PHYLOGENETIC ANALYSIS OF CAUGHT RAT BY USING CYTOCHROME OXIDASE 1 FRAGMENT

WAN MUHAMMAD IMRAN BIN WAN ISMAIL

Final Year Project Report Submitted in
Partial Fulfillment of the Requirement for the
Degree of Bachelor Science (Hons.) Biology
in the Faculty of Applied Sciences
University Teknologi MARA

JULY 2018

This Final Year Project Report entitle "**Phylogenetic Analysis of Caught Rat by using Cytochrome Oxidase 1 Fragment**" was submitted by Wan Muhammad Imran bin Wan Ismail, in partial fulfillment of the requirements for the Degree of Bachelor of Science (Hons.) Biology, in the Faculty of Applied Sciences, and was approved by

_____

Sarah Shazwani binti Zakaria
Supervisor
Faculty of Applied Sciences
Universiti Teknologi MARA (UiTM)
Negeri Sembilan, Kampus Kuala Pilah,
Pekan Parit Tinggi, 72000 Kuala Pilah
Negeri Sembilan.

_____

Lili Syahani Binti Rusli
Coordinator FSG661 AS201
Faculty of Applied Sciences
Universiti Teknologi MARA (UiTM)
Negeri Sembilan, Kampus KualaPilah,
Pekan Parit Tinggi, 72000 Kuala Pilah
Negeri Sembilan.

_____

Dr. Aslizah Binti Mohd Aris
Head of Biology School
Faculty of Applied Sciences
Universiti Teknologi MARA (UiTM)
Negeri Sembilan, Kampus Kuala Pilah,
Pekan Parit Tinggi, 72000 Kuala Pilah
Negeri Sembilan.

Date:_____

TABLE OF CONTENTS

ABSTRACT

PHYLOGENETIC ANALYSIS OF CAUGHT RAT BY USING CYTOCHROME OXIDASE 1 FRAGMENT

The rats were widely diverse around the world. The identification of rat were difficult since most rats share common morphology characteristics. Thus, the identification through genetic material might help to identify the rat more accurately since the rat species were difficult to identify through the morphology characteristic. The aim of this study was to identify the unknown caught rats using phylogeny-based identification and further compared rat identification through morphological characteristics. Five rats' samples were obtained from five different areas and the morphological characteristics of each sample were recorded to identify their species. The five rats' tails were taken for DNA extractions by using high-salt method. The extracted DNA were amplified and sequenced for cytochrome oxidase 1 region. A total of 745 base pair were successfully sequenced for all samples and were aligned with 77 sequences retrieve from GenBank. Three phylogenetic trees were reconstructed Neighbor-Joining, Bayesian inferences and maximum likelihood method. Based on the morphological characteristics, the five samples were most likely identified as *Rattus norgevicus* for Rat 1, Rat 2 as *Rattus tiomanicus*, Rat 3 as *Rattus andamanensis*, Raat 4 as Rattus norvegicus and Rat 5 as *Rattus exulans*. However, further identification through phylogeny-based identification from the three phylogenetic tree shows that Rat 1 highly probably identified as *Rattus norvegius*, while Rat 2, Rat 3, Rat 4 and Rat 5 as *Rattus kandianus* and/or *Rattus andamanensis.*