Complete mitochondrial genome and phylogeny of Microhyla butleri (Amphibia: Anura: Microhylidae)

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The whole mitochondrial genome of Microhyla butleri was determined by next-generation sequencing of mitochondrial DNA. It had a total length of 16,720 bp, consisting of 13 protein-coding genes, 2 rRNA genes, 22 tRNA genes and 2 non-coding regions (L-strand replication origin and control region). The control region (1338 bp) was flanked by cob and trnL1 genes. The start codons included 11 ATG, 1 ATA and 1 GTG. Three PCGs had TAA, 3 had AGG, 1 had TAG and 6 had incomplete T stop codons. The cloverleaf structure for trnS1 lacked the DHU-stem, and that of trnC lacked the DHU-loop. Molecular phylogeny based on 12 protein-coding genes (without nad6 on L-strand) was congruent with 13 protein-coding genes. It was not concordant with 37 mitochondrial genes and rrnL and rrnS genes. In all mitochondrial markers, M. butleri was basal to its congeners. The genera Microhyla and Kaloula of Microhylidae were monophyletic. The whole mitogenome of M. butleri will serve as a useful dataset for studying the genetics, systematics and phylogenetic relationships of the Microhyla species in particular, and Microhylidae in general.

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1. Introduction

The painted chorus frog Microhyla butleri Boulenger, 1900 is a member of the Microhylidae. It occurs in northeastern India, Myanmar, southern China, Taiwan, Hong Kong, Laos, Cambodia, Vietnam, Thailand, Peninsular Malaysia and Singapore (Frost, 2015). It inhabits disturbed open areas and cultivated land. The genus Microhyla is represented by 38 species. M. butleri is listed as 'Least Concern' in the IUCN (Red List) Status.

Mitochondrial and nuclear genes have been used to study the phylogeny of Microhyla taxa (Matsui et al., 2005, 2011; van der Meijden et al., 2007; Pyron and Wiens, 2011; de Sá et al., 2012; Oliver et al., 2013; Howlader et al., 2015). The phylogenetic relationships based on these molecular markers remain unresolved.

To date, the complete mitochondrial genomes of four species of Microhyla (Microhyla heymonsi, Microhyla fissipes (listed as Microhyla ornata), Microhyla okinavensis and Microhyla pulchra) are available in GenBank. Of these, the mitogenomes of M.

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