Online journal ISSN - 1676-5680
GMR Genetics and Molecular Research
EVOLUTION AND TECHNOLOGY

Phylogenetic relationships of Malaysian monkeys, Cercopithecidae, based on mitochondrial cytochrome c sequences

B.M. Md-Zain[1], M. Mohamad[1], M.A. Ernie-Muneerah[1], A. Ampeng[1,4], A. Jasmi[2], M. Lakim[3] and M.C. Mahani[1]

[1]School of Environmental and Natural Resource Sciences, Faculty of Science and Technology, Universiti Kebangsaan Malaysia, Bangi, Selangor, Malaysia
[2]Department of Wildlife and National Parks, Peninsular Malaysia, Kuala Lumpur, Malaysia
[3]The Board of Trustees of Sabah Parks, Kinabalu Park, Kota Kinabalu, Sabah, Malaysia
[4]Sarawak Forestry Department, Kuching, Sarawak, Malaysia

Corresponding author: B.M. Md-Zain
Email: abgbadd@ukm.my / abgbadd1966@yahoo.com

Genet. Mol. Res. 9 (4): 1987-1996 (2010)
Received June 2, 2010
Accepted July 20, 2010
Published October 5, 2010
DOI 10.4238/vol9-4gmr942

ABSTRACT. Mitochondrial DNA cytochrome c oxidase II (COII) gene sequences of Malaysian Cercopithecidae were examined to ascertain their phylogenetic relationships. Colobinae were represented by the genera *Presbytis*, *Trachypithecus* and *Nasalis*, while the genus *Macaca* represented Cercopithecinae. DNA amplification and sequencing of the COII gene was performed on 16 samples. *Symphalangus syndactylus* (Hylobatidae) was used as the outgroup. Data were analyzed using both character (maximum parsimony) and distance (neighbor-joining) methods. Tree topologies indicated that Colobinae and Cercopithecinae have their own distinct monophyletic clade. This result was well supported by bootstrap values and genetic distances derived from the Kimura-2-parameter algorithm. Separation of *Macaca nemestrina* from *M. fascicularis* was also well supported by bootstrap values. In addition,

tree topologies indicate a good resolution of the Colobinae phylogenetic relationships at the intergeneric level, but with low bootstrap support. The position of *Nasalis* remained problematic in both trees. Overall, COII is a good gene candidate for portraying the phylogenetic relationships of Malaysian primates at the inter- and intra-subfamily levels.

Key words: Malaysian primates; COII gene; Molecular phylogeny; Cercopithecinae; Colobinae

