403/D

Genetic variation in *Mycalesis* from Sri Lanka based on analysis of the mitochondrial DNA COI gene

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Butterflies of the genus *Mycalesis* display a variety of phenotypes in relation to changes in seasonal and geographical variations. As a result, there is morphological disparity within species and a remarkable similarity between species, which makes this genus difficult to identify with the aid of standard taxonomic keys alone.

The objective of this study was to investigate the genetic variability in *Mycalesis* from Sri Lanka, by analysis of the cytochrome c oxidase I (COI) gene. Multiple samples of four *Mycalesis* species in Sri Lanka (*M. subdita,M. perseus, M. patnia, M. mineus*), were collected from across the island. COI gene was sequenced to obtain the 658bp barcode region and the standard indices of genetic variation and pairwise genetic distances were calculated. COI sequences of local specimens were supplemented with those found in GenBank to better understand relationships with species in other countries.

This study has established a preliminary reference library of 27 COI DNA barcodes of the local *Mycalesis* species. The haplotype tree of *Mycalesis* formed barcode clusters permitting reliable identification of the four local species. A total of 18 unique haplotypes were identified from the COI sequences analysed from the local species and all were unique to the island. A majority of these haplotypes were observed only in a single butterfly (66.7%) and restricted in location except for one shared haplotype of *M. perseus* found more frequently (18.52%) and observed in samples from Galle, Kalutara and Kurunegala. A higher level of haplotype variability was shown in *M. subdita, M. patnia* and *M. mineus.* Nucleotide diversity was lower for *M. perseus* and *M. subdita* species indicating only smaller nucleotide differences between haplotypes. Tajima's *D* values were negative for all populations, but were significant only for *M. mineus* ($P < 0.01$) and *M. subdita* ($P < 0.001$) populations. Pairwise F_{ST} values showed a significant genetic distance between all four local species with the least distance (0.198) shown between morphologically very similar *M. mineus* and *M. subdita*.

In conclusion, this study presents the preliminary data obtained for haplotype and nucleotide diversity of COI gene of *Mycalesis* populations from Sri Lanka. The preliminary genetic data suggests that the *Mycalesis* population in Sri Lanka is not consistent with a neutral model of evolution. Further studies are necessary to determine the genetic structure and phylogeographic relationships of the *Mycalesis* populations in Sri Lanka.

Keywords: COI gene, DNA barcode, genetic variation, mitochondrial DNA, *Mycalesis*
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