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Differences in Moth Diversity in Two Types of Forest Patches in an Agricultural Landscape in Southern Korea - Effects of Habitat Heterogeneity -

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ABSTRACT: This research focused on the effects of fragmentation on moth diversity in an agricultural landscape by comparing moth species richness and abundance between hillocks and young secondary forests. We examined five sites from the southwestern part of South Korea: three sites from hillock forest and two from secondary forest. We collected moths bi-weekly from April to October for a 2-year period (2006-2007) with a UV light trap that usually attracts moths within 30 meters. Tree species richness and abundance in 20 m × 20 m plots at each moth sampling site showed a substantial difference in tree diversity between the two types of forest habitats. The total abundance and richness of moth species were higher in secondary forests (541 species with 4,998 individuals) than in hillock forests (423 species with 3,913 individuals), irrespective of the distance among the sites. An ordination analysis with NMDS showed that habitat is the most important factor of grouping sites. The food preferences of the dominant moth species in each habitat were closely related to the habitat type.

Key words: Agricultural landscape, Biodiversity, Food plant, Fragmentation, Habitat heterogeneity, Lepidoptera

INTRODUCTION

Globally, there have been rapid and vast structural changes in agricultural landscapes in the last century caused by the intensification and mechanization of agriculture, which has, in turn, reduced biodiversity (Duelli 1997, Benton et al. 2003, Weilbull et al. 2003). Agroecosystem biodiversity and ecosystem functions may depend on both landscape heterogeneity and farmers' attitudes (Benton et al. 2003, Weilbull et al. 2003, Tscharntke et al. 2005). Declines in biodiversity in agricultural landscapes have also been observed in eastern Asia, where the traditional agricultural landscape in rural areas (called 'Satoyama' in Japan) is comprised of a mosaic of rice paddy fields and diverse non-crop habitats, including secondary oak and pine forests, bamboo groves, grasslands, ponds, streams, and reservoirs for irrigation. Biodiversity in these agricultural landscapes results from the network of diverse habitats and human management of the landscape. Changes in rural areas, however, such as shifts in sources of fuels and fertilizers, as well as depopulation during the last 20～40 years, have caused succession of secondary forests and decreased heterogeneity, leading to a loss of biodiversity (Washitani 2001, Takeuchi et al. 2003, Senior 2005).

Studies measuring biodiversity in mosaic patches have focused on a few groups of animals, including butterflies. The species richness of butterflies in a Satoyama, when compared to native forests or urban parks, vary widely and depend on the site's characteristics and the presence or absence of secondary forests (Tanaka 1988, Ishii 1996, Inoue 2003). Secondary forests in a Satoyama play an important role as sources of a diverse set of foods for butterfly larvae, resulting in high species diversity (Natuhara et al. 1999, Ohwaki et al. 2007). Species richness and abundance of butterflies are closely related to large- and small-scale habitat heterogeneity (Weibull et al. 2000).

As host-specific herbivores, moths and butterflies are good indicators of vegetative structure and local management. Moths are often preferred to butterflies in ecological monitoring studies in temperate and tropical regions, because moths have much higher species richness and are easily captured by light traps (Usher and Keiller 1998, Kitching et al. 2000, Summerville et al. 2004). Site comparisons of night-flying insects through light traps provide valid results as long as the sampling method is standardized across the habitats to be compared, since the attraction radii of light traps for moths are small, less than 30 meters in most situations (Beck and Linsenmair 2006).

In this study, we compared the moth faunas of hillock forests in agriculture-dominated landscapes to the faunas in young secondary

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forests on a mountain in the same region. Over the past couple of decades in Korea, the hillock forests in agricultural landscapes have been largely neglected, whereas forests in mountain areas have been extensively managed. Here species richness, abundance, and similarity in moth species composition were compared between the habitats. The aims of the present study were: (1) to investigate the diversity and abundance of moths in hillock forests and young secondary forests in an agricultural landscape and (2) to investigate the relationship between moth occurrences and habitat type.

METHODS

Study Sites

A total of five sampling sites in the southwestern part of South Korea were studied: three sites (ck1, ck2, ck3) from hillock forests in an agricultural landscape and two sites (sd1, sd2) from young secondary forests on a nearby mountain (Fig. 1). Only two sites from young secondary forests were included due to the inavailability of additional comparative data from the two study years. All of the study sites were located close together: average distances between sites in the hillock habitats and the young secondary forests were 2.5 km and 0.5 km, respectively, and the largest distance between sites, that between site ck1, a hillock forest and sd1, a young secondary forest, was approximately 4.7 km. However, the forest composition and surrounding landscapes of the sampling sites were quite different.

