

MITOGENOME ANNOUNCEMENT**Sequence and organization of complete mitochondrial genome of the firefly, *Aquatica leii* (Coleoptera: Lampyridae)**

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Abstract

The firefly *Aquatica leii* (Coleoptera: Lampyridae) is widely distributed in China. In this study, we sequenced and characterized the first complete mitochondrial genome of the firefly from the subfamily Luciolinae. The circular genome of 16,856 bp in length contains 13 protein-coding genes, 22 transfer RNA genes, 2 ribosomal RNA genes and a non-coding AT-rich region. Overall base composition of the genome is 42.28% A, 34.80% T, 13.91% C and 9.01% G, with an AT bias of 77.08%. All protein-coding genes start with an ATN codon, and terminate with the typical stop codon TAA, TAG or a single T. The non-coding AT-rich region is unusually long (2239 bp), containing six 113 bp tandem repeats and a microsatellite-like (TA)₇ element. The genome sequence is useful for studying the evolution of sexual signaling and many ecological specializations in fireflies.

Keywords

Aquatica leii, firefly, Lampyridae, Luciolinae, mitochondrial genome

History

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The beetle family Lampyridae (>2000 species), commonly called fireflies or lightning bugs, are well known for their bioluminescent courtship signals (Lewis & Cratsley, 2008). All firefly larvae use a faint glow at night to warn against predators, while adults employ light signals for species recognition, sexual selection and location (Branham & Wenzel, 2001; Lloyd, 1971). Although most fireflies produce light as adults, some species are not luminous at all and may rely exclusively on pheromones for mate choice. In other firefly species, both pheromones and light signals are used for sexual selection (Lloyd, 1997). The diversity of sexual signaling permits fireflies to be an excellent group for studying the evolution of animal communication signals and sexual selection (Lewis & Cratsley, 2008). Mitochondrial (mt) genome sequences are valuable molecular markers and will be helpful to reconstruct the evolutionary history of firefly sexual signaling, however, only one complete mt genome of *Pyrocoelia rufa* (Lampyridae: Lampyrinae) has been determined (Bae et al., 2004). Here, we report the first complete mt genome of *Aquatica leii* (Lampyridae: Luciolinae), a firefly species widely distributed in China, from another subfamily Luciolinae (Fu & Ballantyne, 2006; Fu et al., 2010), aiming to expand our knowledge of firefly mt genomes.

Genomic DNA was isolated from thoracic muscle of an adult male of *Aquatica leii* using DNeasy Blood & Tissue Kit (QIAGEN, Hilden, Germany). The complete mitochondrial genome was amplified with two pairs of universal primers (Folmer et al., 1994; Vogler & DeSalle, 1993) and 12 pairs of newly designed primers based on the mt genome of *Pyrocoelia*

rufa (Bae et al., 2004). All primer information will be provided upon request. PCR amplification and sequencing procedure were followed our previous work (Wang et al., 2013).

The complete mt genome of the firefly *Aquatica leii* (GenBank accession number: KF667531) is a circular double-stranded molecule of 16,856 bp in length, which is shorter than the other firefly *Pyrocoelia rufa* (Bae et al., 2004) but longer than the two luminous beetles closely related to fireflies (Li et al., 2007). Its gene content, arrangement and orientation are identical to those of most insects (Table 1), containing 13 protein-coding genes (PCGs), 2 ribosomal RNAs, 22 transfer RNAs and a non-coding AT-rich region (Beard et al., 1993). Overall base composition of the genome is 42.28% A, 34.80% T, 13.91% C and 9.01% G, which appears to show an AT bias of 77.08%. Seven intergenic spacers ranging from 1 to 65 bp and 12 overlapping sequences from 1 to 8 bp are scattered over the genome (Table 1).

