

#### 53 0 Distance-driven species turnover in Bornean rainforests: homogeneity and heterogeneity in primary and post-logging forests 55

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Sel is v of ass the Fiv Py in in pri A the ho ovv the sel	lective logging is practiced extensively within tropical rainforests of south-east Asia, and its impact on local biodiversity well documented. Little is known, however, about the impact of selective logging on patterns of spatial heterogeneity species. We set out to test the hypothesis that selective logging will lead to a homogenization of the associated faunal semblages, using moths (Lepidoptera) as our subject taxa. Large-scale transects were established within primary and post-logging lowland mixed dipterocarp rainforests around e Danum Valley Conservation Area and surroundings, Sabah, Malaysia (4°50'N–5°00'N and 117°35'E–117°45'E). we study sites were located within each habitat with geometrically increasing inter-site distances. Macro-moths plus raloidea were sampled by light trapping in 2007 and 2008. Vegetation state was also measured at each site. A clear distance–decay relationship (decreasing assemblage similarity with increasing geographic distances) was observed primary forest but was absent in the post-logging forest. Large, comparable numbers of macro-moth species were found both primary and post-logging forests. There were no significant differences in moth assemblage composition between imary and post-logging forests. There were no significant differences in moth assemblage composition between is important structural differences between primary and post-logging forests reflected in the moth assemblages. two-stage hypothesis combining both neutral and niche concepts is probably the most parsimonious explanation of ese results. First, the composition of the moth assemblage probably reflects clumping and, in turn, dispersal capacity of e commoner plants in each forest type. Although the impact of selective logging may be subtle, this study suggests that lective logging results in the spatial homogenization of macro-moth assemblages.
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The physical disruption caused by logging operations on tropical rainforests has produced evidence that the biodiver-35 sity and ecology of such post-logging forests may be seriously impacted (Sist et al. 2003a, b, Meijaard et al. 2006, Paoli et al. 2008, Corlett 2009). In terms of increases or decreases in species richness, a range of studies of taxon- or habitatspecific assemblages have given mixed results (Holloway

- 40 et al. 1992, Hill 1999, Willott 1999, Davis 2000, Willott et al. 2000, Schulze et al. 2004, Deblauwe and Dekoninck 2007, Dumbrell et al. 2008, Sodhi et al. 2010). Given the vast biological diversity associated with tropical rainforests such studies still concern a small proportion of taxa, loca-
- 45 tions and time periods. Further studies will shed light on the generality or otherwise of these earlier results.

In addition, anticipated post-logging impacts may be considerably more subtle than simple changes in species richness. As the physical structure of the forest is altered, so

- 50 corresponding changes may be induced in community parameters such as food-web structure, guild partitioning,
- 52 habitat diversity and, most pertinent to the present paper,

99, Hill and patterns of Hamer 200 changes can occur without changing species richness and yet may have dramatic impacts upon ecosystem functioning and service 90 provision. In other words it is the composition and patterning of the richness which may change rather than the absolute richness itself.

One hypothesis derived from these concerns, is that the disturbance regime associated with the logging process may 95 impose a spatial homogeneity on species assemblages, in place of a distance-mediated dynamic turnover in species composition which might be expected to occur within an intact 'primary' rainforest (Nekola and White 1999, Chave and Leigh 2002, Morlon et al. 2008). Should this prove to 100 be the case then questions arise as to what sorts of ecological processes may produce these patterns. The current neutrality/ niche differentiation debates (Chesson 2000, Hubbell 2001, Leibold and McPeek 2006) are pertinent here, as are related issues of spatial scale as it relates to pattern in emergent 105 properties of ecological communities. If neutrality is the

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- 0 dominant process determining place to place turnover in community composition, then once spatially explicit processes are taken into account, a distance decay curve may be expected with steepness associated with the clumping regime of the underlying plants (Chave and Leigh 2002,
- Morlon et al. 2008). Of course, such a relationship may 5 also arise if there is spatial habitat heterogeneity and the sort of compartment-based specialisation of communities noted for arthropods by, among others, Walter et al. (1998) for mite assemblages, and C. Wardhaugh et al. (pers. comm.) for
- 10 beetles in rainforests. Further, if place to place turnover is examined on too small a scale vis-à-vis the inherent or feasible vagility of the organisms being studied, then again no distance-decay relationship may be detected.

