

Molecular phylogenetics and phylogeography of Malaysian mousedeer (*Tragulus Kanchil*) based on mitochondrial dna sequences of the d-loop region

ABSTRACT

Two sympatric mousedeer species, *Tragulus kanchil* and *Tragulus napu*, inhabit the Malaysian tropical rainforests. Previous studies have established their phylogenetic relationships based on morphological variations; however, comprehensive genetic data have yet to be extensively used to relate the relationships especially from different populations. The main objectives of this study were to determine the phylogenetic relationships, population genetics, and phylogeography of mousedeer species based on DNA sequences of the mitochondrial D-loop region. DNA from 32 mousedeer samples, representing various populations in Malaysia, was sequenced and analyzed using NeighborJoining, Maximum Parsimony, and Bayesian Inference approaches. The phylogenetic analyses showed two main clades representing the populations of *T. kanchil* and *T. napu*. The results also showed that the *T. kanchil* populations in Borneo was separated from Peninsular Malaysia taxa in MP and BI phylogenetic tree. However, Borneo population was nested in east population of Peninsular Malaysia in NJ tree. In addition, the *T. kanchil* population in Peninsular Malaysia further separated into east and west coast populations of Titiwangsa Range. It was supported with finding in population genetic relation that showed relatively low levels among population. This is expected because some of the populations are isolated geographically. The divergence of these populations is likely due to the Titiwangsa Range which acts as a barrier separating the east and west Peninsular Malaysia populations, and the South China Sea separates the populations of Peninsular Malaysia and Borneo. Molecular clock tree reconstruction showed that the separation of *T. kanchil* and *T. napu* occurred around 17.11 million years ago (MYAs). Furthermore, the *T. kanchil* populations from the east and west Peninsular Malaysia showed a branching pattern from those of Borneo of about 11.04 and 9.14 MYAs, respectively. The results of this study increase our understanding of Malaysian mousedeer phylogeny and phylogeography