. Santos, M. Tabarelli, and I. R. Leal. 2015. Chronic
498 anthropogenic disturbance drives the biological impoverishment of the Brazilian Caatinga
499 vegetation. Journal of Applied Ecology 52:611–620.

500 Rodal, M. J. N., E. V. S. Sampaio, and M. A. Figueiredo. 1992. Manual sobre métodos de estudo
501 florístico e fitossociológico: ecossistema caatinga. Sociedade Botânica do Brasil, Brasília,
502 Brazil.
503 Roeder, M., M. McLeish, P. Beckschäfer, M. de Blécourt, E. Paudel, R. D. Harrison, and F. Slik.
504 2014. Phylogenetic clustering increases with succession for lianas in a Chinese tropical montane
505 rain forest. Ecography 38:1–10.
506 Sagar, R., A. S. Raghubanshi, and J. S. Singh. 2003. Tree species composition, dispersion and
507 diversity along a disturbance gradient in a dry tropical forest region of India. Forest Ecology
508 and Management 186:61–71.
509 Santos, B. A., V. Arroyo-Rodríguez, C. E. Moreno, and M. Tabarelli. 2010. Edge-related loss of
510 tree phylogenetic diversity in the severely fragmented Brazilian Atlantic forest. PloS ONE
511 5:e12625.
512 Santos, B. A., M. Tabarelli, F. P. L. Melo, L. C. Camargo, A. Andrade, S. G. Laurance, and W. F.
513 Laurance. 2014*a*. Phylogenetic impoverishment of amazonian tree communities in an
514 experimentally fragmented forest landscape. PloS ONE e113109.
515 Santos, M. G., M. T. Oliveira, K. V. Figueiredo, H. M. Falcão, E. C. P. Arruda, J. Almeida-Cortez,
516 E. V. S. B. Sampaio, J. P. H. B. Ometto, R. S. C. Menezes, A. F. M. Oliveira, M. F. Pompelli,
517 and A. C. D. Antonino. 2014*b*. Caatinga, the Brazilian dry tropical forest: can it tolerate climate
518 changes? Theoretical and Experimental Plant Physiology 26:83–99.
519 Schmidt, I. B., and T. Ticktin. 2012. When lessons from population models and local ecological
520 knowledge coincide – Effects of flower stalk harvesting in the Brazilian savanna. Biological
521 Conservation 152:187–195.

522 Shaanker, R. U., K. N. Ganeshaiah, M. N. Rao, and N. A. Aravind. 2004. Ecological consequences
523 of forest use: from genes to ecosystem: a case study in the Biligiri Rangaswamy temple wildlife
524 Sanctuary, South India. Conservation and Society 2:347–363.
525 Silvério, D. V, P. M. Brando, J. K. Balch, F. E. Putz, D. C. Nepstad, C. Oliveira-Santos, and M. M.
526 C. Bustamante. 2013. Testing the Amazon savannization hypothesis: fire effects on invasion of
527 a neotropical forest by native cerrado and exotic pasture grasses. Philosophical Transactions of
528 the Royal Society B 368:20120427.
529 Simmons, M. 2012. Phylogeny of Celastraceae subfamilies Cassinoideae and Tripterygioideae
530 inferred from morphological characters and nuclear and plastid loci. Systematic Botany 37:456–
531 467.
532 Singh, S. P., Y. S. Rawat, and S. C. Garkoti. 1997. Failure of brown oak (*Quercus semecarpifolia*)
533 to regenerate in central Himalaya: A case of environmental semisurprise. Current Science
534 73:371–374.
535 Singh, S. P. 1998. Chronic disturbance, a principal cause of environmental degradation in
536 developing countries. Environmental Conservation 25:1–2.
537 Tripathi, N., and R. S. Singh. 2012. Impact of savannization on nitrogen mineralization in an
538 indian Tropical forest. Forest Research 1:1–10.
539 Vamosi, S. M., S. B. Heard, J. C. Vamosi, and C. O. Webb. 2009. Emerging patterns in the
540 comparative analysis of phylogenetic community structure. Molecular Ecology 18:572–92.
541 Vandelook, F., M. Verdú, and O. Honnay. 2012. The role of seed traits in determining the
542 phylogenetic structure of temperate plant communities. Annals of Botany 110:629–636.

543 Van Lent, J., J. C. Hernandez-Barrios, N. P. R. Anten, and M. Martínez-Ramos. 2014.
544 Defoliation effects on seed dispersal and seedling recruitment in a tropical rain forest
545 understorey palm. Journal of Ecology 102:709–720.
546 Webb, C. O., D. D. Ackerly, M. A. McPeek, and M. J. Donoghue. 2002. Phylogenies and
547 community ecology. Annual Review of Ecology and Systematics 33:475–505.
548 Webb, C. O., D. D. Ackerly, and S. W. Kembel. 2008. Phylocom: software for the analysis of
549 phylogenetic community structure and trait evolution. Bioinformatics 24:2098–2100.
550 Webb, C. O., D. D. Ackerly, and S. W. Kembel. 2011. Phylocom 4.2 users' manual. Available
551 from http://phylodiversity.net/phylocom/
552 Willis, C. G., B. Ruhfel, R. B. Primack, A. J. Miller-Rushing, and C. C. Davis. 2008. Phylogenetic
553 patterns of species loss in Thoreau's woods are driven by climate change. Proceedings of the
554 National Academy of Sciences 105:17029–17033.
555 Willis, C. G., M. Halina, C. Lehman, P. B. Reich, A. Keen, S. McCarthy, and J. Cavender-Bares.
556 2010. Phylogenetic community structure in Minnesota oak savanna is influenced by spatial
557 extent and environmental variation. Ecography 33:565–577.
558 Winter, M., V. Devictor, and O. Schweiger. 2013. Phylogenetic diversity and nature conservation:
559 where are we? Trends in Ecology & Evolution 28:199–204.
560

Table 1. Differences in plant phylogenetic metrics among ontogenetic classes (adult trees, saplings and seedlings) sampled in 29 sites from the Brazilian Caatinga forest, Parnamirim municipality, Pernambuco, Brazil. Different letters indicate significant differences among classes after post hoc comparisons (Tukey tests).

