

HOW BEETLE DIVERSITY CHANGES ACROSS YEARS AT PANGKOR ISLAND, MALAYSIA

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Abstract: Tropical islands such as Pangkor Island in western Malaysia have been recently subject to numerous land cover modifications and urban development. It threatens biodiversity and their effects remain unstudied for many taxa. In this study, we assessed the abundance, species richness, and diversity of beetles at Pangkor Island, at three different years, from 2009 to 2017. Also, we analyzed species composition between years, and the specific association of beetle families and species to each year was evaluated. A total of 578 specimens, 155 species and 34 families of Coleoptera were collected from the island after three years of sampling. A significant increase in abundance, species richness, and diversity were observed from 2009 to 2016; changes between 2016 and 2017 were non-significant. However, the comparison between 2009 to 2016 indicated a higher faunistic similarity than 2016-2017. Results observed in 2009 may be originated by the increasing disturbance since 2004 as a result of land clearing for tourism development; also, changes from 2016 to 2017 may be evidence of new disturbances. The biodiversity changes and their influence on species are necessary to detect the increasing pressure on biodiversity at the island ecosystems in Malaysia.

Key words: abundance, composition, disturbance, forest, species richness.

INTRODUCTION

Recent changes in land use cover, as well as the increase in the human population, drive major disturbances in natural ecosystems, due to the increase in forest and natural vegetation clearing for urban settlements in the last years. The impact of such

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modifications is more important in small land areas, such as tropical islands, where species have a smaller to disperse and recolonize after major disturbance (Velmurugan 2018).

The tropical islands of Malaysia are subjects of these changes since several have becoming tourist destinations in the last years (Selamat et al. 2016). Although it has benefits for local economies, however, bad planning and infrastructure design may result in changes in the spatio-temporal dynamics of communities, populations, and ultimately biodiversity loss (Mohamad et al. 2015). These effects are more serious in high biodiversity taxa, such as Coleoptera, whose species also have very important ecological functions, and their diversity is associated with other plant and animal taxa (Bouchard et al. 2009). However, despite its relevance, inventories, and diversity assessments of this group are inexistent or remain unstudied for several islands of Malaysia, such as Pangkor Island (Rooijen et al. 2011).

Pangkor constitutes an island classified as a coastal hill forest with a high conservation status (Ghollasimood et al. 2011). Nonetheless, several landscape modifications have been occurring due to the increase in economic development, land clearing, and the number of tourists between 2004 and 2014 (Sadatiseyedmahalleh et al. 2016, Selamat et al. 2016). Such changes due to the tourism development may be having further larger physical environmental impacts in the near future (Mohamad et al. 2015). Some studies exist on other taxa such as vegetation (Ghollasimood et al. 2011), herpetofauna (Rooijen et al. 2011, Norhayati et al. 2019), rodents (Jayaraj et al. 2019) and beetles (Abdullah & Musthafa 2019). However, none of these studies didn't compare the changes in species composition and distribution. This study was undertaken to assess the species composition and diversity of Coleoptera at three different years to detect changes in species composition.

MATERIALS AND METHODS

Study sites

Pangkor island is located at the Western coast of Peninsular Malaysia lay at 4° 13' 12" N; 100° 33' 18" E coordinates with a total area of 8 km² with a maximum elevation from sea level being 340 m. The sampling points are shown in Figure 1 and the collections were made at the same points in 2009, 2016, and 2017.

