

ABSTRACT

(Morphometric and phylogenetic analyses were done on six species of genus *Tupaia* from Malaysia. Morphological study was done on *T. montana*, *T. tana*, *T. minor*, *T. glis*, *T. gracilis*, and *T. picta*. The primary objective of this study was to examine the intraspecific and interspecific relationships of the genus *Tupaia* using molecular and morphological analyses. The secondary objective was to validate any probable cryptic species and clarify the similar morphological characteristics among the taxa under study. The third objective was to document the taxonomic composition of small mammal in Malaysia especially the *Tupaia* species. A total of 24 characters of the cranial, dental and external were taken from 46 adult individuals of *Tupaia*.) Two separate analyses were done on the morphological data namely discriminant function analysis (DFA) and un-weighted pair groups method average (UPGMA). The upper molar row length (UMR), molar 1 to molar 1 length (M1M1), and palatal length (PL) were identified as important characters contributing to high factor loading. The findings from all these analyses supported the groupings of the *Tupaia* into six different groups as showed in UPGMA clustering. Phylogenetic analyses were done on five available *Tupaia* species represented by 40 individuals utilising three partial mitochondrial DNA (mtDNA) genes; 882 base pair (bp) of mtDNA 12S rRNA, 398 bp of mtDNA cyt *b*, and 474 bp of mtDNA COI. The reconstructions of phylogenetic trees depicting the relationships of *Tupaia* were retrieved using all four inferring methods through neighbor-joining (NJ), maximum parsimony (MP), maximum likelihood (ML) and Bayesian analyses. All analyses consistently showed a monophyletic clade which is further divided into two major groups where *T. montana*, *T. tana*, and *T. minor* were clustered together in Group 1 while *T. glis* was clustered together with *T. picta* in Group 2. The phylogenetic trees showed that *T. tana* was more closely related to *T. montana* compared to *T. minor* which were strongly supported with

high to moderate bootstrap values. It was suggested that partial mtDNA 12S rRNA gene have better resolution in elucidating the phylogenetic relationships of genus *Tupaia*. However, it was observed that in morphological analyses that *T. montana* was closely related to *T. glis* while *T. tana* was closely related to *T. picta*. On the other hand, *T. minor* was closely related to *T. gracilis*. The rough estimation of time of divergence resulting in the diversification of *Tupaia* species began about not later than 7 Mya and predating the Pleistocene events.

Keywords: *Tupaia*, morphological, molecular, phylogenetic, relationships.

KAJIAN HUBUNGAN FILOGENETIK TERHADAP GENUS *Tupaia* (SCANDENTIA:
TUPAIIDAE) MENGGUNAKAN KAEDAH ANALISIS MORFOLOGI DAN
MOLEKULAR

ABSTRAK

Kajian tentang hubungan filogenetik menggunakan kaedah analisa secara morfometrik dan molekular telah dilakukan ke atas enam spesies yang mewakili genus *Tupaia* iaitu *T. montana*, *T. tana*, *T. minor*, *T. glis*, *T. gracilis*, dan *T. picta* telah dijalankan dengan menggunakan kaedah analisis secara morfometrik dan molekular. Objektif utama kajian adalah untuk mengkaji pertalian filogeni *Tupaia* dari aspek morfologi dan genetik. Objektif kedua adalah untuk mengenalpasti kebarangkalian wujudnya spesies samar-samar dan untuk menjelaskan persamaan dari segi karakter morfologi dalam kalangan taxa yang dikaji. Objektif yang ketiga adalah untuk mendokumenkan taburan dan komposisi haiwan mamalia kecil di Malaysia terutamanya spesies *Tupaia*. Sebanyak 24 karakter telah digunakan dan sebanyak 46 individu telah digunakan dalam kajian ini. Dua kaedah telah digunakan dalam analisi data morfologi iaitu discriminant function analysis (DFA) dan un-weighted pair groups method average (UPGMA). Ukuran barisan gigi molar atas (UMR), kepanjangan molar 1 ke molar 1 (M1M1), dan kepanjangan lelangit (PL) adalah antara karakter yg terbaik dan berkesan untuk membezakan spesies *Tupaia*. Penemuan ini menyokong pengelasan kumpulan spesies *Tupaia* ke dalam kumpulan masing-masing seperti yang ditunjukkan dalam pengelasan UPGMA. Analisa filogenetik menggunakan mtDNA 12S rRNA, cyt *b*, COI telah dijalankan ke atas 40 individu yang mewakili 5 spesies *Tupaia*. Hubungan filogenetik antara spesies telah diterangkan melalui hubung kait antara spesies seperti yang ditunjukkan dalam neighbor-

joining (NJ), maximum parsimony (MP), maximum likelihood (ML) and Bayesian. Kesemua analisis menyokong penemuan bahawa hubungan antara spesies *Tupaia* adalah monofiletik di mana *T. tana* adalah lebih rapat kepada *T. montana* berbanding kepada *T. minor*. Walau bagaimanapun, *T. montana* adalah lebih rapat kepada *T. glis* sementara *T. tana* pula lebih rapat kepada *T. picta* dalam analisa secara morfologi. *T. minor* pula adalah lebih rapat dengan *T. gracilis*. Berdasarkan analisis menggunakan data genetik, didapati bahawa mtDNA separa 12S rRNA merupakan gen yang paling sesuai untuk menunjukkan hubungan di antara serta di kalangan spesies. Spesies *Tupaia* adalah dianggarkan telah berevolusi sejak tidak kurang daripada 7 Mya. Oleh itu, dapat disimpulkan bahawa evolusi genus *Tupaia* adalah dipengaruhi oleh peristiwa Pleistosen.

Kata kunci: *Tupaia*, morfologi, molekular, filogenetik, hubungkait