Ontogenetic stage	Phylogenetic metric							
	${}^{0}\overline{D}$(T)		${}^{2}\overline{D}$(T)		MPD		NRI	
	Mean ± SD	Max – Min	Mean ± SD	Max – Min	Mean ± SD	Max – Min	Mean ± SD	Max – Min
Adults	10.0[a] ± 1.5	13.0 – 7.1	2.3[a] ± 0.8	5.1 – 1.3	106.1[a] ± 33.3	184.1–50.0	2.7[a] ± 1.1	4.7 – 0.3
Saplings	4.9[b] ± 1.4	7.2 – 1.3	2.5[a] ± 0.7	4.1 – 1.0	120.0[a] ± 44.5	191.1 – 22.7	1.7[a] ± 1.8	6.1 – (-0.8)
Seedlings	4.3[b] ± 1.2	7.0 – 1.9	2.8 [a] ± 0.8	4.2 – 1.3	126.5[a] ± 51.7	203.9 – 15.6	1.8[a] ± 1.8	5.2 – (-0.85)

Table 2. Results of linear models fitted to test the effect of chronic disturbance index on phylogenetic metrics of plant assemblages (adults, saplings and seedlings) from the Brazilian Caatinga vegetation, Parnamirim municipality, Pernambuco, Brazil†. Phylogenetic metrics: ${}^{0}\overline{D}$(T) - mean phylogenetic diversity of total lineages, ${}^{2}\overline{D}$(T) - mean phylogenetic diversity of dominant lineages, MPD - mean phylogenetic distance and, NRI - nearest relatedness index. Model factors codes: CDI – chronic disturbance, OS - ontogenetic stage, A – stem relative abundance of the plot.

	Whole model		Model factors			
Phylogenetic metric	R^2_{adj}	*F*	CDI	OS	A	CDI × OS
${}^{0}\overline{D}$(T)	0.78	51.58*	6.36*	7.26*	$2.86^{n.s.}$	$0.66^{n.s.}$
${}^{2}\overline{D}$(T)	0.12	2.96*	5.99*	$0.29^{n.s.}$	$0.67^{n.s.}$	$0.14^{n.s.}$
MPD	0.21	4.93*	23.65*	$0.09^{n.s.}$	$0.38^{n.s.}$	$0.84^{n.s.}$
NRI	0.18	4.16*	7.33*	$1.27^{n.s.}$	$0.76^{n.s.}$	5.63*

†We indicate the *F* values and significance level ($^{n.s.}P > 0.05$;* $P < 0.05$). Degrees of freedom: whole model (6,86), CDI (1,86), OS (2,86), A (1,86) and CDI×OS (2,86).

Figure legends

FIG. 1. Relationships between each phylogenetic metric and the chronic disturbance index in old-growth Caatinga forests in Parnamirim municipality, Brazil. The 'r' values in each line are the Pearson's correlation coefficient used to illustrate the strength of relationships between phylogenetic metrics by ontogenetic stage with chronic disturbance.

FIG. 2. Relationships between adults' (A), saplings' (B) and seedlings'(C) relative individual densities per plant family and the chronic disturbance index. Families acronyms - Ana: Anacardiaceae; Apo: Apocynaceae; Bix: Bixaceae; Bor: Boraginaceae; Bur: Burseraceae; Cac: Cactaceae; Cap: Capparaceae; Cel: Celastraceae; Com: Combretaceae; Eup: Euphorbiaceae; Ery: Erythroxylaceae; Fab; Fabaceae; Nyc: Nyctaginaceae; Mal: Malvaceae; Ola: Olacaceae; Rha; Rhaminaceae; Rub; Rubiaceae; Sal: Salicaceae;Ver: Verbenaceae.

Figure 1.