The open reading frames of the 13 PCGs were inferred from a sequence alignment of published mt genome sequences of coleopteran insects. All PCGs use standard ATN (ATT, ATG or ATA) as the start codon. Whereas six PCGs (*ATP8*, *ATP6*, *ND4L*, *ND6*, *ND1* and *ND2*) use the typical stop codon TAA or TAG, the remaining seven PCGs terminate with a single T (Table 1). The non-coding AT-rich region is unusually long (2239 bp) and is located between *12S rRNA* and *tRNA^{Met}*, containing six 113-bp tandem repeats and a microsatellite-like (TA)₇ element. All 22 tRNAs could be folded into classic clover-leaf secondary structures except for *tRNA^{Ser}* (AGN).

Nucleotide sequence accession number

The complete genome sequence of *Aquatica leii* has been submitted to GenBank under accession number KF667531.

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Table 1. Organization of the complete mitochondrial genome of the firefly *Aquatica leii*.

Gene	Direction	Position	Size (bp)	Intergenic length*	Start codon	Stop codon
<i>tRNA^{Ala}</i>	F	1–63	63	0		
<i>tRNA^{Gln}</i>	R	61–129	69	–3		
<i>tRNA^{Met}</i>	F	129–194	66	–1		
<i>ND2</i>	F	195–1208	1014	0	ATA	TAG
<i>tRNA^{Trp}</i>	F	1210–1274	65	1		
<i>tRNA^{Cys}</i>	R	1340–1402	63	65		
<i>tRNA^{Tyr}</i>	R	1402–1465	64	–1		
<i>COI</i>	F	1458–2997	1540	–8	ATT	T + tRNA
<i>tRNA^{Leu} (UUR)</i>	F	2998–3061	64	0		
<i>COII</i>	F	3063–3741	679	1	ATG	T + tRNA
<i>tRNA^{Lys}</i>	F	3742–3812	71	0		
<i>tRNA^{Asp}</i>	F	3812–3874	63	–1		
<i>ATP8</i>	F	3875–4030	156	0	ATT	TAA
<i>ATP6</i>	F	4024–4698	675	–7	ATG	TAA
<i>COIII</i>	F	4698–5481	784	–1	ATG	T + tRNA
<i>tRNA^{Gly}</i>	F	5482–5545	64	0		
<i>ND3</i>	F	5546–5897	352	0	ATT	T + tRNA
<i>tRNA^{Ala}</i>	F	5898–5961	64	0		
<i>tRNA^{Arg}</i>	F	5961–6025	65	–1		
<i>tRNA^{Asn}</i>	F	6025–6090	66	–1		
<i>tRNA^{ser} (AGN)</i>	F	6091–6157	66	0		
<i>tRNA^{Glu}</i>	F	6158–6221	64	0		
<i>tRNA^{Phe}</i>	R	6220–6283	64	–2		
<i>ND5</i>	R	6284–8012	1729	0	ATT	T + tRNA
<i>tRNA^{His}</i>	R	8013–8075	63	0		
<i>ND4</i>	R	8076–9402	1327	0	ATG	T + tRNA
<i>ND4L</i>	R	9396–9686	291	–7	ATG	TAA
<i>tRNA^{Thr}</i>	F	9688–9749	62	1		
<i>tRNA^{Pro}</i>	R	9750–9815	66	0		
<i>ND6</i>	F	9817–10,305	489	1	ATA	TAA
<i>CYTB</i>	F	10,305–11,436	1132	–1	ATG	T + tRNA
<i>tRNA^{Ser} (UCN)</i>	F	11,437–11,502	66	0		
<i>ND1</i>	R	11,520–12,464	945	17	ATT	TAG
<i>tRNA^{Leu} (CUN)</i>	R	12,472–12,534	63	7		
<i>16S rRNA</i>	R	12,535–13,797	1263	0		
<i>tRNA^{Val}</i>	R	13,798–13,867	70	0		
<i>12S rRNA</i>	R	13,868–14,617	750	0		
AT-rich region		14,618–16,856	2239			

*The positive number indicates the length of intergenic spacers, while the negative number indicates the overlapping length between genes.

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Declaration of interest

The authors report no conflict of interest. The authors alone are responsible for the content and writing of the article. This study was supported by a start-up fund from Wuhan University to HZ.

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