A MORPHOLIGICAL AND MOLECULAR PHYLOGENETIC ANALYSIS OF MALAYSIAN Kerivoula (Chiroptera: Vespertilionidae)

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A Morphological and Molecular Phylogenetic Analysis of Malaysian Kerivoula (Chiroptera: Vespertilionidae)

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DECLARATION

I hereby declare that no portion of the work referred to this thesis has been submitted in support of an application for another degree or qualification to this or any other university or institute of higher learning.

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(Noor Haliza binti Hasan @ Ahmad)

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Abstract

(Morphometric and phylogenetic analyses were done on six species of Kerivoula from Malaysia.)

(Morphological studies could only be done on five out of the six Kerivoula species available for this research, namely K. papillosa, K. lenis, K. pellucida, K. hardwickii and K. minuta.) No sample of K. intermedia was available for morphological analysis.

(Thirty-one characters of the external body, skull and dentition were taken from 47 adult individuals of Kerivoula.)

(Three separate analyses were done on the morphological data; (1) clustering analysis, (2) principal component analysis (PCA) and (3) discriminant function analysis (DFA) were applied to the data.)

(The findings from all the three analyses supported the groupings of the Kerivoula samples into six different groups; namely, K. minuta, K. hardwickii, K. pellucida, K. lenis and K. papillosa.) Cryptic samples of K. papillosa were further separated into two types; K. papillosa type small (K. papillosa type S) and K. papillosa type large (K. papillosa type L). Phylogenetic analysis was done on six available Kerivoula samples utilising three mitochondrial genes; 409 basepair (bp) of cytochrome b (cyt b), 478 bp of cytochrome oxidase I (COI) and 1044 bp of NADH dehydrogenase subunit 2 gene (ND2). This was followed by another analysis utilising one nuclear gene - 1054 bp of recombinant activating gene subunit 2 (Rag2). The reconstructions of phylogenetic trees depicting the relationship of Kerivoula were retrieved using all four inferring methods through three analyses namely, neighbor-joining (NJ), maximum parsimony (MP) and maximum likelihood (ML). All analyses consistently resulted in seven groups, namely K. minuta, K. pellucida, K. hardwickii, K. lenis and K. papillosa, with K. papillosa further separated into two different subgroups which were congruent with those of morphological analyses, and also the addition of K. intermedia samples. The same samples were used in both analyses and out of 17 samples identified as K. papillosa, five were classified as K.
papillosa type L (forearm length of 44.5 mm to 49.0 mm); with one sample from the Madai Cave in Sabah and the other four from the Niah National Park of Sarawak. Another 12 samples were classified as K. papillosa type S (forearm length of 40.0 mm to 44.5 mm) with their distribution scattered around Sarawak and Peninsular Malaysia. The separation of these two types of K. papillosa were also supported by a notable genetic distance of >10% which was comparable to those of biologically different species. This suggested the presence of cryptic species within the K. papillosa groups. It was also noted that K. hardwickii samples were separated into the Eastern and the Western Borneo samples with 100% support of bootstrap for the cyt b and the ND2 genes analyses. The existence of a potential phylogroup was suggested with a genetic distance of 4.6% to 6.0% in the cyt b as >5% was the value proposed by Baker and Bradley (2006) for such definition. Separation of K. minuta samples into two subgroups was also observed using at least three analyses and the existence of a subspecies was suggested. It was concluded that the analysis using ND2 gene gave the best tree in depicting the phylogenetic relationship of Kerivoula. The comparison of the K. papillosa type S and the K. papillosa type L identified in this study to the type specimen would justify the taxonomic revision of the cryptic species within the genus. Population studies of K. papillosa, K. hardwickii and K. minuta were suggested to further verify the findings of the present study. Further analysis onto both forms of K. papillosa together with the other nine Kerivoula species occurring in Malaysia would provide better insights into the phylogenetic relationship of genus Kerivoula. (The findings of this study were expected to aid in the taxonomy and future management and conservation plans for this genus.)

Keywords: Kerivoula, Malaysia, morphology, molecular phylogenetic, cryptic species
Analisis morfologi dan filogenetik molekul *Kerivoula* (Chiroptera: Vespertilionidae) dari Malaysia

Abstrak


Kata kunci: Kerivoula, Malaysia, morfologi, filogenetik molekul, spesies kriptik
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