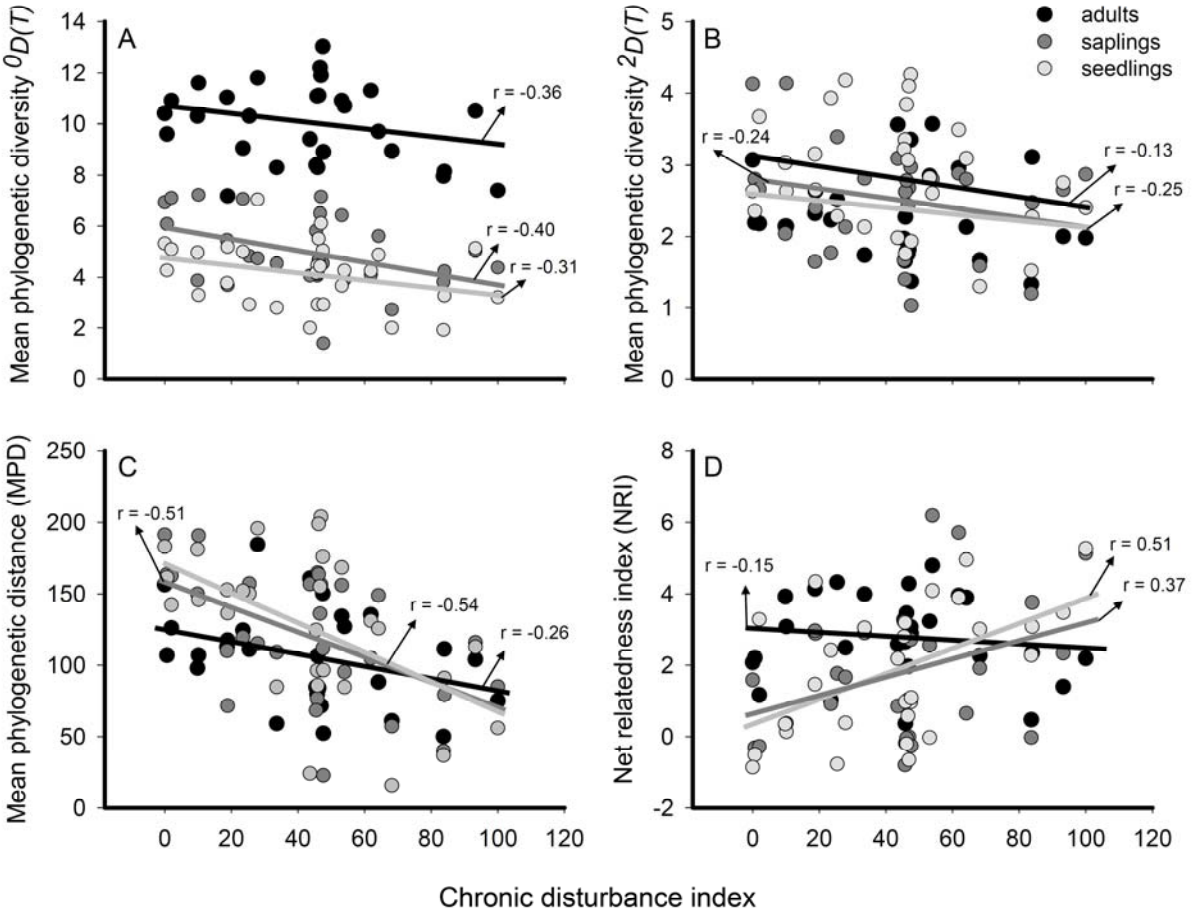
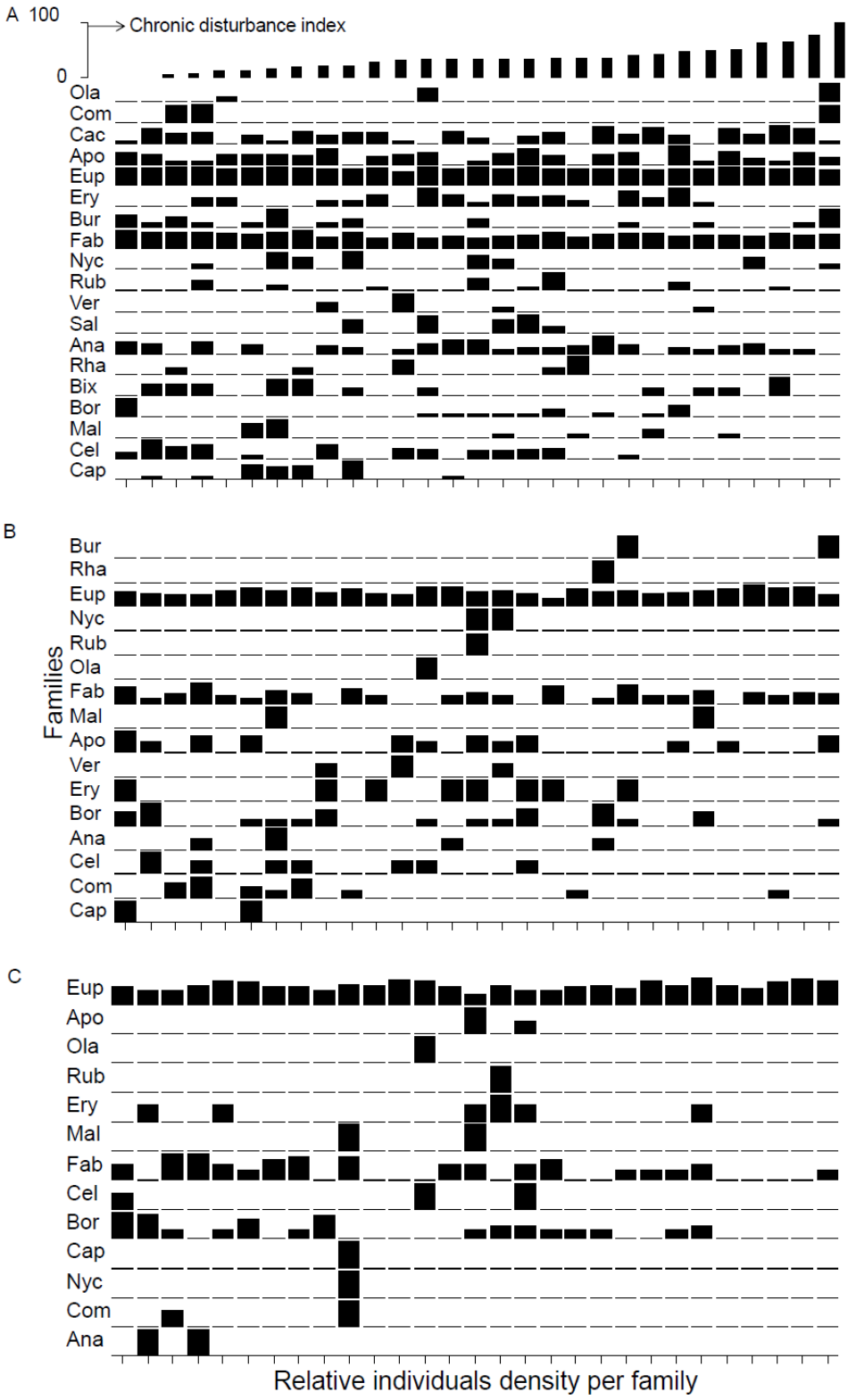

A
B
C
D
adults
saplings
seedlings
Mean phylogenetic diversity $^0D(T)$
Mean phylogenetic diversity $^2D(T)$
Mean phylogenetic distance (MPD)
Net relatedness index (NRI)
Chronic disturbance index
r = -0.36
r = -0.40
r = -0.31
r = -0.24
r = -0.13
r = -0.25
r = -0.51
r = -0.54
r = -0.26
r = -0.15
r = 0.51
r = 0.37

Figure 2.

