Hemerobiidae, the brown lacewings, is the third largest family of Neuroptera, with about 650 species in the world and widely distributed. The genus Hemerobius is the largest genus of family Hemerobiidae, with about 250 species in the world (Oswald 1993, 2019; Monserrat 2000). In this study, we present the complete mitochondrial genome of the Chinese species *Hemerobius spodipennis* Yang, 1987, which belongs to genus *Hemerobius* and important natural enemies because both their adults and larvae prey on aphid, scale insect, worm eggs, and mollusk insects (Yang 1981). The samples were collected in Purang County, Xizang, China (30°12′4″N, 81°15′10″E). Voucher specimen (No. HEME-00813) was deposited at the Entomological Lab of Nanjing Institute of Agricultural Sciences.

This mitochondrial genome is 16,343 bp long (GenBank accession number: MT268963). It includes the entire set of 37 genes (i.e. 13 protein-coding genes, 22 transfer RNA genes, and 2 ribosomal RNA genes) usually present in animal mitochondrial genomes and a control region. Gene order is identical to that of the putative ancestral arrangement of insects and other lacewings. All protein-coding genes initiate with ATN, except COI use CGA as start codons and terminate with TAG or TAA, except ND5 and ND4 use TA— or a single T— residue as the stop codon. All tRNAs, ranging from 63 to 72 bp, can be folded into typical clover-leaf secondary structure except for tRNA<sup>ser(AGN)</sup>, in which the dihydouridine (DHU) arm did not form a stable stem-loop structure. The control region is 1433 bp long with an A+T content of 91.4%. In the sampled families of Neuroptera, each family showed a monophyletic cluster and Polystoechotidae + Rapismatidae, Hemerobiidae + (Chrysopidae + (Polystoechotidae + Rapismatidae)), are recovered in phylogenetic analyses with high supports.
Rapismatidae; and (2) Hemerobiidae + (Chrysopidae + (Polystoecotidae + Rapismatidae)).

Acknowledgements

In particular, we thank Dr. Yunpeng Gai from Zhejiang University for his valuable contributions in technical support.

Disclosure statement

No potential conflict of interest was reported by the author(s).

Funding

This research was supported by the Exploratory and Innovation Project of Jiangsu Academy of Agricultural Sciences (Project No. ZY (17) 2005).

Data availability

The data that support the findings of this study are openly available in NCBI at https://www.ncbi.nlm.nih.gov/, reference number MT268963.

References

Cameron SL. 2014. Insect mitochondrial genomics: implications for evolution and phylogeny. Annu Rev Entomol. 59(1):95–117.

Haruyama N, Mochizuki A, Sato Y, Naka H, Nomura M. 2011. Complete mitochondrial genomes of two green lacewings, Chrysoperla nipponensis (Okamoto, 1914) and Apochrysa matsumurae Okamoto, 1912 (Neuroptera: Chrysopidae), Mol Biol Rep. 38(5):3367–3373.

Monsenat VJ. 2000. New data on the Brown Lacewings from Asia (Neuroptera: Hemerobiidae). J Neuropterol. 3:61–97.

Oswald JD. 1993. Revision and cladistic analysis of the world genera of the family Hemerobiidae (Insecta: Neuroptera). J New York Entomol S. 101:143–299.

Oswald JD. 2019. Neuropterida species of the world. Version 3.0. [cited 2019 Nov 31]. http://lacewing.tamu.edu/Species-Catalogue/

Winterton SL, Hardy NB, Wiegmann BM. 2010. On wings of lace: phylogeny and Bayesian divergence time estimates of Neuropterida (Insecta) based on morphological and molecular data. Syst Entomol. 35(3):349–378.

Wolstrnholme DR. 1992. Animal mitochondrial DNA: structure and evolution. Int Rev Cytol. 141:173–216.

Yang JK. 1981. The brown lace-wings (Neuroptera: Hemerobiidae) of Wuyi Mountain. Wuyi Sci. 1:191–196.

Yang JK. 1987. Agricultural insects, spiders, plant diseases and weeds of Xizang. Xizang: Xizang Renmin Press House. 1:463. pp.

Zhang J, Wang XL. 2016. The complete mitochondrial genome of Mymelonia immanis Walker, 1853 (Neuroptera: Myrmeleontidae) Mitochondrial DNA. 27(2):1439–1440.

Zhao J, Li H, Winterton SL, Liu ZQ. 2013. Ancestral gene organization in the mitochondrial genome of Thyridomyus langii (McLachlan, 1870) (Neuroptera: Osmiidae) and implications for lacewing evolution. PLOS One. 8(5):e62943.

Zhao Y, Chen YJ, Zhao J, Liu ZQ. 2016. First complete mitochondrial genome from the brown lacewings (Neuroptera: Hemerobiidae). Mitochondrial DNA Part A. 27(4):2763–2764.

Zhao Y, Shao HP, Zhang NN, Jing JQ. 2020. First complete mitochondrial genome of Hemerobius japonicus (Neuroptera: Hemerobiidae). Mitochondrial DNA Part B. 5(1):879–880.