



## RESEARCH PAPER

# Species richness and abundance among macromoths: A comparison of taxonomic, temporal and spatial patterns in Oregon and South Korea

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### Abstract

The present study aims to establish a long-term intercontinental collaboration based on a sampling protocol using standardized repeated measures at permanent sites to document macromoth species richness and abundance through time and across the landscape. We pooled the data from two continental regions providing a total of 12 trap sites: Mt. Jirisan National Park in South Korea (2005–2007) and HJ Andrews Experimental Forest in Oregon, USA. (2004–2006). A synthesis of our data indicated that: (i) noctuids (43–52%) and geometrids (33–39%) dominated the measures of species richness; (ii) using our sampling protocols more than three years would be needed to obtain a value of 90% of empirical species richness relative to Chao-1 estimated species richness; (iii) temperature alone could not explain the peak pattern in moth abundance and species richness; (iv) the highest/lowest proportion of species richness and abundance were present in similar elevation and forest sites. These observations established a foundation for developing a network-oriented database for assessing biotic impact of environmental and contributed to identifying species at high risk to environmental change based on empirical measures of temporal and spatial breadth.

**Key words:** biodiversity, database, environmental change, Lepidoptera, long-term monitoring.

### Introduction

Insect biodiversity and ecosystem dynamics are interdependent via numerous mechanisms such as decomposition of litter, pollination, suppression of plant growth and serving as prey for carnivores (Janzen 1987; Kim 1993; Hammond & Miller 1998). In general, these functions may be placed into three categories according to their role in ecosystem dynamics: (i) exploiter, in the role of herbivore, parasite or predator; (ii) provider, serving as host or prey for a predator or parasite; and (iii) facilitator, performing functions such as pollination, phoresy, or vector of a pathogen (Miller 1993). Among insects, the Lepidoptera (butterflies and moths) exist as a diverse and abundant taxon found in many different ecosystems, playing a role as herbivores, pollinators and prey (Barlow & Woiwod 1989; Summerville & Crist 2002;

Summerville *et al.* 2004). Moths are an important group for ecological and conservation research since most of the species are nocturnal and are easily surveyed in large numbers with standardized light traps, allowing relatively efficient estimation of geographic patterns of diversity and abundance. In addition, moths play a role as indicators of plant diversity and local land management because many are generally host-restricted (Usher & Keiller 1998; Kitching *et al.* 2000; Ricketts *et al.* 2001) and less mobile (Truxa & Fiedler 2012). Therefore, moth assemblages in diverse forests are promising indicators of overall biodiversity and forest composition (Kitching *et al.* 2000; Summerville *et al.* 2004; Choi 2011; Itämies *et al.* 2011; Fox 2012).

Consistent and uniform sampling methods are essential for addressing environmental issues such as land-use policies and the biological impacts resulting from the dynamics

of climate change (Kitching *et al.* 2000; Miller *et al.* 2003; Choi 2008; Pöyry *et al.* 2011; Fox 2012). The ability to conduct a standardized and consistent sampling program is inherently simple when the scale of the project is restricted to local sites. However, on a regional scale the ability to conduct standardized and consistent sampling among all sites becomes more difficult due to logistical problems associated with long distance travel by a given sampling team or the need to train multiple sampling teams to follow an identical protocol. On a global scale the ability to conduct standardized and consistent sampling methods becomes even more challenging. Thus, we created a set of standardized protocols for the execution of a global-scale study founded on basic taxonomic practices, ecological concepts and statistical tests regarding the biodiversity of macromoths.

The aims of the present study comprised three questions. The first question related to creating a standardized benchmark measure for long-term monitoring: Which macromoths comprised the majority taxon at family and species level? And how does an empirical measure of species richness compare to an estimated (Chao-1) value?

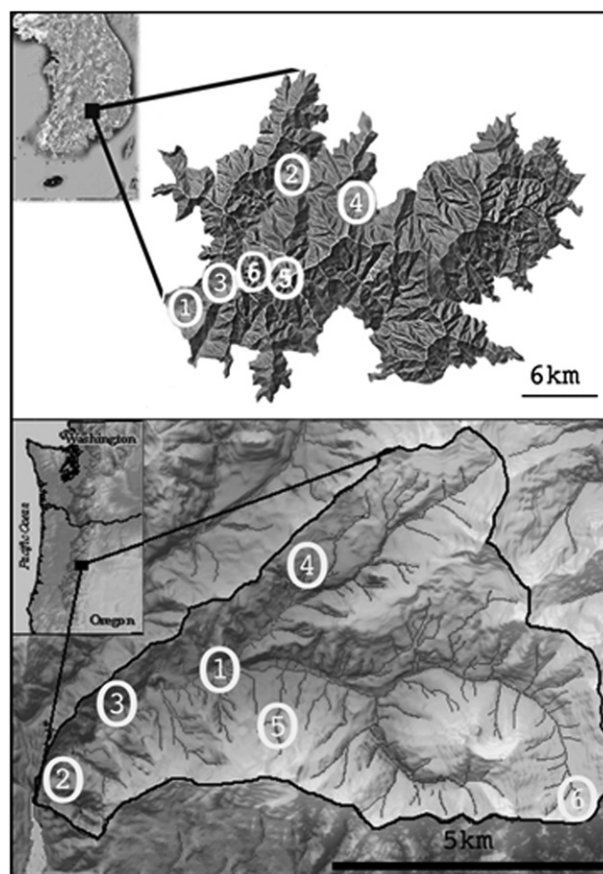
The second question concerned temporal patterns in species richness and abundance: What is the seasonal pattern of species abundance and species richness? We also questioned what combinations of climatic factors define the period of peak species richness? This question was related to understanding the role of climate dynamics in seasonal and inter-annual trends in phenology for individual species.