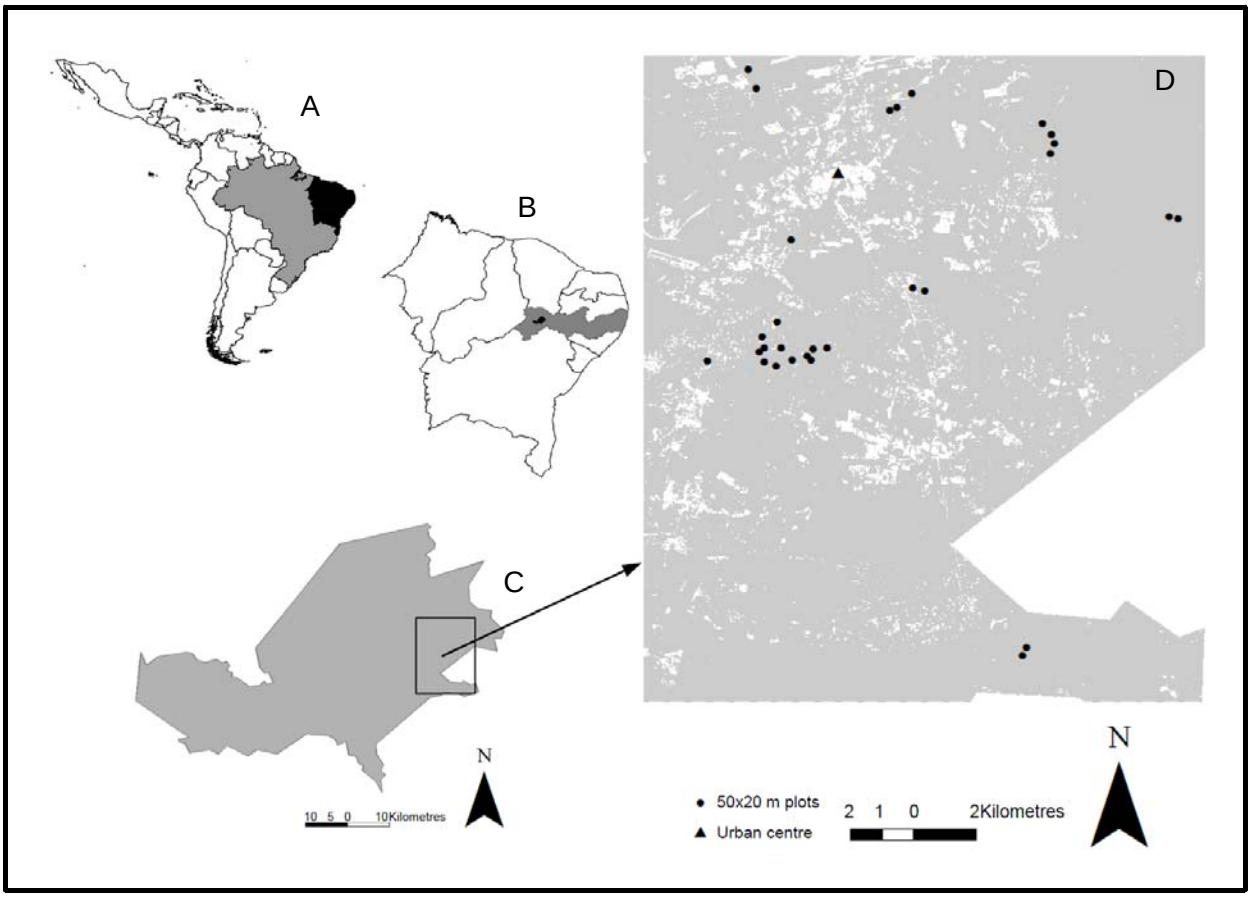

A 100
0
Chronic disturbance index
Ola
Com
Cac
Apo
Eup
Ery
Bur
Fab
Nyc
Rub
Ver
Sal
Ana
Rha
Bix
Bor
Mal
Cel
Cap
B
Families
Bur
Rha
Eup
Nyc
Rub
Ola
Fab
Mal
Apo
Ver
Ery
Bor
Ana
Cel
Com
Cap
C
Eup
Apo
Ola
Rub
Ery
Mal
Fab
Cel
Bor
Cap
Nyc
Com
Ana
Relative individuals density per family

Ecological Archives

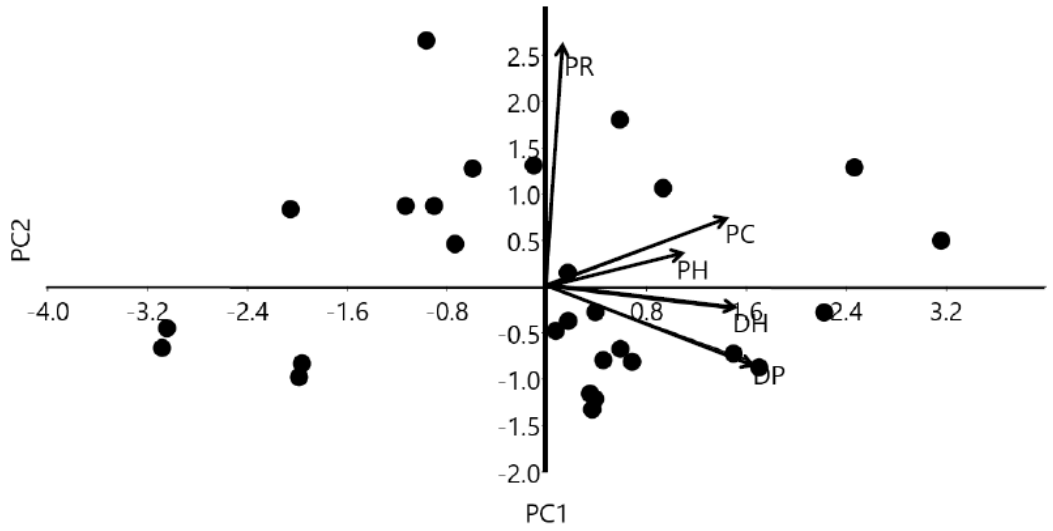
Appendices A, B, C, D, F, G, H, I, J, K, L and a Supplement are available online:

http://dx.doi.org/

Appendix A. Location of the study area in northeastern Brazil (A).We indicate the Parnamirim municipality (in black) within the Pernambuco state (in gray) (B). We also show the study landscape (C) in which we located 29 50 × 20-m plots, and the urban center of Parnamirim (black triangle) (d). The white areas in (D) represent deforested areas.



Appendix B. Principal component analysis biplot illustrating the relationship between the chronic disturbance index (PC1, which explained 41% of variation), the chronic disturbance predictors (DP: density of people; DL: density of livestock; PR: proximity to nearest road; PC: proximity to urban center; PH: proximity to the nearest house) and sample distributions (black circles). Positive values of PC1 scores represent the most chronically disturbed sites, while negative values represent the least disturbed sites.



Appendix C. Correlation matrix showing relationships between chronic disturbance index (CDI) and chronic disturbance predictors (DP: density of people; DL: density of livestock; PR: proximity to nearest road; PC: proximity to urban center; PH: proximity to the nearest house). Cell values correspond to the Pearson's correlation coefficient (below the empty diagonal) and its associated *P*-value (above the diagonal). Bold cases emphasize significant relationships ($P<0.05$).

	PR	PC	DH	DP	DL	CDI
PR		0.967	0.647	0.399	0.487	0.151
PC	-0.008		0.075	**0.014**	0.077	**0.005**
DH	-0.090	0.341		**0.019**	0.595	**0.002**
DP	-0.165	**0.456**	**0.439**		**0.011**	**0.000**
DL	-0.136	0.339	-0.104	**0.472**		**0.000**
CDI	-0.278	**0.744**	**0.553**	**0.865**	**0.610**	

Appendix D. Differences in plot size and sample completeness.

To address this potential problem, we calculated the inventory completeness for each plot and ontogenetic class using the coverage estimator recommended by Chao & Shen (2010). Sample coverage was greater in adults than saplings and seedlings, averaging 98.6% ± 1.1% for adult (mean ± SE), 87.7% ± 1.2% for saplings and 72.6% ± 3.3% for seedling plots. This suggested that our results could be biased by differences in sample completeness among ontogenetic stages (Chao & Shen 2010; Chao & Jost 2012). However, when we correlated plot sample completeness with their respective phylogenetic metrics, no pattern rose. Of the 12 correlations performed (four metrics by three ontogenetic stages), only two were statistically significant [correlations of completeness with $^{0}D(T)$ and MPD for saplings] and even so quite weak ($r < 0.5$). Seedling and adult assemblages, which had the lowest and greatest abundance per plot, respectively, did not show correlation between phylogenetic metrics and sample completeness. To completely discard the influence of sampling completeness, we also correlated the metrics with species richness predicted by rarefaction curves. None but one of the 12 possible correlations between predicted richness and the phylogenetic metrics was statistically significant. The only significant correlation rose between predicted richness and the adult NRI ($r = -0.456$, $p = 0.015$). Based on these analyses we conclude that differences in plot size and their effects on abundance did not significantly affect our results.

