

GENETIC DIVERSITY OF THE CAVE ROOSTING DUSKY FRUIT BAT, *Penthetor lucasi* FROM SARAWAK

YUVARAJAN MANIVANNAN^{1*}, MOHD RIDWAN ABD RAHMAN², ROBERTA CHAYA TAWIE TINGGA²
and FAISAL ALI ANWARALI KHAN^{1*}

¹Faculty of Resource Science and Technology, Universiti Malaysia Sarawak,
94300 Kota Samarahan, Sarawak

²Centre for Pre-University Studies, Universiti Malaysia Sarawak,
94300 Kota Samarahan, Sarawak

*E-mail: yuvanyuv7@gmail.com; akfali@unimas.my

Accepted 20 December 2018, Published online 30 June 2019

ABSTRACT

Previous studies have revealed a high genetic divergence in *Penthetor lucasi* population in Sarawak, indicating it may consist of multiple genetic lineages. However, these studies are not accompanied by morphological data from the studied population suggesting this may be an effect of isolation by distance, especially with small sampling coverage. Here, we provide information based on D-loop sequence analysis from 32 individuals of *Penthetor lucasi* collected from four different regions in Sarawak. Our results revealed a high haplotype diversity and low nucleotide diversity, suggesting that these populations are possibly recovering from a recent geological and climatic event. However, neutrality test and mismatch distributions showed long-term population stability with no population subdivision observed among the studied populations. The moderate to high level of gene flow found in this study indicates that *Penthetor lucasi* population is likely panmictic. Meanwhile, the low level of genetic divergence value among and within populations could account for the absence of species complexity in this study. Our result highlighted the importance of sampling coverage in proper assessment of species diversity especially in species with wide distribution.

Key words: Complexity, D-Loop, divergence, gene flow, panmictic

INTRODUCTION

Bats from the Order Chiroptera represent the second most diverse order from the class Mammalia. In term of global diversity, a total of 131 species of bats from different feeding diet is known to be from Malaysia (Francis 2008; Payne *et al.*, 1985; Phillips & Phillips, 2016). From this, 81 species of insectivorous bats and 18 species of frugivorous and nectarivorous bats can be found in Sarawak (Phillips & Phillips, 2016). Besides controlling global insect population, bats play an important role in balancing the ecosystem through pollination and seed dispersal in the tropical region (Fujita and Tuttle 1991). However, anthropogenic disturbances such as cave closures and forest clearings have affected much of the bats' roosting and foraging activities (Mildenstein *et al.*, 2005; Struebig *et al.*, 2007; Epstein *et al.*, 2009). This leads to bat population

clearing or fragmentation which may result in bat population decline or segregation that can potentially intrude the overall forest ecosystem (Russel, 2005). Therefore, studies involving bat population structure and genetic diversity are important to indirectly inform the sustainable management of caves and forest (Mohd-Ridwan & Abdullah, 2012).

Population genetic studies provide means to address the above issues through the understanding of the genetic diversity of a population affected by environmental changes and habitat loss (Clark *et al.*, 2008; Pruett *et al.*, 2008; Renshaw *et al.*, 2006; Steiper, 2006; Bryja *et al.*, 2009). These studies also inform the genetic make-up of a population over time by revealing which gene is constant and which gene has changed due to environmental factors or other mutation factors through generations (Burland & Worthington-Wilmer, 2001). This is crucial because these unique and rare genes within a gene pool can be an important source of natural selection

* To whom correspondence should be addressed.