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Ecological Study of Braconid Wasps in Different Logged over Forests with Special Emphasis on the Microgastrines (Hymenoptera:Braconidae)

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Abstract: An ecological study of braconid wasps with special emphasis on the subfamily microgastrinae was conducted in three different logged and fragmented forests (HSUKM, HSKLU and HSKLS). Sampling was done for one week per month starting from July to November 2001 using nine Malaise traps per forest. A total of 953 braconidae individuals comprising 19 subfamilies and 91 species (morphospecies) were collected. Of this, 195 individuals were collected at HSUKM, 414 individuals at HSKLU and 344 individuals at HSKLS. The microgastrinae, gnampthodontinae and rogadinae individuals were the most abundant in all forests having 427, 133 and 98 individuals respectively. Of the eight Microgastrinae species recorded, Sp4 was the most abundant in all forests but did not clearly indicate its preference to either older or younger regeneration forests. However, its presence seemed to be related to the forest size. Although HSUKM had the lowest microgastrines individuals, it had the highest diversity of microgastrines species compared with other forests. Results also showed that using value of H' (Shannon diversity index) this group of parasitoid has potential to be used as a biological indicator of environmental health or habitat disturbance status. Species similarity between the forests is somewhat higher (> 70%) but results suggested that the closer the forests the higher would be percent of species overlapped (shared). There were two different microgastrines community assemblages between the forests observed. The possible effect of size and distances between the logged over forests on the parasitoid abundance, diversity and species similarity are discussed.

Key words: Braconidae, microgastrinae, parasitoid, diversity, habitat disturbance

Introduction

The threat to global biodiversity through disturbance of tropical forests is an issue of current concern (Sutton and Collins, 1991), and that over half of global diversity in terms of number of species is represented by insects (Stock, 1991; 1993; Kim, 1993). Severe forest disturbance due to human alteration of the landscape for urban development and agriculture usually result in forest fragmentation (Sauer and Andropogon, 1998), a reduction of a large habitat area into small and isolated from one patch to another when surrounding land cleared (Smith and Smith, 2001) and presents barriers to dispersal for plants and animals. Differential size of the isolated forests and distance between them may influence animal diversity especially when there is no corridor (strips of vegetation linking one patch with another on the landscape) exists (Forman, 1995).

This study explored the differential effect of logged forests on braconid diversity and population abundance and to infer the results whether or not the braconid parasitoid wasps (Hymenoptera:Braconidae) is potentially be used as biological indicator of habitat disturbance. Braconid wasps represent one of the most diverse and abundant of the parasitoid groups (Shaw and Huddleston, 1991; LaSalle and Gauld, 1993). They are typically parasitoids of other insects, parasitizing and ultimately killing their hosts. Their most common hosts are the larvae of Lepidoptera, Coleoptera and Diptera (Wahl and Sharkey, 1993). Braconids are solitary or gregarious parasitoids, worldwide distribution with 52 genera, occur in very diverse habitats with no striking preference for tropical or temperate regions or for wet or dry habitat (Wahl and Sharkey 1993). Braconid species tend to attack and feed on a very narrow range of hosts and they are limited by specialized biological and behavioral adaptation (Wharton, 1993). Within Braconidae, subfamily Microgastrinae is the most conspicuous single group of parasitoids of Lepidoptera in the world, both in species richness and in economic importance. Over 1500 species have been described, and Mason (1981) has estimated that the actual world total may reach 5 000 - 10 000 species when the rich tropical and south temperate faunas are fully known. Microgastrines are found worldwide from tropical to arctic climates, and attack virtually the entire taxonomic and biological spectrum of Lepidoptera - many of them are pests of crops of economic importance. More than 100 species in this group have been used in the biological control of lepidopteran pests, and this total is likely to rise (Whitfield, 1995, 1997). Recently, microgastrines have become the focus genetic interest as carriers of polydnaviruses (Stoltz and Whitfield, 1992; Whitfield, 1997); these remarkable virus like entities are hereditary (Fleming and Summers, 1987) and play essential roles in the process of host parasitism by the wasps.

