

UNIVERSITI PUTRA MALAYSIA

MORPHOLOGICAL AND MOLECULAR SYSTEMATICS OF Shorea SECTION Richetoides (DIPTEROCARPACEAE) IN PENINSULAR MALAYSIA

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FH 2018 2



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Thesis Submitted to the School of Graduate Studies, Universiti Putra Malaysia, in Fulfillment of the Requirements for the Degree of Master of Science

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DEDICATIONS

Dedicated With My Love to My Late Father

Ana

To My Beloved Mother, Her Love, Support, and Constant Prays Have Sustained

Me throughout My Life

To My Dear Sisters and My Brothers for Their Endless Love, Support and Sacrifices.



Abstract of thesis presented to the Senate of Universiti Putra Malaysia in fulfillment of the requirement for the degree of Master of Science

MORPHOLOGICAL AND MOLECULAR SYSTEMATICS OF Shorea SECTION Richetoides (DIPTEROCARPACEAE) IN PENINSULAR MALAYSIA

By

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November 2017

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A phylogenetic study of the *Shorea* section *Richetioides* (Meranti Damar Hitam) was conducted by using morphological characters and molecular technique. Shorea is one of the largest genera in the family of Dipterocarpaceae with an estimated 300 species worldwide and there are more than 150 species in Malaysia, of which more than one third is found in Peninsular Malaysia. This genus is distributed from India and Sri Lanka, through western Malaysia, to Philippines and Maluku. The identification of dipterocarps species including Shorea based on morphological characters is not an easy task due to similarities of vegetative characters, and taxonomic classification in deipterocarp have not been supported by their monophyletic origins. Therefore, comprehensive analysis using morphology and molecular studies is required to ascertain their status. Nine fresh samples of Shorea sect. Richetioides were collected from different areas in Peninsular Malaysia and were identified to the species level based on morphological characters. In addition, a new population of Shorea with similar feature of S. kuantanensis that was found in Terengganu, Peninsular Malaysia was included. Shorea kuantanensis, a member of Shorea sect. Richetioides classified as critically endangered species by IUCN Red List and was presumably extinct. This study will clarify the identity and providing a taxonomic evaluation of members in Shorea sect. Richetioides in Peninsular Malaysia because to date, there is no study on the phylogenetic relationship among all Shorea species within Shorea sect. Richetioides.

Morphological and molecular analyses were conducted for *Shorea* sect. *Richetioides* together with other sections in *Shorea*. Morphological analysis was done using distance method of Neighbor Joining Method (NJ), and molecular analysis was carried out using two phylogenetic analyses methods, NJ and Maximum Parsimony (MP).

Two non-coding regions from chloroplast (trnL intron, and trnL-F IGS) were used to construct the phylogenetic trees and rooted with genus Hopea. The morphological analysis confirmed that the newly rediscovered population of Shorea species is S. kuantanensis, and part of monophyletic group of Shorea sect. Richetioides. The monophyly of groups in Shorea is also consistent with the artificial grouping of wood in Shorea i.e., Red Meranti, White Meranti, Balau and Yellow Meranti (Meranti Damar Hitam). Phylogenetic analysis using molecular data also showed similar results on the monophyly of Shorea sect. Richetioides. The use of cpDNA (trnL intron and trnL-F IGS) has provided good resolution in phylogenetic trees and also confirm that the newly found population of Shorea as S. kuantanensis as been found with the morphological analysis.



Abstrak tesis yang dikemukakan kepada Senat Universiti Putra Malaysia sebagai memenuhi keperluan untuk ijazah Master Sains