We have used the relatively well-known moth fauna of 15 Sabah in northern Borneo to compare the patterns of species turnover across primary and post-logging lowland forest. We have used a mass sampling programme based on geometrically increasing inter-site distances from 100 to 80000 m in each forest type to test the hypothesis outlined above.

- 20 We began with the a priori expectation that species turnover would be related to inter-site distance in undisturbed forest whereas place to place change in post-logging forest would show no such relationship.
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## Study site and methods

### Study area

- The Danum Valley Field Centre is located on the Segama 30 River in north-eastern Borneo in the Malaysian state of Sabah. The Field Centre is adjacent to the 43 800 ha Danum Valley Conservation Area (4°50'N-5°00'N and 117°35'E-117°45'E) – a fully conserved region of undisturbed primary
- lowland dipterocarp forest. Both the Field Centre and the 35 Conservation Area are embedded with the 1 million ha Yayasan Sabah logging concession. This surrounding area has experienced various intensities of logging from the 1960s until very recently. Most of the post-logging areas have been allowed to regenerate naturally although some restoration 40
- by interplanting using dipterocarp saplings has occurred in a few areas.

In general the primary forest has a high density of dipterocarp trees frequently forming a closed canopy with relatively open understory. In contrast post-logging areas have

- relatively open canopies and a dearth of dipterocarp species (these being the primary targets of the logging industry). The few large trees left standing are those less favoured by the industry such as Koompasia excelsor (although following
- some logging regimes a small number of dipterocarp 'seed 50 trees' also remain). The understory is frequently dense with mass thickets of gingers, climbing bamboos Dinochloa spp. and smothering vines as well as tree genera such as Macaranga, Octomeles and Neolamarkia characteristic of
- disturbed areas (Willott 1999). Detailed descriptions of the 55 flora and vegetation of the primary rainforests close to our study areas are provided by Newbery et al. (1992). Studies of the vegetation of the forests after logging are few but Woods (1989), Brearley et al. (2004) and Bischoff et al. (2005) provide useful introductions and some survey data. 60
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### Sampling design

We selected ten study sites, five in undisturbed primary forest and five in post-logging forest, at each of which we located three Pennsylvania-style light traps hung at about 65 head height (Frost 1957, Kitching et al. 2005). Figure 1 shows the approximate location of each group of traps. All sites were at < 300 m a.s.l. (primary forest sites 152–279 m a.s.l.; logged-over sites 124-215 m a.s.l.). Traps were arranged about a focal point such that no trap was visible from 70 any other. At each site three traps were run for several nights, until a moth sample of at least 1000 individuals of macromoths with a wingspan greater than circa 8 mm, had been accumulated. We have not used each trap as an independent sample, first, because of their proximity to each other (gener-75 ally < 20 m) and, second, because accumulating a sufficiently large, statistically powerful, sample in each trap (rather than sets of three traps) would have extended the sampling period beyond the time resources available. We used this approach as a way of circumventing the inherent 80 variability in nightly catches associated with light trapping.

Sampling was carried out during two field trips in the same period (December-March) in 2007 and 2008. Simple logistics prevented all 10 sites being sampled in the same year, and this is an acknowledged weakness in the study. 85 Accordingly we sampled four primary forest and two postlogging forest sites in 2007, and two primary and four post-logging forest sites in 2008. We resampled one primary and one secondary site in each year so that the year-to-year variation in diversity could be assessed (see below). 90

Within each forest type, sampling foci were located at geometrically increasing inter-site distances. From a base location and set of samples (point 0), further samples were collected at ca 100, 1000, 10000 and 80000 m distance (the most distant sites were located in the adjacent 95 Imbak Canyon Conservation Area). This design gave us the ability to calculate assemblage similarities for inter-site distances within each forest 'treatment'. All sites occurred within a more or less continuous forest matrix.