The third question addressed spatial patterns in species richness and abundance: How many species occurred at only one site, two sites, etc? Did similar patterns in species composition occur among the species in both regions? These data are pertinent to assessing the breadth of geographical range in each species in the context of the current trapping transects and proposing which species may be at risk given rapid environmental change.

## Materials and methods

### Study sites

This project was conducted at two locations, North America and South Korea (Fig. 1). The site selection was based on the availability of consistent moth sampling data for a period of three years. In North America the study was based within the HJ Andrews Experimental Forest (HJA) in the Willamette National Forest, Lane County, Oregon (<http://andrewsforest.oregonstate.edu/>). In South Korea the study was based within the Mount Jirisan National Park (JIRI), the tallest mountain on the mainland of South Korea and the oldest national park (<http://english.knps.or.kr/knp/jirisan/intro/introduction.aspx>).

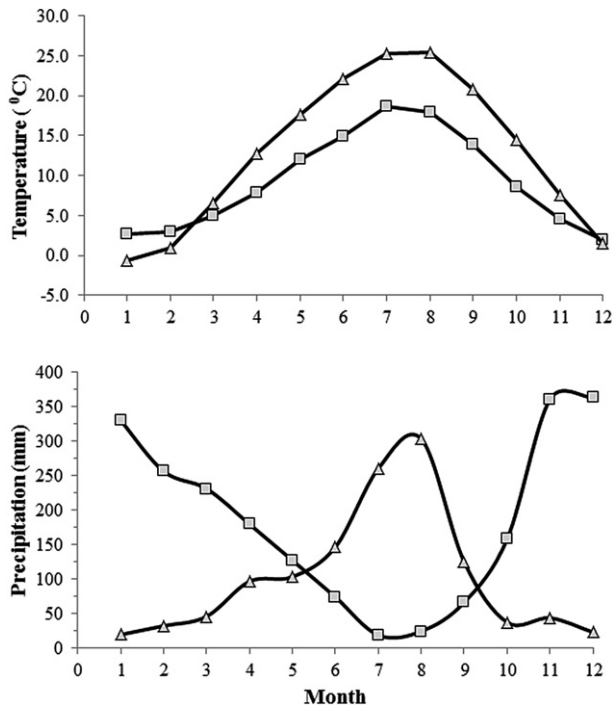


**Figure 1** Map of study locations for sampling macromoths at six sites within transects located at Mt. Jirisan National Park, South Korea (2005–2007) (top) and the HJ Andrews Experimental Forest, USA (2004–2006) (bottom).

The HJA study was located on the west slope of the Oregon Cascade Mountains, 80 km east of Eugene, and consists of 64 000 ha representing the entire Lookout Creek watershed. The valley of the watershed starts at an elevation of 425 m on the west end, rising to 1620 m along a north–south ridge that divides the Lookout Creek drainage from the valley of the Mackenzie River to the east. High elevation ridges range from 1000–1500 m and also mark the boundaries of the HJA to the north and the south.

The JIRI study was located on the southern tip of the Baekdu Mountain Range, about 250 km south of Seoul, and consists of 44 000 ha. High elevation occurs in the northern part and a major mountain ridge lies east–west. This ridge produces northeast and southwest valleys. Two watersheds start from each aspect: the valley from northeast follows the Imcheon River and the valley from southwest follows the Seomjin River.

The weather conditions characteristic of each region are relatively similar when comparing temperature, but very



**Figure 2** Mean monthly temperatures (°C) and mean monthly precipitation (mm) for study locations located at Mt. Jirisan National Park (triangles), South Korea (2005–2007) and the HJ Andrews Experimental Forest (squares), USA (2004–2006).

different when comparing annual rainfall pattern (Fig. 2). Average monthly temperatures exhibited a similar pattern in both forests: from 2 to 18°C at the HJA and from –1 to 26°C at JIRI. Thus, JIRI is much warmer during the late spring and summer months and much colder during winter months. Annual average precipitation was much lower at JIRI, 1600 mm, and was distributed with the majority of moisture occurring during the hot summer months (June to August). In stark contrast, HJA precipitation averages 2300 mm with a majority of the moisture occurring during the cold winter months. Thus, the HJA is a wetter site but the precipitation occurs when temperatures are low.

The flora comprising the temperate forests at each study site is structurally and taxonomically different. The HJA is a conifer-based forest while at JIRI the forest contains hardwoods as the dominant species. At the HJA study site the plant communities at the lower elevations, below 1000 m, are dominated by an overstory of Douglas fir, *Pseudotsuga menziesii* (Mirb.) Franco; and western hemlock, *Tsuga heterophylla* (Raf.) Sarg., with most of the trees creating a canopy 60–80 m high. The understory vegetation at the lower elevations consists of a wide diversity of deciduous hardwood trees and shrubs, including maples (*Acer* spp.), willows (*Salix* spp.), alders (*Alnus* spp.), blueberries (*Vaccinium* spp.) and hazelnut (*Corylus cornuta* Marsh).

