

Effects of Forest Changes after the Abandonment of Slash-and-Burn Cultivation on the Beetle Diversity in Sarawak, Malaysia

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Introduction

Human impacts on the biodiversity of tropical forests are a widespread concern. To date, several studies have estimated these impacts by using various kinds of insect as indicators (e.g., Lawton et al. 1998; Liow et al. 2001). Such insect indicators have revealed a loss of species in secondary forests and cultivated fields compared to the original species diversity in tropical primary forests (e.g., Chey et al. 1997; Vasconcelos et al. 2000; Davis et al. 2001).

Slash-and-burn agriculture is an important and problematic human impact on forests, leading to significant changes. Around the primary forest of Sarawak, Malaysia, various kinds of forests have developed that represent different developmental stages after the abandonment of slash-and-burn cultivation. Microhabitat structures such as canopy openness, tree species richness, and tree density differ among these forests (Nakagawa et al. 2006). Have these forest changes affected on the insect diversity? Unfortunately, the effects of the different ages of the regenerated forests that resulted from the abandonment of slash-and-burn cultivation on insect diversity are poorly understood.

Since beetles exhibit extreme diversity in form and function, we chose the diversity of this taxon as a useful indicator of the effects of forest changes on biodiversity. In this study, we estimated the species richness, abundance, and composition of beetle assemblages in primary forests and in forests at different stages of regeneration after the abandonment of slash-and-burn cultivation.

Methods

Study Site

The study was conducted from August to September 2003 in and around Lambir Hills National Park, Sarawak, Malaysia (4°20'N, 113°50'E, 150 to 200 m a.s.l.). We established 12 study plots (100x20 m) in each of six forest types representing different stand ages: primary forest (plots H2 and H5), fragmented primeval forest (P2, P7), new fallow (1 year after abandonment; B1, B4), young fallow (5 to 6 years after abandonment; T1, T4), old fallow (>20 years after abandonment; F4, F5), and rubber plantation (G0, G9). Details of the study plots are provided by Nakagawa et al. (2006).

Insect Collections

The beetles were collected in the 12 study plots using a net with a 150-cm stretch at its longest extent. At

each plot, we selected 100 thickets and swung a net 10 times in each thicket so that the sweeping covered ca. 196.25 m² foliage in total at each plot. The collected beetles were sorted to the family and morphospecies level on the basis of external characteristics.

Diversity and Similarity indices

Simpson's index of diversity (Lande 1996) was adopted to understand what degrees of the beetle diversity were at the 12 study plots. We also calculated Morishita's similarity index (C_s) (Morishita 1959) to assess the similarity of the chrysomelid fauna between pairs of plots in all combinations of the 12 study plots.

Results and Discussion

Beetle family composition, species richness, and abundance

Of the 166 coleopteran families listed by Lawrence and Newton (1995), 54 families were recorded in the 12 study plots. In terms of the number of species, Chrysomelidae was the most abundant family (ca. 23% of the total) caught throughout the study period, followed by Curculionidae (9%) and Anthicidae (7%). In terms of the number of individuals, Chrysomelidae was the most abundant (32%), followed by Anthicidae (16%) and Coccinellidae (7%). In Sabah, Malaysia, the most abundant coleopteran families were Staphylinidae and Pselaphidae (Chung et al. 2000). The differences in family composition may have resulted from the sampling methods; Chung et al. used three different methods to collect beetles, including ground-dwelling beetles. The most abundant families in the present study were the plant-associated beetles (Chrysomelidae and Curculionidae) and potential predators of herbivorous insects (Anthicidae and Coccinellidae).

The total number of individuals captured during our study was 1937, representing at least 556 species. The number of species was lowest in the primary forest and new fallow plots, but the abundances (number of individuals) shown in the new fallow plots were high (Table 1). The diversity indices were lower in the new fallow plots than in the other plots; in all plots except the new fallow plots, the diversity indices tended to be high (> 0.95; Table 1). A previous analysis at our study site using various microhabitat structure variables (Nakagawa et al. 2006) distinguished three groups of forest types: (A) primary forest plots, (B) new fallow plots, and (C) other plots. Since the plots for groups A and C were characterized by relatively high basal area, tree density, and tree species richness, the resulting microhabitat structures may enhance the beetle diversity in these plots. The primary forest plots were relatively shady, with a thick canopy layer, and we never included any of the gaps that occasionally appeared in primary forests in our study. Thus, we may