All conventionally designated macro-moths (that is: 100 members of the clade 'Macrolepidoptera' together with Hepialoidea, Zygaenoidea and Cossoidea) plus Pyraloidea and Thyridoidea (Grimaldi and Engel 2005) were removed from the samples and counted. This group of moths comprises a large portion of Lepidoptera in Borneo, representing 105 more than 6800 recognised species (Holloway 1986-2011, Whitaker unpubl.). All moths were identified to morphospecies and a substantial fraction have subsequently been named using the 18 volumes of Holloway (1986-2011), Robinson et al. (1994) and treatments in preparation for 110 [AQ2] the Pyraloidea and Thyridoidea (Whitaker et al. unpubl.).

Lepidoptera are almost universally herbivorous in their larval stages (Scoble 1992) and hence information on plant assemblages is useful in trying to explain moth diversity patterns. Accordingly plants were surveyed within a circle of 115 20 m diameter, centred on each of the three light traps per site. The number of trees and their size classes ('large' >50 cm dbh, 'medium' 25-50 cm dbh, 'small' <25 cm dbh) were recorded, and abundance levels of other vegetation including seedlings and herbs were estimated using the semi-quantitative DAFOR scale where 5 = dominant, 121



Figure 1. Map of the study sites and their locations on the island of Borneo. Sites in primary forest are indicated as open symbols and numbered with the prefix 'P', sites in logged-over forest are indicated by closed symbols numbered with the prefix 'L'. Spot heights are in feet above sea level. Topographic categories range from 0 to 150 m a.s.l. (mid-green) and then in 300 m steps through to >1500 m (pale green to increasing shades of brown). The base map is reproduced with permission from the Sarawak/Sabah/Brunei 1:650000 sheet of the International Travel Maps produced by ITMB Publishing (< www.itmb.com >), Vancouver, Canada who retain its copyright.

4 = abundant, 3 = frequent, 2 = occasional, and 1 = rare (Butterfield et al. 1991). All plants were identified to families and, where possible, to genus and/or species.

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#### Data analysis

- We first compared moth species richness between primary 40 and secondary forests. Although sampling intensity was standardized at approximately 1000 individuals, exact numbers varied from 1036 to 1269. Species richness was therefore adjusted to a sample size of N = 1000 individuals, using individual-based species rarefaction curves generated for
- 45 each site, based on the expected richness function (Mao Tau) using EstimateS ver. 8.2.0 (Colwell 2009). Total species richness was estimated using the abundance-base coverage estimator (ACE) of Chazdon et al. (1998), based on a standard sample of n = 1000 individuals per site.
- 50 As year-to-year variation was evident (Results), statistical analyses treated sampling year as a random factor and habitat type as a fixed factor. For both univariate (species richness) and multivariate analyses (assemblage composition), we used a permutational multivariate analysis of variance
- (PERMANOVA) implemented in PRIMER 6 (ver. 6.1.13, Clarke and Gorley 2006) and PERMANOVA + (ver. 1.0.3, Anderson et al. 2008) add-on software. The PERMANOVA routine tests for the effects of factors on one (such as species richness) or more (for example, assemblage composition)
   response variables, based on pseudo-F statistics of the

distance measures. Although PERMANOVA was developed primarily for multivariate analysis, univariate analysis is possible using Euclidean distances which yield Fisher's 95 traditional univariate *F* statistic (Anderson et al. 2008). Type III sums of squares were used to calculate *F* statistics. Due to the limited number of possible permutations, Monte Carlo tests were conducted to obtain *P* values using 4999 permutations of residuals under a reduced model. 100

