The complete mitochondrial genome of *Micromus paganus* (Linnaeus, 1767) (Neuroptera: Hemerobiidae: Microminae) with phylogenetic analysis

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ABSTRACT

The complete mitochondrial (mt) genome of *Micromus paganus* (Linnaeus, 1767) (Neuroptera: Hemerobiidae: Microminae) was assembled and the phylogenetic analysis of Chrysopoidea was conducted. The mt genome was 16,607 bp long including 13 protein-coding genes (PCGs), 22 tRNA genes, 2 rRNA genes, and a control region (CR). Twelve PCGs started with typical ATN, but COI initiated with TCG. The control region was 1335 bp long and the base composition was 89.66% of A + T. Phylogenetic analysis revealed that *M. paganus* was the sister group to *Micromus* sp. + *M. angulatus*. Hemerobiinae and Microminae were recovered monophyletic with high support values. However, the monophyly of Drepanepteryginae was not recovered, which needed more samplings from this subfamily in the further study. The closer relationship between Microminae and Drepanepteryginae was supported. Hemerobiidae was demonstrated monophyletic and being the sister group to Chrysopidae.

This mt genome was a traditional double-strand circular molecule with 16,607 bp long including 22 tRNA genes, 13 protein-coding genes (PCGs), 2 rRNA genes, and a control region (CR). Meanwhile, 23 genes were encoded at the major strand while the remaining 14 genes were encoded at the minor strand. The overall base composition was 39.77% for A, 12.60% for C, 8.88% for G, and 38.74% for T. Twelve PCGs used the typical initiation codon ATN, while COI used TCG as the start codon. There were six genes ended with the incomplete stop codon (T-trNA for COI, ND2, NDS, CytB and TA-trNA for COII, ND4) and seven PCGs terminated with the stop codon TAA. The length of tRNAs varied from 64 bp to 72 bp. The length of *rml* and *rms* was 1327 bp and 790 bp, respectively. The CR was 1335 bp in length with an A + T content of 89.66%.

The phylogenetic trees were reconstructed by MrBayes 3.2.2 (Ronquist et al. 2012) and RAxML 8.2.4 (Stamatakis 2014) based on the first and second codon positions of the PCGs inferring the same topology (Figure 1). *Ditaxis biseriata* (NC_013257) and *Euclimacia badia* (NC_039773) from Mantispidae were selected as outgroups. Phylogenetic analysis showed that *M. paganus* grouped with *Micromus* sp. + *M. angulatus*, all belonging to *Micromus* genus with high support values (PP = 1, BS = 100). Hemerobiinae and Microminae were recovered as monophyletic. Drepanepteryginae was recovered being the sister group to Microminae. However, the monophyly of Drepanepteryginae was not recovered, which needed further studies with more

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Yuyu Wang (Email: hebau_entmus@126.com) under the voucher number HEM001. It was sequenced by Illumina NovaSeq 6000 platform with 150 bp paired-end reading strategy. Raw reads about 3 Gb were checked by FastQC 0.11.9 (Andrews 2010) and low-quality reads were filtered by Trimmomatic 0.32 (Bolger et al. 2014). The mt genome was assembled using IDBA-UD 1.1.3. (Peng et al. 2012) and annotated by MITOS Web Server (Bernt et al. 2013) and then checked by manual proofreading.
comprehensive samplings. Hemerobiidae was demonstrated monophyletic being the sister group to Chrysopidae.

Disclosure statement

No potential conflict of interest was reported by the authors.

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Data availability statement

The genome sequence data that support the findings of this study are openly available in GenBank of NCBI at https://www.ncbi.nlm.nih.gov under the accession MW800748. The associated BioProject, SRA, and BioSample numbers are PRJNA707120, SRR14066566, and SAMN18437193, respectively.

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