Literature cited

Chao, A., and T.J. Shen. 2010. Program SPADE: Species Prediction and Diversity Estimation. Program and User's Guide. CARE, Hsin-Chu, Taiwan.

Chao, A., and L. Jost. 2012. Coverage-based rarefaction and extrapolation: standardizing samples by completeness rather than size. Ecology 93:2533–47.

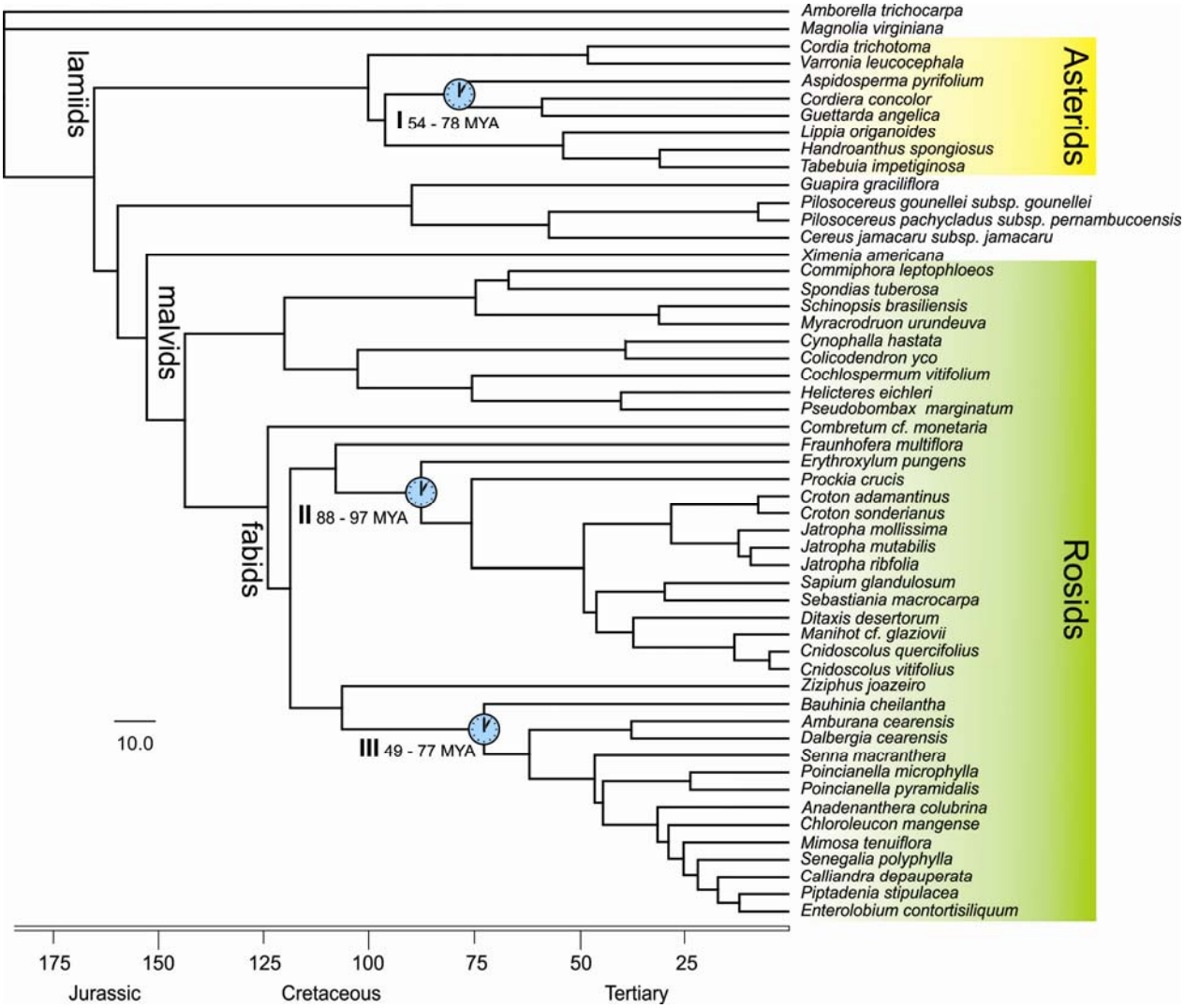
Appendix E. Correlation matrix showing relationships between phylogenetic metrics: ${}^{0}\bar{D}$(T) - mean phylogenetic diversity of total lineages, ${}^{2}\bar{D}$(T) - mean phylogenetic diversity of dominant lineages, MPD - mean phylogenetic distance and, NRI - nearest relatedness index. We can observe a weak relationship between NRI and ${}^{0}\bar{D}$(T), which indicates that the increase of lineages can result in phylogenetic clustering. Cell values correspond to the Pearson's correlation coefficient (below the empty diagonal) and its associated *P*-value (above the diagonal). Bold cases emphasize significant relationships ($P<0.05$). As NRI is a standardized measure of MPD, the increase in clustering degree result in the decrease in phylogenetic distances between the species. We can also observe that the increase in MPD values can be related to the increase of dominant lineages (${}^{2}\bar{D}$(T)).

	${}^{0}\bar{D}$(T)	${}^{2}\bar{D}$(T)	MPD	NRI
${}^{0}\bar{D}$(T)		0.500	0.258	**0.043**
${}^{2}\bar{D}$(T)	0.073		**0.000**	0.969
MPD	0.122	**0.781**		**0.000**
NRI	**0.217**	0.004	**-0.400**	

Appendix F. Methods used to build our time-calibrated phylogeny.

Initially we searched for four DNA regions [ribulose-bisphosphate carboxylase gene (*rbc*L), maturase K (*mat*K), 5.8S ribosomal RNA gene, and *trn*L-*trn*F intergenic spacer (*trn*L-F)] from sequence data available in GenBank and in *Amborella* Genome Database (see Appendix G). When sequence data for a species were not available, we used a randomly chosen alternative species within the genus to estimate the relatedness to that genus (see Appendix F). The effect on branch length of using these substitute species is expected to be minimal given the breadth of phylogenetic sampling (Cadotte et al. 2008, 2009). We used *Amborella trichocarpa* and *Magnolia virginiana* to root the tree and increase the depth of taxon sampling (Burns and Strauss 2011). Sequences were aligned for each region independently and later combined into a single supermatrix using Geneious version 7.1.4 (Kearse et al. 2012). The Bayesian inference search was performed using Mr. Bayes v3.1.2 (Ronquist and Huelsenbeck 2003), 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. We then created a time-calibrated phylogeny adopting fossil calibration points derived from Bell et al. (2010) using BEAST v1.8.2 (Drummond et al. 2012). 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.