The hillock forests were mainly composed of mixed conifer and oak forests, surrounded by a traditional agricultural landscape. The agricultural landscapes evaluated in this study are used for year-round extensive cultivation, predominantly of onion (*Allium cepa*), which is cultivated from late autumn to spring, and rice, which is cultivated from spring to autumn. The two young secondary forests on the mountain, One of the young secondary forest sites (sd1) was a deciduous forest located on the eastern slope of the mountain and the other (sd2) was a mixed conifer forest on the western slope. Both secondary forests were 20～40 years old.

Moth Sampling

A light trap consisting of a 22-watt ultraviolet light with a 12V battery (BioQuip Co., USA) was used to collect insects at each survey site. We sampled moths bi-weekly from April to October in 2006 (14 samples) and 2007 (16 samples), collecting a total of 30 samples. Moth sampling was conducted for five hours after dusk. The Lepidopteran species targeted for the present analysis were moth families traditionally included in the informal category macrolepidoptera, in addition to a few of the more readily identifiable families of microlepidoptera (e.g. Pyralidae, Limacodidae, Thyrididae). We identified moths to the species level and preserved them for a

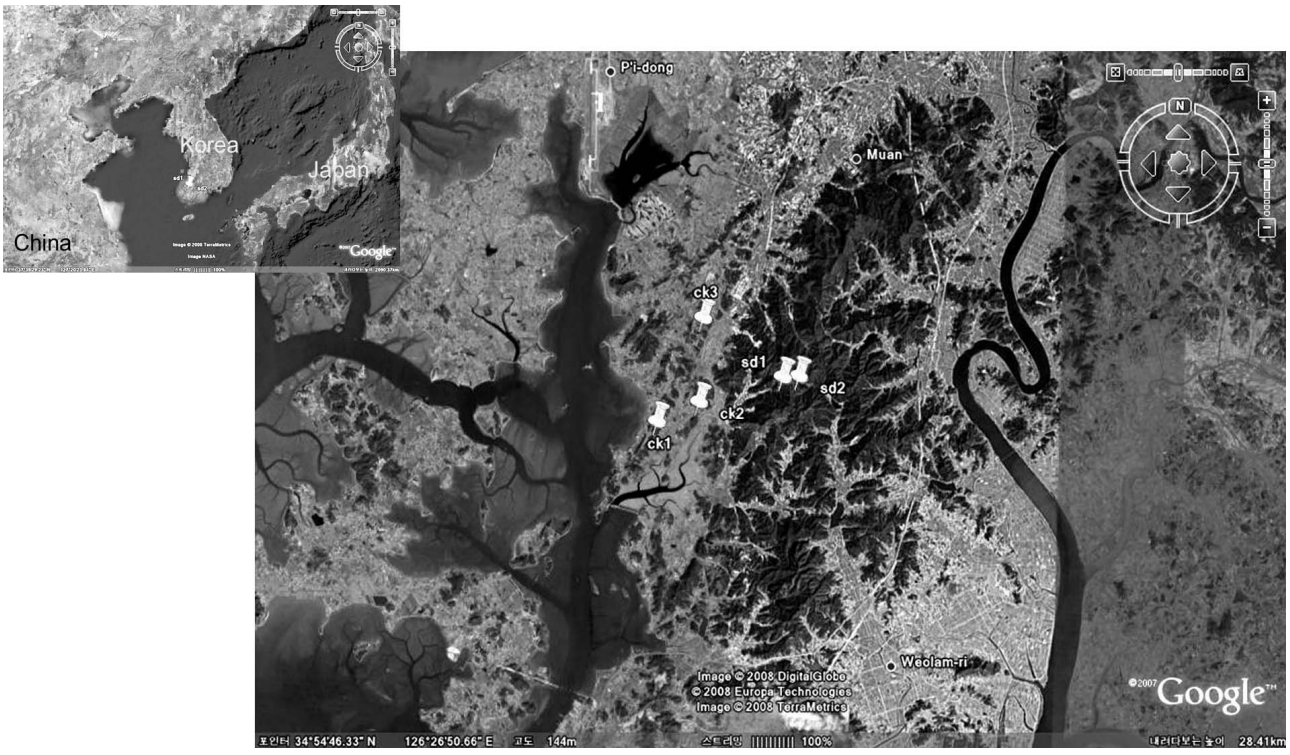

Fig. 1. Site map. Hillock forest sites (ck1, ck2 and ck3) and secondary forests sites (sd1 and sd2) in an agricultural landscape in South Korea.