Steep south-facing slopes occur in various areas throughout the watershed, and the vegetation in these warmer and drier habitats consists of a distinct flora including evergreen hardwood trees and shrubs such as manzanita (*Arctostaphylos* spp.), rhododendron (*Rhododendron macrophyllum* G. Don) and chinquapin (*Chrysolepis chrysophylla* Douglas). The plant communities at higher elevations, above 1000 m, on the eastern ridges support a subalpine forest with a 50–70 m overstory dominated by Pacific silver fir (*Abies amabilis* (Dougl.) Forbes) and noble fir (*Abies procera* Rehder). In addition, extensive subalpine meadows and barren rocky ridge tops occur along the eastern boundary and support a rich diversity of herbs and grasses. The total floral inventory of HJA contains ca. 440 species of vascular plants.

At the JIRI study site the vegetation at lower elevations, below 600 m, is dominated by *Quercus variabilis* Bl. and *Pinus densiflora* Siebold & Zucc. The plant communities at middle elevations, between 600–1000 m, are dominated by *Carpinus laxiflora* (Siebold & Zucc.) Bl., *Quercus serrata* Thunb., *Acer mono* Maxim., *Larix leptolepis* (Siebold & Zucc.) Gordon and *Pinus koraiensis* Siebold & Zucc. The plant communities at higher elevations, above 1000 m, are dominated by *Quercus mongolica* Fisch. ex Ledeb., *Agrostis clavata* Trin., *Rhododendron mucronulatum* Turcz. and *Abies koreana* Wils. The floral inventory of JIRI contains ca. 1500 species of vascular plants (Yim & Kim 1993).

### Sampling transects and processing

A total of 12 permanent sampling locations were established along a transect representing an elevational gradient within each forest. The general environmental conditions at the sampling locations are described (Table 1). Each transect was designed to include a variety of environmental conditions typical of each forest, including riparian, upland, open canopy, closed canopy, deciduous, conifer and mixed deciduous-conifer habitats.

The macromoths were collected in UV-blacklight bucket traps (BioQuip model #2851, 22-watt circle line bulb, powered by a 12-volt battery and equipped with a killing agent) after a single night of deployment, once per month during the same night within each forest from May through October. Thus, we acquired a total of 36 trap-night samples (6 sites × 6 months) per year. The study reported here involved three consecutive years of sampling (HJA: 2004–2006; JIRI: 2005–2007).

The specimens from each trap-night sample were identified to species/subspecies with a corresponding measure on abundance that related to sample location and date. The main species of Lepidoptera included in this study belonged to 19 moth families traditionally classified in the informal category of macro-lepidoptera and several more readily identifiable families of micro-lepidoptera (Limacodidae, Thyrididae,

**Table 1** A comparison of elevation and habitat conditions among six sample sites selected for an assessment of macromoth species richness and abundance within a transect at the HJ Andrews Experimental Forest, USA (HJA), 2004–2006, and Mt. Jirisan National Park, South Korea (JIRI), 2005–2007

Site	Elevation	Aspect	Habitat
HJA: latitude 43°N; 440 species of vascular plants			
1	485 m	West	Riparian, mixed conifer-deciduous woodland
2	789 m	East	Upland, conifer forest
3	789 m	Southeast	Upland, meadow
4	909 m	Southeast	Upland, conifer forest
5	1091 m	Northwest	Upland, meadow
6	1394 m	North	Upland, conifer forest
JIRI: latitude 35°N; 1526 species of vascular plants			
1	302 m	Southeast	Upland, conifer forest
2	525 m	Southwest	Riparian, deciduous woodland
3	650 m	North	Riparian, deciduous woodland
4	745 m	Northwest	Upland, mixed conifer-deciduous woodland
5	1330 m	North	Upland, conifer forest
6	1350 m	North	Upland, mixed conifer-deciduous woodland

Zygaenidae)(Kristensen 1999). A voucher collection of moths used as exemplars for each species exists at Oregon State University (HJA) and Mokpo National University (JIRI).

### Data analysis

Species richness (the total number of species), abundance (total number of individuals), Chao-1 estimated species richness and singleton percentage were calculated for each sample site. The Chao-1 index is the sum of the observed number of species and the quotient  $a^2/2b$ , where  $a$  and  $b$  equal the number of singletons (one individual in a sample) and doubletons (two individuals in a sample), respectively (EstimateS ver. 8.0; Colwell 2006). The Chao 1 estimator is widely accepted as reliable in biodiversity studies since this estimator uses information on the number of rare or infrequent species in the collection to estimate the number of undetected species (Chao *et al.* 2009; Colwell *et al.* 2012; Eren *et al.* 2012).

Moth abundance, numbers of observed and estimated species and singleton ratio between two survey areas were analyzed by t-test using SPSS statistics package (SPSS Inc 2009). Regression among abundance, number of species, Chao-1 number of estimated number of species and percentage of singletons in each study site and combined were analyzed and the slope and elevation of each regression line were statistically compared using the method of Zar (2010).