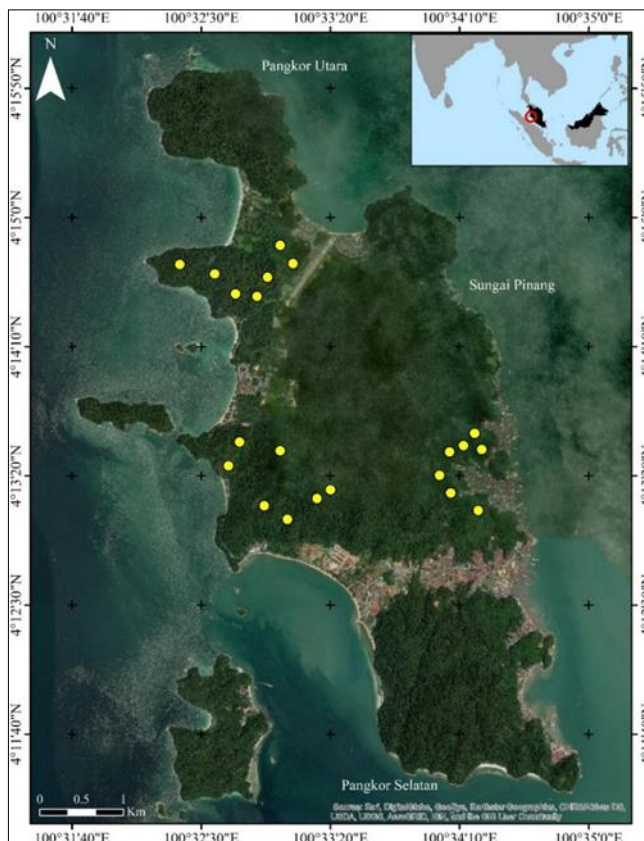


Figure 1. Sampling localities at Pangkor Island during this study over the years. The top-right box indicates the location of Pangkor Island (circled area) within Malaysia (black areas). Yellow points indicate sampling points.

Sample Trapping Methods

The two light traps, two Malaise traps, and 25 pitfall traps were fixed at Pangkor Utara, Sungai Pinang, and Pangkor Selatan in all three years from June to September. Malaise trap was made up of nylon net (black/white) with a collection jar half filled with 70% alcohol. Malaise traps were fixed at a branch of a tree not more than 1.0 m from the ground level. Malaise traps were set for 48 hours while pitfall traps were set in the site for 24 hours starting from 0800. Pitfall traps are 200 ml plastic cups (65 mm diameter, 9.5 cm depth) sunk into the ground with the brim at the same level as

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the ground. Beetles were sampled using pitfall traps partially filled with 70% alcohol. Large leaves were positioned to protect the traps from rain. Light traps were made of mosquito net with a 160-watt mercury bulb connected to a Honda EU10i portable power generator. The beetles attracted to the light were stuck on the net and they were collected using pill bottles.

Specimens and taxonomic identification

All the collected samples were sorted and tallied to Family level based on Triplehorn and Johnson (2005) and then cross-checked with the Wildlife Department of Malaysia, University of Malaya, National University of Malaysia and Forestry Department of Malaysia museum collections. Previous collections at the Toxicology Lab, University of Malaya were used to assign consistent morphospecies labels to specimens. The voucher specimens of each morpho-species had been retained in Toxicology Lab, University of Malaya insect collection.

Statistical Analysis

Differences in the abundance of beetles between years were compared by using the Kruskal-Wallis test, and Mann-Whitney for specific pairwise comparisons, after discarding normality of data. Species richness was measured as the number of species observed in each sampling year; dominance and diversity were measured with the Simpson index and Shannon index, respectively; differences in the three parameters were determined by analyzing the overlap in confidence intervals of the mean values. The faunistic similarity between years was assessed by using the Bray-Curtis index. The analysis was conducted in PAST 3.22 (Hammer et al. 2001). The abundance of families and species of beetles was associated, independently, with the year in which they occurred, according to the abundance values, by using simple correspondence analysis. Through this multivariate technique, the association between rows (families/species) and columns (year) was analyzed by a chi-square test (Beh 2004); values with a $p < 0.05$ indicate a significant association. The analysis was conducted in STATISTICA 8.0 (StatSoft Inc. 2007).

RESULTS

This study collected a total of 578 specimens from 155 species and 34 families of Coleoptera from the island after three years of sampling (Table 1). Only 37 species from 15 families were obtained in 2009. Overall numbers increased to 2016, when 91

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species from 24 families were collected. Finally, 108 species and 24 families were recorded in 2017. Significant differences in abundance were found between years (Kruskal-Wallis $H=42.26$; $p<0.001$). Specifically, the number of specimens increased significantly from 2009 (100 individuals) to 2016 (207) (Mann-Whitney $U=8120.5$; $p<0.001$) and from 2009 (100) to 2017 (270 specimens) (Mann-Whitney $U=7131$; $p<0.001$); changes in abundance from 2016 (207 individuals) to 2017 (270) were not significant (Mann-Whitney $U=11322.5$; $p=0.3485$).

Table 1. Checklist and abundance of beetles at Pangkor Island in 2009, 2016 and 2017.