The responses of some insect groups such as butterfly and beetle to forest disturbance in the tropic have been comparatively well documented (Hamer et al., 1997; Sajap et al., 1999; Hill et al., 2001), but no data are available that show the effect of forest disturbance on the parasitoid wasps such as the braconid. This is particularly unfortunate because many parasitoids may response to disturbance more rapidly than the vertebrates or other insect groups, giving them potential as early biological indicators of environmental and ecological change (Kremen et al., 1993). However, the role of parasitoid communities the tropical rainforest ecosystem dynamic was studied in detail by Memmott et al. (1994).

The changes in forest structure, size and fragmentation resulting from human disturbance such as logging may represent a particular threat to biodiversity of a particular habitats or ecosystem (Harris, 1984) such as in the Langat Basin ecosystem. The objectives of this study were (1) to investigate the differential abundance of braconid wasps, (2) to find out the effect of forest's edge and distances between fragmented forest on diversity and abundance focusing on the subfamily microgastrinae and (3) to determine whether or not the age of regeneration forests have species in common (species similarity) in three logged over forests of the Langat Basin in Selangor, Malaysia. Results of the study are expected to serve as guideline for the policy makers and forest managers' decision in approving the land development projects and managing the Malaysian forests.

Materials and Methods

Study aites: Study was conducted at three different logged and fragmented forests of the Langat Basin in Selangor, Malaysia. The forests selected were UKM Forest Reserve (HSUKM), the Northern Kuala Langat Forest Reserve (HSKLU) and Southern Kuala Langat Forest Reserve (HSKLS) in Selangor, Malaysia. The HSUKM is a lowland dipterocarp forest with 50 – 200 m altitude and total area of 105 ha. It was logged twice, first between 1941 and 1945, and second in 1969 (Noraini, 1990). The HSKLU and HSKLS are peat

swamp forests with total area of 1107 and 7198 ha respectively. The HSKLU was logged in 1945, 1949 and 1993, and dominated by early succession plants while the HSKLS was logged in 1954 and 1976. The Diptherocarpaceae and Euphorbiaceae are the dominant plants in old and recently logged forests respectively (Bakri and Latiff, 2000). The climate of the study area is equatorial with high but uniform annual temperature, humidity, and rainfall throughout the year. Dry and wet seasons are not particularly well marked. The distances were approximately 20 km, 35 km and 75 km between HSKLU and HSKLS, HSKLU and HSUKM, and HSUKM and HSKLS. The villages and the scattered small agricultural areas, oil palm plantation, housing estates, Kuala Lumpur International Airport, and industrial areas are main features surrounding these

Experimental layout: Nine transects (three per forest = three replicates) were randomly established from each forest edge up to 500 m into the forest (Idris and Soon, 2002). The distance between transects was 600-700 m depending on the accessibility in installing the traps in each forest. Malaise traps were installed along each transect line namely at 5, 250 and 500 m from the forest edge respectively. Insects were collected from the traps 7-8 days later. The samplings were done for a week per month from July to November 2001 with sampling interval between 25-34 days (= four sampling occasions). Samples were brought to laboratory, placed in vials filled up with 70% ethanol and temporary kept in freezer before sorted out. The specimens were identified following Goulet and Huber (1993) and Achterberg (1993). Numbers of braconid individuals per subfamily or number of microgastrines individual per morphospecies per forest or distances from forest edges were recorded.

Data analysis: Data of four samplings were pooled before analysis to reduce error related to sampling time effect. Chi-square test was used to analyze total number of braconid individual among forests. A 2-way analysis of variance (ANOVA) was used to analyze differences in the number of braconid individual or number of microgastrines individual per species collected among forests and/or distances of trap from forest edge (MINITAB Version 13.0). When ANOVA was significant means were separated using Tukey's test at $\alpha=0.05$. A multivariate analysis (Anonymous, 1999) were used to find out percent species similarity (species assemblages) among species within forest and among forests. GW basic program (Robinson, 1991) was used to analyze the species diversity, richness and evenness.

