

MITOGENOME ANNOUNCEMENT

Characterization of the mitochondrial genome of the montane grasshopper, *Qinlingacris elaeodes* (Orthoptera: Catantopidae)

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Abstract

Qinlingacris elaeodes is the dominant grasshopper at an altitude of 3000 meters and above, and is a representative species of the genus *Qinlingacris* endemic to China. The sequenced mitochondrial genome of this grasshopper is 14,818 bp in length, including 13 protein-coding genes (*ND1-6*, *COI-III*, *ATP6*, *ATP8*, *ND4L*, *CTYB*), 21 transfer RNAs, and 2 ribosomal RNAs (*12S* and *16S*). The orientation and gene order of these genes are identical to those found in the putative ancestral insect mitogenome. The 13 PCGs start with a typical ATN codon as their start codons. The usual TAA and TAG termination codons are found for 12 PCGs. However, the *ND5* gene has an incomplete termination codon (T).

Keywords

Acridoidea, mitogenome, Orthoptera, *Qinlingacris elaeodes*

History

Received 31 August 2014
Accepted 7 September 2014
Published online 25 September 2014

The genus *Qinlingacris* (Orthoptera: Catantopidae) is first published in 1979, and is endemic to Taibai Mountain in Shaanxi Province, China (Yin & Chou, 1979). To date, there are three known species within this genus (Li et al., 1991; Yin & Chou, 1979). *Qinlingacris elaeodes* is the dominant species at an altitude of 3000 meters and above, and is a representative species of the genus *Qinlingacris*.

At the last count, about fifty complete or nearly complete mitogenomes in Acridoidea species have been published in GenBank (<http://www.ncbi.nlm.nih.gov>, ending on August 30, 2014), among them only two species, *Shirakiacris shirakii* and

Kingdonella bicollina, belong to the Catantopidae. In this study, we described the characterization of mitogenome of *Q. elaeodes*. The adult specimens were collected in Shaanxi, China.

The nearly complete mitogenome sequence of the *Q. elaeodes* was 14,818 bp long, which comprised of 13 protein-coding genes (PCGs), 9 (*ND2*, *COI*, *COII*, *ATP8*, *ATP6*, *COIII*, *ND3*, *ND6* and *CYTB*) of them were distributed on the majority strand, while the rest (*ND5*, *ND4*, *ND4L*, *ND1*) were distributed on the minority strand. All of the PCGs in the *Q. elaeodes* mitogenome were initiated by typical ATN codons (eight with ATG, two with ATT, two with ATC and one with ATA). Twelve of 13 PCGs share the

Table 1. Annotation and gene organization of the *Q. elaeodes* mitogenome.

Gene	Strand	Nucleotide no.	Size(bp)	IN	Anticodon	Start codon	Stop codon
<i>tRNA^{Gln}</i>	N	52–120	69	0	TTG	–	–
<i>tRNA^{Thr}</i>	J	122–191	70	1	TGT	–	–
<i>ND2</i>	J	192–1214	103	0	–	ATG	TAA
<i>tRNA^{Trp}</i>	J	1213–1279	67	–2	TCA	–	–
<i>tRNA^{Cys}</i>	N	1272–1336	65	–8	GCA	–	–
<i>tRNA^{Tyr}</i>	N	1345–1410	66	8	GTA	–	–
<i>COI</i>	J	1403–2940	1538	–8	–	ATC	TAG
<i>tRNA^{Leu(UUR)}</i>	J	2943–3008	66	2	TAA	–	–
<i>COII</i>	J	3011–3694	684	2	–	ATG	TAA
<i>tRNA^{Asp}</i>	J	3693–3757	65	–2	GTC	–	–
<i>tRNA^{Lys}</i>	J	3760–3830	71	2	CTT	–	–

(continued)

Table 1. Continued.