Family	Species	Key	2009	2016	2017	Total
Anthribidae (Anth)	<i>Acorynus pictus</i>	Acp	1	2		3
	<i>Anthribus</i> sp. 1	Ant1			1	1
Bostrichidae (Bost)	<i>Amphicerus malayanus</i>	Ampm			41	41
	<i>Amphicerus</i> sp. 1	Amp1			4	4
	<i>Amphicerus</i> sp. 2	Amp2			2	2
	Anobiinae A	AnobA		5	1	6
	Anobiinae B	AnobB			1	1
	Anobiinae C	AnobC			1	1
	<i>Apoleon</i> sp. 1	Apo1			2	2
	<i>Bostrychus</i> sp. 1	Bo1			1	1
	<i>Calonistes</i> sp. 1	Cal1			5	5
	<i>Calonistes</i> sp. 2	Cal2			2	2
	<i>Dinoderus</i> sp. 1	Di1			1	1
	<i>Heterobostrychus</i> sp. 1	Het1			1	1
	<i>Lyctoxylon</i> sp. 1	Lyc1		2	1	3
	<i>Lyctoxylon</i> sp. 2	Lyc2			3	3
	<i>Minthea</i> sp. 1	Min1			1	1
	<i>Minthea</i> sp. 2	Min2			1	1
	<i>Paraxylion</i> sp. 1	Par1			1	1
<i>Sinoxylon</i> sp. 1	Sin1		2	1	3	
<i>Xylopsocus</i> sp. 1	Xyl1			1	2	
<i>Xylothrips</i> sp. 1	Xylo1		10	1	11	
<i>Xylothrips</i> sp. 2	Xylo2			15	15	
Bothrideridae (Both)	Bothrideridae A	BotA			1	1
	Bothrideridae B	BotB			1	1

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Table 1. (Continued)

Family	Species	Key	2009	2016	2017	Total	
Brentidae (Bren)	<i>Cerobates sexsulcatus</i>	Cers		2	1	3	
	<i>Stereodermus</i> sp. 1	Ste1		1	1	2	
Buprestidae (Bupr)	<i>Chrysochroa</i> sp. 1	Chr1		1		1	
Cantharidae (Cant)	<i>Falsomalthinus</i> sp. 1	Fal1		2		2	
	<i>Themus</i> sp. 1	The1		1		1	
Carabidae (Cara)	<i>Calleida</i> sp. 1	Call1	1	7	1	9	
	Carabidae H	CaraH			1	1	
	<i>Cylindera viduata</i>	Cit		3	1	4	
	<i>Collyris</i> sp. 1	Coll1		1		1	
	<i>Colpodes</i> sp. 1	Col1		9		9	
	<i>Colpodes</i> sp. 2	Col2			1	1	
	<i>Cyclosomus</i> sp. 1	Cy1			33	33	
	<i>Macrocheilus</i> sp. 1	Mac1			1	1	
	<i>Orthogonius</i> sp. 1	Ort1	1	14	2	17	
	<i>Orthogonius</i> sp. 2	Ort2		1		1	
	<i>Stenolophus smaragdulus</i> (Fabricius, 1798)	Sts	2	27	15	44	
	<i>Therates dimidiatus</i> Dejean, 1825	Thd		1	1	2	
	Cerambycidae (Cera)	<i>Ceresium furtivum</i> Pascoe, 1869	Cef	1			1
		<i>Demonax algebraicus</i>	Dea	1	1		2
<i>Glenea suturalis</i>		Gls			1	1	
<i>Hoplocerambyx</i> sp. 1		Hop1	1			1	
<i>Praonetha propinqua</i>		Prp	1	1		2	
<i>Trirachys aurifaber</i>		Tra	1	1		2	
Chrysomelidae (Chry)	<i>Aulacophora antennata</i>	Aua		3	1	4	
	Chrysomelidae C	ChrysoC	2	1	2	5	
	Chrysomelidae F	ChrysoF	1			1	
	<i>Dercetisoma concolor</i>	Derc			1	1	
	<i>Luperodes</i> sp. 1	Lup1	1	5	1	7	
	<i>Monolepta</i> sp. 1	Mon1		4	1	5	
	<i>Nodina malayana</i>	Nom		1	1	2	
	<i>Nodostoma</i> sp. 1	Nod1	1	1	2	4	
	<i>Ochralea nigripes</i>	Ocn	1	3	1	5	

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Table 1. (Continued)