Bellow we show the time-calibrated tree which illustrates our regional phylogeny and the tree calibration points derived from Bell et al. (2010): I Gentianales (54-78 MY), (II) Malphighiales (88-97 MY) and Fabaceae (49-77 MY).



Literature cited

Bell, C. D., D. E. Soltis, and P. S. Soltis. 2010. The age and diversification of the angiosperms re-revisited. American Journal of Botany 97:1296–303.

Burns, J. H., and S. Y. Strauss. 2011. More closely related species are more ecologically similar in an experimental test. Proceedings of the National Academy of Sciences U.S.A. 108:5302–5307.

Cadotte, M. W., B. J. Cardinale, and T. H. Oakley. 2008. Evolutionary history and the effect of biodiversity on plant productivity. Proceedings of the National Academy of Sciences U.S.A. 105:17012–17017.

Cadotte, M. W., J. Cavender-Bares, D. Tilman, and T. H. Oakley. 2009. Using phylogenetic, functional and trait diversity to understand patterns of plant community productivity. PLoS ONE 4:e5695.

Drummond, A. J., M. A. Suchard, D. Xie, and A. Rambaut. 2012. Bayesian phylogenetics with BEAUti and the BEAST 1.7. Molecular Biology and Evolution 29:1969–1973.

Kearse, M., R. Moir, A. Wilson, S. Stones-Havas, M. Cheung, S. Sturrock, S. Buxton, A. Cooper, S. Markowitz, C. Duran, T. Thierer, B. Ashton, P. Mentjies, and A. Drummond. 2012. Geneious basic: an integrated and extendable desktop software platform for the organization and analysis of sequence data. Bioinformatics 28:1647–1649.

Ronquist, F., and J. P. Huelsenbeck. 2003. MRBAYES 3: Bayesian phylogenetic inference under mixed models. Bioinformatics 19:1572–1574.

Appendix G. Sequences used to estimate the Bayesian tree (Appendix D). We used four DNA regions maturase K (*mat*K), 5.8S ribosomal RNA gene (5.8S), ribulose-1,5-carboxylase/bisphosphate gene (*rbc*L), and intergenic spacer (*trn*L-*trn*F). Data from sequences available in GenBank and in *Amborella* Genome Database (http://amborella.huck.psu.edu/shortstack). NA – Cases where information was absent for the species and its genera.

Species	Species used for matK	matK	Species used for 5.8S	5.8S	Species used for rbcL	rbcL	Species used for trnL-trnF	trnL-trnF
Amborella trichocarpa	*Amborella trichocarpa*	AF543721	*Amborella trichocarpa*	AmTr_v1.0_scaffold 03396	*Amborella trichocarpa*	L12628	*Amborella trichocarpa*	AY14532
Amburana cearensis	*Amburana cearensis*	JX846614	*Amburana cearensis*	KJ813615	NA	NA	*Amburana cearenses*	EF466144
Anadenanthera colubrina	*Anadenanthera colubrina*	EU812064	*Anadenanthera colubrina*	JQ910930	*Anadenanthera peregrina*	KJ082119	*Anadenanthera peregrina*	EU811875
Aspidosperma pyrifolium	*Aspidosperma pyrifolium*	JX850029	*Aspidosperma marcgravianum*	FJ037794	*Aspidosperma cylindrocarpon*	DQ660633	*Aspidosperma quebracho-blanco*	AF214165
Bauhinia cheilantha	*Bauhinia tomentosa*	AY386893	*Bauhinia cheilantha*	DQ787410	*Bauhinia guianensis*	JQ626034	*Bauhinia forficata subsp. pruinosa*	FJ801053
Calliandra depauperata	*Calliandra rhodocephala*	JQ587534	*Calliandra depauperata*	JX870682	*Calliandra vaupesiana*	KR082842	*Calliandra ulei*	JX870815

Cereus jamacaru subsp. jamacaru	*Cereus alacriportanus*	AY015313	*Cereus alacriportanus*	AY064344	*Cereus fernambucensis*	AY875240	*Cereus aethiops*	JQ779665
Chloroleucon mangense	*Chloroleucon mangense*	AY386921	*Chloroleucon mangense*	EF638183	NA	NA	*Chloroleucon mangense*	AF278517
Cnidoscolus quercifolius	*Cnidoscolus aconitifolius*	AB268041	NA	NA	*Cnidoscolus aconitifolius*	AB267937	*Cnidoscolus tubulosus*	EU518895
Cnidoscolus vitifolius	*Cnidoscolus spinosus*	KM219793	NA	NA	*Cnidoscolus urens var. stimulosus*	AY794874	*Cnidoscolus albomaculatus*	EU518894
Cochlospermum vitifolium	*Cochlospermum vitifolium*	JQ587264	NA	NA	*Cochlospermum vitifolium*	JQ591114	NA	NA
Colicodendron yco	*Capparis spinosa*	AY491650	*Capparis acutifolia*	KP092569	*Capparis spinosa*	AY167985	*Capparis spinosa*	AY122422
Combretum cf. *monetaria*	*Combretum elaeagnoides*	KC130317	*Combretum fragrans*	FJ381754	*Combretum apiculatum subsp. apiculatum*	KC158546	*Combretum paniculatum*	AY905455
Commiphora leptophloeos	*Commiphora schlechteri*	KF147383	*Commiphora schimperi*	JN882702	*Commiphora falcata*	GU246030	*Commiphora leptophloeos*	KM516816

Cordia trichotoma	*Cordia torrei*	JX517572	*Cordia revoluta*	HM443775	*Cordia trichotoma*	EU599827	*Cordia lutea*	KF158215
Cordiera concolor	*Alibertia myrciifolia*	KF981358	*Gardenia hansemannii*	HM443775	*Alibertia myrciifolia*	KF981281	*Alibertia edulis*	AF201029
Croton adamantinus	*Croton dichogamus*	KR735055	*Croton guildingii subsp. tiarensis*	AY971254	*Croton maestrense*	EF405857	*Croton grangerioides*	KP878425
Croton sonderianus	*Croton menyharthii*	JF270729	*Croton cupulifer*	EU478063	*Croton setiger*	EF405853	NA	NA
Cynophalla hastate	*Cynophalla hastata*	KJ012557	*Capparis acutifolia*	KP092569	*Cynophalla hastata*	KJ082259	NA	NA
Dalbergia cearensis	*Dalbergia monetaria*	KJ593846	*Dalbergia miscolobium*	EF451070	*Dalbergia hupeana*	U74236	*Dalbergia hupeana*	KP338261
Ditaxis desertorum	*Ditaxis montevidensis*	AB233761	*Ditaxis guatemalensis*	DQ997792	*Ditaxis montevidensis*	AB233865	*Ditaxis simoniana*	AY794742
Enterolobium contortisiliquum	*Enterolobium contortisiliquum*	JX495708	*Enterolobium contortisiliquum*	EF638190	*Enterolobium contortisiliquum*	JX571823	*Enterolobium timbouva*	JX870876

