Sequencing and characterization of mitochondrial genome of *Idaea effusaria* (Lepidoptera: Geometridae)

Jian-Lin Xie
Taiyuan University of Science and Technology, Taiyuan, China

**ABSTRACT**

The *Idaea effusaria* belongs to Geometridae in Lepidoptera. The complete mitogenome of *I. effusaria* was described in this study, which is typically circular duplex molecules and 16,161 bp in length, containing the standard metazoan set of 13 protein-coding genes, 22 transfer RNA genes, 2 ribosomal RNA genes, and an A + T-rich region. The gene order is same with other lepidopterans. Except for *cox1* started with CGA, all other PCGs started with the standard ATN codons. Most of the PCGs terminated with the stop codon TAA, whereas *cox2* has the stop codon CAT. The phylogenetic tree showed that Larentiinae is close to Sterrhinae. The species of Ennominae form a monophyly.

*Idaea effusaria* (Christoph) is a moth of the family Geometridae. Geometridae is one of the most species-rich groups in Lepidoptera, include more than 26,000 described species (Liu et al. 2014). However, mitochondrial genomes of only 13 species in Geometridae were reported. This group is so large and should be studied by more mitochondrial genomes information.

In this study, the samples were collected by light trapping in Taiyuan city of China (37°83′33″N, 112°66′61″E) in July 2019, some of these specimens were immediately frozen in −80°C on board for mitogenome analysis and others were preserved by spreading wings in the Herbarium of Institute of Plant Protection, Shanxi Academy of Agricultural Sciences, and their numbers is 2019TYKD1706-1710. Total genomic DNA was extracted from tail tip using the Ezup pillar genomic DNA extraction kit (Sangon Biotech, Shanghai, China). The mitogenome was sequenced by Illumina HiSeq 4000. Gene annotation was performed and circularity was checked using the MITOS2 webserver (Bernt et al. 2013, http://mitos.bioinf.uni-leipzig.de/).

The mitochondrial genome of *I. effusaria* has a total length of 16,161 bp (GenBank accession No. MN646772), consisting of 13 PCGs, 22 tRNA, 2 rRNA genes, and an A + T-rich region. The major strand encodes a larger number of genes (9 PCGs and 14 tRNAs) than the minor strand (4 PCGs, 8 tRNAs, and 2 rRNA genes). Gene content and arrangement are highly conserved and typical of Lepidoptera (Wu et al. 2016). The mitogenome is highly biased toward A/T, contains 41.02% T, 41.07% A, 10.70% C, and 7.20% G, which is a feature common in Lepidoptera insects (Garey and Wolstenholme 1989). The 16S rRNA is 1286 bp in length and the 12S rRNA is 720 bp in length. The A + T-rich region is 771 bp long located between 12S rRNA and tRNA-Met and it is longer than other most Lepidoptera insects. There is a motif ATAGA in downstream of 12S rRNA followed by an 17 bp Poly-T stretch.

The phylogenetic position of *I. effusaria* was inferred using sequences of the 13 PCGs of 14 species. Thirteen of them belong to Geometridae and a species from Pyraloidea (which is used as outgroup) (Figure 1). The sequences were aligned with MAFFT v7.2 software (Katoh and Standley 2013), the evolutionary analyses were conducted with RAxML v8.2.10 (Stamatakis 2014) on the CIPRES Science Gateway (Miller et al. 2010). The result showed that *I. effusaria* and *Operophtera brumata* are clustered into a clade, Larentiinae is close to Sterrhinae. Other moths belong to Ennominae and form a monophyly. The result is consistent with morphological classification.

**Nucleotide sequence accession number**

The complete mitochondrial genome sequence of *I. effusaria* was deposited in the GenBank under the accession number MN646772.

**Disclosure statement**

The authors report no conflicts of interest. The authors alone are responsible for the content and writing of the paper.

**Funding**

This work was supported by the Key R & D Projects of Shanxi Province (Social Development) [201903D321058] and the Open fund of Shanxi
References

Bernt M, Donath A, Juhling F, Externbrink F, Florentz C, Fritzsch G, Putz J, Middendorf M, Stadler PF. 2013. MITOS: improved de novo metazoan mitochondrial genome annotation. Mol Phylogenet Evol. 69(2):313–319.

Boore JL. 1999. Survey and summary: animal mitochondrial genomes. Nucleic Acids Res. 27(8):1767–1780.

Garey JR, Wolstenholme DR. 1989. Platyhelminth mitochondrial DNA: Evidence for early evolutionary origin of a tRNA ser AGN that contains a dihydrouridine arm replacement loop, and of serine-specifying AGA and AGG codons. J Mol Evol. 28(5):374–387.

Katoh K, Standley DM. 2013. MAFFT multiple sequence alignment software version 7: improvements in performance and usability. Mol Biol Evol. 30(4):772–780.

Liu X, Yang C, Han H, Ward R, Zhang A. 2014. Identifying species of moths (Lepidoptera) from Baihua Mountain, Beijing, China, using DNA barcodes. Ecol Evol. 4(12):2472–2487.

Miller MA, Pfeiffer W, Schwartz T. 2010. Creating the CIPRES science gateway for inference of large phylogenetic trees. Proceedings of the Gateway Computing Environments Workshop (GCE); Nov 14; New Orleans, Louisiana: Institute of Electrical and Electronics Engineers (IEEE), p. 1–8.

Stamatakis A. 2014. RAxML version 8: a tool for phylogenetic analysis and post-analysis of large phylogenies. Bioinformatics. 30(9):1312–1313.

Wu YP, Zhao JL, Su TJ, Luo AR, Zhu CD. 2016. The complete mitochondrial genome of Choristoneura longicollina (Lepidoptera: Tortricidae) and phylogenetic analysis of Lepidoptera. Gene. 591(1):161–176.

Figure 1. Maximum-likelihood tree of evolutionary relationships I. effusaria based on the complete mitogenomes of 14 Lepidopteran moths.