Complete mitochondrial genome of *Actias dubernardi* (Lepidoptera: Saturniidae)

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**ABSTRACT**

The complete mitochondrial genome of *Actias dubernardi* (Lepidoptera: Saturniidae) is 15,270 bp in length, containing 13 protein-coding genes, 22 transfer RNAs, 2 ribosomal RNAs, and a putative control region. All of the protein-coding genes (PCGs) use the standard start codon ATN, except for cox1 which starts with CGA. The Bayesian phylogenetic analysis was performed using a dataset matrix containing 13 PCGs concatenated from the mitogenomes of 14 Saturniidae species. The monophyly of the five *Actias* species was highly supported and *Antheraea* was inferred as the sister group of *Actias*.

Furthermore, we checked the coding sequences (CDSs) by nucleotide BLAST and the CDS feature display.

The complete mitogenome of *A. dubernardi* is 15,270 bp in size, composed 37 genes as in most insect mitogenomes (Cameron 2014), including 13 protein-coding genes (PCGs), 2 ribosomal RNAs (16S and 12S), 22 transfer RNAs (tRNAs), along with the noncoding control region, termed in insects as A + T rich region (GenBank accession no. MW133617). The gene arrangement of the *A. dubernardi* was identical to the majority of the Lepidoptera (Wan et al. 2013), with the order *trnM/trnL/trnQ* between the A + T rich region and *nad2*. The overall base composition is 38.7% A, 39.5% T, 13.5% C, and 8.3% G. The nucleotide composition of the *A. dubernardi* mitogenome is biased toward A + T (78.2%). All of the PCGs use the standard start codon ATN, except for cox1 which starts with CGA. The 16S is located between *trnL*1 and *trnV*, with a length of 1371 bp. The *12S* is located between *trnV* and the control region, with a length of 779 bp. The control region is 330 bp in length, and is located between 12S and *trnM*.

Phylogenetic analysis was performed on concatenated nucleotide sequences of the 13 PCGs of five *Actias* species, along with nine Saturniidae species as an outgroup (Langley et al. 2020). Sequences of the 14 species of each PCG were aligned using CLUSTAL X (Thompson et al. 1997) with the default settings and refined manually. The alignment of each PCG was deliberately trimmed to equal length before concatenating. Phylogenetic inference was performed using MrBayes 3.2.7 (Ronquist et al. 2012) with 10,000,000 generations, which are sufficient to meet the 0.01 criteria of standard deviation of split frequencies. The best-fit nucleotide substitution models (GTR + I + G) were determined by AIC implemented in jModelTest 2 (Darriba et al. 2012).
As expected, the monophyly of Actias species was supported with 100% bootstrapping rates. A. dubernardi was inferred as the sister group of a subclade including A. luna, A. selene, and A. artemis, while A. maenas had the basal status in the genus (Figure 1). In addition, Antheraea was inferred as the sister group of Actias, consistent with that previously described (Langley et al. 2020).

Disclosure statement

No potential conflict of interest was reported by the authors.

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Data availability statement

The mitogenome 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 no. MW133617. The associated BioProject, SRA, and Bio-Sample numbers are PRJNA687294, SRR13329533, and SAMN17141016, respectively.

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