### Results

A total of 19 families were included in our combined studies (Table 2). All but one family, Diopsideae, occurred at the JIRI

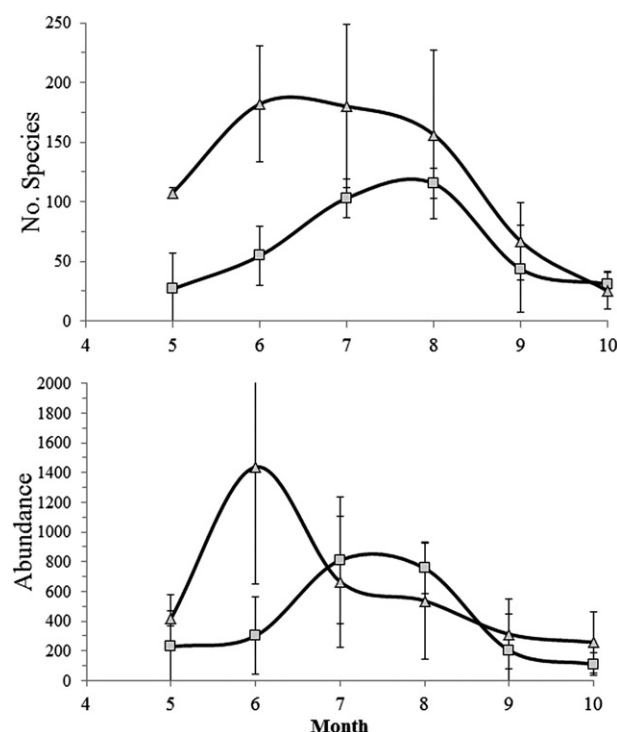
study site, while, 12 families were present at the HJA study site. The seven families that occurred uniquely to JIRI also accounted for a total of 18 genera and 182 moth species out of a combined total of 608 genera and 18 102 individuals. Likewise, the only unique family to the HJA, Diopsideae, represented only one genus and a total of nine individuals. Four (Noctuidae, Geometridae, Arctiidae and Notodontidae) of the 11 families with representative species at both study sites comprised ca. 98% of HJA fauna and 89% of JIRI fauna. Furthermore, a total of 505 genera, 83.1% of the grand total of genera, occurred in two families, Noctuidae and Geometridae. Similarly, the number of species representing the Noctuidae and Geometridae totaled 858, 80.3% of the entire sample. The total number of individual Noctuidae and Geometridae was 15 060 individuals, 83.2% of the total sample.

Comparisons of species occurring at each of the six sites in the two survey areas, HJA and JIRI showed that JIRI exhibited higher values for overall numbers of families, genera and species (Table 2). The total numbers of observed and estimated species, abundance and singleton rate were statistically different between the two survey areas (number of species,  $t = -4.416$ ,  $df = 34$ ,  $P < 0.001$ , number of estimated species,  $t = -4.560$ ,  $df = 34$ ,  $P < 0.001$ , abundance,  $t = -2.888$ ,  $df = 34$ ,  $P < 0.01$ , singleton percentage  $t = -5.504$ ,  $df = 34$ ,  $P < 0.001$ ).

A comparison based on three-year means at JIRI and HJA showed that the peak value for moth abundance and species richness occurred at different times of the year (Fig. 3). At JIRI, mean moth abundance/species richness increased rapidly from May into June, peaked in June and decreased rapidly into July and August, with further declines into

**Table 2** Total abundance and richness among macromoths at six sites within a transect located at the HJ Andrews Experimental Forest, USA (HJA), 2004–2006, and Mt. Jirisan National Park, South Korea (JIRI), 2005–2007

Family	Abundance		No. of Genera		No. of Species	
	HJA	JIRI	HJA	JIRI	HJA	JIRI
Noctuidae	2032	4 467	87	177	169	321
Geometridae	4593	3 968	70	135	127	245
Arctiidae	228	596	6	13	9	24
Notodontidae	180	534	4	35	6	51
Lymantriidae	12	304	1	12	2	23
Drepanidae	5	272	1	10	2	13
Thyatiridae	26	240	4	7	5	13
Sphingidae	5	154	2	13	2	18
Limacodidae	–	149	–	9	–	10
Saturniidae	14	31	2	3	2	3
Epiplemlidae	9	18	1	1	1	2
Lasiocampidae	106	17	2	6	2	8
Bombycidae	–	13	–	3	–	3
Thyrididae	–	10	–	2	–	4
Zygaenidae	–	5	–	1	–	1
Cyclididae	–	2	–	1	–	1
Uraniidae	–	2	–	1	–	1
Endomidae	–	1	–	1	–	1
Diopitidae	9	–	1	–	1	–
<b>Total</b>	<b>7219</b>	<b>10 883</b>	<b>181</b>	<b>430</b>	<b>328</b>	<b>742</b>



**Figure 3** Timing of macromoth mean species richness (top) and abundance (bottom) at six sites within a transect located at Mt. Jirisan National Park (triangles), South Korea (2005–2007) and the HJ Andrews Experimental Forest (squares), USA (2004–2006). Bars indicate standard deviation.

September and October. In contrast, at HJA mean moth abundance/species richness remained relatively low in May and June, peaked in July–August and decreased rapidly into September and October.