Family	Species	Key	2009	2016	2017	Total
	<i>Phyllotreta</i> sp. 1	Phyl	1	2	1	4
	<i>Pseudocophora</i> sp. 1	Pse1		1	1	2
Cleridae (Cler)	<i>Omadius clytiformis</i>	Omc	5		1	6
	<i>Omadius seticornis</i> Westwood, 1855	Oms	1		1	2
Coccinellidae (Cocc)	Coccinellidae F	CocciF		1		1
	Coccinellidae G	CocciG		1		1
	<i>Coccinella</i> sp. 1	Coc1		3		3
	<i>Coccinella</i> sp. 2	Coc2		1		1
	<i>Cryptogonus fulvoterminalis</i>	Crf		1		1
	<i>Epilachna indica</i> Mulsant	Epi		1	1	2
	<i>Verania discolor</i> Fabricius	Ved		1	1	2
Curculionidae (Curc)	<i>Alcidodes</i> sp. 1	Al1		2	1	3
	<i>Alcidodes</i> sp. 2	Al2		1		1
	<i>Platypus</i> sp. 1	Pla1		1		1
	Scolytinae C	ScolC	3			3
	<i>Trigonopterus</i> sp. 1	Tri1		1	1	2
	<i>Xyleborus affinis</i>	Xya	4			4
	<i>Xyleborus schutzer</i>	Xys	3	1	1	5
Dryopidae (Dryo)	<i>Geoparnus</i> sp. 1	Geo1	6			6
	<i>Geoparnus</i> sp. 2	Geo2	1			1
Dytiscidae (Dyti)	Bidessini 1	Bi1	2	4	1	7
	<i>Hydroporus</i> sp. 1	Hyd1	1			1
Elateridae (Elat)	<i>Anathesis laconoides</i>	Anl	1	1		2
	<i>Anathesis</i> sp. 2	An2		1		1
	<i>Melanotus</i> sp. 1	Mel1	2	1	1	4
	<i>Melanotus</i> sp. 2	Mel2		1		1
Endomychidae (Endo)	<i>Amphisternus</i> sp. 1	Amph1			1	1
	<i>Cacodaemon</i> sp. 1	Cac1		1	1	2
	Endomychidae F	EndoF			1	1
	<i>Eumorphus</i> sp. 1	Eum1			1	1
	<i>Gerstaeckerus</i> sp. 1	Ger1			1	1
Eucnemidae (Eucn)	<i>Cebriorhipis</i> sp. 1	Ceb1		1		1
	<i>Cebriorhipis</i> sp. 2	Ceb2		1		1

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Table 1. (Continued)

Family	Species	Key	2009	2016	2017	Total
	<i>Euliches subocellata</i>	Eus		1		1
	<i>Fornax</i> sp. 1	For1		1		1
Histeridae (Hist)	<i>Nicotikis</i> sp. 1	Nic1		1		1
Hydrophilidae (Hydr)	<i>Helochares</i> sp. 1	Hel1			1	1
	<i>Omicrogiton</i> sp. 1	Omi1		2	2	4
Lampyridae (Lamp)	<i>Lucernuta</i> sp. 1	Luc1		1		1
	<i>Lucernuta</i> sp. 2	Luc2		1		1
Lucanidae (Luca)	<i>Figulus scaritiformis</i> Parry	Fis		1		1
Lycidae (Lyci)	<i>Cautines nervosus</i> Klne	Can		2		2
	<i>Conderis signicollis</i>	Cos		1		1
Lymexylidae (Lyme)	<i>Atractocerus</i> sp. 1	At1			2	2
Mordellidae (Mord)	<i>Gilpa</i> sp. 1	Gil1	6	1	1	8
	<i>Mordella</i> sp. 1	Mor1	6	1	2	9
	<i>Mordella</i> sp. 2	Mor2		1	1	2
	<i>Mordellistena</i> sp. 1	Mord1		1	1	2
	<i>Mordellistena</i> sp. 2	Mord2		2		2
	<i>Mordellistena</i> sp. 3	Mord3		2		2
Nitidulidae (Niti)	<i>Brachypeplus</i> sp. 1	Br1		3	1	4
	<i>Brachypeplus</i> sp. 2	Br2		1	2	3
	<i>Carpophilus</i> sp. 1	Carp1		2	1	3
	<i>Eपुरaea</i> sp. 1	Epu1		1	1	2
	<i>Eपुरaea</i> sp. 2	Epu2		1	1	2
	<i>Urophorus</i> sp. 1	Uro1		3	5	8
Passalidae (Pass)	<i>Leptaulax</i> sp. 1	Lep1			1	1
Phalacridae (Phal)	<i>Entomocnemus</i> sp. 1	Ent1			1	1
	<i>Grouvelleus</i> sp. 1	Gro1			1	1
	<i>Litostilbus</i> sp. 1	Lit1			1	1
	<i>Phalacrinus</i> sp. 1	Pha1			1	1
	Phalacridae F	PhlaF			15	15
Propalticidae (Prop)	<i>Propalticus</i> sp. 1	Pro1			1	1
Ripiphoridae (Ripi)	<i>Ohananomla</i> sp. 1	Oha1	23			23

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Table 1. (Continued)