Gene	Strand	Nucleotide no.	Size(bp)	IN	Anticodon	Start codon	Stop codon
<i>ATP8</i>	J	3845–4006	162	14	–	ATC	TAA
<i>ATP6</i>	J	4000–4677	678	–7	–	ATG	TAA
<i>COIII</i>	J	4682–5469	788	4	–	ATG	TAA
<i>tRNA^{Gly}</i>	J	5476–5542	65	6	TCC	–	–
<i>ND3</i>	J	5543–5896	354	0	–	ATT	TAA
<i>tRNA^{Ala}</i>	J	5896–5961	66	–1	TGC	–	–
<i>tRNA^{Arg}</i>	J	5964–6027	64	2	TCG	–	–
<i>tRNA^{Asn}</i>	J	6028–6096	69	0	GTT	–	–
<i>tRNA^{Ser(AGN)}</i>	N	6097–6163	67	0	GCT	–	–
<i>tRNA^{Glu}</i>	J	6164–6231	68	0	TTC	–	–
<i>tRNA^{Phe}</i>	N	6230–6295	66	–2	GAA	–	–
<i>ND5</i>	N	6303–8015	1713	7	–	ATT	T--
<i>tRNA^{His}</i>	N	8029–8093	65	13	GTG	–	–
<i>ND4</i>	N	8100–9434	1335	6	–	ATG	TAA
<i>ND4L</i>	N	9428–9721	294	–7	–	ATG	TAA
<i>tRNA^{Thr}</i>	J	9724–9793	70	2	TGT	–	–
<i>tRNA^{Pro}</i>	N	9794–9859	66	0	TGG	–	–
<i>ND6</i>	J	9862–10,383	522	2	–	ATG	TAA
<i>Cytb</i>	J	10,390–11,529	1140	6	–	ATG	TAA
<i>tRNA^{Ser(UCN)}</i>	J	11,537–11,607	71	7	TGA	–	–
<i>ND1</i>	N	11,630–12,574	945	22	–	ATA	TAG
<i>tRNA^{Leu(CUN)}</i>	N	12,578–12,643	66	3	TAG	–	–
<i>16S</i>	N	12,643–13,956	1314	–1	–	–	–
<i>tRNA^{Val}</i>	N	13,956–14,025	71	–1	TAC	–	–
<i>12S</i>	N	14,026–14,818	793	0	–	–	–

Strand of the genes is presented as J for majority and N for minority strand. IN, negative numbers indicate that adjacent genes overlap, positive number indicate that intergenic sequences.

usual termination codon TAN (ten with TAA and two with TAG), and the remaining one PCG possesses the incomplete termination codons T for *ND5* gene (Table 1). The common interpretation of this phenomenon is that TAA termination was caused by posttranscriptional polyadenylation (Clary & Wolstenholme, 1985). The base composition in this mitogenome was: A = 42.6%, T = 33.1%, G = 10.4% and C = 13.9%. Although the A + T-rich region could not be amplified, the rate of A + T presented was also reaching a common level as high as the completely sequenced insect mitogenomes (Erler et al., 2010; Nardi et al., 2003).

Two ribosomal *rRNA* genes (*rRNA*) were presented in *Q. elaeodes*. The length of the *16S* was 1314 bp, and the partial of *12S* was 793 bp. Twenty-one transfer *rRNA* genes (*tRNA*) varied from 64 bp (*tRNA^{Arg}*) to 71 bp (*tRNA^{Lys}*, *tRNA^{Ser}* and *tRNA^{Val}*) in size. The mitogenome of *Q. elaeodes* contained a total of 39 bp gene overlaps in 10 locations, the regions of which ranges from 1 to 8 bp in size. The length of the intergenic spacers varied from 1 to 22 bp. And the longest intergenic spacer was located between *tRNA^{Ser}* (*UCN*) and *ND1*.

The mitochondrial genes have been widely used as an informative molecular marker for diverse evolutionary studies of animals, including phylogenetics and population genetics. In this study, the mitogenome of *Q. elaeodes* was first analyzed. Therefore, we expect this mitogenome sequence to provide further insights into the phylogenetic relationships within and among families of the superfamily Acridoidea. What is more, it will provide more inspiration for us to study the movement differences and evolution of poly-type wings among the interesting grasshoppers.

Nucleotide sequence accession number

The mitogenome sequence of *Q. elaeodes* has been assigned GenBank accession number No. KM363599.

Acknowledgements

We thank Wan-Wei Dong and Yu-Xiang Liu for additional assistances.

Declaration of interest

The authors report no conflicts of interest. The authors alone are responsible for the content and writing of the article. This work was supported by grants from the National Natural Sciences Foundation of China (No. 30970339) to Guo-Fang Jiang, and the National Basic Research Program of China (973 Program) (Grant no. 2011CB302102) to Ai-Ping Liang.

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