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Genetic variations and population structure of the genus *Cynopterus* in Malaysia

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ABSTRACT

Nuclear microsatellite analysis of *Cynopterus* was aimed at characterising the microsatellite genotypes and the population structure of this genus especially in the large form of *C. brachyotis* and the small form of *C. brachyotis*. Nine pairs of existing microsatellite primers isolated from Indian *C. sphinx* were used. A total of 51 alleles and 97 genotypes were documented from four forms of *Cynopterus*. Genetic variations revealed from AMOVA analysis showed that there was low genetic variation among the four forms. The interspecies Global AMOVA comparison analysis showed that the genetic variation between the large and small forms of *C. brachyotis* was the lowest among interspecies comparisons. This resulted in low genetic structure in the UPGMA tree, and species boundary of each form was not clearly defined. This might due to the microsatellite primers that were isolated from Indian *C. sphinx* being low in sensitivity to detect variations in Malaysian cynopterans.

Keywords: Microsatellite analysis, *Cynopterus*

INTRODUCTION

Microsatellites or Simple Sequence Repeats (SSRs) are nuclear markers, as well as co-dominant Mendelian markers (DeWoody and Avise, 2000; Srikwan *et al.*, 2002; Scandura, 2004). In microsatellites, sequences are composed of repeated units of sequences; these repeats are generally two to five base pairs in length and are called di-, tri-, tetra- or pentanucleotides (Srikwan *et al.,* 2002). The dinucleotide CA repeats are most commonly found in many eukaryotes (Page & Holmes, 1998; Scandura, 2004).

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