
Genetic diversity of *Macaca fascicularis* (Cercopithecidae) from Penang, Malaysia as inferred from mitochondrial control region segment

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ABSTRAK

Keanekaragaman genetic kera ekor panjang (*Macaca fascicularis*) dari Penang, termasuk Pulau Jerejak dan daratan utama Negeri Penang Malaysia telah dianalisis dengan menggunakan 1.042 bp control region (CR) segment DNA mitochondria (mtDNA). Dua puluh haplotipe menunjukkan adanya satu haplotipe tunggal yang sama antara daratan utama dan pulau, hal ini menandakan bahwa ini merupakan genetic yang diterima dari daratan. Dibandingkan dengan penelitian sebelumnya yang dilakukan berdasarkan CR, semua haplotipe dari Penang merupakan gambaran baru dan tidak ada yang sama dengan populasi *M. fascicularis* lainnya di wilayah ini. Adanya satu deletion mutasi unik pada contoh dari penang (Kelompok I dan II) bisa menjadi indicator yang baik untuk upaya konservasi keunikan genetic dan mungkin bisa dikelola sebagai satu unit pengelolaan. Sebuah ringkasan pohon filogenetik (NJ, MP, ML dan Bayesian) mendukung pengelompokan monofiletik dari *M. fascicularis* seperti digambarkan pada penelitian sebelumnya. Pemisahan topologi dari haplotype Penang kedalam tiga kelompok utama secara umum berhubungan dengan distribusi geografis mereka. Penelitian ini juga mencatat bahawa haplotipe Penang memiliki garis keturunan dari wilayah continental yang telah terpisah dari garis keturunan insular sekitar 1.04 juta tahun yang lalu. Penelitian ini juga menunjukkan bahwa CR dari mtDNA sangat baik digunakan untuk mengkuantifikasi keanekaragaman genetic intraspesifik pada *M. fascicularis*.

ABSTRACT

The genetic diversity of the long-tailed macaques (*Macaca fascicularis*) from Penang, Malaysia, including Jerejak Island and the mainland area of the state of Penang, Seberang Perai were examined using 1,042 bp control region (CR) segment of the mitochondrial DNA (mtDNA). Twenty haplotypes were described with a single haplotype sharing between the mainland and the island which suggests that it is a remnant of the genetic makeup from the mainland. Compared to previous studies based on the CR, all the Penang haplotypes are newly described with none shared with the other regional populations of *M. fascicularis*. A single deletion mutation unique to the Penang samples (Groups I and II) could be a good indicator for the conservation of the genetic uniqueness and possibly should be managed as a management unit (MU). A summarised phylogenetic tree (NJ, MP, ML and Bayesian) supports the monophyletic clustering of the *M. fascicularis* as described in previous studies. The topology separates the Penang haplotypes into three major groups, which generally corresponds to their geographical distribution. We also noted that the Penang haplotypes are of the continental lineage which separated from the insular lineage at around 1.04 mya. Finally, we showed that the CR of the mtDNA is powerful and suitable for the quantification of intraspecific diversity in *M. fascicularis*.

Keywords: *Macaca fascicularis*, Penang Island, phylogenetics, hypervariable segments I and II

INTRODUCTION

THE LONG-TAILED MACAQUE, *MACACA FASCICULARIS*, also known as the cynomolgus macaques, are widely distributed in nature and occupies vast areas of mainland

southeast Asia (Thailand, Cambodia, Vietnam, Laos, Myanmar, Peninsular Malaysia and Singapore) and the Greater and Lesser Sunda Islands (Indonesia, Brunei, and the Malaysian Borneo) and the Philippines (Eudey, 2008; Fooden, 1995). They can be found almost everywhere especially at low elevations preferring the mangrove and swampy forests, river banks, and

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