Complete mitochondrial genome of *Lelecella limenitoides* (Lepidoptera: Nymphalidae: Apaturinae) and phylogenetic implication

Li Jun Fang\(^a\), Shao Li Mao\(^a\) and Ya Lin Zhang\(^b\)

\(^a\)Shaanxi Engineering Research Centre for Conservation and Utilization of Botanical Resources, Xi’an Botanical Garden of Shaanxi Province (Institute of Botany of Shaanxi Province), Xi’an, China; \(^b\)Key Laboratory of Plant Protection Resources and Pest Management, Ministry of Education, Entomological Museum, Northwest A&F University, Shaanxi, China

**ABSTRACT**

The length of *Lelecella limenitoides* complete mitogenome was 15,203 bp and contained the typical gene arrangement, base composition, and codon usage found in other related species. The overall base composition exhibited obvious anti-G (7.5%) and AT bias (81.6%). The initiation codons of all PCGs were typical ATN (ATA/ATG/ATT), and the termination codons were TAA, TAG, or incomplete stop codon T—a. All tRNAs could be folded into typical cloverleaf secondary structures, except tRNA\(^{\text{Ser}}\) (AGN). Phylogenetic analysis showed that *L. limenitoides* was clustered with the clade of *Sasakia*, *Euripus*, and *Apatura*.

Figure 1  Phylogenetic reconstruction of the Apaturinae using mitochondrial PCGs and rRNA of the concatenated dataset.
tRNAIle-tRNAGln-tRNAMet gene cluster and 448 bp in length. It is located at the conserved position between 12S rDNA and ND2. There are 13 overlaps with all of 41 bp. The overall base composition of the whole mitochondrial genome is 39.8% A, 41.8% T, 10.9% C, and 7.5% G, obvious anti-G and AT bias (81.6%).

The initiation codons of all PCGs are typical ATN (COII, ATP6, COIII, ND1, ND4, ND4L, and Cytb with ATG, ND2, ATP8, ND5, ND6 with ATT; ND3 with ATA). Nine protein genes (ND2, COI, ATP8, ATP6, COII, ND4L, ND6, Cytb, and ND1) use TAA as the termination codons, and only one gene (ND3) is stopped with TAG. COII, ND5, and ND4 have an incomplete stop codon T—in. The length of tRNA genes ranked from 61 bp (tRNA^{Ser}_{AGN}) to 73 bp (tRNA^{Leu}_{CUN}). All tRNAs exhibit typical cloverleaf secondary structures, except tRNA^{Ser}_{AGN} lacks the DHU arm, a feature generally present in all Lepidoptera insects as well as in other metazoan mitochondomes (Lavrov et al. 2000). The length of 12S rRNA and 16S rRNA are 713 bp and 1324 bp respectively, separated by 113 bp of intergenic spacer sequences, which are spread over 12 regions and the longest one locates between tRNAGln and ND2. There are 13 overlaps with all of 41 bp. The overall base composition of the whole mitochondrial genome is 39.8% A, 41.8% T, 10.9% C, and 7.5% G, obvious anti-G and AT bias (81.6%).

Phylogenetic analysis of Apaturinae species was performed on the concatenated datasets of 13 PCGs and two rRNA genes by IQ-tree (Nguyen et al. 2015). Phylogenetic topology of the genera was congruent with previous study (Wang et al. 2017). The new sequenced species L. limenitoides clustered with the genera of Sasakia, Euripus, and Apatura and then clustered together with the clade of Herona, Chitoria, and Timelaea.

Disclosure statement

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

Funding

This study was supported by the National Natural Science Foundation of China [31750002], the Natural Science Foundation of Shaanxi Province [2019JQ-195] and Key Projects of Shaanxi Academy of Sciences [2016K-06].

References

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

Cao TW, Wang JP, Xuan SB, Zhang M, Guo YP, Ma EB. 2013. Analysis of complete mitochondrial genome of Timelaea maculate (Lepidoptera, Nymphalidae). Acta Zootaxon Sin. 38(1):468–475.

Chen M, Tian LL, Shi QH, Cao TW, Hao JS. 2013. Complete mitogenome of the Lesser Purple Emperor Apatura ilia (Lepidoptera: Nymphalidae) and comparison with other nymphaid butterflies. Zool Res. 33(2):191–201.

Kearse M, Roir A, Wilson A, Stones-Havas S, Cheung M, Sturrock S, Buxton S, Cooper A, Markowitz S, Duran C, et al. 2012. Geneious Basic: an integrated and extendable desktop software platform for the organization and analysis of sequence data. Bioinformatics. 28(12):1647–1649.

Lavrov DV, Brown WM, Boore JL. 2000. A novel type of RNA editing occurs in the mitochondrial tRNAs of the centipede Lithobius forficatus. Proc Natl Acad Sci USA. 97(25):13738–13742.

Meng G, Li Y, Yang C, Liu S. 2019. MitoZ: a toolkit for animal mitochondrial genome assembly, annotation and visualization. Nucleic Acids Res. 47(11):e63.

Nguyen LT, Schmidt HA, von Haeseler A, Minh BQ. 2015. IQ-TREE: a fast and effective stochastic algorithm for estimating maximum likelihood phylogenies. Mol Biol Evol. 32(1):268–274.

Wang JP, Cao TW, Xuan SB, Wang H, Zhang M, Ma EB. 2013. The complete mitochondrial genome of Sasakia funebris (Lecih) (Lepidoptera: Nymphalidae) and comparison with other Apatnutinae insects. Gene. 526(2):336–343.

Wang JP, Cao TW, Zhang Y, Fan RJ, Zhang M, Shi BM, Peng FC. 2017. Sequencing and analysis of the complete mitochondrial genome of Limenitis helmanni (Lepidoptera: Nymphalidae). Acta Entomol Sin. 60(8):950–961.

Wang JP, Nie XP, Cao TW, Zhang M, Guo YP, Ma EB, Zhang XN. 2012. Analysis of complete mitochondrial genome of Sasakia charonda coreana (Lepidoptera, Apatnutinae). Acta Zootaxon Sin. 37(1):1–9.

Wang JP, Xuan SB, Cao LM, Hao JS, Cao TW. 2016. The complete mitochondrial genome of the butterfly Herona marathus (Lepidoptera: Nymphalidae). Mitochondr DNA A. 27(6):4399–4400.

Wang JP, Xuan SB, Zhang YP, Yang J, Cao TW, Ma EB. 2015. Sequencing and analysis of the complete mitochondrial genome of Chitoria ulupi (Lepidoptera: Nymphalidae). Acta Entomol Sin. 58(3):319–328.

Xuan SB, Song F, Cao LM, Wang JP, Li H, Cao TW. 2016. The complete mitochondrial genome of the butterfly Euripus nectiellus (Lepidoptera: Nymphalidae). Mitochondr DNA A. 27(4):2563–2565.

Zhang M, Nie X, Cao T, Wang J, Li T, Zhang X, Guo Y, Ma EB, Zhong Y. 2012. The complete mitochondrial genome of the butterfly Apatura metis (Lepidoptera: Nymphalidae). Mol Biol Rep. 39(6):6529–6536.