Erythroxylum pungens	*Erythroxylum rufum*	KJ012581	*Erythroxylum amplifolium*	DQ787423	*Erythroxylum confusum*	L13183	*Erythroxylum sp.*	KC428510
Fraunhofera multiflora	*Fraunhofera multiflora*	JF410097	NA	NA	NA	NA	*Fraunhofera multiflora*	JF410055
Guapira graciliflora	*Guapira fragrans*	KJ012616	*Guapira fragrans*	JX844233	*Guapira fragrans*	KJ082334	NA	NA
Guettarda angelica	*Guettarda scabra*	KJ012627	*Guettarda uruguensis*	DQ063692	*Guettarda acreana*	JQ626041	*Guettarda speciosa*	KJ906574
Handroanthus spongiosus	*Handroanthus albus*	KF981308	*Handroanthus impetiginosus*	JX856460	*Handroanthus albus*	KF981207	*Handroanthus guayacan*	EF105094
Helicteres eichleri	*Helicteres baruensis*	JQ589303	*Helicteres guazumifolia*	AF233300	*Helicteres angustifolia*	AY082356	NA	NA
Jatropha mollissima	*Jatropha curcas*	KJ663789	*Jatropha gossypiifolia*	KF551972	*Jatropha curcas*	JX571853	*Jatropha integerrima*	AY794685
Jatropha mutabilis	*Jatropha integerrima*	AB233775	*Jatropha integerrima*	EU340795	*Jatropha integerrima*	AY794902	NA	NA
Jatropha ribfolia	*Jatropha podagrica*	KJ150223	*Jatropha curcas*	EU700455	*Jatropha zeyheri*	JQ025058	NA	NA
Lippia origanoides	*Lippia*	HM853860	*Lippia salsa*	FJ867399	*Lippia javanica*	JX572735	*Lippia sidoides*	AY945838

	integrifolia							
Magnolia virginiana	*Magnolia virginiana*	GQ248153	*Magnolia virginiana*	DQ499097	*Magnolia virginiana*	GQ248639	*Magnolia virginiana*	AY145354
Manihot cf. *glaziovii*	*Manihot esculenta*	JQ587466	*Manihot esculenta*	GU214953	*Manihot esculenta*	AB233880	*Manihot tristis*	EU518925
Mimosa tenuiflora	*Mimosa tenuiflora*	JX850057	*Mimosa guatemalensis*	AF458784	*Mimosa strigillosa*	KJ773686	*Mimosa quitensis*	AF278514
Myracrodruon urundeuva	*Astronium graveolens*	JQ586471	*Myracrodruon urundeuva*	DQ787397	*Astronium ulei*	JQ625995	*Myracrodruon urundeuva*	AY594560
Pilosocereus gounellei subsp. *Gounellei*	*Pilosocereus rosae*	JX683850	NA	NA	NA	NA	*Pilosocereus chrysacanthus*	HM041340
Pilosocereus pachycladus subsp. *Pernambucoensis*	*Pilosocereus floccosus*	JX683847	NA	NA	NA	NA	*Pilosocereus aureispinus*	JN035566
Piptadenia stipulacea	*Piptadenia flava*	JQ587930	NA	NA	*Piptadenia flava*	JQ592113	*Piptadenia moniliformis*	AF278496
Poincianella microphylla	*Caesalpinia coriaria*	JQ587523	*Poincianella pluviosa*	KP003693	*Poincianella mexicana*	JX856662	*Poincianella eriostachys*	EF177389

Poincianella pyramidalis	*Poincianella pyramidalis*	JX850053	*Poincianella gaumeri*	KP003692	*Caesalpinia calycina*	AM234236	*Poincianella caladenia*	EF177383
Prockia crucis	*Prockia crucis*	EF135588	NA	NA	*Prockia crucis*	JQ592133	*Prockia costaricensis*	AY757056
Pseudobombax marginatum	*Pseudobombax septenatum*	GQ982072	*Pseudobombax marginatum*	AF028521	*Pseudobombax septenatum*	GQ981847	*Pseudobombax croizatii*	HQ696749
Sapium glandulosum	*Sapium glandulosum*	JQ589779	*Sapium sebiferum*	AF537586	*Sapium glandulosum*	AY794841	*Sapium glandulosum*	AY794626
Schinopsis brasiliensis	*Schinopsis brasiliensis*	AY594477	*Schinopsis brasiliensis*	AY531203	NA	NA	*Schinopsis brasiliensis*	KP055559
Sebastiania macrocarpa	*NA*	NA	*Sebastiania cornuta*	AF537587	*Sebastiania klotzschiana*	AY794850	*Sebastiania hexaptera*	AY794645
Senegalia polyphylla	*Senegalia tenuifolia*	KJ593761	*Senegalia caffra*	JQ265905	*Senegalia tenuifolia*	KJ594092	*Senegalia berlandieri*	HM020797
Senna macranthera	*Senna macranthera var. nervosa*	AM086873	*Senna hirsuta*	KJ638428	*Senna macranthera var. micans*	JX856680	*Senna pleurocarpa*	AF367007
Spondias tuberosa	*Spondias mombin*	AY594480	*Spondias mombin*	AF445882	*Spondias tuberosa*	KP774626	*Spondias tuberosa*	GU943750

Tabebuia impetiginosa	*Tabebuia impetiginosa*	JQ587045	*Tabebuia impetiginosa*	JX497689	*Tabebuia impetiginosa*	JQ590850	*Tabebuia impetiginosa*	EF105097
Varronia leucocephala	*Varronia guanacastensis*	JQ589896	*Varronia revoluta*	HM443774	*Varronia bullata*	KF158132	*Varronia bullata*	KF158211
Ximenia Americana	*Ximenia americana*	KJ012821	*Ximenia americana*	DQ333869	*Ximenia americana*	DQ790149	*Ximenia americana*	DQ340620
Ziziphus joazeiro	Ziziphus rignonii	KJ012831	Ziziphus lloydii	JN900312	*Ziziphus nummularia*	JX856807	*Ziziphus glabrata*	AJ225799

Appendix H. Results of Shapiro-Wilk tests used to test the normal distribution of response variable errors. Response variables: ($^{0}\bar{D}$(T) - mean phylogenetic diversity of total lineages, $^{2}\bar{D}$(T) - mean phylogenetic diversity of dominant lineages, MPD - mean phylogenetic distance and, NRI - nearest relatedness index). Model factors: CDI - chronic disturbance, OS - ontogenetic stage, A - stem abundance in the plot.

