

**ISLAND BIOGEOGRAPHY OF TERRESTRIAL
SNAIL FROM ISLANDS OF SABAH,
MALAYSIA**



PHUNG CHEE CHEAN

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**INSTITUTE FOR TROPICAL BIOLOGY AND
CONSERVATION
UNIVERSITI MALAYSIA SABAH
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**ISLAND BIOGEOGRAPHY OF TERRESTRIAL
SNAIL FROM ISLANDS OF SABAH,
MALAYSIA**

PHUNG CHEE CHEAN



**THESIS SUBMITTED IN FULFILLMENT FOR
THE DEGREE OF MASTER OF SCIENCE**

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CONSERVATION**

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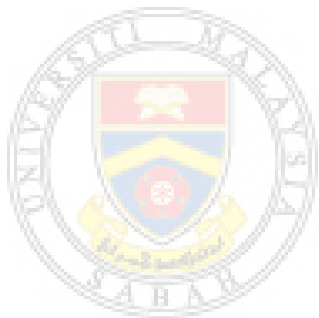
2018

DECLARATION

I hereby declare that the material in this thesis is my own except for quotations, excerpts, equations, summaries, and references, which have been duly acknowledged.

30 NOVEMBER 2017

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ABSTRACT

Islands always held special attraction to scientist as model systems in biogeography and evolutionary studies. In Sabah, there are about 500 islands with various degree of isolation and size, and have experienced different climatic or historical processes. These attributes promise high research potential particularly in the field of island biogeography. Unfortunately, the up-to-date knowledge about the island biodiversity in Sabah is scarce in spite of the fact that Sabah is situated within one of the megabiodiversity hotspots. In addition, the geographical, ecological and evolutionary factors that shaped the Sabah's islands biodiversity pattern are yet to be tackled. Using land snail as subject, an annotated checklist of land snail from 24 west coast islands of Sabah was presented and was explained the effect of island area, isolation on species composition and species richness. The phylogeography pattern of selected land snail species (i.e. *Leptopoma pellucidum*) from northwest islands was also demonstrated to understand the present genetic distribution and structure, and infer underlying historical processes by calibrating the phylogenetic tree with molecular clock. A total of 67 land snail species were documented from 24 west coast islands of Sabah based on 133 systematic sampling plots, collection database and published records. Land snail composition pattern was influenced by both isolation and area. The results of this study demonstrated that the species richness on Sabah's island was largely determined by interaction among island area and isolation. With respect to phylogeography of *L. pellucidum* from northwest islands, the results revealed that its genetic structure was categorised into three major lineages. Surprisingly, time-calibrated tree showed that the genetic divergence time does not correspond with island isolation due to sea level rising during Last Glacial Maximum. The lineages were estimated to have diverged during the middle and late Pleistocene. Earlier periodic interglacials and Pleistocene climate fluctuation might caused intra-specific divergence. This study reveals biogeography and evolutionary processes of Borneo's island. This study also contribute to island biodiversity management plan as island size can be the relevant variable in conserving land snail diversity.

