

Phylogenetic relationships of Malaysia's long-tailed macaques, *Macaca fascicularis*, based on cytochrome *b* sequences

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Abstract

Phylogenetic relationships among Malaysia's long-tailed macaques have yet to be established, despite abundant genetic studies of the species worldwide. The aims of this study are to examine the phylogenetic relationships of *Macaca fascicularis* in Malaysia and to test its classification as a morphological subspecies. A total of 25 genetic samples of *M. fascicularis* yielding 383 bp of Cytochrome *b* (Cyt *b*) sequences were used in phylogenetic analysis along with one sample each of *M. nemestrina* and *M. arctoides* used as outgroups. Sequence character analysis reveals that Cyt *b* locus is a highly conserved region with only 23% parsimony informative character detected among ingroups. Further analysis indicates a clear separation between populations originating from different regions; the Malay Peninsula versus Borneo Insular, the East Coast versus West Coast of the Malay Peninsula, and the island versus mainland Malay Peninsula populations. Phylogenetic trees (NJ, MP and Bayesian) portray a consistent clustering paradigm as Borneo's population was distinguished from Peninsula's population (99% and 100% bootstrap value in NJ and MP respectively and 1.00 posterior probability in Bayesian trees). The East coast population was separated from other Peninsula populations (64% in NJ, 66% in MP and 0.53 posterior probability in Bayesian). West coast populations were divided into 2 clades: the North-South (47%/54% in NJ, 26/26%