Family	Species	Key	2009	2016	2017	Total	
Scarabaeidae (Scar)	<i>Anomala</i> sp. 1	Anom1			1	1	
	<i>Anomala</i> sp. 2	Anom2			4	4	
	<i>Anomala</i> sp. 3	Anom3			2	2	
	<i>Apogonia</i> sp. 1	Ap1		1	1	2	
	<i>Aserica</i> sp. 1	As1	4	1	2	7	
	<i>Onthophagus proletarius</i>	Onp	2	1	1	4	
Silvanidae (Silv)	<i>Airaphilus</i> sp. 1	Ai1			1	1	
	<i>Psammoecus</i> sp. 1	Psa1			1	1	
	<i>Silvanus</i> sp. 1	Sil1			1	1	
	<i>Silvanus</i> sp. 2	Sil2			1	1	
Staphylinidae (Stap)	<i>Aenictocleptis</i> sp. 1	Ae1		1	2	3	
	<i>Amaurodera</i> sp. 1	Ama1		1	3	4	
	<i>Bledius</i> sp. 1	Bl1		2	1	3	
	<i>Coproporus</i> sp. 1	Cop1		6	3	9	
	<i>Euconnus</i> sp. 1	Euc1		1		1	
	<i>Hesperus</i> sp. 1	Hes1		1	1	2	
	<i>Leptogenonia</i> sp. 1	Lept1	5	4	1	10	
	<i>Lispinus</i> sp. 1	Lis1		5	1	6	
	<i>Lispinus</i> sp. 2	Lis2		1	1	2	
	<i>Malaiseium</i> sp. 1	Mal1			1	1	
	<i>Orphnebius</i> sp. 1	Orp1		2	1	3	
	<i>Orphnebius</i> sp. 2	Orp2		2	1	3	
	<i>Paederus</i> sp. 1	Pae1		1	1	2	
	<i>Paederus</i> sp. 2	Pae2		1	2	3	
	Tenebrionidae (Tene)	<i>Ceropia</i> sp. 1	Cero1			17	17
		<i>Hemicera alternicolor</i>	Hea	1			1
<i>Leiochrodes glabratus</i>		Leg	2			2	
<i>Luprops</i> sp. 1		Lupr1		1	1	2	
<i>Luprops</i> sp. 2		Lupr2			1	1	
<i>Mesomorphus</i> sp. 1		Mes1	2			2	
<i>Obriomaia subcostata</i>		Obs	1			1	
<i>Strongylium</i> sp. 1		Str1		3		3	
<i>Uloma tufilabris</i>		Ult	1			1	
Trogidae (Trog)	Trogidae A	TrogA	1			1	

Regarding species richness, values were significantly different between all year comparisons (Fig. 2A). Dominance values were overall low for the three sampled

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years (under 0.1), but were significantly lower in 2016 when compared to 2017 and 2009 (Fig. 2B). Shannon entropy was different between all years, is significantly higher in 2016 than any other year; however, all values ranged from 3.0 to almost 4.0 (Fig. 2C).

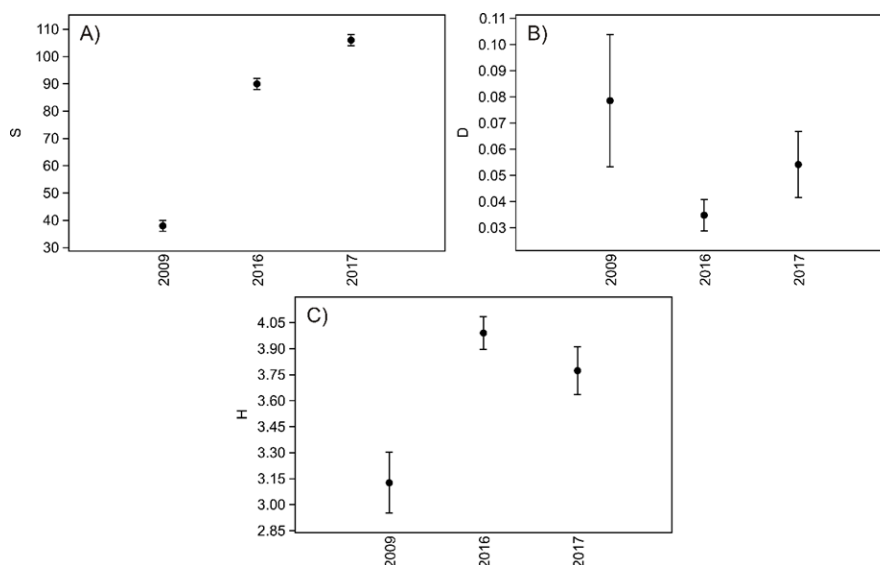


Figure 2. Diversity values of beetle communities in Pangkor Island in three sampling years. A) Species richness (S); B) Simpson Dominance (D); C) Shannon entropy (H).

