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Notes:
Rapid decay of tree-community composition in Amazonian forest fragments


State University, Baton Rouge, LA 70803

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Forest fragmentation is considered a greater threat to vertebrates than to tree communities because individual trees are typically long-lived and require only small areas for survival. Here we show that forest fragmentation provokes surprisingly rapid and profound alterations in Amazonian tree-community composition. Results were derived from a 22-year study of exceptionally diverse tree communities in 40 1-ha plots in fragmented and intact forests, which were sampled repeatedly before and after fragment isolation. Within these plots, trajectories of change in abundance were assessed for 267 genera and 1,162 tree species. Abrupt shifts in floristic composition were driven by sharply accelerated tree mortality and recruitment within ~100 m of fragment margins, causing rapid species turnover and population declines or local extinctions of many large-seeded, slow-growing, and old-growth taxa; a striking increase in a smaller set of disturbance-adapted and abiotically dispersed species; and significant shifts in tree size distributions. Even among old-growth trees, species composition in fragments is being restructured substantially, with subcanopy species that rely on animal seed-dispersers and have obligate outbreeding being the most strongly disadvantaged. These diverse changes in tree communities are likely to have wide-ranging impacts on forest architecture, canopy-gap dynamics, plant–animal interactions, and forest carbon storage.

Results and Discussion

At least during the initial decades after isolation, edge effects (i.e., the diverse environmental changes associated with the abrupt, artificial boundaries of forest fragments) appear to be the most important drivers of ecological change in fragmented Amazonian forests. Of particular significance is that tree mortality is chronically elevated within ~100 m of forest edges as a result of greater desiccation stress and wind turbulence. Large (>60 cm in diameter) trees are especially vulnerable, dying nearly three times faster near edges than in forest interiors. Rapid tree death reduces forest biomass and leads to increased treefall gaps, wood debris, fine litter, and climbing vines in fragmented forests.

At the outset, we estimated the rate of change in tree species richness for each of our 40 plots by regressing the number of species recorded in each census against the time in years since the initial census and then using the slope term as our response variable (supporting information (SI) Tables 1–3). Rates of change did not differ significantly (P = 0.22, Mann–Whitney U-test) between forest edges (mean ± SD: 0.00 ± 1.23 species ha⁻¹ year⁻¹) and interiors (−0.36 ± 0.58 species ha⁻¹ year⁻¹), or among 1-, 10-, and 100-ha fragments and intact forest (P = 0.33, Kruskal–Wallis test). Results were similar (P > 0.24 in all tests) when rates of change were based on Fisher’s alpha diversity index (SI Tables 1 and 2), which is insensitive to variation in sample size. Thus, at least during the initial two decades after fragmentation, tree species richness did not decline significantly in edge or fragment plots.

These simple patterns, however, obscure many striking changes in tree communities. First, the density of trees fluctuated considerably over time in many fragment plots (SI Tables 1–3), especially near forest edges, as a result of major episodes of tree mortality from windstorms or droughts, often followed by large pulses of tree recruitment. As a consequence, coefficients of variation (CV) in tree number were much higher (P < 0.0001, Mann–Whitney U test) for individual edge plots (6.0 ± 4.8%) than for interior plots (1.7 ± 1.2%).

Second, the rate at which species disappeared (being absent from samples of ≥10-cm-diameter trees) rose dramatically in forest fragments on one of the world’s most diverse tree floras.
edge and fragment plots (Fig. 1a). These losses were largely countered by elevated recruitment of new species, leading to rapid species turnover (Fig. 1b). As a result of such volatility, species richness fluctuated markedly over time in individual edge plots, which had significantly ($P < 0.005$; Mann–Whitney $U$ test) higher CVs in species richness (3.5 ± 2.4%) than did interior plots (1.5 ± 0.7%). Hence, despite the fact that species number did not decline consistently in fragments, the tree communities were much less stable, with accelerated species losses and turnover and temporally varying species richness (SI Tables 1–3).

Third, the size distributions of trees changed markedly in edge plots, with small (10- to 20-cm diameter) trees increasing in number, whereas trees in all larger size classes declined (Fig. 2). These changes were highly significant in edge plots ($\chi^2 = 56.4$, df $= 5$, $P < 0.00001$; $\chi^2$ test for independence) and nonsignificant in forest-interior plots ($\chi^2 = 1.58$, df $= 5$, $P = 0.90$) (see SI Table 4). Because of the large proliferation of small trees, total tree density increased in many (13 of 19) edge plots but varied little over time in the interior plots.