MORFOLOGI DAN SISTEMATIK MOLEKUL Shorea SEKSYEN Richetoides (DIPTEROCARPACEAE) DI SEMENANJUNG MALAYSIA

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Kajian filogenetik Shorea seksyen Richetioides (Meranti Damar Hitam) dilakukan dengan menggunakan ciri morfologi dan kaedah molekul. Shorea adalah salah satu genera terbesar dalam keluarga Dipterocarpaceae dengan kira-kira 300 spesies di seluruh dunia dan terdapat lebih daripada 150 spesies di Malaysia, di mana lebih daripada satu pertiga ditemui di Semenanjung Malaysia. Genus ini tertabur dari India dan Sri Lanka, melalui Malaysia barat, ke Filipina dan Maluku. Pengecaman spesies dipterokarp termasuk Shorea berdasarkan karakter morfologi bukanlah tugas yang mudah kerana persamman dalam ciri vegetatif, dan pengelasan taksonomi dalam dipterokarp tidak disokong oleh leluhur monofiletik. Oleh itu, analisis menyeluruh menggunakan kajian morfologi dan molekul diperlukan bagi menentukan status spesies ini. Sembilan sampel segar dari Shorea seksyen Richetioides dikutip dari beberapa kawasan di Semenanjung Malaysia dan dicamkan ke peringkat spesies berdasarkan ciri morfologi. Di samping itu, satu populasi Shorea yang mempunyai ciri serupa dengan S. kuatanensis ditemui di Terengganu, Semenanjung Malaysia turut dikaji. Shorea kuantanensis merupakan ahli Shorea seksy. Richetioides dikategorikan sebagai spesies terancam dalam Senarai Merah IUCN dan dikatakan mungkin telah pupus. Kajian ini cuba untuk menjelaskan identiti dan memberikan penilaian taksonomi Shorea seksy. Richetioides di Semenanjung Malaysia kerana sehingga kini tiada kajian perhubungan filogeni yang telah dijalankan pada ahli Shorea seksy. Richetioides.

Analisis morfologi dan molecular dijalankan pada *Shorea* seksy. *Richetioides* termasuk beberapa lagi seksyen yang ada pada *Shorea*. Analisis morfologi menggunakan kaedah perbezaan jarak iaitu kaedah *Neighbor Joining* (NJ) an analisis molekular dengan kaedah Parsimoni Maksima (MP). Dua kawasan bukan berkod dari

kloroplas DNA (*trn*L intron dan *trn*L-F IGS) digunakan bagi membina pokok filogeni yang ditambat dengan genus *Hopea*. Analisis morfologi mengesahkan bahawa populasi *Shorea* yang baru dijumpai adalah spesies *S. kuantanensis* yang merupakan sebahagian daripada kumpulan monofiletik *Shorea* seksy. *Richetioides*. Kumpulan monofiletik dalam genus *Shorea* adalah konsisten dengan pengelasan artifisial pada kumpulan kayu dalam *Shorea* iaitu Meranti Merah, Meranti Putih, Balau dan Meranti Kuning (Meranti Damar Hitam). Analisis filogeni menggunakan data molekular pula memberikan keputusan yang sama dengan monofili *Shorea* seksy. *Richetioides*. Penggunaan cpDNA (*trn*L intron dan *trn*L-F IGS) telah memberikan resolusi yang baik dalam pokok filogeni dan mengesahkan yang populasi baru dijumpai *Shorea* adalah *S. kuantanensis* sama seperti keputusan dalam analisis morfologi.



ACKNOWLEDGEMENTS

Alhamdulillah, all praises to Allah S.W.T., The greatest and the most merciful for his guidance and blessing, because without it I can't finish this research. This dissertation would not have been possible without the guidance and the help of several individuals who in one way or another contributed and extended their valuable assistance in the preparation and completion of this study. First and foremost, my utmost gratitude to my main supervisor Associate Prof. Dr. Nazre Saleh whose sincerity and encouragement I will never forget. I would like to express my sincere appreciation to him for the continuous support of my Master study and research, for his patience, motivation, enthusiasm, and immense knowledge. His guidance helped me in all the time of research and writing of this thesis. I could not have imagined having a better advisor and mentor for my Master study. Beside my supervisor, I would like to thank my co-supervisor Associated Prof. Dr. Mohamad Azani Alias for his advice, and valuable feedback throughout my study. My sincere thanks also go to all my laboratory colleagues for their patience in guiding and information sharing for the molecular applications; and to the staff from the Faculty's herbarium, for their help in providing information in terms of botany studies. My appreciation also extended to all academic and non-academic members of the Faculty of Forestry for their warm heart cooperation during my stay in Universiti Putra Malaysia. I also wish to thank to the Forest Department of Peninsular Malaysia, especially the Forest Department of Terengganu State and the Forest Department of Johor State whom provided help and assistance in sample collection and botanical information for my study. Last but not least, I would like to display my sincere appreciation towards Mr. Mohammed Zain Al-Abdeen Mohammed Raoof the director general of State Board for Seed Testing and Certification in the Ministry of Agriculture of Iraq for his support and encouragement. Heartfelt acknowledgement is expressed to my family without their guidance, support, encouragement, and advices I may have never overcome this long journey in my studies. I also would like to thank to my friends and all the people that directly or indirectly help me in finishing the thesis.