Results and Discussion

Abundance and species composition: A total of 953 braconid individual comprising 19 subfamilies and 95 morphospecies were successfully collected from all three forests (Table 1). This had added the number of braconid subfamilies recorded from Malaysia from 18 (Idris and Nor Zaneedarwarty, 2000) to 21, i.e. 72.4% of the total braconid subfamilies recorded worldwide (29) (Wahl and Sharkey, 1993). There was a relatively no difference in the total number of subfamily collected among forests. However, there was a significant difference (x² analysis, df = 36, P ≤ 0.05) in the total number of individual collected among forests; the number of individuals collected was relatively higher in the older regeneration forests (HSUKM and HSKLS) than in the younger regeneration forest (HSKLU). This indicates that braconid was more abundant in the older forests than the younger forests and that disturbance negatively affected the braconid communities in the Langat Basin forests. Of the 19 subfamilies recorded the microgastrinae had the most abundant individuals (427) representing 43.7% of the total braconid individual collected while Braconinae, Agathidinae, Euphorinae, Dirrhopinae, Doryctinae and Alysiinae were the least abundant (rare) subfamily in these forests. In addition, the microgarstrinae had a relatively higher number of individuals per forest compared with other subfamilies (Table 1). Idris and Nor Zaneedarwarty (2000) also reported that microgastrines were

Table 1: Number of braconid individual per subfamily collected from three different logged over forest habitats from July to November 2001

	Forests*			
Cubénmilue				.
Subfamilys	HSKLU	HSKLS	HSKUKM	Total
Microgastrinae	66	171	190	427
Gnamptodontinae	32	52	89	173
Roganidae	29	31	38	98
Opiinae	27	33	28	88
Cheloninae	13	2,3	23	59
Aphidinae	3	17	16	36
Helconidae	7	4	11	22
Khaoikhoiinae	1	4	5	10
Macrocentrinae	4	1	4	9
Orgolinae	6	0	1	7
Miracinae	0	3	2	5
Trachypetinae	0	2	3	5
Meteoriinae	4	0	0	4
Braconinae	0	1	1	2
Agathidinae	1	0	1	2
Euphorinae	0	0	2	2
Dirrhopinae	0	2	0	2
Doryctinae	1	0	0	1
Alysiinae	1	0	0	1
Total subfamily	14	13	15	-
Total Individual	195	344	414	953
Chi-square (calculated)	127.0*	188.4*	246.9*	•

Table 2: Jaccard's coefficient index (similarity index) of microgastrinae collected from UKM forest reserve (HSUKM), the Northern Kuala Langat forest reserve (HSKLU) and the Southern Kuala Langat forest reserve (HSKLU)

- Lui	gat rorest reserve (ri		
Forest	HSUKM	HSKLU	HSKLS
HSUKM	1	0.753	0.751
HSKLU	0.753	1	0.714
HSKLS	0.751	0.714	1

*HSUKM, UKM forest reserve; HSKLU, Northern Kuala Langat forest reserve and HSKLS, Southern Kuala Langat forest reserve;

the most conspicuous group of braconid parasitoids in various habitats of Peninsular Malaysia. The microgastrines were species rich and abundant parasitoid group worldwide attacking the entire taxonomic of Lepidoptera as compared with other subfamilies of braconid (Manson, 1981). The Braconinae, Agathidinae, Euphorinae, Dirrhopinae, Doryctinae and Alysiinae species were reported to be more abundant in the temperate regions than in the tropical regions (Wahl and Sharkey, 1993).

