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Arthropod inventories can provide good indicators of habitat biodiversity because arthropods respond quickly to environmental changes and are a highly diverse taxon (Landau, 1999). Lepidoptera, one of the largest groups of insects, can yield large sample sizes and many species are relatively easily identified due to their conspicuous wing color and pattern. Thus, Lepidoptera are particularly appropriate for biodiversity surveys (Fisher, 1998). Moths, especially, are relatively easy to survey within the order because most species can be collected with simple light traps. In addition, the comprehensive databases based on fairly reliable systematics are available across the world (Holloway and Barlow, 1992; Landau et al., 1999).

The purpose of the present study was to investigate the differences of faunal composition of larger moths between rural, semi-natural and natural habitats in the southwestern part of the Korean peninsula. Study areas comprised three types of habitats: rural habitat or Satoyama, a small hill surrounded by agricultural lands and nearby village; semi-natural habitat, a mountain nearby university campus and mainly composed of secondary forest; and natural habitat, one of Long-Term Ecological Research Monitoring sites in Korea, Mt. Jiri, the oldest national park in Korea.

Field collecting to rural and semi-natural habitats was operated twice a month from March to November since 2004. Field collecting to Mt. Jiri was operated from April to October once a month since 2005. All specimens were collected with UV light traps. Each trap consisted of a 22-W light set within a funnel and baffle apparatus. Traps were operated with 24-hour timer switches and were powered by 12-V d/c batteries. Moths collected in traps were inspected in the following morning. All specimens were placed in envelopes and taken to the laboratory to be processed and identified. Moths were identified using taxonomic literatures (Inoue et al., 1982; Kononenko et al., 1998; Park, 2000; Kim et al., 2001).

Species diversity was measured by α, β, γ diversity: α diversity is a measure of microhabitat within a homogeneous community; β diversity is change between communities or change between microhabitats within homogeneous communities; and γ diversity is total diversity of all sampled communities within a geographic area (Cody, 1986). To calculate β diversity, the total number of species (γ diversity) was divided by the average number of species (α diversity) per each different habitat. The Shannon-Wiener diversity index was calculated as well as the Simpson diversity index (Krebs, 1999).

A total of 5,023 moths were identified in this study, 696 from rural habitat, 1385 from semi-natural habitat and 2942 from natural habitat. Moths from 20 families were identified. Each value in three different habitats is presented (Table 1). Total numbers of species in different habitats were the highest in natural habitat with 354 followed by semi-natural (275) and rural (163) habitats.

Table 1 Summary values for rural, semi-natural and natural habitats in the southwestern part of Korea

Value	Rural	Semi-natural	Natural
No. species	163	275	354
No. singletons	125	186	211
No. doubletons	26	54	80
Shannon-Wiener Diversity (H')	6.576	2.181	5.354 ± 0.489
Simpson Evenness	0.328	0.051	0.158 ± 0.100

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Unlike total number of species, the indices of diversity and evenness showed a different pattern: higher value in the rural habitat and natural habitat; and lower value in the semi-natural habitat.

Total number and β diversity between species and families in three different habitats showed significant positive relationships (spearman's rho 0.920 (P < 0.01) in total number, 0.903 (P < 0.01) in beta diversity; Figure 1). This result suggested that the composition of taxonomic groups in different categories and ecological functional groups were closely related in all three habitats. Although the β diversity was strongly correlated between species and families, one of natural habitat, Mt. Jiri #6 was negatively correlated.
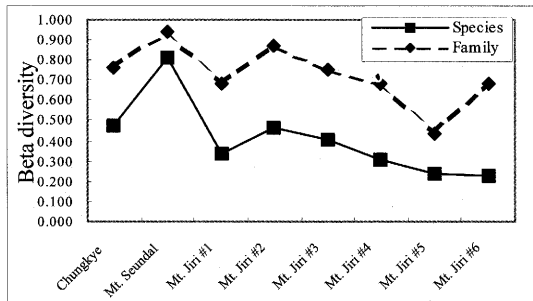

Figure 1 Beta diversity of different levels between species and families at eight surveyed sites.
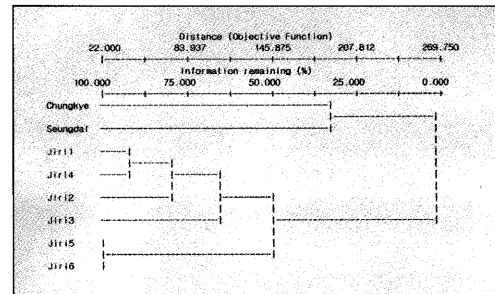
Figure 2 Dendrogram of species similarity among eight surveyed sites

To compare the faunal similarity of larger moths in three habitats, cluster analysis by PC-ORD (McCune and Grace, 2002) was attempted and the dendrogram based on Ward's method is presented (Figure 2). The dendrogram grouped geographically neighboring habitats such as rural (Chungkye) and semi-natural (Mt. Seungdal) and six sites in the natural habitat (Mt. Jiri). In the natural habitat, the similarity between sites Mt. Jiri #1 and Mt. Jiri #4 was resulted mainly not from the geographical closeness, but from the floral composition, mainly *Pinus* forest. This result suggested that both geography and host-plant composition were played in the composition of larger moths community.

The different pattern of moth assemblages may be explained on the basis of broad known and expected host-plant patterns. The present study will focus on how moth assemblages are powerful indicators by the forest types and environment.

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