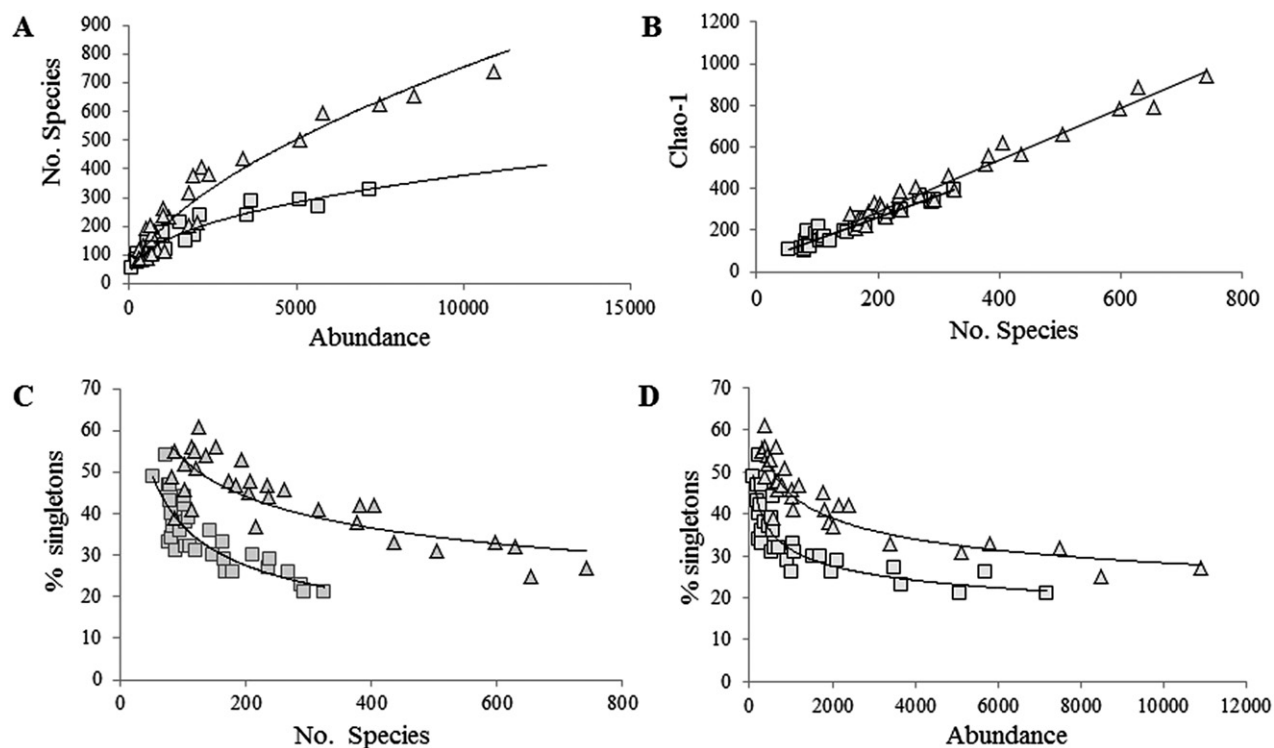
A comparison of abundance, species richness, percent singleton species and the Chao-1 index among each trap site showed the highly variable pattern among years and trap sites within the same survey area (Table 3, Fig. 4). The range in abundance varied from two-three-fold to four-fold differences: HJA trap site #2 ranged from 294 to 1080 individuals and JIRI trap site #4 spanned 285 to 1010. The range in species richness was relatively constant, certainly exhibiting less fluctuation from year to year. However, the highest range in species richness was observed in middle elevation sites: 78–121 at HJA trap site #2 and 119–236 at JIRI trap site #4. The relatively low abundance and species richness were observed at high elevation sites: 97–233 and 53–83 at HJA trap site #6 and 310–1044 and 87–115 at JIRI trap site #6.

## Discussion

The present study is part of a project with the goal of establishing a long-term intercontinental collaboration based on a sampling protocol using standardized repeated measures at permanent sites to document macromoth species richness and abundance through time and across the landscape.

Site	No. indiv. (range)	No. species (range)	% Singletons	Chao-1
<b>HJA</b>				
1	1036 (193;287;556)	163 (81;97;103)	33 (43;36;44)	211 (146;183;214)
2	1967 (294;593;1080)	169 (78;112;121)	26 (33;32;31)	254 (101;151;166)
3	902 (299;229;374)	167 (81;82;105)	29 (47;34;38)	227 (123;123;148)
4	1702 (453;527;722)	149 (85;88;104)	30 (37;31;32)	192 (121;125;167)
5	1014 (202;268;544)	179 (78;102;109)	26 (47;42;39)	223 (105;152;191)
6	560 (97;230;233)	144 (53;83;74)	36 (49;40;54)	197 (106;111;194)
All	7181 (1538;2134;3509)	326 (212;238;236)	21 (30;29;27)	393 (263;300;301)
<b>JIRI</b>				
1	1201 (438;414;349)	234 (102;136;113)	47 (52;54;56)	370 (153;229;235)
2	2147 (638;1013;496)	405 (153;262;194)	42 (56;46;53)	619 (276;408;332)
3	1798 (348;763;687)	316 (126;184;172)	41 (61;47;48)	460 (265;291;259)
4	1927 (285;1010;632)	378 (119;236;206)	38 (55;44;48)	518 (193;385;314)
5	1779 (370;854;555)	204 (83;120;87)	45 (49;51;39)	327 (131;222;114)
6	2031 (310;1044;677)	216 (87;115;102)	38 (55;41;46)	290 (181;175;156)
All	10883 (2389;5098;3396)	742 (381;504;436)	27 (42;31;33)	941 (558;665;565)

**Table 3** A comparison of three-year totals (yearly totals) for abundance, species richness, percent singleton species and estimated species richness (Chao-1) among macromoths at six sites within a transect located at the HJ Andrews Experimental Forest, USA (HJA), 2004–2006; and Mt. Jirisan National Park, South Korea (JIRI), 2005–2007. Numbers in the parenthesis (range) indicate each value of first, second and third year, respectively



**Figure 4** Relationships between species richness and (A) macromoth abundance and (B) Chao-1 estimated number of species, between percent singleton species and (C) species richness and (D) abundance at six sites within a transect located at Mt. Jirisan National Park (triangles), South Korea (2005–2007) and the HJ Andrews Experimental Forest (squares), USA (2004–2006).