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collection being made at Mokpo National University, Korea.

Tree species richness and abundance were counted in a 20 m × 20 m plot at each moth sampling site in hillock or secondary forests. Food plant records for moths sampled in the present study were obtained from Sugi (1987) and other literature (Teramoto 1993, Scoble 1999, Sohn 2006).

Data Analysis

The species richness and abundance for each habitat were calculated. Light trapping has been widely used to determine moth assemblages for specific habitats; however, it does not guarantee recording of the total moth ensemble for a site (Gotelli and Colwell 2001). A species diversity index, Fisher's α, was calculated, because it is relatively unaffected by changes in the abundance of the most abundant species and variation in size, and is independent of sample size (Magurran 2003). To estimate the total species richness of moths, We calculated the Chao 1 estimator. The Chao 1 is the sum of the observed number of species and the quotient $a^2/2b$, where a and b equal the number of singletons and doubletons, respectively (Colwell 2006). We used EstimateS (ver. 8.0; Colwell 2006) for calculation of Fisher's α and the Chao 1 estimator.

The relationship between moth assemblages and distance between sites was examined using the Mantel test. Mantel test was undertaken with a first matrix of 5 sites and 405 species (after deleting unique species across the five sampling sites) and a second matrix of distances (in km) among sampling sites. The distance measures for the first and second matrices were Sørensen (Bray-Curtis) and Euclidean distances, respectively. We applied a Monte Carlo randomization test with 999 runs using PC-ORD (ver. 5.12; McCune and Mefford 2006).

A conventional measure of beta diversity based on sample observations (sites) is computed as $\beta w = (\gamma / \alpha) - 1$, where γ is the number of species in a region and α is the average number of species occurring in n local sites within the region (Whittaker 1972).

An alternative method for measuring beta diversity is to determine the dissimilarity between two assemblages. An ordination method - non-metric multidimensional scaling (NMDS), which is appropriate for ecology studies (McCune and Grace 2002) - was used to compare the dissimilarity in composition and abundance among samples. The NMDS procedure was undertaken after a data transformation: (1) deletion of singletons (species with one individual, 251 species) and (2) relativization by the maximum value for each species. Therefore a data matrix with 10 sampling units (five sites in two years) and 434 species was produced. The significance of clusters in the NMDS space was calculated using the multi-response permutation procedure (MRPP) in PC-ORD (ver. 5.12; Mc Cune and Mefford 2006).

RESULTS

Tree species richness and abundance within a 20 m × 20 m plot for each moth sampling site from hillock and secondary forests showed that richness and abundance were this similar between the two forest types (Table 1), except for one of the hillock forest sites, ck3, which was densely covered with a conifer tree, *Pinus densiflora*.

A total of 3,913 and 4,998 moths were collected from hillock and young secondary forests, respectively. The total species richness was higher in young secondary forests, where we recorded 541 species, than in hillock forests, in which only 423 species were recorded. Fisher's α was lower in the hillock sites than secondary forest sites (Table 2). The proportion of dominant and rare species in the total catches in each habitat were similar: dominant species

Table 1. Site description and tree diversity in a 20 m × 20 m plot in the moth sampling sites in hillock and secondary forests in a agricultural landscape in South Korea

Site	Habitat type	Altitude (m a.s.l.)	Tree species			
			Richness	Abundance	Total tree dbh	Shannon-Wiener H'
ck1	Hillock forest	20	3	48	418.5	0.80
ck2		44	11	37	342.6	1.81
ck3		71	12	97	882.8	1.27
sd1	Young secondary forest	92	13	49	544.5	1.99
sd2		123	14	38	622.1	1.96

Table 2. Summary of alpha and beta diversity indices for each site. Observed species richness (Spp_{obs}), Fisher's α with standard deviation (SD), Estimated species richness (Spp_{Chao1}) with standard deviation (SD), Whittaker β diversity (βw)

Site	Abundance	Spp_{obs}	Fisher's α (SD)	Spp_{Chao1} (SD)	βw
ck1	1,355	235	82.1 (3.69)	342.56 (30.90)	
ck2	1,541	304	113.44 (4.70)	418.0 (28.25)	
ck3	1,017	248	104.5 (5.22)	386.67 (37.03)	
Total	3,913	423	120.48 (3.48)	562.45 (32.28)	2.61
sd1	2,364	385	130.99 (4.50)	544.40 (35.22)	
sd2	2,634	410	136.54 (4.47)	636.51 (49.28)	
Total	4,998	541	154.56 (3.95)	752.04 (42.28)	1.72

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comprised 25% of the sample in the hillock forests and 28% of the sample in the young secondary forests, and singleton species comprised 31% of the sample in the hillock forests and 33% of the sample in the young secondary forests.

