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ORIGINAL ARTICLE

Genetic diversity and population structure of long-tailed macaque (*Macaca fascicularis*) populations in Peninsular Malaysia

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Abstract

Background The genetic diversity and structure of long-tailed macaques (*Macaca fascicularis*) in Peninsular Malaysia, a widely used non-human primate species in biomedical research, have not been thoroughly characterized.
Methods Thirteen sites of wild populations of long-tailed macaques representing six states were sampled and analyzed with 18 STR markers.
Results The Sunggala and Penang Island populations showed the highest genetic diversity estimates, while the Jerejak Island population was the most genetically discrete due to isolation from the mainland shelf. Concordant with pairwise F_{ST} estimates, STRUCTURE analyses of the seven PCA-correlated clusters revealed low to moderate differentiation among the sampling sites. No association between geographic and genetic distances exists, suggesting that the study sites, including island study sites, are genetically if not geographically contiguous.
Conclusions The status of the genetic structure and composition of long-tailed macaque populations require further scrutiny to develop this species as an important animal model in biomedical research.

Introduction

The long-tailed macaque (*Macaca fascicularis*), which is also known as cynomolgus macaque and crab-eating macaque, is found in Brunei, Cambodia, Indonesia, Malaysia (including the peninsula as well as Sabah and Sarawak in East Malaysia), the Philippines, Singapore, southern Thailand, southern Vietnam, and Nicobar, India [13]. [Correction added on 26 June 2014, after first online publication: The first sentence of the Introduction was edited to include Nicobar, India as one of the places where the long-tailed macaque (*Macaca fascicularis*) can be found.] Long-tailed macaques are desirable for use in medical and scientific research [39] and are primarily used in biotechnological and biomedical research on infectious diseases such as AIDS [50], influenza [22], tuberculosis [5], measles [37], and neurological diseases, including Alzheimer's [47] and Parkinson's [9] diseases. The genetic composition of study subjects is one of several factors known to influence experimental outcomes [16]. An animal's genetic background reflects the genetic variation and structure of the population from which it is derived. Consequently, animals from different source populations can respond differently to the same experimental treatment [7, 44]. Therefore, identifying and quantifying genetic variation and

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