### Taxonomic profile

The taxonomic profile of the two study sites (HJA and JIRI) exhibited a similar pattern in their respective higher taxonomic composition such as the dominance of four (Noctuidae, Geometridae, Arctiidae and Notodontidae)

families. The high generic and species richness and abundance of individuals among the top macromoth families have been generally observed globally (Hebert 1980; Fiedler *et al.* 2008). Recently, in the context of bioinventory and ecologically based studies, a focus on a limited number of taxa, to serve as indicator taxa, has been discussed (Lambeck

**Table 4** Spatial and temporal occurrence of the most abundant species of macromoths among six traps sites at the HJ Andrews Experimental Forest, USA (HJA), 2004–2006; and Mt. Jirisan National Park, South Korea (JIRI), 2005–2007

Trapsite	Year-1	Year-2	Year-3	Overall
<b>HJA</b>				
1	<i>Clemensia albata</i> , 47 <sup>¶</sup>	<i>Clemensia albata</i> , 101 <sup>¶</sup>	<i>Clemensia albata</i> , 178 <sup>¶</sup>	<i>Clemensia albata</i> , 326 <sup>¶</sup>
2	<i>Panthea portlandia</i> , 66 <sup>†</sup>	<i>Macaria signaria</i> , 246 <sup>†</sup>	<i>Macaria signaria</i> , 274 <sup>†</sup>	<i>Macaria signaria</i> , 573 <sup>†</sup>
3	<i>Homorthodes hanhami</i> , 73	<i>Homorthodes hanhami</i> , 39	<i>Melanolophia imitata</i> , 64	<i>Homorthodes hanhami</i> , 125
4	<i>Macaria signaria</i> , 121 <sup>†</sup>	<i>Nepytia umbrosaria</i> , 125	<i>Clemensia albata</i> , 164	<i>Macaria signaria</i> , 332 <sup>†</sup>
5	<i>Macaria signaria</i> , 29 <sup>†</sup>	<i>Macaria signaria</i> , 114 <sup>†</sup>	<i>Macaria signaria</i> , 73 <sup>†</sup>	<i>Macaria signaria</i> , 216 <sup>†</sup>
6	<i>Pero behrensaria</i> , 30	<i>Macaria signaria</i> , 104 <sup>†</sup>	<i>Macaria signaria</i> , 72 <sup>†</sup>	<i>Macaria signaria</i> , 189 <sup>†</sup>
All	<i>Macaria signaria</i> , 285 <sup>†</sup>	<i>Macaria signaria</i> , 622 <sup>†</sup>	<i>Macaria signaria</i> , 553 <sup>†</sup>	<i>Macaria signaria</i> , 1460 <sup>†</sup>
<b>JIRI</b>				
1	<i>Heterothera postalbida</i> , 141 <sup>†</sup>	<i>Alcis angulifera</i> , 48 <sup>¶</sup>	<i>Sophta subrosea</i> , 30 <sup>††</sup>	<i>Heterothera postalbida</i> , 170 <sup>†</sup>
2	<i>Alcis angulifera</i> , 104 <sup>¶</sup>	<i>Hydrillodes morosa</i> , 102 <sup>‡</sup>	<i>Hermonassa arenosa</i> , 19 <sup>‡</sup>	<i>Hydrillodes morosa</i> , 169 <sup>‡</sup>
3	<i>Alcis angulifera</i> , 31 <sup>¶</sup>	<i>Hydrillodes morosa</i> , 62 <sup>‡</sup>	<i>Alcis angulifera</i> , 79 <sup>¶</sup>	<i>Alcis angulifera</i> , 144 <sup>¶</sup>
4	<i>Hydrillodes morosa</i> , 29 <sup>‡</sup>	<i>Hydrillodes morosa</i> , 111 <sup>‡</sup>	<i>Alcis angulifera</i> , 17 <sup>¶</sup>	<i>Hydrillodes morosa</i> , 157 <sup>‡</sup>
5	<i>Telorta edentata</i> , 95 <sup>§</sup>	<i>Hydrillodes morosa</i> , 358 <sup>‡</sup>	<i>Hydrillodes morosa</i> , 158 <sup>‡</sup>	<i>Hydrillodes morosa</i> , 523 <sup>‡</sup>
6	<i>Telorta edentata</i> , 54 <sup>§</sup>	<i>Hydrillodes morosa</i> , 480 <sup>‡</sup>	<i>Hydrillodes morosa</i> , 314 <sup>‡</sup>	<i>Hydrillodes morosa</i> , 800 <sup>‡</sup>
All	<i>Alcis angulifera</i> , 228 <sup>¶</sup>	<i>Hydrillodes morosa</i> , 1117 <sup>‡</sup>	<i>Hydrillodes morosa</i> , 516 <sup>‡</sup>	<i>Hydrillodes morosa</i> , 1755 <sup>‡</sup>

†Conifer-feeder.

‡Detritus-feeder.

§Forb/herb/grass-feeder.

¶Hardwood-feeder.

††Unknown foodplant.