ABSTRAK

BIOGEOGRAFI PULAU BAGI SIPUT DARAT DARI PULAU-PULAU DI SABAH, MALAYSIA

*Pulau merupakan tarikan istimewa kepada saintis sebagai model sistem dalam kajian biogeografi dan evolusi. Di Sabah, terdapat kira-kira 500 pulau yang pelbagai saiz, jarak dari tanah besar dan mengalami proses iklim atau sejarah geologi yang berbeza. Ciri-ciri ini menjanjikan potensi penyelidikan yang tinggi terutamanya dalam bidang biogeografi pulau. Walaupun Sabah merupakan salah satu pusat biodiversiti mega, pengetahuan terkini mengenai kepelbagaian biologi pulau di Sabah masih terhad. Di samping itu, faktor geografi, ekologi dan evolusi yang membentuk kepelbagaian biologi di pulau-pulau Sabah masih belum diketahui. Dengan mengambil siput darat sebagai subjek kajian, di sini saya memberi senarai semak spesies siput darat dari 24 pulau di pantai barat Sabah dan menjelaskan peranan saiz pulau, jarak dari tanah besar dalam pembentukan komposisi dan kekayaan spesies. Selain itu, corak filogeografi siput darat terpilih (iaitu *Leptopoma pellucidum*) juga ditunjukkan untuk memahami struktur genetic dan taburan dengan mengkalibrasikan pokok filogeni menggunakan jam molekul. Sejumlah 67 spesies siput darat telah didokumentasikan dari 24 pulau di pantai barat Sabah berdasarkan 133 plot sistematik, pangkalan data dan rekod yang diterbitkan sebelum ini. Pola komposisi siput darat dipengaruhi oleh saiz pulau dan jarak dari tanah besar. Sementara itu, keputusan menunjukkan bahawa kekayaan spesies di pulau Sabah sebahagian besar ditentukan oleh saiz pulau dan jarak dari tanah besar. Pokok filogenetik *L. pellucidum* dari pulau menunjukkan bahawa struktur genetic dikategorikan kepada tiga kumpulan geografi utama. Tanpa dijangka, masa pencapahan genetik adalah tidak sepadan dengan tempoh pengasingan pulau yang disebabkan oleh peningkatan paras laut semasa Maksimum Glasial Terakhir (MGT). Pencapahan intra-spesifik dijangka berlaku di antara pertengahan dan akhir Pleistosen. Inter-glasia sebelum MGT dan iklim Pleistosen yang tidak konsisten mungkin merupakan sebab pencapahan intra-spesifik tersebut. Kajian ini telah mendedahkan proses biogeografi dan evolusi di Kepulauan Borneo.*

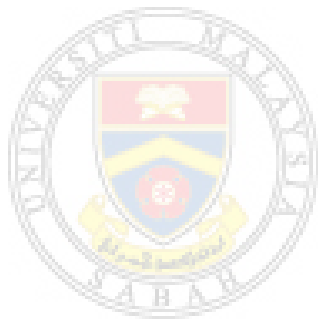
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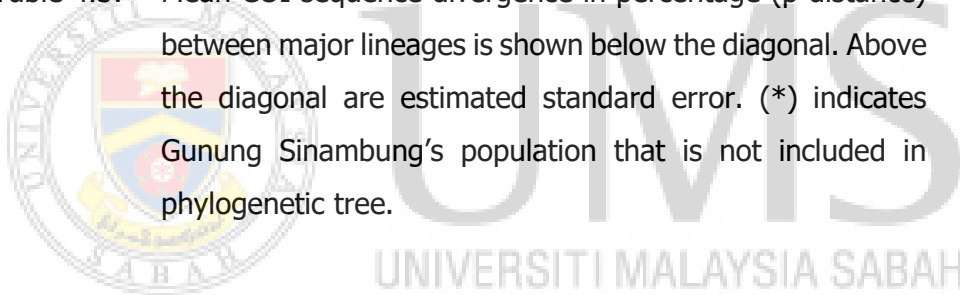
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LIST OF ABBREVIATIONS

%	-	Percent
AICc	-	corrected Akaike's Information Criterion
BEAST	-	Bayesian evolutionary analysis by sampling trees
BI	-	Bayesian Inference
BOLD	-	Barcode of Life Data System
COI	-	Cytochrome C Oxidase subunit I
DNA	-	Deoxyribonucleic Acid
ETIB	-	Equilibrium Theory of Island Biogeography
e.g.	-	for example; Latin phrase <i>exempli gratia</i>
et al.	-	and others; Latin phrase <i>et alia</i>
ISAR	-	Island species-area relationship
ITS-1	-	First internal transcribed spacer
Ka	-	Thousand years ago
LMM	-	Linear mixed model
LRT	-	Likelihood ratio test
ML	-	Maximum likelihood
Ma	-	Million years ago
nMDS	-	non-metric dimensional scaling
PCR	-	Polymerase Chain Reaction
PFM	-	Power function model
R²m	-	marginal R ²
sp.	-	species
Taq	-	<i>Thermus aquaticus</i>
TBE	-	Tris Borate-EDTA
χ²	-	Chi-square

