

Haplotype analysis of long-tailed macaques in TNB Bukit Selambau, Peninsular Malaysia, leads to inferences of fission-fusion social structure

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Abstract

Long-tailed macaques have been roaming near Tenaga National Berhad Bukit Selambau Solar (TBSS) causing human-macaque conflicts. This study reveals the social organization and genetic variation of these macaques. Macaques' groups were determined via direct observation and closed-circuit television. Genomic DNA from 29 fecal samples were extracted and proceeded with amplification of the D-loop region of mitochondrial DNA. There are four main groups of primates at TBSS. Some members of the Kuil group and the Pekan group shared haplotype 1, forming a fission-fusion society. This finding can be used for TNB in mitigation plans involving human-macaque conflict.

Keywords: *Macaca fascicularis*, pest, nuisance, phylogeny, Mitochondrial DNA

Introduction

A long-tailed macaque (*Macaca fascicularis*) is considered to be one of the most successful primate species because of its widespread distribution (Abegg & Thierry, 2002). In Malaysia, the long-tailed macaque is locally known as *kera* and is highly adaptable to anthropogenic environmental changes (Osman et al., 2022). It is the most prevalent macaque species in Malaysia and has a wide distribution across Peninsular Malaysia and Borneo (Md-Zain et al., 2022). Long-tailed macaques have recently been classified as endangered in the International Union for Conservation of Nature Red List (Hansen et al., 2022) due to their population declines over time. Human activities are believed to be the primary cause of this decline and subsequent species extinctions (Estrada et al., 2017).

Macaques that live near human interface may cause property damage in rural, urban, and semi-urban areas (Hambali et al., 2012, 2014). Conflict at the human–macaque interface area arises as long-tailed macaques are frequently seen intruding on TNB Bukit Selambau Solar Station (TBSS), causing much damage to TNB properties such as lamp posts and closed-circuit television (CCTV) cameras. This site can be easily accessed by macaques because it is surrounded by oil palm plantations. To determine the human–macaque conflict status, the basic ecological data of long-tailed macaques such as group size, gender, and age structure should be obtained. We also need to determine the genetic structure of the existing long-tailed macaque group to see how they are related to each other.

The noninvasive molecular approach has made significant progress in primate genetics research. DNA can be extracted from feces, hairs, feathers, skin, or saliva without the subject being captured, restrained, or even observed (Abdul-Latiff et al., 2019). The development of molecular techniques, such as polymerase chain reaction (PCR) has allowed primatologists to investigate and study primate systematic and social structure in greater depth (Md-Zain et al., 2010a). Several genes of interest have been amplified using the mitochondrial genome for species identification, phylogenetic, and population genetics studies (Abdul-Latiff et al., 2019; Md-Zain et al., 2018). This study aims to determine the social organization and genetic structure among long-tailed macaque groups in TNB Bukit Selambau Solar Station, Peninsular Malaysia. The D-loop region was selected as a locus candidate based on its suitability in the genetic analysis at the population level (Abdul-Latiff et al., 2014; Abdul-Latiff & Md-Zain, 2021; Aifat et al., 2020) and closely related taxa (Abdul-Latiff et al., 2019). The D-loop region is also known as a suitable candidate locus for studying the complex social structure in primates (Fredsted et al., 2004). Genetic information is important for operational activities and managing human–macaque conflict at