Table 1 The number of species, abundances (number of individuals), and Simpson's index of diversity (SID) of beetles in the 12 study plots

Forest type Plot	No. of species	No. of individuals	SID
Primary forest			
H2	23	28	0.980
H5	35	51	0.980
Fragmented primeval forest			
P2	51	85	0.980
P7	96	208	0.946
New fallow			
B1	38	172	0.710
B4	37	114	0.930
Young fallow			
T1	100	218	0.990
T4	70	129	0.975
Old fallow			
F4	61	183	0.950
F5	84	236	0.950
Rubber plantation			
G0	98	213	0.960
G9	100	262	0.960

have underestimated the species richness on the primary forest floor, because shady floor and brighter gaps are often mixed on the primary forest floor.

Species richness and abundance (number of individuals) data revealed that Chrysomelidae dominated most of the study plots (Table 2). Carabidae, most of which are carnivores, were abundant in one primary forest plot, but their numbers were low in other plots.

Table 2 List of top two abundant families in regard of species number and abundances in the 12 study plots

Top two abundant families in regard of species richness					
H2	H5	P2	P7	B1	B4
1 Curculionidae (38%)	Chrysomelidae (23%)	Chrysomelidae (24%)	Chrysomelidae (19%)	Chrysomelidae (32%)	Chrysomelidae (34%)
2 Elateridae (14%)	Carabidae (11%)	Anthicidae (20%)	Anthicidae (18%)	Anthicidae (13%)	Coccinellidae (10%)
Chrysomelidae (14%)					
T1	T4	F4	F5	G0	G9
1 Chrysomelidae (28%)	Chrysomelidae (27%)	Chrysomelidae (38%)	Chrysomelidae (30%)	Chrysomelidae (14%)	Chrysomelidae (22%)
2 Anthicidae (7%)	Coccinellidae (11%)	Anthicidae (11%)	Anthicidae (10%)	Anthridae (10%)	Coccinellidae (11%)
Curculionidae (7%)					
Top two abundant families in regard of abundances					
H2	H5	P2	P7	B1	B4
1 Curculionidae (38%)	Carabidae (22%)	Chrysomelidae (25%)	Anthicidae (23%)	Anthicidae (59%)	Chrysomelidae (48%)
2 Chrysomelidae (10%)	Chrysomelidae (20%)	Anthicidae (22%)	Ptinidae (20%)	Chrysomelidae (27%)	Anthicidae (12%)
Coccinellidae (10%)					
Elateridae (10%)					
T1	T4	F4	F5	G0	G9
1 Chrysomelidae (23%)	Chrysomelidae (40%)	Chrysomelidae (42%)	Chrysomelidae (50%)	Chrysomelidae (30%)	Chrysomelidae (30%)
2 Anthicidae (18%)	Phalacridae (9%)	Cantharidae (16%)	Cantharidae (9%)	Anthicidae (12%)	Cantharidae (15%)

Numbers in the parentheses represent the proportion of the family to total species or individuals captured in each plot

Distribution of species-abundance in the 12 study plots

The species rank-abundance curves showed that the primary forest plots and one of the fragmented primeval forest plots had relatively shallow curves compared to those of the other plots (Fig. 1). This suggests that the evenness of the species abundance in the former plots is high. A single species of Anthicidae dominated (more than half of all individuals) in one new fallow plot (B1; Fig. 1). Such dominant species may be rare in primary forests and forests that retain most of the characteristics of primary forests.

