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

ABSTRACT

DNA sequencing of the Y-chromosome testis-specific protein locus (TSPY) and sexdetermining 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 Ychromosome 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.

Keyword: Macaca fascicularis; Y-chromosome; TSPY and SRY; Isthmus of Kra; Genetic barrier