Before assemblage-level analyses, moth species were subdivided into 'common' and 'rare' species. Common species were selected following Novotny et al. (2007) who calculated the probability of observing a species (P) given N individuals from n sites, under an assumption of the extreme case where 105 there is no beta-diversity within a given habitat, using the following equation:  $P = 1 - (1 - 1/n)^N$ . Threshold minimum abundance of common species (N = 14) was calculated with P = 95% chance of detection from n = 5 sites within each habitat type. Abundances of 'common' moth 110 species were then transformed to presence/absence binary data, and a Sørensen similarity index was used to measure assemblage similarities among pairs of sites. Only common species were incorporated into the calculation of these similarity measures, as inadequate sampling of rare species 115 results in overestimation of beta-diversity (Novotny et al. 2007). In addition we used the relative abundance of both common and rare species to calculate Chao's abundancebased Sørensen similarity index (Chao-Sørensen index, Chao et al. 2005) in order to cross-validate the results obtained using the Sørensen index of common moth species 121

- 0 (executed by EstimateS, ver. 8.2.0, Colwell 2009). Unlike other similarity indices that measure assemblage similarities using observed samples, the Chao-Sørensen index estimates the extent of shared species taking into account unseen shared species, based on the number of observed rare, shared
- species between two sites. The Chao-Sørensen index is 5 effective when samples are undersampled and contain a substantial fraction of rare species (Chao et al. 2005).

Variations in moth assemblage composition were also investigated visually using non-metric multi-dimensional

- 10 scaling (NMDS) ordination using PRIMER 6 software. Based on the triangular matrix of between-site similarity values, an NMDS ordination was generated using 25 random restarts with the first Kruskal fit scheme.
- Pairwise comparisons among the five locations within 15 each forest type are not wholly independent of each other (because the data from each location is involved in calculating similarities with several other sites). Accordingly we investigated distance-decay relationships between moth assemblage similarities and inter-site distances using Mantel
- 20 tests calculated in R ver. 2 (R Development Core Team) and the vegan community ecology package ver. 2 (Oksanen et al. 2008). Mantel tests investigate whether two different matrices show similar patterns of inter-site variation using a correlation between two dissimilarity matrices (a Pearson
- 25 correlation coefficient was used here), and test the significance of the statistic using Monte Carlo techniques. We tested the relationships between moth assemblage compositions and geographic distances between sites (in metres, log-transformed and measured as Euclidean distances). We
- carried out these analyses using Sørensen indices based on 30 the presence or absence of species and the Chao-Sørensen metric which takes into account relative abundance of species. We repeated this analysis for the plant assemblages using Sørensen indices alone. Finally we examined the correlation
- between the moth assemblage and the tree assemblage. 35

### Results

Primary forests were characterised by greater proportion of 40 large trees and larger number of large and medium size tree species (Table 1). The proportion of dipterocarp trees was also greater within primary than secondary forest across all size classes. These differences, however, were not significant due to large between-site variations (Supplementary material 45

Appendix 1). In total, we sampled 13562 moths (6992 in primary forest and 6570 in post-logging forest), representing 1996 species (1393 in primary forest and 1468 in post-logging

forest). Of these individuals, 7089 (1298 species) were 50 caught in year 1 and 6473 (1465 species) in year 2. The similarity of abundances reflects the fact that we sampled each site until at least the requisite 1000 individuals were encountered (Table 2).

Two outcomes are of particular note based on the mean 55 values of standardised species richness and ACE (both estimated at N = 1000 individuals) (Table 2). First, these values in primary and post-logging forest were comparable with no significant effect of habitat type (Table 3). Second, both standardized species richness and ACE in primary 60

Table 1. Mean and standard error (in parentheses) of: proportion of 61 large trees to all other size classes (viz. large, medium and small trees); species richness of trees with different size classes, and seedlings and other vegetation; and proportion of Dipterocarp trees across three size classes between primary and post-logging forests.

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	Primary forest	Post-logging forest
Proportion of large trees	0.420 (0.097)	0.267 (0.090)
Species richness		
Large trees	4.2 (0.9)	2.8 (0.9)
Medium trees	8.4 (1.9)	7.8 (1.0)
Small trees	1.8 (0.7)	3.2 (1.0)
Seedlings and other vegetation	10.2 (1.0)	8.8 (1.1)
All	19.0 (1.6)	18.2 (2.8)
Proportion of Dipterocarp trees		
Large trees	0.776 (0.091)	0.562 (0.167)
Medium trees	0.352 (0.088)	0.192 (0.041)
Small trees	0.400 (0.187)	0.107 (0.066)

forest were higher in year 2 than in year 1 although there was 80 no significant effect of year, nor interaction between habitat and year (Table 3).