The estimated number of species was higher than the observed number of species. The Chao 1 estimators of species richness were 752 species in the young secondary forests and 563 species in the hillock forests. The observed regional species richness in hillock and secondary forests together was 684, and the estimated total richness (Chao 1) was 905; however, neither the observed nor the estimated species richness reached an asymptote (Fig. 2).

Species richness and abundance were analyzed according to families (Table 3). A total of 18 families were collected in the secondary forests, while only 12 families were collected in the hillock forests. In both types of sites, the family Noctuidae was the most abundant in both species richness and abundance. However, the second-most-abundant family differed between the habitat types: Pyralidae was the second-most-abundant family in the hillock forests and Geometridae was the second-most-abundant family in the secondary forests. Moths belonging to the families Bombycidae, Cossidae, Cyclididae, Lasiocampidae, Saturniidae, and Zygaenidae were not collected in the hillock forest samples.

The Sørensen index shows that the similarity in moth composition between sites of the same habitat type (mean 0.52 ± 0.06) was significantly higher than that across different habitats (mean 0.30 ± 0.03) (Table 4, ANOVA $F_{1,8} = 56.21$, $p < 0.001$). The Mantel test showed that moth species assemblages and distances between sites are not significantly correlated (Mantel $r = 0.78$, $P = 0.07$). This suggests that moth assemblages in different habitats do not vary as a function of distance.

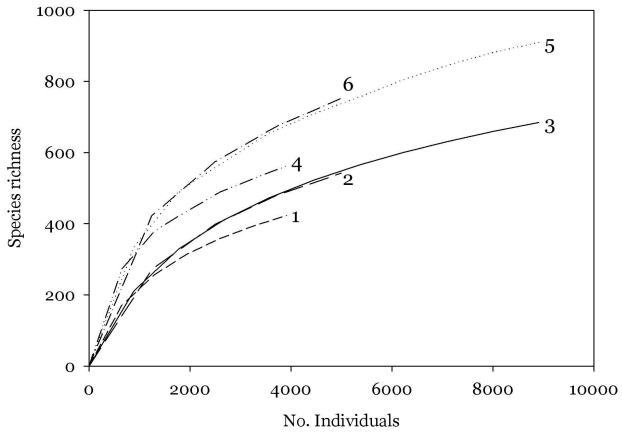

Fig. 2. Observed and estimated species richness versus abundance of moths in hillock and secondary forests in an agricultural landscape in South Korea. 1. Hillock forests, observed; 2. secondary forests, observed; 3. regional, observed; 4. Hillock forests, estimated Chao 1; 5. regional, estimated Chao 1; 6. secondary forests, estimated.

Ordination by the NMDS produced two axes and explained a total of 89% of the total variance: the first axis explained 58% of the total variance and the second axis explained 31% of the total variances. A correlation between species composition and habitat type revealed that habitat (MRPP $r = 0.78$, $P < 0.005$) was significant factor leading to the clustering of the two different groups (Fig. 3). Whittaker's beta diversity of hillock forests was 2.61, and that of secondary forests was 1.72, indicating higher displacement of moth assemblages among sites in hillock forests (Table 2).

The 10 most abundant species in each habitat are listed in Table 5. The species recorded include 10 species in the family Noctuidae and 4 in the family Pyralidae, and 1 species in each of families Drepanidae, Epiplemidae, Geometridae, and Limacodidae. A drepa-

Table 3. Number of moth species collected in hillock (ck1, ck2, ck3) and the secondary (sd1, sd2) forests in an agricultural landscape in South Korea

Family	Hillock		Secondary	
	Species richness	Abundance	Species richness	Abundance
Arctiidae	19	109	16	116
Bombycidae	0	0	1	2
Brahmaeidae	1	1	1	3
Cossidae	0	0	1	1
Cyclididae	0	0	1	5
Drepanidae	8	51	15	269
Epiplemidae	2	66	2	60
Geometridae	80	675	125	1,373
Lasiocampidae	0	0	3	10
Limacodidae	6	49	10	96
Lymantriidae	11	95	13	73
Noctuidae	180	1,890	204	,1504
Notodontidae	19	95	21	53
Pyralidae	90	867	108	1,329
Saturniidae	0	0	1	1
Sphingidae	3	5	12	85
Thyrididae	3	3	5	13
Zygaenidae	0	0	1	1
Total	423	2,913	541	4,998

