

Microsatellite DNA polymorphism of *Macaca fascicularis* populations in Malaysia

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Abstract: A total of 386 long-tailed macaques (*M. fascicularis*) from 17 populations in Malaysia was analysed using eight polymorphic microsatellite loci on a microfluidic-based platform (Agilent DNA 1000 Chips on the Agilent 2100 bioanalyzer) to identify and evaluate the genetic polymorphism and population structure. The microfluidic-based chip platform provides simple, reliable and cost effective approach for microsatellite studies. Genetic diversity estimates showed that the Peninsular Malaysian populations are slightly more diverse than their Bornean conspecifics. Furthermore, weak population structuring among the peninsula populations suggest that they comprise of genetically contiguous populations. The Sarawak and Labuan populations were differentiated from the peninsula populations except for the Sabah population which is due to the low sample number from the latter. Interestingly, no matching genotype was found among all samples indicating that the loci set can be used for individual identification of *M. fascicularis*.

Key words: : Long-tailed macaques, sex bias dispersal, population structure, short tandem repeats, cross-species amplifications, microfluidic-based chip

INTRODUCTION

Macaca fascicularis in the wild demonstrates an extreme biased dispersal behaviour. Males exhibit highly dispersal nature while females remain sedentary once occupying a particular area (Pusey and Packer 1987; Melnick and Hoelzer 1992). This condition would lead to contrasting findings when observed using different genetic markers. While uniparental genetic markers such as Y-chromosomal DNA (Y-DNA) and mitochondrial DNA (mtDNA) could only provide information on either side of the sexes, microsatellite loci are biparentally inherited and contain fourfold of effective population size (N_e) compared to Y-DNA and mtDNA (Avisé 2009). Therefore, the use of biparental genetic markers such as microsatellite loci provides unbiased genetic information especially in a taxon that exhibits biased dispersal behaviour.

Microsatellite loci which are also known as short tandem repeats (STRs) are vastly distributed in the genome, contain abundant variations, and easy to genotype making them a valuable genetic marker (Perwitasari-Farajallah et al. 2010). Co-dominantly inherited, these markers had been frequently used to identify and quantify genetic variations and often being used in population genetic studies of *M. fascicularis* (Bonhomme et al. 2005; Kawamoto et al. 2008; Kanthaswamy et al. 2013; Nikzad et al. 2014; Smith et al. 2014). Furthermore, due to their high levels of polymorphisms, STRs are suitable for the investigation into past population demography such as bottlenecks and expansion events (Goossens et al. 2006; Bonhomme et al. 2008).

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