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Phylogenetic Position of *Tarsius bancanus* Based on Partial Cytochrome *b* DNA Sequences

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Abstract: This study was carried out to ascertain the molecular phylogenetic position of *Tarsius bancanus* among Malaysian primates based on the partial of Cytochrome *b* (cyt *b*) gene sequences. A total of five samples of *Tarsius bancanus* from Sabah, Malaysia, were used in this study. Several other Malaysian primates were also included in the analysis (Leaf monkeys (*Presbytis* and *Trachypithecus*), Macaques (*Macaca*), Siamang (*Symphalangus*) and Slow loris (*Nycticebus*). We also included DNA sequences of several prosimians (*Galago*, *Cheirogaleus*, *Daubentonia*, *Indri*, *Avahi*, *Lemur* and *Lepilemur*) from GenBank. In addition, one individual of orang utan (*Pongo pygmaeus*) and human (*Homo sapiens*) were used as outgroups to root the tree. All taxa were analysed using character method (Maximum Parsimony, MP) and distance method (Neighbor-Joining, NJ). From the 375 examined characters, 43.2% were constant characters while 4.8% characters were parsimony uninformative whereas 52.0% characters were parsimony informative. Tree topologies discriminated three major clades in which primitive primates, Old World Monkeys and Anthropoids belongs to their own monophyletic clades. Both MP and NJ trees showed that *T. bancanus* was placed in primitive primates group.

Key words: *Tarsius bancanus*, molecular systematics, Malaysian primates, cytochrome *b*, Tarsiers

INTRODUCTION

The Bornean tarsier, *Tarsius bancanus* is a nocturnal primate (Napier, 1970), which is classified under the family Tarsiidae (Brandon-Jones *et al*., 2004; Szalay and Delson, 1979). They can be found on the island of Borneo (Groves, 2001). Tarsiers have sometimes been called ‘living fossils’. The proportions of the limbs, which indicate their tree-hopping gait, are very similar to those of early primates of the Eocene period (Napier, 1970). Tarsier possesses problem in the primate systematics. Its evolutionary position is hard to be clarified. Mittermaier *et al*. (1999) stated that there are evidence suggesting tarsiers to be most closely related to the monkeys and apes than prosimians. For example, like anthropoid, tarsiers have a short muzzle rather than typical prosimians that externally have relatively long muzzles terminating in a naked, moist snout (Mafham and Mafham, 1992).

Recent developments in molecular techniques allow evolutionary biologists with an additional tool for making phylogenetics inferences, by comparing DNA sequences between homologous DNA segments using mitochondrial genes (Shahrom *et al*., 2005; Lim *et al*., 2010). These mitochondrial DNA (mtDNA) genes are widely used to infer phylogenetic relationships on primates (Masters *et al*., 2007; Roos *et al*., 2008). Cyt *b* gene of the mitochondrial is well-known as rapidly evolve gene and can shows variations within and between species and has been used in phylogeny and biogeography studies (Caine´ *et al*., 2006; Karanth *et al*., 2008).

Many molecular systematic researches have studied on primates focusing on Great Apes (Steiper, 2006; Gonder *et al*., 2006) and Old World Monkeys (Karanth *et al*., 2008; Osterholz *et al*., 2008). In addition, there are also many molecular studies on primitive primates particularly tarsiers (Raina *et al*., 2005; Uddin *et al*., 2008). Andrew *et al*. (1998) have looked on cyt *b* gene of *T. bancanus* and Murayama *et al*. (1998) worked on D4 dopamine receptor (D4DR) genes of prosimians (including tarsier) and tree shrew. In addition, Schmitz *et al*. (2002) had sequenced the entire mitochondrial genome of *T. bancanus*. Most of the molecular systematic studies on Malaysian primates focused only at the genus level, for instance the genus

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