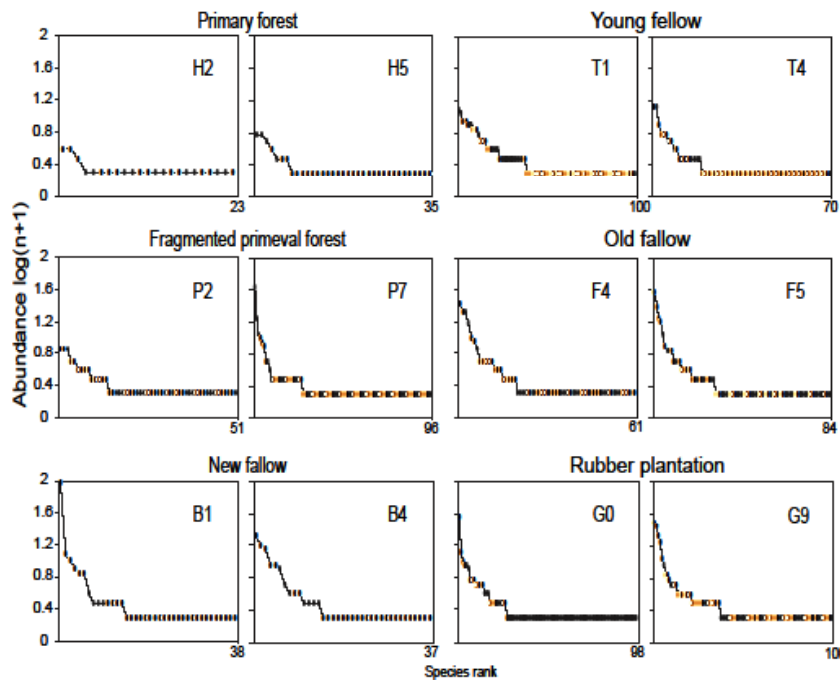


Fig. 1 Species rank-abundance curves for the beetles at the 12 study plots

Chrysomelid fauna in the 12 study plots

For the paired combinations of the same forest type, we found high similarity indices for the chrysomelid fauna in primary forest, new fallow, and old fallow, but the similarity indices were low between the two plots belonging to the fragmented primeval forest, young fallow, and rubber plantation (Table 3). The highest similarity index (0.990) was between H5 and G9 (Table 3), suggesting that the chrysomelid faunas in these plots strongly resemble each other; however, the microhabitat structures of these two plots were not particularly similar (Nakagawa et al. 2006). The chrysomelid species found in the new fallow plots rarely appeared in other plots and never appeared in primary forest and fragmented primeval forest (Fig. 2). Only two species caught in some plots (P7, T1, F4, G0, G9) were found in the primary forest plots (Fig. 2), suggesting that few species that inhabit deforested areas can invade primary forests.

Table 3 Similarity of chrysomelid fauna (C_s) of the 12 study plots

	H2	H5	P2	P7	B1	B4	T1	T4	F4	F5	G0	G9
H2	-	-	-	-	-	-	-	-	-	-	-	-
H5	0.950	-	-	-	-	-	-	-	-	-	-	-
P2	0.000	0.000	-	-	-	-	-	-	-	-	-	-
P7	0.000	0.690	0.000	-	-	-	-	-	-	-	-	-
B1	0.000	0.000	0.000	0.000	-	-	-	-	-	-	-	-
B4	0.000	0.000	0.070	0.000	0.680	-	-	-	-	-	-	-
T1	0.000	0.250	0.170	0.150	0.130	0.110	-	-	-	-	-	-
T4	0.000	0.000	0.000	0.010	0.390	0.410	0.170	-	-	-	-	-
F4	0.000	0.160	0.630	0.280	0.006	0.060	0.210	0.050	-	-	-	-
F5	0.000	0.380	0.730	0.340	0.008	0.070	0.220	0.010	0.700	-	-	-
G0	0.000	0.030	0.000	0.030	0.000	0.008	0.130	0.070	0.130	0.020	-	-
G9	0.000	0.990	0.020	0.420	0.070	0.060	0.230	0.060	0.290	0.330	0.080	-

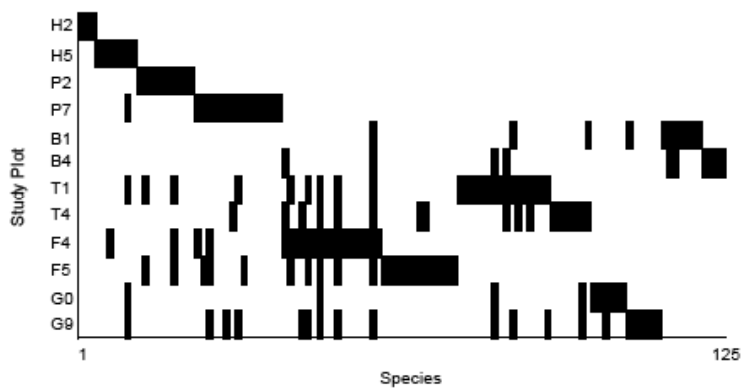


Fig. 2 Species overlap of chrysomelid assemblages among the 12 study plots

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