According to the similarity in species composition, each sampled year corresponded to a distinct faunistic assemblage, since all comparison was below 50%. The higher similarity value was obtained between 2009 and 2016 (30.3%). Lower values were found between 2009 and 2017, as well as between 2016 and 2017 (7.1% and 17.8% of faunistic similarity, respectively).

The Correspondence analysis indicated a significant association between the abundance of beetles and the year when they occurred (Eigenvalues: 0.4865, 0.2147; Total chi-square=405.328; df=66; p=0.000). Several families were most associated with 2009 than other years, such as Ripiphoridae, Dryopidae, Trogidae, and Cleridae. Others such as Curculionidae, Cerambycidae, Chrysomelidae, Mordellidae, Scarabaeidae, or Tenebrionidae were distributed along all sampling period, from 2009 to 2017. Phalacridae, Silvanidae, Passalidae, Endomychidae, or Bostrichidae were mainly associated with 2016; by the contrary, Coccinellidae, Buprestidae,

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Eucnemidae, Lampyridae, Lycidae, Lucanidae, or Cantharidae, were dominant in 2017 (Fig. 3).

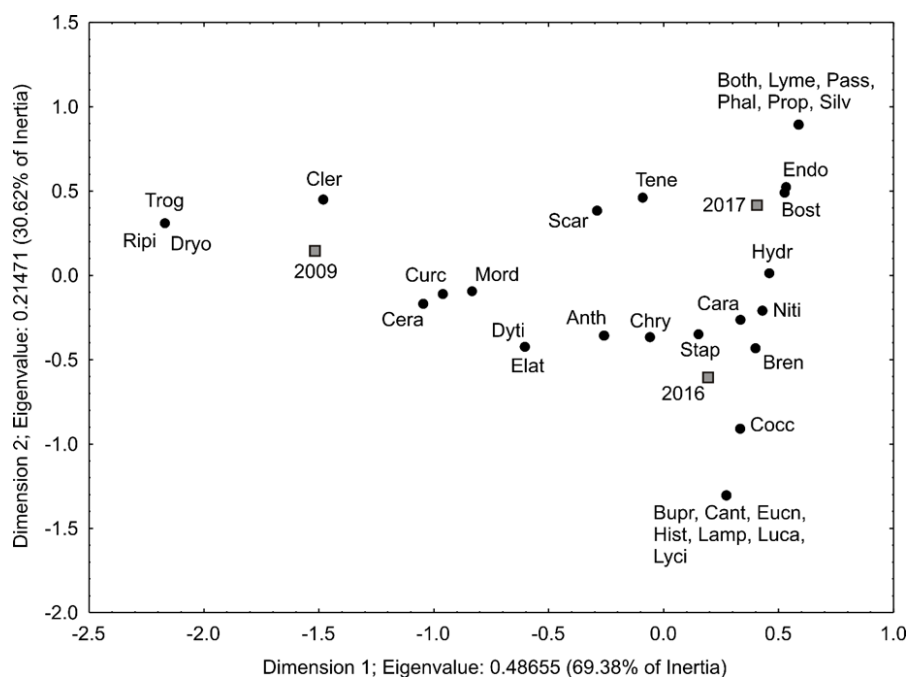


Figure 3. Correspondence analysis for Coleoptera families in three sampling years at Pangkor Island. The name of the families is in Table 1.

Similarly, species of beetles were significantly associated with the sampling years (Eigenvalues: 0.7161, 0.5543; Total chi-square=734.260; df=308; p=0.000). Clear tendencies were observed in the dispersion plot, according to the closeness between species and years. In the extreme left of the origin of the dispersion, species such as *Gilpa* sp. 1 (Gil1), *Mordella* sp. 1 (Mor1) and *Omadius clytiformis* Westwood, 1855 (Omc), and also all taxa within the dotted square, from *Ceresium furtivum* Pascoe, 1869 (Cef) to *Xyleborus affinis* Eichhoff 1868 (Xya), were highly associated with 2009. Species at the right-upper area of the plot, were closely related to the sampling year of 2017; these were *Aenictocleptis* sp. 1 (Ae1), *Amaurodera* sp. 1 (Ama1), *Brachypeplus* sp. 2 (Br2), *Paederus* sp. 2 (Pae2), *Urophorus* sp. 1 (Uro1), *Xylopsocus* sp. 1 (Xyl1), and all species in the upper dotted square, from *Airaphilus* sp. 1 (Ai1) to *Xylothrips* sp. 2 (Xylo2). Species in the lower area of the plot had their abundance concentrated in the year of 2016; examples of these were *Stenolophus*

