

USING Y-CHROMOSOME TO ELUCIDATE THE EVOLUTION AND DISPERSAL PATTERN OF THE LONG-TAILED MACAQUES (*Macaca fascicularis*) IN SOUTHEAST ASIA

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ABSTRACT

We employed a combined segment of the testis-specific protein (TSPY) and the sex-determining region (SRY) of the Y-chromosome gene to elucidate the evolutionary pattern of the long-tailed macaques (*Macaca fascicularis*) in Southeast Asia. A maximum-likelihood (ML) tree and a phylogenetic network were constructed using 147 sequences of *M. fascicularis* from the Peninsular Malaysia and Sarawak including sequences from the other regions of the species range taken from the other previous studies. Measurements of standard genetic diversity indices were calculated. Our findings revealed that the *M. fascicularis* are separated into two major groups of the continental and the insular lineages. Furthermore, the continental lineage is separated into two faunal regions demarcated at the Isthmus of Kra. The Y-chromosome dataset revealed a dominant haplotype emerging at around 0.25 (± 0.1) million years ago (mya) which was shared by 82 samples from the southern region of the Isthmus of Kra which ranges from Songkhla, Thailand, the Malay Peninsula and downwards to Sumatra, Indonesia. The insular lineage emerged at around 0.61 (± 0.4) mya which occupied the island of Borneo and the Philippines. We also confirmed that the introgression of the *M. mulatta* Y-chromosome into the Indochinese *M. fascicularis* (Vietnam and Cambodia) are absent in the *M. fascicularis* haplotypes from the southern region of the Isthmus of Kra.

Keywords: *Macaca fascicularis*, Y-chromosome, phylogenetic tree and network, dispersal route, time estimates.