Thank you very much

Ikhlas Hussain

This thesis was submitted to the Senate of Universiti Putra Malaysia and has been accepted as fulfillment of the requirement for the degree of Master of Science. The members of Supervisory Committee were as follows:

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LIST OF ABBREVIATIONS

μg/ml Microgram per Milliliter

μl Microliter

BLAST Basic Local Alignment Search Tool

bp Base Pairs

cpDNA Chloroplast DNA

DNA Deoxyribonucleic Acid

EDTA Ethylenediaminetetraacetic acid

EtBr Ethidium bromide

g Gravitational force

IGS Intergenic Spacer

Indel Insertion / Deletion

IUCN International Union for Conservation of Nature

KEP Kepong Herbarium

MEGA Molecular Evolutionary Genetics Analysis

ML Maximum Likelihood

ml Milliliter

MP maximum parsimony

NCBI National Center for Biotechnology Information

NHN-L Netherlands- Leiden university branch

NJ Neighbor-Joining

nm nanometer

OTUs Operational Taxonomic Units

PAUP Phylogenetic Analysis Using Pasimony

PCR Polymerase Chain Reaction

RAPD Random Amplified Polymorphic DNA

RFLP Restriction Fragment Length Polymorphism

RNase A Ribonuclease A

Taq Thermus aquaticus Super Therm DNA Polymerase

TBE Tris borate EDTA

UKM University Kebangsaan Malaysia

UPGMA Unweighted Pair Group Method with Arithmetic Mean

UPM Universiti Putra Malaysia

UV Ultra Violet

w/v Weight per volume



CHAPTER 1

INTRODUCTION

Taxonomy has been in development for more than 250 years, but according to Costello, *et al.*, (2013), only about 1.5 million species have been identified. Thus, it can be stated that despite the introduction of the modern taxonomic system by Carolus Linnaeus in the mid-1700s, only about 86% of the species on earth are identified (Mora *et al.*, 2011; Stork, 1993). Typically, species identification can be accomplished by classical taxonomic practices, mainly based on morphological characters by using dichotomous keys, or by morphological comparisons with herbarium specimens, besides working with experienced botanists. Indeed, plant identification requires experience, technical skills and knowledge on native flora including new and exotic species (Newmaster *et al.*, 2009; Funk *et al.*, 2005).

Apart from relying on morphological traits, plant taxonomists have progressively used DNA markers with many studies conducted on the reliability of molecular genetic methods to identify plant species (Nuroniah *et al.*, 2010; Finkeldey *et al.*, 2010; Wesselink and Kuiper, 2008). For the past 20 years, the rapid development of DNA sequencing technologies has further allowed resolving the problems of species identification, especially for tropical rainforest plants. Southeast Asia tropical rainforests are distinguished by high species diversity of trees (Morley, 2000). Within those forest communities, Bawa (1998) pointed out that the family of Dipterocarpaceae dominated a large area of tropical rainforest, with 92% of the area and 510 species mainly restricted to Asia.

Dipterocarpaceae is an important pantropical large tree family that plays essential roles in the international timber industry and in other wood products from the tropical rainforests of Southeast Asia. The evergreen rainforests of Peninsular Malaysia, Sumatra and Kalimantan (Borneo) have been seen showing the highest species diversity and abundance of Dipterocarpaceae (Ashton, 1982; Symington, 1943). In the past, the conservation of dipterocarps was not highlighted since they were considered as a common species that are not threatened. Nevertheless, Saw and Sam (2000) mentioned in their study that there over 57% of this species were observed to have distribution patterns restricted to Peninsular Malaysia. In addition to that, there are 30 species that are endemic to Peninsular Malaysia with 12 of them considered rare. It is worth mentioning that many rare plants are endangered due to their small population. However, the identification of the dominant trees in a tropical rain forest, particularly dipterocarps, is not an easy task. Standard morphological characters, such as shape of the canopy, height of the tree, shape and size of bole and buttress, texture and colour of bark pattern, and the typical shape size of leaf shape, are not enough to recognize Dipterocarpaceae species because of the sheer size, similar shapes and near-identical leaf morphologies displayed in several genera of this family. Likewise, dipterocarps trees have infrequent flowering and fruiting seasons. In addition, Symington (1943) mentioned that most forest characters vary with the age of the tree, and sometimes