Model	*W*	*P*
$^{0}\bar{D}$(T) = CDI + OS + A + OS×CDI	0.990	0.752
$^{2}\bar{D}$(T) = CDI + OS + A + OS×CDI	0.973	0.07
MPD= CDI + OS + A + OS×CDI	0.986	0.506
NRI= CDI + OS + A + OS×CDI	0.987	0.558

Appendix I. Differences in species richness and stems abundance (mean ± SD) among ontogenetic stages (adults, saplings and seedlings). Different letters indicate significant differences among stages (Tukey tests).

Ontogenetic stage	Species richness	Stem abundance
Adults	$18.5^{a} \pm 3.6$	$362^{a} \pm 92.1$
Saplings	$6.7^{b} \pm 2.2$	$11.6^{b} \pm 6.5$
Seedlings	$5.1^{b} \pm 1.8$	$10.6^{b} \pm 3.5$

Appendix J. Model coefficients for each factor model included in the linear models fitted to test the effect of chronic disturbance index on phylogenetic diversity metrics of plant assemblages (adults, saplings and seedlings) from the Brazilian Caatinga, Parnamirim municipality, Pernambuco, Brazil. Model factors codes: CDI – chronic disturbance, OS – ontogenetic stage, A – individuals abundance in each plot. Significance level ($^{n.s.}P > 0.05$;* $P < 0.05$).

	Phylogenetic metrics							
	$^{0}\overline{D}$(T)		$^{2}\overline{D}$(T)		MPD		NRI	
Model factors	Estimate	t - ratio	Estimate	t - ratio	Estimate	t - ratio	Estimate	t - ratio
CDI	-0.014*	-2.58	-0.007*	-2.22	-0.804*	-4.98	0.001*	2.57
A	$0.005^{n.s.}$	1.69	$-0.002^{n.s.}$	-1.12	$-0.047^{n.s.}$	-0.53	$-0.004^{n.s.}$	-1.15
CDI × OS (adults)	$0.007^{n.s.}$	0.85	$-0.001^{n.s.}$	-0.07	$0.290^{n.s.}$	1.23	-0.02*	-2.99
CDI × OS (saplings)	$-0.007^{n.s.}$	-0.90	$0.000^{n.s.}$	0.11	$-0.04^{n.s.}$	-0.21	$0.00^{n.s.}$	1.08
CDI × OS (seedlings)	$-0.000^{n.s}$	-0.00	$-0.000^{n.s.}$	-0.04	$-0.244^{n.s.}$	-1.09	0.01*	2.07

Appendix K. Results of NODESIG procedure showing clades that contributed to non-random phylogenetic structure in adult, sapling and seedling communities. With this method we identified clades that contributed significantly to non-random phylogenetic structure, considering each ontogenetic stage. Based on a randomization test, NODESIG assesses whether a particular NODE in the sample has significantly more or less descendent taxa than expected by a null model (indicated as SIG in the Tables). **Abbreviations:** A = adult; Sa = sapling; Se = seedlings. **References:** Webb, C.O., Ackerly, D.D. & Kembel, S.W. (2008) Phylocom: software for the analysis of phylogenetic community structure and character evolution. Bioinformatics, **24**, 2098–2100.

Adult assemblage				**Sapling assemblage**				**Seedling assemblage**			
Plot	*Disturbance value*	*Node*	*SIG*	*Plot*	*Disturbance value*	*Node*	*SIG*	*Plot*	*Disturbance value*	*Node*	*SIG*
1	53.9	30, 50	more	1	53.9	30, 50,	more	1	53.9	30, 50, 53, 57, 58, 59	more
2	25.3	30, 50	more	2	25.3	51, 53, 57,58,59	more	2	25.3	51, 53, 57, 58, 59	more
3	53.1	28, 30, 50, 80	more	3	53.1	83	more	5	45.4	53	more
5	45.4	30, 50, 58	more	5	45.4	51, 53	more	7	61.8	53, 57, 58, 59	more
6	43.5	30, 50, 82	more	7	61.8	53, 57, 58, 59, 62	more	8	33.5	51, 53	more
7	61.8	30, 50, 78, 82	more	8	33.5	50, 51, 53	more	9	64.4	89	more
10	18.8	30, 53	more	9	64.4	89	more	10	18.8	89	more
11	47.4	30, 50, 78, 80, 82	more	10	18.8	89	more	11	47.4	88, 22	more
12	46.8	58	more	11	47.4	86, 88	more	20	46.1	59	more

15	9.8	28, 30, 50, 78, 80, 88	more	20	46.1	59	more	23	27.8	30	more
17	0.6	30	more	23	27.8	30	more	24	83.9	30, 53, 57, 75	more
19	47.5	28, 30, 50	more	24	83.9	30, 53, 57, 75	more	25	100	30, 50, 51, 53, 53,57, 58, 62	more
20	46.1	50	more	25	100	30, 50, 51, 53, 57 73	more	27	93.2	53	more
21	1.9	39	more	27	93.2	53	more	28	83.6	86, 88	more
23	27.8	28, 30	more	28	83.6	82	more	29	18.1	58, 59	more
23	27.8	7	less								
24	83.9	73	more								
26	68.1	73	more								
29	18.7	28, 30, 86	more								

Node codes

Assemblages	*Node*	*Clade*
A/	7	Lamiids (Gentianales and Lamiales)
A/	28	Core Eudicots
A/Sa/Se	30	Rosids (Fabids and Malvids)
A	39	Malvales to Brassicales
A/Sa/Se	50	Fabids (Celastrales, Malpighiales, Fabales and Rosales)
Sa/Se	51	Celastrales to Malphigiales
A/Sa/Se	53	Malphighiales
Sa/Se	57	Euphorbiaceae
A/Sa/Se	58	*Croton* to *Jathopha*
Sa/Se	59	*Croton*
Sa/Se	62	*Jatropha*
A/Sa	73	*Manihot* and *Cnidoscolus*
Sa/Se	75	*Cnidoscolus*
A	78	Fabids
A	80	Fabaceae
A/Sa/Se	82	Papilionoideae and Mimosoids

Sa	83	*Amburana* to *Dalbergia*
A/Sa/Se	86	Palpilionoideae
A/Sa/Se	88	Mimosoids
Sa/Se	89	*Poncianella*

Appendix L. Correlations between the chronic disturbance index and the abundance of each species for adult (A), sapling (B) and seedling (C) plant assemblages. Gray rectangles highlight species abundances that are significantly ($p < 0.05$) higher or lower due to chronic disturbance.