The total number of microgastrinae individuals collected was 66, 189 and 171 for HSUKM, HSKLU and HSKLS respectively. In contrast to the braconid as a group, this result suggested that HSKLU (younger regeneration forests) had a relatively more abundant microgastrinae individuals than that of HSKLS and HSUKM (older regeneration forest). A total of eight microgastrinae species was successfully collected from HSUKM while HSKLU and HSKLS had six species each. There was a significant difference (F = 8.7, df = 2 and 14; P < 0.05) in the mean number of microgastrine individuals per species among forests. The mean number of species Sp4 individuals was significantly higher (P ≤ 0.05) in HSKLU (136) and HSKLS (110) than in the HSUKM (40) (Fig. 1). However, the number of individual of Sp8 was significantly higher (P ≤ 0.05) in HSKLU than the other two forests. The number of microgastrines individual collected was also significantly (P ≤ 0.05) influenced by interaction between forests and number of species collected.

The number of ichneumonid species in particular the Xanthopimpla species is also higher in HSKLU than in HSKLS and HSUKM (Idris et al., 2002). The recently disturbed forest (HSKLU) seemed to have less canopy cover allowing more vegetation to grow which eventually provides plenty of food for the microgastrines and its

^{*} Significant at P ≤ 0.05

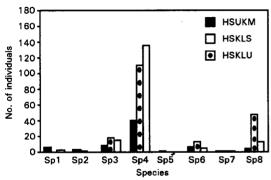


Fig. 1: Mean number of individuals per microgastrinae species collected from UKM forest reserve (HSUKM), Northern Kuala Langat Forest Reserve (HSKLU) and Southern Kuala Langat forest reserve (HSKLS) between July and November 2001

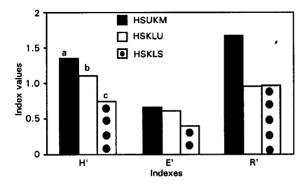


Fig. 2: Shannon-Weiner diversity index (H¹), evenness index (E¹) and Margalef¹s richness index (R¹) of microgastrines in three logged and fragmented forests (HSUKM, UKM forest reserve; HSKLS, the Northern Kuala Langat forest reserve; HSKLS, the Southern Kuala Langat forest reserve) of the Langat Basin in Selangor, Malaysia

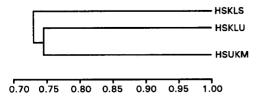


Fig. 3: Dendrogram from a cluster analysis based on the presence and absence of each microgastrine species recorded at different forests (HSKLS. Southern Kuala Langat forest reserve; HSKLU, Northern Kuala Langat Forest reserve; and HSKLS, Southern Kuala Langat forest reserve), utilizing Jaccard's coefficient index (similarity index) and the unweighted-pair groups method (UPGMA)

insect hosts (Shahabuddin, 2000; Thomas and Mallorie, 1985). In addition, the species recorded at HSKLU are most probably the area-insensitive species that favor disturbed habitat (Smith and Smith, 2001). High number of individuals Sp4 suggests that it prefers bigger size fragmented forest like HSKLU and HSKLS and not small size fragmented (or isolated) forest such as HSUKM. In contrast, Sp8 is clearly prefers bigger size and younger regeneration forest like HSKLU. Although the HSUKM is smaller in

size (105 ha) than HSKLU (1107 ha) and HSKLS (7198 ha), it had two more microgastrine species than that of HSKLU and HSKLS. The HSUKM might have served as refuge for many microgastrines species affected by the high degree of disturbances of the surrounding areas. It is expected that this extra species will not permanent here but rather will be migrated to other suitable habitats (such as HSKLU) or perish as a result of lack of resources for living and reproduction as well as high degree intra and interspecific competition.