In both forest types across both years of sampling there were very large numbers of 'rare' species. In primary forest, 94% (1308 species) of all species encountered fell into this 85 category, in secondary forest, 95% (1394 species). This is not an unexpected outcome given the size of the Bornean moth fauna.

Figure 1 represents the results of our ordination analysis based on Sørensen similarity measures of common moth 90 species. Although within-year points for primary and post-logging forest cluster separately from each other, the introduction of two samples from the additional year in each case obfuscates these differences especially in the primary forest samples. A PERMANOVA test suggests that the year 95 to year differences are significant whereas the forest type differences and any interaction, are not (Table 3). Similar results were found when we used Chao-Sørensen similarity measures of both common and rare species.

The situation, however, is much clearer and more inter-100 esting when we examine the relationship between species

Table 2. Mean and standard error (in parentheses) of moth abundance, species richness, estimated species richness (ACE) and the number of common and rare species per site. Values are also subdivided for the data collected in year 1 and 2.

	Primary forest	Post-logging forest
Number of individuals	1165 (40.9)	1095 (22.8)
Year 1	1211 (44.3)	1081 (24.1)
Year 2	1075 (33.0)	1124 (55.5)
Species richness at 1000 individuals	468 (17.5)	501 (8.3)
Year 1	453 (23.1)	500 (11.6)
Year 2	497 (7.6)	503 (15.0)
ACE at 1000 individuals	1236 (80.5)	1213 (39.2)
Year 1	1146 (90.3)	1182 (44.9)
Year 2	1415 (3.5)	1273 (73.8)
Number of common species	94 (2.2)	93 (0.8)
Year 1	96 (3.0)	93 (1.3)
Year 2	91 (1.5)	94 (0.5)
Number of rare species	362 (17.1)	397 (15.3)
Year 1	343 (18.5)	404 (19.4)
Year 2	402 (7.5)	383 (30.5)

0 Table 3. Summary results of PERMANOVA, showing pseudo-*F* and p values (p values obtained from Monte-Carlo permutations) of habitat, year and their interaction effects on species richness (univariate) and assemblage (multivariate) data. Degrees of freedom for habitat, year, interaction and error were 1, 1, 1 and 8 respectively.

		Habitat		Habitat Year		Interaction			
_		Pseudo-F	р	Pseudo-F	р	Pseudo-F	р	65	
5	Univariate data								
	Standardised species richness	1.26	0.453	1.09	0.324	1.40	0.282		
	ACE	0.09	0.813	1.27	0.300	5.19	0.053		
	Multivariate assemblage data								
	Sørensen similarity measures on 'common' species only	3.34	0.083	4.98	0.005	0.69	0.640	70	
10	Chao-Sørensen abundance-based estimated similarity measures	9.22	0.039	6.18	0.004	0.33	0.776		

turnover and inter-site distance within primary and post-logging forest types (Fig. 2). We note, first, that the similarity values of moth assemblages in both forest types were remarkably high, ranging between 71 and 91% for Sørensen (that is: based on 'common' species only) and 65 and 95% for Chao–Sørensen similarity values (that is: based on all species). There was a negative relationship between assemblage similarity and the log of inter-site distance for primary forest. However, no such relationship existed for post-logging forests. Mantel tests confirmed the observed patterns, showing significant relationships

between geographic distance and moth assemblages of primary, but not post-logging forest (Table 4). Plant assemblages, similarly, were significantly correlated with geographic distances within primary (r = 0.85, p = 0.040), but not post-logging forest (r = -0.18, p = 0.749). Moth assemblage composition was also correlated to those of plant assemblages. The relationships, however, were only

30 plant assemblages. The relationships, however, were only significant for moth assemblage composition based on Chao–Sørensen index values (Table 4).