Finally, fragmentation caused important changes in species composition and abundances. We initially assessed these changes with Euclidean distances (19) to estimate floristic dissimilarity between the initial and final abundances of all 267 tree genera in our plots. We found much larger Euclidean distances near forest edges (54.5 ± 28.8) than in forest interiors (22.9 ± 6.8), revealing a breakdown of compositional stability in many fragment plots (Fig. 3).
positions in ordination space that reflect their relative floristic composition, such that changes in the position of individual plots over time describe trajectories of change in floristic composition. The ordination analysis revealed three major gradients in floristic composition and explained 67% of the total variation in the dataset (see SI Table 6). Axis 3 did not differ significantly between edge and interior samples and was not considered further.

Although one would expect fragment plots, because of their considerable instability, to have longer trajectories than intact-forest plots, there is no a priori reason to assume that the fragment plots would move in any consistent direction. Neutral-community models, for example, predict largely random deviations from initial species composition, with communities becoming increasingly dominated after fragmentation by locally abundant species (2, 21).

However, most fragment and edge plots exhibited similar trajectories of change, increasing along both the first and second ordination axes (Fig. 4). In contrast, intact-forest plots clustered around zero (little or no change) on both axes. The likelihood of this pattern arising by chance is minuscule ($P = 0.0001$, $\chi^2 = 22.83$, df = 4; Fisher’s log-probability test).

A key driver of these nonrandom compositional changes is elevated tree mortality in forest fragments. This is illustrated by highly significant relationships between the first two ordination vectors, which describe trajectories of floristic change in plots, and the mean rate of tree mortality in each plot (axis 1: $P < 0.0001$, $R^2 = 49.4\%$; $F_{1,38} = 37.15$; axis 2: $P < 0.0001$, $R^2 = 42.4\%$, $F_{1,38} = 27.98$; linear regressions). Even among edge and fragment plots, tree mortality varied considerably as a result of factors such as varying local topography, the spatial patchiness of windstorms, and differing distances of plots from the forest edge (14, 22), and these differences account for substantial variation in the floristic trajectories of different plots. In addition, spatial variability in the modified vegetation surrounding our fragments (pastures and different types and ages of regrowth forest), which provides a seed rain of disturbance-adapted tree dispersers, has obligate outbreeding systems (dioecious, gynodioecious, or androdioecious species), and tend to be relatively abundant in intact forest (see SI Text: Univariate Tests of Old-Growth Genera). Hence, even among old-growth species, ecological and life-history differences often cause large variations in responses to habitat fragmentation. Edge effects probably underlay at least some of these changes, given that many old-growth subcanopy trees are slow-growing and physiologically specialized for the low-light conditions of the intact-forest understory (24, 25) and thus are likely to be poorly adapted for exploiting edge conditions. However, the declines of genera that require obligate outbreeding and animal seed-dispersers suggest that losses of key pollinators and seed dispersers in fragments (26–31) could also be affecting tree communities.

Our findings suggest that habitat fragmentation will have pervasive, long-term impacts on the species and functional composition of Amazonian forests. Trees that increase in abundance in fragments are very different at higher taxonomic levels than are trees that decline (SI Fig. 7). These changes could affect many aspects of forest ecology and functioning. Wood density, for example, is strongly and negatively related to the responses of tree genera to fragmentation (Fig. 5), suggesting that compositional shifts are reducing carbon storage in fragmented forests, above and beyond the carbon losses that result from elevated tree mortality (16, 17). Compositional changes in tree communities are also likely to affect forest architecture, canopy-gap dynamics, nutrient cycling, and plant–animal interactions in fragmented forests (9–11, 26–31).

A key finding of this study is that habitat fragmentation provokes surprisingly rapid changes in the composition of Amazonian tree communities. In less than two decades after fragmentation, nearly a fifth of the more-common tree genera have declined significantly ($P < 0.01$) in abundance, whereas over a tenth of the common genera have increased significantly. Such abrupt shifts are surprising. First, individuals of many Amazonian tree species can live for centuries or even millennia (32, 33), at least in intact old-growth forests, and thus one might expect
threat to tropical biodiversity, given the myriad ecological linkages among rainforest trees and their many dependent animal, plant, and fungal species.