with the habitat. These specific characteristics are frequently undeveloped before maturity, and may be atypical after senility has commenced, or when the tree has been subjected to abnormal environmental conditions. Moreover, it is frequently difficult to decide whether any given tree is mature or senile, and whether it has grown under normal conditions.

1.1 Problem Statement

Massive loss of valuable plant species in the past centuries and its adverse impact on environmental and socioeconomic values has triggered the conservation of plant resources. Appropriate identification and characterization of plant materials is essential for the successful conservation of plant resources and to ensure their sustainable use. Molecular tools developed in the past few years provide easy, less laborious means for assigning known and unknown plant taxa. These techniques answer many new evolutionary and taxonomic questions, which was not previously possible with only phenotypic methods.

The Meranti Damar Hitam group (*Shorea* section *Richetioides*) is one of the sections in Dipterocarpaceae, and can be found in Peninsular Malaysia, with (10) species, namely *S. balanocarpoides* Sym., *S. blumutensis* Foxw., *S. hopeifolia* (Heim) Sym., *S. faguetiana* Heim., *S. gibbosa* Brandis, *S. longisperma* Roxb., *S. maxima* (King) Sym., *S. multiflora* (Burck) Sym., *S. peltata* Sym., and *S. kuantanensis*. Only a few studies have been done on the *Shorea* section *Richetioides* relationship in Peninsular Malaysia, and the research was mainly restricted to taxonomy by Symington (1943) and Ashton (1982). Thus; information and understanding of the native *Shorea* section *Richetioides* is still insufficient, particularly on the phylogeny of the species. The much-developed area in Peninsular Malaysia and difficulties in accessing the forests are the main factors that have led to a lack of records.

According to the IUCN Red List (www.iucnredlist.org), S. kuantanensis is a critically endangered endemic species in Peninsular Malaysia, and many consider that S. kuantanensis is already an extinct species. This is because the type of specimens and the only specimens collected of S. kuantanensis were collected in the forest of Bukit Goh, Kuantan, in Peninsular Malaysia, which was fully converted into palm oil plantation. However, during a forest trip in one of the confined forests in Terengganu, the staff from the Forest Department of Peninsular Malaysia found a population of Shorea that resembles S. kuantanensis with a few variations from the type of materials that were encountered.

Molecular studies in particular phylogenetic relationships may play an important role in confirmation of the identity of the newly rediscovered population of so-called *S. kuantanensis*. This is because the molecular markers-based on DNA analysis will provide much more powerful and convenient means for distinguishing the different

species of *Shorea* for both endemic and more commonly widespread species and help to understand the phylogeny and relationship of the species.

1.2 Justification of Study

With the increasing rate of environmental degradation and current issues on biodiversity, the documentation of the country's flora is deemed important before they disappear or become totally unknown to science. Basic data on flora, which especially employs systematic studies, is useful and fundamental to many fields.

1.3 Objectives of Study

The primary goal of the present study was use of nucleotide sequences of two non-coding regions in Chloroplast DNA along with a set of morphological characters to construct a phylogenetic tree of *Shorea* species of section *Richetioides* in Peninsular Malaysia to provides a working set of relationships that can be used in future studies to address questions of character evolution within the study group.

The objectives of the study are:

- I. To identify species of genus *Shorea* section *Richetioides* in Peninsular Malaysia.
- II. To study the relationships among section *Richetioides* species by using numerical taxonomy and molecular approach.
- III. To examine the identity of newly rediscovered population of thought to be extinct of *Shorea kuantanensis* and its relationship with *Shorea* section *Richetioides*.

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