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Table 4. Similarity of the moth fauna among sites in hillock and secondary forests in an agricultural landscape in South Korea. Similarity values are (1-Sørensen dissimilarity). Hillock forest sites: ck1, ck2, ck3; secondary forest sites, sd1 and sd2. The mean similarity index is significantly different ($F_{1,8} = 56.21$, $p < 0.001$)

Category	Site pair	Distance (km)	Similarity
Same habitat	ck1 - ck2	1.47	0.47
	ck1 - ck3	3.52	0.47
	ck2 - ck3	2.57	0.57
	sd1 - sd2	0.51	0.58
	Mean	2.02	0.52
Different habitat	ck1 - sd1	4.24	0.29
	ck1 - sd2	4.71	0.32
	ck2 - sd1	2.79	0.28
	ck2 - sd2	3.27	0.35
	ck3 - sd1	3.12	0.26
	ck3 - sd2	3.54	0.32
	Mean	3.61	0.30

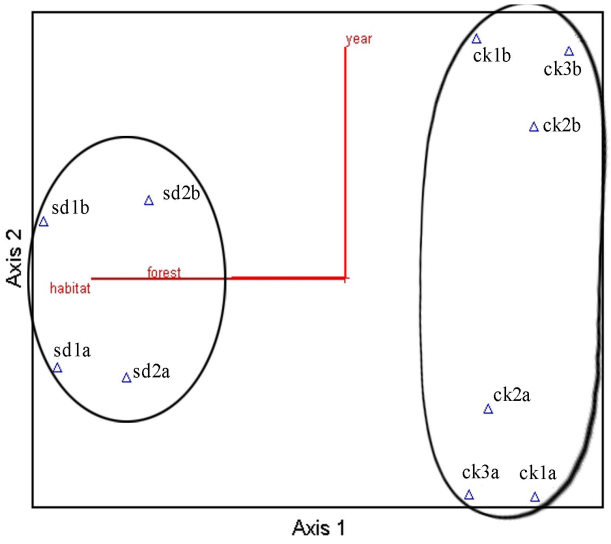

Fig. 3. Ordination in two-dimensional similarity space based on moths collected in light traps in young secondary forests (sd1 and sd2) and hillock forests (ck1, ck2, ck3). Small letters a, b indicate 2006 and 2007, respectively. We used NMDS analysis of Bray-Curtis similarity matrices based on relativization by the maximum value for each column (species) (418 moth species, final stress = 6.46). Each habitat was significantly different (MRPP, $P < 0.001$). The graph is rotated 125 degrees.

nid species, *Pseudalbara parvula* (Leech), was only caught in the secondary forests, while a noctuid, *Spodoptera exigua* (Hübner), was predominantly found in the hillock forests. The food preference of the dominant species in each habitat included a nearly equal distribution of mono-, oligo- and polyphagous species. Three noctuid species, *Herminia arenosa* (Butler), *Hipoea fractalis* (Guenée), and *Hydrillodes morosa* (Butler), were classified as detritivores, because they feed on dead leaves (Sugi 1987).

DISCUSSION

The fauna of the young secondary forest in the mountains was richer in families and species than the fauna of the hillock forest in the agricultural landscape, irrespective of the relatively short distances between survey sites. It was also shown that moth assemblages in the two different habitats do not vary as a function of distance (Mantel test, $p > 0.05$), and moth assemblages in different habitats were separated into different clusters (Fig. 3).

The species richness of insect communities tend to be correlated with the species richness of the plant communities in their habitats (Cunningham et al. 2005, Ohwaki et al. 2007). For example, Kwaiser and Hendrix (2008) showed that bee diversity was significantly different in native and rural grasslands due to differences in the availability of floral resources. In this study, we also found a close relationship between plant species richness and moth diversity: the highest moth diversity was found in the young secondary forest with the highest tree species richness.