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CHAPTER 1

INTRODUCTION

1.1 Background of study

Island biogeography is a study of the geographical distribution patterns and diversity of island or isolated organisms in space and time and the underlying forces for such patterns. Among a variety of natural geographical features, islands always held special attraction to scientist as one of the key model systems in studies of biogeography and evolution (Warren *et al.*, 2015) particularly after publications of Charles Darwin's and Wallace's work on the Galapagos island and Malay Archipelago (Darwin, 1859; Wallace, 1869). Unique island biotas are shaped under predictable processes due to special attributes of island like geographical isolation, relatively small size and young geological age (Losos & Ricklefs, 2009). Such circumstances allow testing of theories or hypotheses on processes of speciation, taxonomic diversity and composition. In particular, the ultimate goal of the island biogeography is to decipher the determinants of island biodiversity patterns.

A critical progress in the field of island biogeography is based on a relatively simple but comprehensive model by MacArthur and Wilson (1967), namely the Equilibrium Theory of Island Biogeography. The theory postulated that island biodiversity is shaped through dynamic equilibrium between immigration rate and extinction rate. The Equilibrium Theory also postulated that species richness increase with island area and decrease with isolation. With the equilibrium theory as a paradigm, a spawning number of studies have supported species-area and species-isolation relationship (Whittaker & Triantis, 2012 and reference therein; Parent, 2012). Despite the wealth of island biogeography studies, key determinants of island biodiversity patterns and how the determinants function are still not fully understood and the field requires a new theoretical framework instead of relying on the model

proposed half century ago (Brown & Lomolino, 2000). In view of this, continued testing of the theories on wide range of organisms from different geographical regions are required to provide novel insights into island biogeography.

Beside the island biogeography, island system also serves as the ideal site for the study of effect of geographical isolation, paleogeographical event or historical climate change on the genetic diversity and genetic distribution of island biotas (Bittkau & Comes, 2005). Study of phylogeography and population genetics on island biotas allows gaining insights into microevolutionary patterns and its underlying processes (e.g. Emerson *et al.*, 1999; Nakamura *et al.*, 2010; Ruedi & Fumagalli, 1996). Recent advancement on molecular techniques and theories allows comprehensive investigations of evolutionary histories of organism such as calibration of molecular clock that enables estimation of divergence times (Avice, 2009; Avice *et al.*, 1987, 1998). Thus, events that responsible for genetic divergence can be postulated and enables better understanding on evolution of island biotas.

Land snails are informative model organism for island biogeography (Holland & Cowie, 2009) and phylogeography study. Their sedentary behavior and passive dispersal ability that prevent them from escaping unfavorable environmental conditions allow scientists to track genetic variation patterns that arose in the past (Davison, 2002; Pfenninger & Posada, 2002). Moreover, the empty shells are well preserved in forest leaf litter which can be used to reveal their present geographical distribution. Therefore, the study of land snails can reveal the underlying biodiversity, evolutionary processes and biogeography patterns of islands.

Among the mega-biodiversity hotspot regions of the world (Myers *et al.*, 2000; Woodruff, 2010), the island of Borneo is the ideal natural laboratory for testing island biogeography theories. Borneo is the third largest island in the world (743,330km²) and also member of the most geographically complex tropical regions in the world, namely the Malay Archipelago (Lohman *et al.*, 2011). West coast of Sabah in northern Borneo was extensively connected to Sumatra, Java, Malay Peninsular and Indochina compare to northeastern part of Sabah during Last Glacial Maximum (LGM) which is about 20,000 years ago and periodic glaciations before LGM for relatively long periods