# 35 Discussion

 In trying to erect hypotheses to underpin our observations on both richness and turnover, we first suggest that, almost without exception, local richness and assemblage structure for Lepidoptera will reflect locally available larval host plants. Although there are celebrated exceptions,



Figure 2. NMDS ordination based on Sørensen similarity measures of 'common' moth species, collected from primary (triangle) and post-logging forest (circle) in year 1 (closed symbols) and year 2 (open symbols).

(Williams 1930) most adult Lepidoptera are not very vagile (Wilson and Thomas 2002) and probably spend their 75 lives within a few tens or, at most, hundreds of meters of their birth sites. A large proportion is also specialized by forest stratum with mixing between ground and canopy being the exception rather than the rule (Schulze et al. 2001, Schulze and Fiedler 2003, Brehm 2007, Ashton and 80 Kitching unpubl.). In addition, most species are narrowly oligophagous often being restricted to a single genus or genus-group within a particular plant family (Basset 1992, Novotny et al. 2002, 2003, Dyer et al. 2007). If we accept these three generalisations as axiomatic, then explanations 85 of spatial pattern are best sought in ideas about the spatial



Figure 3. Relationships between geographical distance and (a) Sørensen and (b) Chao–Sørensen similarity values using moth assemblages collected from primary (triangles) and post-logging secondary (circles) forest. Shaded points represent similarity values based on comparisons of moth assemblages across the two years of the study. Trend lines were drawn for primary (solid line) and secondary (dotted line) forests.

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0 Table 4. Summary results of Mantel tests showing r and p values of the matrix correlation between moth assemblages and distance matrix, and between moth and vegetation assemblages.

		Dis	tance	Veget	Vegetation		
_		r	р	r	р		
5	Primary forest						
	Sørensen	0.96	0.041	0.80	0.087		
	Chao–Sørensen	0.82	0.043	0.67	0.042		
	Secondary forest						
	Sørensen	0.06	0.631	0.07	0.668		
0	Chao–Sørensen	0.18	0.452	-0.50	0.872		
0	Chao–Sørensen	0.18	0.452	-0.50	0.		

patterning of the plant species which make up the local vegetation. Here a rich and informative literature is available (Hubbell 2001, Condit et al. 2002, Losos et al. 2004).

Our comparisons of the species' totals in primary and post-logging secondary forests confirm earlier observations on Lepidoptera that each forest type presents similar levels of richness (Willott 1999, Hamer et al. 2003). Likewise we detected no significant overall differences in assemblage

- composition between these two habitat types, despite strong evidence of year-to-year variations. The similar levels of species richness encountered in primary and post-logging forest may be explained when we take into account the range of food-plant driven opportunities provided for estab-
- 25 failing of food-plant driven opportunities provided for establishment of specific moth populations. The species composition in the understorey of primary forest is likely driven by the availability of ombrophilous shrubs, seedlings of canopy trees, woody and non-woody vines, plus vascular
- 30 and non-vascular epiphytes, plus a few species will originate in the leaf litter and fallen timber. Herbaceous plants are relatively rare under closed canopies. In contrast, in postlogging forests, the canopy is almost always substantially disturbed and simplified with concomitant loss of woody
- 35 vines and epiphytes (Johns 1988). This may be compensated for, however, by vastly increased availability of non-woody vines, herbs, and ferns. Grasses, gingers, scrambling palms and other vigorous monocotyledons are a much more apparent part of the flora in these post-logging forests. It seems likely that this compensates for the inevitable loss
- of the canopy components of the fauna to produce the closely similar richness measures across the two forest types.

