Abstract

Dragonflies have been used in an extensive array of studies dealing with the functional morphology, behavior, ecology, and evolution. They have been indicated to be important in functioning as bioindicators. The major aim of this study is to investigate the dragonfly population in the Selangor areas and to conduct the analysis on the molecular systematic and phylogenetics. Field sampling was done in 22 sites for the odonate biodiversity studies and the mitochondrial gene – partial regions of *NADH dehydrogenase subunit 1* (*ND1*) was utilized for the molecular aspects.

The results revealed a total of 1298 individuals belonging to 54 species from 9 families of Odonata which showed a significant preference for tropical lowland rainforest (TLR) in contrast to the open areas (OP). This was supported by the higher indices of richness (R) diversity (H') and evenness (E) for TLR. The phylogenetic trees were constructed from 40 samples using the neighbor joining (NJ) and maximum parsimony (MP) algorithms which were implemented by MEGA 4.0.2. One consistent result across all the analyses was the Suborder Anisoptera as a monopyletic group. Opposite to suborder Zygoptera, they were resolved clustered into 2 clusters, paraphyletic group. The distinct separation between cluster Anisoptera and Zygoptera with confidence level 72% in the NJ analyses while 90% in MP analyses.

It is suggested that *ND1* gene sequences can serve as a reference for DNA-based identification purposes, especially when in doubt for the larvae identification. The population aspects provided a baseline information for the future monitoring of Odonata in the Selangor areas related to diversity, abundance, distribution as well as the effects of physical parameter of the study sites.

Abstrak

Pepatung telah digunakan dalam pelbagai kajian yang luas yang berkaitan dengan morfologi, tingkah laku, ekologi dan juga evolusi. Mereka sangat penting dalam berfungsi sebagai bioindikator. Tujuan utama kajian ini adalah untuk mengkaji populasi pepatung di kawasan Selangor dan untuk menjalankan analisis pada sistematik molekul dan juga filogenetik. Persampelan telah dijalankan di 22 lokasi untuk kajian biodiversiti pepatung dan gen mitokondria - kawasan separa *NADH dehidrogenase subunit 1 (ND1)* telah digunakan untuk aspek-aspek yang berkaitan dengan molekul.

Sebanyak 1298 individu telah berjaya diperolehi yang diwakili oleh 54 spesies daripada 9 keluarga Odonata, yang menunjukkan keutamaan habitat di kawasan tanah rendah hutan hujan tropika (TLR) berbanding dengan kawasan terbuka (OP). Ini disokong oleh indeks yang lebih tinggi di TLR pada nilai kekayaan (R), kepelbagaian (H') dan keserasian, (E). Pokok-pokok filogenetik telah dibina daripada 40 sampel menggunakan algoritma *Neighbor-joining* (NJ) dan *Maximum Parsimony* (MP) melalui perisian MEGA 4.0.2. Satu hasil yang konsisten di semua analisis molekular adalah suborder Anisoptera sebagai kumpulan *monopyletic* iaitu sebagai 1 kumpulan, berbeza dengan suborder Zygoptera yang mempunyai 2 kelompok (*paraphyletic*). Pemisahan antara kelompok Anisoptera dan Zygoptera adalah pada tahap keyakinan 72% dalam analisis NJ manakala 90% dalam analisis MP.

Dicadangkan urutan gen *ND1* boleh dijadikan sebagai rujukan untuk tujuan pengenalan yang berasaskan DNA, terutamanya untuk mengenal pasti pepatung pada peringkat larva. Aspek populasi pepatung juga boleh dijadikan maklumat asas yang berkaitan dengan diversiti, kelimpahan dan taburan, serta kesan parameter fizikal di kawasan kajian.

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Table of Contents

Contents Page

APPENDICES

List of Figures

Figures **Page**

List of Tables

Tables **Page**

List of Abbreviations

~ ……. Approximately

^{o}C ……. Degree celcius

-ve ……. Negative

bp ……. Base pairs

µg ……. Microgram

µl ……. Microliter

µM ……. Micromolar

A ……. Adenine

C ……. Cytosine

CO1 ……. Mitochondrial Cytochrome oxidase 1 gene

dH_2O ……. Desterilized water

DNA ……. Deoxyribonucleic acid

DNase ……. Deoxyribonuclease

dNTP ……. Deoxyribonucleotide triphosphate

et al. ……. Others

EtBr ……. Ethidium bromide

fw ……. Forward

G …… Guanine

g …… Gram

GPS …… Global Positioning System

H' …… Shannon Weiner Index

HCl …… Hydrochloric acid

Leu …… Leusine

M …… Molar

mg …… Miligram

Mg^{2+} …… Magnesium ions

$MgCl_2$ …… Magnesium chloride

ml …… Mililiter

mM …… Milimolar

MP …… Maximum Parsimony

mtDNA ……. Mitochondrial Deoxyribonucleic acid

ND1 …… *NADH dehydrogenase 1*

ng …… Nanogram

nm …… Nanometer

PCR …… Polymerase chain reaction

RAPD ……...……. Random Amplification of Polymorphic DNA

rev …… Reverse

rpm …… Rotations per minute

rRNA …… Ribosomal RNA

T …… Thymine

Taq …… *Thermus aquaticus*

TBE …… Tris – Borate EDTA

T_m …… Melting Temperature

tRNA …… Transfer RNA

UV …… Ultraviolet

V …… Voltage