

The complete mitochondrial genome of *Lyssa zampa* (Lepidoptera: Uraniidae)

Ge-Ge Yuan^{a,b} , Yuan-Wen Du^{a,b} , Lu Chen^{a,b} , Lang Ming^{a,b} , Gong Chen^{a,b}  and Xing Wang^{a,b} 

^aCollege of Plant Protection, Hunan Agricultural University, Changsha, China; ^bHunan Provincial Key Laboratory for Biology and Control of Plant Diseases and Insect Pests, Hunan Agricultural University, Changsha, China

ABSTRACT

The complete mitochondrial genome (mitogenome) of *Lyssa zampa* was first reported. It is 15,314 bp in length (GenBank accession number: MW435592) and consists of 13 protein-coding genes (PCGs), 22 transfer RNA (tRNA) genes, two ribosomal RNA (rRNA) genes. The nucleotide composition is A (41.5%), C (11.1%), G (7.4%), and T (40.0%). Based on the sequences of complete mitogenome from 12 geometroid species and three drepanoid species as ingroups, and two noctuid species as outgroups, the phylogenetic tree was constructed. The results showed that the closest relationship between Uraniidae and Epicopeiidae was strongly supported by Bayesian posterior probabilities values of 0.99.

ARTICLE HISTORY

Received 8 January 2021
Accepted 7 April 2021

KEYWORDS

Lyssa zampa; mitochondrial genome; phylogenetic position

Lyssa zampa, which is broadly distributed from the Himalayas to Borneo and the Malay Peninsula, belongs to the family Uraniidae (Lepidoptera: Geometridae) (Nazari et al. 2016). Its larvae feed on *Endospermum* and other members of the rubber tree in the family Euphorbiaceae (Tokeshi and Yokoo 2007), and its genetic information is rarely known. Here, the complete mitochondrial genome (mitogenome) of *L. zampa* was first obtained and reported in the family Uraniidae, and the phylogenetic tree for understanding its phylogenetic position and relationships within the superfamily Geometridae was constructed. All the specimens and the genomic DNA in this study were deposited at the Insect Museum of Hunan Agricultural University, Changsha City, Hunan Province, China.

The specimens of *L. zampa* were collected on 21 July 2019 from Xiajinchang Town (23°N, 105°E, elevation of 1395 m) in Malipo County, Yunan Province, China. The complete genomic DNA was extracted following the methods in Wang et al. (2019) from the legs of the adult (collection number: HAUHL033878) by using TaKaRa MiniBEST Universal Genomic DNA Extraction Kit Ver.5.0 (Shiga Prefecture, Kusatsu City, Japan), and was sequenced on the Illumina HiSeq platform with 150 bp paired-end reads at Novogene (Beijing, China). For Illumina TruSeq library, 6 Gb of clean data were obtained. The contigs and scaffolds of highly qualified sequences were determined using IDBA-1.1.3 (Peng et al. 2012; Chen et al.

2020). The mitogenome was annotated on the ORF finder (<https://www.ncbi.nlm.nih.gov/orffinder/>) and MITOS web server (<http://mitos.bioinf.uni-leipzig.de/index.py>) (Bernt et al. 2013).

The complete mitogenome of *L. zampa* is a circular DNA molecule of 15,314 bp in length (GenBank accession number: MW435592) and consists of 13 protein-coding genes (PCGs), 22 transfer RNA (tRNA) genes, two ribosomal RNA (rRNA) genes, and an AT-rich region, in which 23 genes are transcribed on the J strand and the remaining 14 are transcribed on the N strand. The nucleotide composition is A (41.5%), C (11.1%), G (7.4%), T (40.0%), and the AT nucleotide content is 81.5%. There are 76 bp intergenic nucleotides that were dispersed in between 14 pairs of neighboring genes with their length varying from 1 to 24 bp. The length of the AT-rich region that located between *rns* and the *trnM* is 436 bp.

To construct the phylogenetic tree, the complete mitogenomes from 12 geometroid species and three drepanoid species as ingroups, and two noctuid species as outgroups were used. Bayesian inference (BI) analysis was executed using MrBayes on XSEDE (3.2.6) (<https://www.phylo.org/portal2/home.action>), with the Markov chain Monte Carlo analysis run for 10,000,000 generations, sampled every 1000th generation and with a burn-in of 25%. The results are shown in Figure 1. The family Uraniidae belongs to the superfamily