Diversity: The value of Shannon-Weiner diversity index (H') for microgastrinae between forests was different significantly (Fig. 2). The HSUKM had significantly (P ≤ 0.05) higher H' value (1.36) than H' value of HSKLU (1.12) and HSKLS (0.76) (Fig. 2). However, the H' of HSKLU was also significantly different from that of HSKLS. The higher H' values in HSUKM is probably due to a higher species number (R') at HSUKM than the R' at HSKLU and HSKLS and not the evenness (E') (Pielou, 1975). This indicates that microgastrines diversity was positively influenced by the degree of habitat disturbance and the size and degree of isolation of a particular forest. HSUKM is much smaller in size and clearly isolated fragmented forests compared with the HSKLU and HSKLS. Disturbances to certain extend may be a better habitat for braconid (Idris and Nor Zaneedawarty, 2000; Idris et al., 2001) as well as for some other parasitoids (Noves, 1989; Idris et al., 2002). Although the recently regeneration forest of HSKLU was observed to have abundant of young trees, shrubs and herb plants that harbor food for microgastrines and their insect hosts compared to HSUKM, it had significantly (P < 0.05) lower H' value than that of HSUKM. Our hypothesis is that the close distance between HSUKM and HSKLU plus some existing plants that act as a 'corridor' between the two forests had allowed species movement, as suggested by Smith and Smith (2001) for vertebrate animals movement between fragmented habitats within landscape. A low H' value at HSKLS, the biggest of the three forests and as old as HSUKM with respect to time after last logged, indicates that HSKLS had less lepidopterans insects than that of HSUKM or HSKLU. Most microgastrine parasitizing larvae of lepidopterans that normally associated with the more open forests or disturbed habitat (Sahabuddin, 2000; Wahl and Sharkey, 1993). Diversity could be used as an indicator of environmental health (Noss, 1993). Result of this study showed that the more disturbed habitat like HSKLU and highly fragmented and isolated forests like HSUKM had high microgastrine diversity. As such microgastrine could be used as a potential biological indicator of environmental changes or health status.

Species similarity: The Jaccard's coefficient index (percent species similarity) among forests was between 0.714 (71.4%) and 0.751 (75.3%) (Table 2); similarity (shared or overlapping species) was 71.4%, 75.1 and 75.3 between HSKLS and HSKLU, HSKLS and HSUKM and HSUKM and HSKLU respectively. This indicates that the microgastrine species at the HSUKM comprising 75.3 and 75.1% of the species assemblages of HSKLU and HSKLS respectively, while only 71.4% species in HSKLU are somewhat similar with species of HSKLS. The higher percent similarity between HSUKM and HSKLS or HSKLU compared to between HSKLU and HSKLS suggests that the relative size of the forests might not the important factor in influencing the species shared among forests but rather the combination of age of the regeneration forests (eg., between HSUKM and HSKLS) and distance between them (eg., HSUKM and HSKLU). However, this observation is still preliminary and that repeated experiment of the same or different forests of similar features need to be done. Many species shared by HSUKM and HSKLS are probably specialist

braconid that are highly sensitive to habitat disturbance as compared to species inhabit the HSKLU (Hawkin and Sheehan, 1994). Higher species similarity between HSUKM and HSKLU is probably due to its proximate distant and that species between two forests may move freely through the existing corridor (Forman, 1995). Based on Jaccard's coefficient index there seemed to exist two community assemblages between these three forests. First is between HSKLU and HSUKM and another one is between HSKLU and the other two forests (Fig. 3). This suggests that bigger species assemblages occurred between to adjacent forests irrespective of their age after being lastly logged.

The braconids are more abundance in the older logged over forests but the microgastrinae indicates otherwise. There exist microgastrine species that are more abundant in certain forests but their present seems to be related the forest size; the abundance is higher in the older than the younger regeneration forests. However, diversity did not necessarily higher in either younger or bigger size forests. Species similarity between the forests is somewhat higher (> 70%) but results suggested that closer the forest the higher percent of species overlapped. Result of this study showed that the more disturbed habitat like HSKLU and highly fragmented and isolated forests like HSUKM had lower microgastrine diversity than that of less disturbed and isolated habitat like HSKLS. We found that the microgastrines could be used as a potential biological indicator of environmental changes or health status. These results could be proved useful information for policy makers and forest managers for the benefit of all of us.

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