Methods

Study Design. The Biological Dynamics of Forest Fragments Project is a 1,000-km² experimental landscape in central Amazonia. Within this landscape, nine forest fragments ranging from 1 to 100 ha in area were isolated from nearby intact forest during the early 1980s by clearing and burning the intervening vegetation to create cattle pastures. Some of the pastures have been abandoned and now support 2- to 15-year-old regrowth forest. Detailed descriptions of the project, including its study design, fragment histories, the matrices of modified vegetation surrounding fragments, and the methods used for censusing and identifying trees, are provided elsewhere (e.g., refs. 12–18).

Before fragment isolation, permanent 1-ha plots were established within each fragment and in eight comparable sites in nearby intact forest. The present study incorporates tree demography data from 40 1-ha plots, 24 of which were located in forest fragments or near forest edges (plot center <100 m from the nearest edge), whereas the other 16 were in intact-forest interiors (170–3,000 m from the edge). After an initial, exhaustive inventory of tree communities, each plot was resampled after fragmentation at typical intervals of 4–6 years to assess tree mortality, damage, and growth, and the recruitment of new trees (14–16). Altogether, the fates of nearly 32,000 trees were followed for periods of up to 18 years (mean = 14.7 years).

Species Loss, Gain, and Turnover. On average, 95.3% of all trees in each plot were identified to the species or morphospecies level; nonidentified trees were not included in species-level analyses. For each plot, mean rates of species loss (% year⁻¹) were derived by first calculating, for each census interval, ([N(t)/N(0)]/t) × 100, where N(t) is the number of local extinctions during the interval, N(0) is the number of species at the beginning of the interval, and t is the census duration in years. Data from multiple censuses of each plot were then weighted by census duration and averaged. Rates of species gain were calculated similarly, except that N(t) was replaced by N(t)g (number of new species during the interval) and N(0) was replaced by Nt (total number of species at the end of the interval). Species turnover for each interval was [(N(t) + N(t)g)/(N(t) + N(t)g)] × 100, with data for multiple intervals weighted by census duration and averaged as above.

Floristic Composition. Analyses of floristic composition were conducted at the genus level, rather than the species level, because this greatly reduced the number of rare taxa that can confound statistical comparisons [88% of tree species in our study area have a mean density of <1 individual (≥10 cm in diameter at breast height) per hectare]. Several studies have shown that Amazonian and other tropical trees tend to show a high degree of ecological and life-history similarity at the genus level (45–50), although certain genera, such as Inga, are relatively more variable. The abundances of tree genera were quantified by using importance values (19), which combine relativized measures of density and basal area for each taxon and provide a more representative measure of the contribution of each genus to forest stands than do either density or basal-area data alone. (Frequency data were not incorporated into the importance values because the values were generated for individual plots.)

Changes in Tree Abundance. Bootstrapping, a robust statistical method that makes no assumptions about the underlying data distributions, was used to test for changes in abundances of tree genera in forest fragments. Our analysis focused on plots in the vicinity of fragment edges (plot center <100 m from the nearest edge) because plots deep in the interiors of large fragments...
to genera initially present in at least five plots. For taxa occurring in a small number of plots, we restricted the analysis to genera with at least 1,000 replicates, the 5th and 995th ranking values of which were taken as the 95% confidence limits. Observed values of A that fell outside this range were considered significant at the P ≤ 0.01 level (using a two-tailed test). Because this method is less reliable for taxa occurring in a small number of plots, we restricted analyses to genera initially present in at least five plots.

**Ordination and Vectors of Floristic Change.** An ordination analysis was used to assess trajectories of change in floristic composition for each plot, based on repeated censuses of all tree genera. Nonmetric multidimensional scaling was used, with Sorensen's distance metric and untransformed tree-abundance data. Ran- domization tests were used to determine the number of significant axes in the analysis. For each 1-ha plot and ordination axis, plot trajectories were calculated by regressing the ordination distance metric against time (the same set of plots was used to find both N and N0). From 1,000 replicates, the 5th and 995th ranking values of A were calculated at random with replacement, and with A calculated each time (the same set of plots was used to find both N1 and N0).

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