

Population Genetics of the Cave-dwelling Dusky Fruit Bat, *Penthetor lucasi*, Based on Four Populations in Malaysia

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ABSTRACT

The population genetics of *P. lucasi* was inferred using 1,061 base pairs (bp) of the Cytochrome *b* mitochondrial gene. A total of 77 individuals were classified *a priori* according to their localities, namely, Miri, Kuching, Sri Aman and Kelantan. Results showed that the populations of *P. lucasi* were separated into two haplogroups, namely, Haplogroup 1 (found in Miri and Kuching populations) and Haplogroup 2 (Miri, Kuching, Sri Aman and Kelantan populations). This separation was supported by bootstrap values in the phylogenetics analyses (94.9% in the maximum likelihood and 100% in Bayesian). A high level of genetic divergence was detected between two haplogroups (3.88%) and this separation could be related to historical events which include multiple colonisation and Pleistocene refugia during the Last Glacial Maximum ice age period. High genetic divergence within Miri (4.93%) and Kuching (4.72%) populations could be due to the presence of a species complex within the *P. lucasi* populations. The presence of haplotypes from both the populations in Haplogroup 1 and Haplogroup 2 might be due to the ability of this particular species of bats to perform long-distance flight for foraging. A high gene flow between these populations suggests a widespread female gene flow of *P. lucasi*, judging from the distance of both localities. Meanwhile, the absence of a deep structure from the haplotype trees further proves that *P. lucasi* may have had a wide dispersal ability since the Pleistocene has allowed for genetic exchange to occur between the regions in Malaysia.

Keywords: *Penthetor lucasi*, population study, genetic diversity, mitochondrial DNA

ARTICLE INFO

Article history:

Received: 17 May 2010

Accepted: 6 July 2011

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INTRODUCTION

An understanding of a species population structure typically provides significant