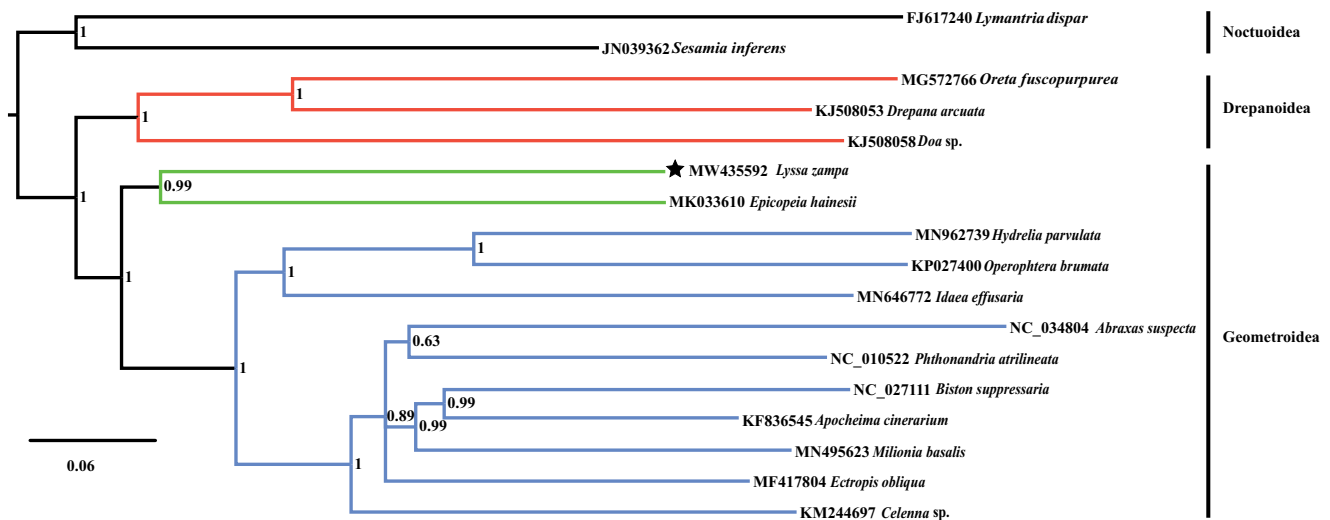


Figure 1. Bayesian (BI) tree of evolutionary relationships for *Lyssa zampa* based on the complete mitogenomes of 17 lepidopteran moths.

Geometridae, which is consistent with Yang et al. (2019). Meanwhile, the closest relationship between Uraniidae and Epicopeiidae was strongly supported by Bayesian posterior probabilities values of 0.99.

Acknowledgements

We thank Mr. Chang-Jin Yang for collecting the specimens.

Disclosure statement

The authors declare that there is no conflict of interest regarding the publication. The authors also are responsible for the content and writing of the paper.

Funding

This study was supported by the National Natural Science Foundation of China [31970450, 31801799], the Hunan Province Natural Science Foundation [2019JJ50274], and the Scientific Research Fund of Hunan Provincial Education Department [18B123].

ORCID

Ge-Ge Yuan  <http://orcid.org/0000-0003-0573-505X>
 Yuan-Wen Du  <http://orcid.org/0000-0002-3573-8094>
 Lu Chen  <http://orcid.org/0000-0002-0706-562X>
 Lang Ming  <http://orcid.org/0000-0002-5391-4629>
 Gong Chen  <http://orcid.org/0000-0002-7199-1396>
 Xing Wang  <http://orcid.org/0000-0001-6815-5912>

Data availability statement

The mitogenome sequence data that support the finding of this study are openly available in GenBank of NCBI at <https://www.ncbi.nlm.nih.gov> under the accession no. MW435592.

References

- Bernt M, Donath A, Juhling F, Juling F, Externbrink F, Florentz C, Fritsch G, Putz J, Middendorf M, Stadler PF. 2013. MITOS: improved de novo metazoan mitochondrial genome annotation. *Mol Phylogenet Evol.* 69:313–319.
- Chen L, Niklas W, Liao CQ, Wang CB, Ma FZ, Huang GH. 2020. Fourteen complete mitochondrial genomes of butterflies from the genus *Lethe* (Lepidoptera, Nymphalidae, Satyrinae) with mitogenome-based phylogenetic analysis. *Genomics.* 112:4435–4441.
- Nazari V, Schmidt BC, Prosser S, Hebert PDN. 2016. Century-old DNA barcodes reveal phylogenetic placement of the extinct Jamaican sunset moth, *Urania sloanus* Cramer (Lepidoptera: Uraniidae). *PLoS One.* 11:1–13.
- Peng Y, Leung HCM, Yiu SM, Chin FYL. 2012. IDBA-UD: a de novo assembler for single-cell and metagenomic sequencing data with highly uneven depth. *Bioinformatics.* 28:1420–1428.
- Tokeshi M, Yokoo M. 2007. New record of the tropical swallowtail moth *Lyssa zampa* (Butler) (Lepidoptera: Uraniidae) from mainland Japan. *Entomol Sci.* 10:103–106.
- Wang X, Chen ZM, Gu XS, Wang M, Huang GH, Zwick A. 2019. Phylogenetic relationships among Bombycidae s.l. (Lepidoptera) based on analyses of complete mitochondrial genomes. *Syst Entomol.* 44:490–498.
- Yang MS, Song L, Shi YX, Li JH, Zhang YL, Song N. 2019. The first mitochondrial genome of the family Epicopeiidae and higher-level phylogeny of Macroheterocera (Lepidoptera: Ditrysia). *Int J Biol Macromol.* 136:123–132.