

Mitogenomes of nine Asian skipper genera and their phylogenetic position (Lepidoptera: HesperIIDae: Pyrginae)

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Abstract

In this study, complete mitochondrial genomes of nine species representing three tribes in the subfamily Pyrginae *sensu lato* were newly sequenced. The mitogenomes are closed double-stranded circular molecules, with the length ranging from 15,232 bp to 15,559 bp, which all encode 13 protein-coding genes (PCGs), two ribosomal RNA (rRNA) genes, 22 transfer RNA (tRNA) genes, and a control region. The orientation and gene order of these nine mitogenomes are identical to the inferred ancestral arrangement of insects. All PCGs exhibit the typical start codon ATN except for *cox1* (using CGA) and *cox2* (using TTG) in *Mooreana trichoneura*. Most of the PCGs terminate with a TAA stop codon, while *cox1*, *cox2*, *nad4*, and *nad5* end with the incomplete codon single T. For the different datasets, we found that the one comprising all 37 genes of mitogenome produced the highest nodal support, indicating that the inclusion of RNAs improves the phylogenetic signal. This study re-confirmed the status of *Capila*, *Pseudocoladenia* and *Sarangesa*, namely *Capila* belongs to the tribe Tagiadini, and *Pseudocoladenia* and *Sarangesa* to the tribe Celaenorrhini. Diagnostic characters distinguishing the two tribes, the length of the forewing cell and labial palpi, are no longer significant. Two population of *Pseudocoladenia dan fabia* from China and Myanmar and *P. dan dhyana* from Thailand are confirmed conspecific.

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