smaragdulus (Fabricius, 1798) (Sts), *Aulacophora antennata* Baly, 1886 (Aua), *Monolepta* sp. 1 (Mon1), *Lispinus* sp. 1 (Lis1), *Orthogonius* sp. 1 (Ort1), *Calleida* sp. 1 (Call1), *Luperodes* sp. 1 (Lup1), as well as the species within the two lowest dotted squares, from *Alcidodes* sp. 1 (Al1) to *Sinoxylon* sp. 1 (Sin1), and *Alcidodes* sp. 2 (Al2) to *Themus* sp. 1 (The1). The right center dotted square contains species from *Apogonia* sp. 1 (Ap1) to *Verania discolor* (Fabricius, 1798) (Ved), which are related both to 2016 and 2017. *Omadius seticornis* Westwood, 1855 (Oms) occurred at 2009 and 2017, but not 2016; contrarily, *Anathesis laconoides* Candèze, 1865 (Anl), *Demonax algebraicus* Pascoe, 1869 (Dea), *Trirachys aurifaber* (Tra) and *Praonetha propinqua* Pascoe, 1865 (Prp) were mainly associated to 2009 and 2016, but not 2017. Other species are located at the center of dispersion, such as Chrysomelidae sp. C (ChrysoC), *Nodostoma* sp. 1 (Nod1), and *Phyllotreta* sp. 1 (Phy1), were beetles whose abundance was not associated with any year at particular, and as such, they were mainly distributed over all sampling period (Fig. 4).

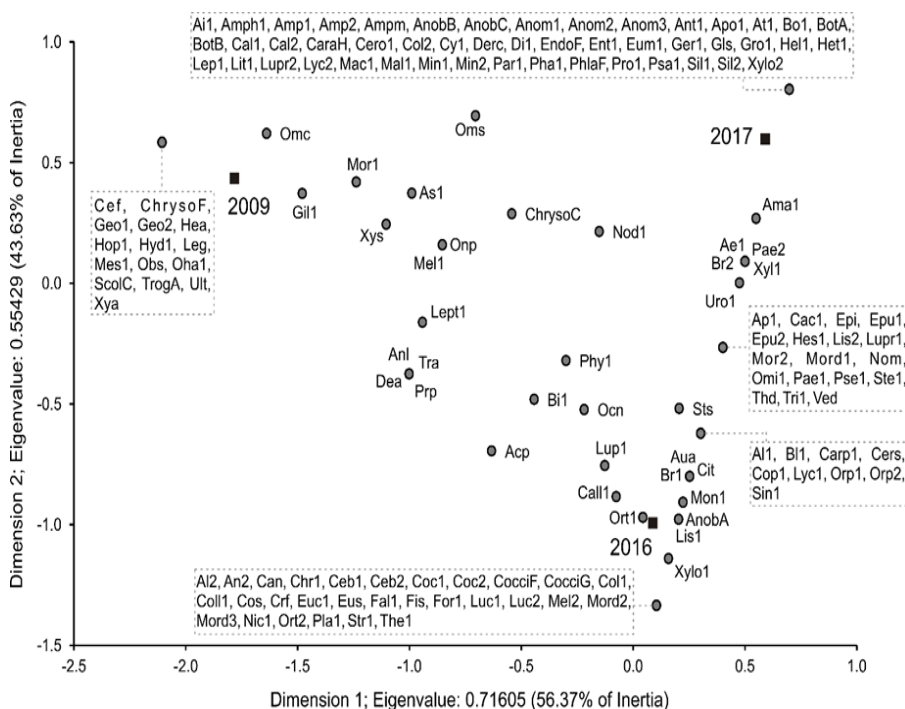


Figure 4. Correspondence analysis for Coleoptera species in three sampling years at Pangkor Island. The name of the species is in Table 1.

DISCUSSION

This study tested the change in beetle species composition through sampling in three different years. Species richness observed in the study area is high when compared with the number of species in other continental areas of tropical Malaysia (Musthafa et al. 2018). Moreover, species abundance, diversity, and richness are determined by climatic factors (temperature, relative humidity, light intensity), which could be shaping the beetle community patterns and the capacity of each species to obtain resources (Escobar et al., 2005; Bouzan et al., 2015).

