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Molecular phylogenetics and systematics of five genera of Malaysian murine rodents (*Maxomys*, *Sundamys*, *Leopoldamys*, *Niviventer* and *Rattus*) inferred from partial mitochondrial cytochrome *c* oxidase subunit I (COI) gene

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Abstract Study on the taxonomy and systematic of Malaysian Murinae is very scarce especially due to the lack of material within the country. We provide an attempt to investigate the phylogenetic relationship and pattern thus identifying species within five genera comprising *Maxomys*, *Sundamys*, *Leopoldamys*, *Niviventer* and *Rattus*. We genetically analysed 50 specimens of Murinae from Peninsular Malaysia and Sarawak, assigned to 12 species. Phylogenetic analyses of partial mitochondrial cytochrome *c* oxidase subunit I (476 base pairs) using four methods, namely, neighbour-joining (NJ), maximum parsimony (MP), maximum-likelihood (ML) and Bayesian method resulted in similar statistically supported clades with minimal change in branching order. The analyses discovered that there were intermediate form of *Maxomys* species within *M. whiteheadi* and *M. ochraceiventer* populations. They display same external morphology as *M. whiteheadi* but genetically closer to *M. ochraceiventer*. Craniodental measurements showed significant differences between the three populations. *Rattus* and *Sundamys* appeared not fully resolved while *Leopoldamys* and *Niviventer* were steadily clustered. The intraspecific geographic variation in some species agrees with previous studies on the vicariance scenario and diversification of flora and fauna in Malaysia and Borneo.

Keywords Murinae – phylogenetics – COI – Genetic Species Concept – geographic structure

INTRODUCTION

Traditionally, taxonomic status of Murinae was based on morphological characteristics. The classification was outdated due to the variation of morphological traits caused by rapid adaptation towards ecological habitats and high rate of evolution in Murinae. The variation of external features sometimes does not indicate the species to be in distinct taxa, at least not in Genetic Species Concept. As closely related species in the subfamily Murinae are morphologically similar to each other, the taxonomic status of Murinae is poorly resolved until recently. Many studies have been done using genetic data, morphology, immunology, albumin and karyotypic analyses but the information of Murinae in Malaysia is still lacking. Examining species boundaries using data from cytochrome *c* oxidase subunit I (COI) is an appropriate method to identify genetically isolated evolutionary units and the phylogenetic relationship estimation of Murinae.

In Peninsular Malaysia, the classical taxonomy of Murinae was based on their morphologies of external features [1-3]. Apart from the genera *Chiropodomys*, *Hapalomys*, *Pithecheir*, *Bandicota* and *Mus*, these authors placed all the remaining species of Murinae in the genus *Rattus*. Subsequent karyotypic and electrophoretic studies emphasised the distinctiveness of some species within the genus *Rattus* with great divergence [4, 5] as that between different genera from North American rodents [6, 7]. Later, the skins, skulls and dental morphology of these species were re-examined and some subgenera were elevated, new genera were named and described such as *Maxomys*, *Leopoldamys*, *Berylmys* and *Sundamys* [8, 9]. Splitting *Rattus* into well-defined genera gives better understanding of phylogenetic relationship among Murinae. Three genera of *Maxomys*, *Sundamys* and *Niviventer* that were previously included in *Rattus* were tested [10]. *Maxomys* was the basal group for these genera and *Rattus* was closely related and