Turning to spatially driven turnover patterns, we found contrasting differences between the two habitat types: the presence of distance-mediated spatial heterogeneity was evident within primary forest but not within the postlogging forests. Effects of year-to-year variation may have confounded our results as the majority of primary and postlogging forests were sampled in different years. Nevertheless, where there were sufficient points available from within

- year samples the contrasts in distance–decay relationship across the two forest treatments was comparable with those seen when all data were considered together. This reinforced our notion that such a relationship exists in primary but not post-logging secondary forests in Bornean rainforests.
- not post-logging secondary forests in Bornean rainforests. Our finding bear direct comparison with those of Novotny et al. (2007) who found low beta diversity in New Guinean tropical rainforests. It is interesting to note that both Novotny et al. and we found relatively high species overlaps among sites (i.e. low beta diversity). Our study,

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however, detected stronger inter-site differences with dis-61 tance than did Novotny et al. (2007). This apparent difference between the two studies probably reflects two factors. First the Novotny study standardised each site for the plant diversity sampled whereas we did not. Indeed that 65 study was based on explicit sampling of trees rather than use of traps. Second, the spatial scales employed in the two studies differed substantially: our study examined inter-site distances of 0.4 to 80 km, whereas Novotny et al. (2007) examined the range, 100 to 600 km. Beck and Khen (2007) 70 found distance-decay relationships in geometrid moth assemblages in Bornean rainforests, but the relationships they observed were more evident at smaller spatial scales with inter-site distances of < 20 km and were only detectable after controlling for other parameters such as elevation 75 and human-mediated disturbances.

The distance-decay relationship that we have identified in primary forest for both moths and plants has been widely supported and debated in the literature (for key references see Introduction). Much recent attention has been 80 focussed on neutral explanations of vegetation in which local diversity is viewed as being drawn from a species pool with little if any determinism concerning local success of particular species (Hubbell 2001, Condit et al. 2002). Recent authors have incorporated explicit spatial dynamics 85 into the fundamental theory of Hubbell (Chave and Leigh 2002, Morlon et al. 2008) showing how the 'traditional' distance-decay curve emerges with only minimal additional parameters related to local, perhaps transient, 'clumping' of species. The most likely driver of such clumping is dispersal 90 limitation. In their model, based on a Poisson cluster process acting upon presence or absence of species, Morlon et al. (2008) show in addition that this pattern is largely generated by the commoner species in any location with rare species playing only a minor role. This insensitivity to 95 rare species even when abundance-based similarity measures are used is also confirmed by Nekola and White (1999). Morlon et al. (2008) also show that the shape of the relationship is insensitive to overall species richness. It is feasible that place to place turnover in plant composition – and, in 100 consequence, of moth assemblages - reflects topographic and pedological heterogeneity with distance producing new opportunities ('niches') for different species. This is not the most parsimonious explanation and, in any case, would not account for the absence of a distance decay relationship 105 in the post-logging forest, where at least most of the topography and gross soil characteristics will persist, albeit in locally rearranged form.

We suggest, therefore, that the clear turnover we observe in moth assemblages in primary forest is adequately 110 explained by neutral explanations of vegetation change. These changes then provide different available niche dimensions (through the availability of food plants) for moths thereby producing the patterns of moth turnover we observe. This combination of neutral and niche drivers of pattern 115 may well have wider applicability for accounting for beta diversity in animal assemblages.

The same logic can be applied in seeking an explanation for the flat (or absent) distance–decay relationship in postlogging forest. Here our argument demands a more or less uniform set of available food plants. Under the spatially 121

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- 0 explicit neutral model the most parsimonious way of positing this is by hypothesising that the post-logging forests are dominated by plant species which have exceptionally well developed dispersal mechanisms. This is not to say that the same aggregative mechanisms would not apply in these
- 5 forests, just that they would operate over a much larger spatial scale. The dominance of regenerating rainforests by plants having a high vagility has been observed by several authors (Willson and Crome 1989, Gorchov et al. 1993, Dalling et al. 2002).
- 10 These results have considerable implications for conservation. They suggest that the effectiveness of ecosystem management for conservation cannot be monitored simply by assessing species richness. Species turnover is a vital marker if vibrant healthy forests are to be maintained. Conceivably
- 15 this requires more landscape management to maintain patches of intact canopies scattered through post-logging forests. Depending on the target taxa this may require particular attention to the spatial scale of these patches.
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