Fragmentation of natural habitats is another cause for the loss of biodiversity in human-affected landscapes (Ewers and Didham 2006). Moths and butterflies behave differently according to patch size (Hambäck et al. 2007): generally moths reach higher densities in large patches, whereas butterflies reach higher densities in small patches. Hambäck et al. (2007) suggested that this difference results from differences in life styles: butterflies are visual searchers and moths are olfactory searchers. Among moth families the requirement of patches was different (Hambäck et al. 2007). Families such as Hepialidae, Notodontidae, Lymantridae, Geometridae and Arctiidae show a higher slope in the density-to-area relationship, requiring large patches to achieve high density. However, the families Zygaenidae, Noctuidae, Lasiocampidae, and Pyralidae showed a relatively low slope for the density-to-area relationship, suggesting that they could achieve high densities in small patches, a pattern observed in the present study as well. Noctuidae was the dominant family in both forest types, while the second-largest family was Geometridae in young secondary forests and Pyralidae in hillock forests (Table 3). This difference can be attributed to differences in patch sizes and environments: hillock forests were smaller in size and surrounded

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by agricultural lands, while the young secondary forests were relatively large and included in a mountain range.

For many species, there may be a positive relationship between population size at a single site and regional distribution, because widespread species are more flexible in their use of resources; generalists are often able to use more resources than specialists (Gaston, 1988). The observed and estimated regional species richness was almost identical to observed and estimated species richness of moths in secondary forests (Fig. 2). The list of most abundant species in each habitat also showed that most species except *Pseudalbara parvula* and *Sopdoptera exigua* occurred in both habitats (Table 5). These results suggest that moths in a secondary forest constitute most of the regional diversity and that these secondary forests may be sources of new immigrants to hillock forests.

Table 5. List of 10 most-abundant species in hillock and young secondary forests in an agricultural landscape in South Korea. Numbers in Hillock and Secondary indicate the number of individuals caught at each site and bold numbers indicate the dominant species. Food preference: Oligophagous (O), Monophagous (M), Polyphagous (P), Detritivore (D), unknown (?), tree (t), herb/ grass (h/g)

Family	Species	Host plant preference		Hillock	Secondary
Drepanidae	*Pseudalbara parvula*	O	t	0	**143**
Epiplemidae	*Epiplema plagifera*	M	**h/g**	**64**	26
Geometridae	*Alcis angulifera*	P	t	**83**	**457**
Limacodidae	*Narosa fulgens*	M	t	5	**60**
Noctuidae	*Gonepatica opalina*	M	t	12	**75**
	Herminia arenosa	D	**–**	**112**	11
	Hipoepa fractalis	D	**–**	**82**	13
	Hydrillodes morosa	D	–	25	**141**
	Koyaga falsa	M	h	38	**75**
	Meganola fumosa	O	t	**68**	51
	Naranga aenescens	O	**h/g**	**87**	8
	Niphonyx segregata	M	**h/g**	**113**	8
	Sophta subrosea	?	**?**	**80**	28
	Spodoptera exigua	P	**h/g**	**88**	1
Pyralidae	*Bradina geminalis*	?	?	52	**98**
	Endotricha consocia	?	**?**	**201**	**220**
	Endotricha olivacealis	?	?	55	**70**
	Endotricha portialis	?	?	29	**63**

The existence of a single species or a group of species in a given habitat may reflect their habitat preferences. For example, *Pseudalbara parvula* and *Sopdoptera exigua* were characteristically found in different habitats (Table 5). The former species, an oligophagous drepanid moth, was only collected from secondary forest, while the latter, a polyphagous noctuid species, was mainly found in the hillock forest. Two species were abundant in both habitats: *Alcis angulifera* (Butler) (Geometridae) and *Endotricha consocia* (Butler) (Pyralidae). *A. angulifera* is a tree-feeding polyphagous species, while the food preferences of *E. consocia* are unknown. In addition, the host plant preferences of abundant moth species differed depending on forest type: the species that were abundant in secondary forests prefer tree species, whereas the species that were abundant in hillock forests prefer herb/grass species.

Forest patches in agricultural landscapes have maintained their biodiversity by serving as refuges for many phytophagous insects such as moths, and providing food for predators such as parasitoid wasps or birds. Tscharntke et al. (2002) emphasized that small habitat fragments in some human-dominated landscapes cover such a wide geographic area that beta diversity and spreading of risk are maximized and that large habitat fragments are close enough to enable dispersal among fragments, to reduce the extinction probability of area-sensitive species and to stabilize predator-prey interactions. The loss of forest patches in agricultural landscapes in South Korea by forest succession or removal might endanger the species that depend on this type of ecosystem.

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