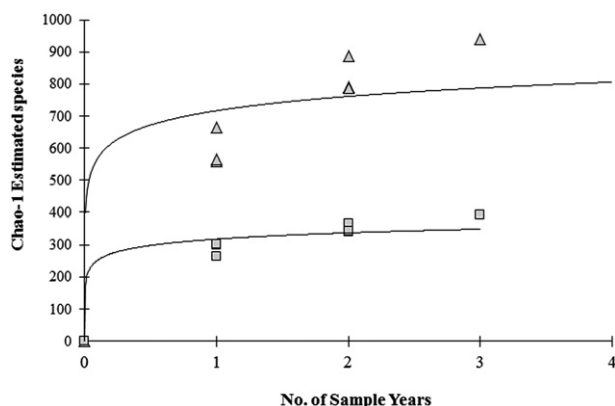
1997; Wiens *et al.* 2008). The question regarding indicator taxa is: Should studies include “extra” taxa (families) instead of the top few (one to four families) in a long-term repeated measures project. Based on the fact that we relied entirely on macromoth taxa as our taxa of interest we do not desire to further restrict our taxonomic base to just the Noctuidae, or Geometridae, or a combination of the two. The reasons we use to justify the inclusion of macromoth taxa beyond the specious groups such as Noctuidae and Geometridae are that we desire to: (i) document and understand the dynamics of a very large species assemblage, as large as is possible with our taxonomic expertise to the species level; (ii) include a wide array of taxa for representation of a broader “universe” of life history strategies; and (iii) compare responses in species that have very different ecological requirements. For instance, food plant relationships and the ability to colonize newly available habitat following a local/regional disturbance may be best examined using a set of species other than Noctuidae and Geometridae. For example, at HJA excluding a drepanid species, *Drepana arcuata*, would eliminate data for a species that is an important member of the alder-feeding guild. On the other hand, if we include too many different moth groups, not only macros but micros as well, we are confronted with practical difficulties such as time, money and expertise for identification. The practical relevance of ranking the families by the number of species is to know which taxa will require the

greatest effort for species identifications over the long-term period of the project and to either develop that expertise or seek existing expert collaborators. For example, the three-year study of all moth inventory projects from JIRI would require at least 1.5 times the current effort.

Although generalized taxonomic patterns appear to be relatively similar between HJA and JIRI (Table 2), significant inter-site differences, in a context of precise taxonomic composition, are evident by an assessment of dominant species and shared species. Only four species were seen in both Oregon and South Korea: *Ectropis crepuscularia*, *Epirrita autumnata*, *Peridroma saucia* and *Xestia c-nigrum*. The most abundant species in the HJA was *Macaria signaria* ( $n = 1460$ ), a geometrid that as a caterpillar feeds on conifer foliage, while the most abundant species in JIRI was *Hydrillodes morosa* ( $n = 1755$ ), a detritivore (Table 4). A profile of the numerically dominant species at each trap site revealed that the HJA site generated a majority of individual moths that belong to a conifer-feeding guild (Miller *et al.* 2003), conifers are the dominant plant in the HJA landscape. The feeding guilds at JIRI have yet to be assessed but the flora is dominated by hardwoods and it is our supposition that a majority of the individual moths at JIRI will be discovered to be associated with a hardwood-feeding guild. The lack of shared species and the higher taxonomic abundance/species richness at JIRI, in part, results from differences in landscape heterogeneity, floral diversity/

composition and energy/moisture inputs, similar to the factors that have been discussed (Summerville & Crist 2008) concerning moth biodiversity in eastern North America.

Relative to moth abundance at each trap site and overall totals of abundance, the percentage of singletons, the number of species detected only once per year, indicates a level of accuracy in empirically measuring species richness (Fig. 4). One of our primary questions was: How did the empirical measure of species richness compare to an estimated (Chao-1) value? The difference between the empirical measure of species richness and an estimated value, the Chao-1 index, indicates the degree of effort needed to assess the overall species richness of a plot, site, or region. The number of species discovered at any site is dependent on the sampling effort and the measure of species richness must be



**Figure 5** Mean estimates of species richness based on the combined totals from annual sampling for macromoths at six sites within a transect located at Mt. Jirisan National Park (triangles), South Korea (2005–2007) and the HJ Andrews Experimental Forest (squares), USA (2004–2006).

standardized. Standardization of species richness data is best addressed by integrating two approaches: (i) establish uniform, consistent, repeated measures sampling protocols to obtain an empirical measure of species richness; and (ii) adjust the empirical measure of species richness via a statistical method involving rarefaction, for instance calculate a Chao-1 index.

A relatively large difference (indicated by a high percentage of singletons) between the empirical measure of species richness and the estimated measure of species richness suggests a greater sampling effort is needed in terms of considering a reduced interval between samples (sampling frequency), more traps per site, and/or more years in the life of the project (Fig. 5). The three-year range in singleton captures among the six trap sites at each location was 27–30% at HJA and 31–42% at JIRI. The Chao-1 index estimated 941 species at JIRI and 393 species at HJA. Thus, the overall empirical species richness represented about 81% of the estimated species richness, 83% at HJA and 79% at JIRI.

