Y-chromosomal gene flow of *Macaca fascicularis* (Cercopithecidae) between the insular and mainland peninsula of Penang state, Malaysia

Jeffrine J. Rovie-Ryan¹²*, Mohd Tajuddin Abdullah², Frankie Thomas Sitam¹, Zaaba Zainol Abidin³, and Soon Guan Tan⁴

¹Wildlife Genetic Resource Bank (WGRB) Laboratory, Ex-Situ Conservation Division, Department of Wildlife and National Parks (DWNP) Peninsular Malaysia, KM 10 Cheras Road, 56100 Kuala Lumpur, Malaysia
²Department of Zoology, Faculty of Resource Science and Technology (FRST), Universiti Malaysia Sarawak (UNIMAS), 94300 Kota Samarahan, Sarawak, Malaysia
³Deputy Director II Office, DWNP, KM 10 Cheras Road, 56100 Kuala Lumpur, Malaysia
⁴Department of Cell and Molecular Biology, Faculty of Biotechnology and Biomolecular Sciences, Universiti Putra Malaysia, 43400 Serdang, Selangor, Malaysia

(*Corresponding author’s email: jeffrine@wildlife.gov.my)

Received 1-7-2013; accepted 28-9-2013

**Abstract** DNA sequencing of the Y-chromosome testis-specific protein locus (TSPY) and sex-determining region (SRY) was conducted on 27 *Macaca fascicularis* individuals from eight insular and two peninsula localities of Penang State, Malaysia. Five haplotypes were discovered from the Penang samples, of which four were unique for that population. These haplotypes constituted of related individuals as observed in the Y-chromosomal gene flow within and between the insular and mainland regions. The occurrence of a dominant haplotype shared amongst *M. fascicularis* from southern Thailand, the Malay Peninsula, and Sumatra could be the result of a recent dispersal event from the common Pleistocene refugia, which had most likely been located in the Malay Peninsula. A combination of nucleotides at 12 sites distinguished the *M. fascicularis* from the northern region of the Isthmus of Kra from those of the southern region including our samples. The molecular phylogenetic tree confirmed that, unlike conspecific populations from regions north of the Isthmus of Kra, *M. fascicularis* from the southern region of the isthmus were free of introgression of Y-chromosome from *M. mulatta*. We dated the last common ancestors shared by the *fascicularis* group at approximately 1.5 million years ago (mya). Also, we estimated the bifurcation between the insular and the continental lineages of *M. fascicularis* as approximately 0.7 mya, which had been estimated as 0.4 mya in a previous study. Finally, similarly to the observations on various taxa by previous authors we recognise the role of the Isthmus of Kra area as a genetic barrier to the dispersal of and to gene flow in *M. fascicularis*.

**Keywords** *Macaca fascicularis* – Y-chromosome – TSPY and SRY – Isthmus of Kra – genetic barrier

**INTRODUCTION**

The long-tailed macaques (*Macaca fascicularis*) like all other macaque species exhibit an extreme level of sex-biased dispersal [1-2] where females are sedentary