Regarding temporal analysis, the lower number of species and individuals during 2009 may be a direct result of the increasing disturbance from 2004 as a result of land clearing for tourism development (Sadatiseyedmahalleh et al. 2016, Selamat et al. 2016). In the following years and due to successional processes, it is possible that species started to recolonize new areas, which was mirrored in the significantly higher number of species and specimens in 2016 and 2017, when compared to 2009. The same pattern must be related to dominance and Shannon index, which were the highest and lowest respectively, in 2009. Both index values may represent evidence of higher disturbance during 2009, as suggested in other studies with the increase in abundance of a few dominant species and a drop-in evenness (Miller et al. 2011), thus reducing diversity (Magurran 2004). This results when compared to 2016 and 2017, which may indicate evidence of the higher disturbance events during the first years after the initial conversion of Pangkor. Therefore, recovery processes may be operating during later years.

However, although these successional changes may be occurring, the communities may not be recovering to their original status, which is a common pattern during successional trajectories (Pulsford et al. 2016). Indeed, for this study, we found a 30% similarity in species composition between 2009 and the sampling that took place in 2016. It suggests a divergent trajectory in species replacement; also, all similarities were below 50%, suggesting unique faunas at each year. On the contrary, a very low similarity was obtained between 2016 and 2017 despite being continuous years. Although higher values of species richness and abundance were obtained in 2017, the species composition was very different from that observed in 2017. Besides, it is evident that dominance increased again, which may be a consequence of new disturbances that are not documented at present. An increase in the number of different species may be attributed to new niches originated by the land clearing for new touristic developments, as well as the formation of forest edges, which are related to an increase in beetle species. Further studies on touristic impacts on Pangkor island

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can be useful to assess the increasing pressure on biodiversity at the island ecosystems in Malaysia.

Results suggest that from 2016 to 2017 at least, the rates of changes in the island were faster, in a sense that even in the next year of sampling, the similarity in species composition was lower than compared with that observed seven years ago. Forest conversion may be exerting a higher and rapid influence on local species extinction and influencing modifications in beetle communities. Such conversion is evident in other tropical ecosystems as well (Hanski et al. 2009).

Evidence of forest conversion may also be related to the families of beetles and their functional habits (Lassau et al. 2005). Chrysomelidae, Curculionidae and other mainly phytophagous families were more abundant at the center of dispersion during all years from 2009 to 2017, which may be explained due to their close association to changes in vegetation along years. The same occurred with the three species located at the center of dispersion, which was leaf beetles. Overall vegetation of Pangkor Island comprises of 57% trees, 13% shrubs, 10% herbs, 9% lianas, 4% palms, 3.5% climbers and 3% ferns according to Ghollasimood et al. (2011). The beetle species diversity fluctuation over the tested years maybe depend upon the habitats provided by these vegetation. The most significant factor contributing to mega diversity of insects in the tropics is the diversity of plants (Zhao et al. 2015, Staunton et al. 2016). Apart from the vegetative change, the massive anthropogenic activities (constructions, tourism, infrastructure developments) were also observed throughout Pangkor island. According to Kubota et al. (2000), good numbers of beetle species have a relatively low dispersal ability compared with other insects and are thus vulnerable to isolation by geographic barriers.

The species richness of endemic and endangered species is a vital indicator of biodiversity conservation efforts (Laurila-Pant et al. 2015). Therefore, there should be more concentrated efforts are required to conserve the endemic beetle species that can be found at Pangkor Island. Further studies should focus on identifying the fluctuations of different endemic species found at Pangkor Island to assess the ecological and evolutionary roles of beetle species.

We documented for the first time a temporal analysis of beetle's biodiversity at Pangkor Island, which is one of the tropical islands from Malaysia. As such, it has been subjected to very fast anthropogenic modifications due to the increase in touristic development, yet studies comparing faunistic changes in different years are scarce for

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the study area. The lowest values of abundance, species richness and diversity found during the first year evaluated may reflect the higher disturbance conditions on the island, which were stronger starting from 2004. Afterward, a significant increase in such values during 2016 could be associated with a recovery of communities. However, the lower values of faunistic similarity between 2016 and 2017 and the increase in dominance at 2017, may suggest that new disturbances are occurring in the area. Families and species of beetles were specifically associated with the sampling years, which reveals the specific conditions occurring at each temporal stage, and which surely are related to each species niche. Such conditions are associated with the changes in vegetation, thus proving the importance of the historical land cover modifications in the area. Therefore, temporal analysis as the one here conducted is useful to document the historical change in biodiversity of a hyperdiverse group, in tropical islands in which tourist development is gaining ground. The results herein obtained may be useful for the responsible and sustainable development of Pangkor Island, as well as other areas of Malaysia.

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