In the context of bioinventory and long-term monitoring the critical question is: Based on statistical analysis how many years are required for adequately assessing the fauna given a certain sampling intensity that is held constant across all years. The sampling effort in HJA and JIRI was almost identical but it resulted in two distinct trajectories for extrapolating future sampling effort (Table 5, Fig. 5). For example, at HJA a second year of sampling provided a 22% gain to a revised estimate of 350 species, a third year of sampling provided a 12% gain to a revised estimate of 393 species. Similarly, at JIRI, a second year of sampling provided a 38% gain in the revised estimate of 822 species and a third year of sampling provided a 13% gain to a revised estimate of 941 species. By combining information on estimates of species richness among any single year, the mixture

**Table 5** Result of the testing for difference between two population regression coefficients and elevation. Data of abundance, species richness and estimated species richness were log-transformed. Calculation was based on Zar (2010). Explanation of each variable: moth abundance (abundance), species richness (no. species), percent singleton (% singleton), estimated species richness (est no. species) and the number of sample years (no. sample yrs). Asterisk (\*) indicates  $P < 0.05$

		a	b	X	Y	t (slope)	t (elevation)
Abundance: no of species	HJA	0.03	0.73	2.86	2.11	-2.25*	-0.23
	JIRI	0.01	0.76	3.07	2.33		
No. species: est no. species	HJA	0.006	1.07	2.11	2.27	-0.33	-0.05
	JIRI	0.008	1.08	2.33	2.52		
Abundance: % singleton	HJA	0.03	0.73	2.86	2.11	-2.25*	-0.23
	JIRI	0.01	0.76	3.07	2.33		
No. of species: % singleton	HJA	1.01	15.84	2.11	34.39	-1.71	-0.24
	JIRI	1.51	18.36	2.33	44.32		
No. sample yrs: est no. species	HJA	0.34	1.27	1.71	2.51	-2.23*	-0.002
	JIRI	-678.64	397.54	1.71	2.86		

HJA, HJ Andrews Experimental Forest, USA; JIRI, Mt. Jirisan National Park, South Korea.



of two-year periods and the three-year total, we found that the annual increment of increase in the Chao-1 value gradually declined with an increase in the number of years assessed. In the context of long-term monitoring this asymptotic curve represents the declining difference between empirical measures of species richness and the estimated values. In the current project, the practice of conducting repeated measures studies, at the stated levels of sampling intensity, indicated a need for our project to occur over a period of more than three years if our goal is to obtain a value of empirical data on species richness relative to Chao-1 that is in excess of 90%.

### Temporal patterns in species abundance and richness

Three questions were fundamental to our assessment of temporal patterns: (i) When was species richness low/high?; (ii) When was abundance low/high?; and (iii) In a comparison of the two study sites how similar/different were the phenological patterns?

The range in abundance typically spanned two-three-fold within a given trap site, but often spanned up to four-fold differences (Table 3). The seemingly high level of variance in inter-annual abundance at any given site suggested that the population dynamics of the local species was highly variable. An understanding of current temporal patterns in moth abundance/species richness creates a baseline for long-term assessment on the dynamics of impacts caused by environmental change (e.g., Itämiies *et al.* 2011; Pöyry *et al.* 2011; Fox 2012). The two study sites (JIRI and HJA) provided an excellent comparison of the influences of climate on moth abundance/species richness. Both JIRI and HJA show a parallel pattern in temperature trends throughout the year, that is, temperatures increase in February from freezing during the winter months of December and January, to gradual warming during the spring months of May and June, with peak temperatures during the summer months of July and August, followed by a drop in temperatures into the fall months of September, October and November (Fig. 2). While the peak moth abundance/species richness corresponds to peak temperatures (summer months) at HJA the same is not shown for peak moth abundance/species richness in JIRI, corresponding to relatively cooler early summer conditions (Fig. 3). The pattern suggests that temperature alone does not appear to offer a consistent explanation regarding the pattern in moth abundance/species richness at the two locations. Seasonal patterns in precipitation at JIRI and HJA are in effect mirror images (Fig. 2). Peak precipitation occurs during the cold winter months at HJA while peak precipitation occurs in the hot summer months at JIRI. Mean moth abundance at HJA coincided with the dry summer months, but peak moth abundance at JIRI coincided

with relatively moderate rainfall before monsoon in July. Therefore, the combined effect temperature and precipitation may play differently to the seasonal pattern of moth abundance/ species richness across the Pacific.

These data will serve as a benchmark for long-term monitoring of moth abundance/species richness with a purpose of assessing inter-annual climate dynamics with special attention given to assessing shifts in the timing and intensity of temperatures and precipitation with corresponding shifts in moth abundance. Future assessment of the climate-moth abundance/species richness relationships will require comparison of calendar-based chronology as well as the development of degree-day models, both aspects of this type of study are in progress.

### Spatial patterns in species abundance and richness

Three questions were fundamental to our assessment of spatial patterns: (i) Where was species richness low/high?; (ii) Where was abundance low/high?; and (iii) In a comparison of the two study sites how similar/different were the geographic (inter-trap) patterns?

The range in species richness was relatively constant (Table 3). However, the highest range in species richness at a given site was 78–121 at HJA trap site #2 and 119–236 at JIRI trap site #4. These sites are located at mid-elevation (about 700 m above sea level) and characterized by conifer or mixed deciduous forest. Meanwhile the relatively low abundance and species richness were observed at high elevation sites. The lowest range in abundance and species richness at a given site was 97–233 and 53–83 at HJA trap site #6 and 310–1,044 at JIRI trap site #6, respectively. Both sites are located at high elevation (more than 1300 m above sea level) and characterized by conifer-dominated forest. The observations that the high/low range in abundance and species richness occurred at the similar elevation and forest types suggested that the diversity pattern is resulted from similar ecological driving force across the globe.

An understanding of spatial patterns in moth abundance/species richness also creates a baseline for long-term assessment on the geographic breadth of each species. Documenting the local distribution of each species is pertinent to assessing the breadth of geographical range in each species in the context of the current trapping transects and proposing which species may be at risk given rapid environmental change.

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