



Mitochondrial DNA Part A

DNA Mapping, Sequencing, and Analysis

ISSN: 2470-1394 (Print) 2470-1408 (Online) Journal homepage: <http://www.tandfonline.com/loi/imdn21>

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To cite this article: Xing Zhao & Ai-Ping Liang (2016) Complete DNA sequence of the mitochondrial genome of the treehopper *Leptobelus gazella* (Membracoidea: Hemiptera), *Mitochondrial DNA Part A*, 27:5, 3318-3319, DOI: [10.3109/19401736.2015.1018202](https://doi.org/10.3109/19401736.2015.1018202)

To link to this article: <http://dx.doi.org/10.3109/19401736.2015.1018202>



Published online: 25 Feb 2015.



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MITOGENOME ANNOUNCEMENT

Complete DNA sequence of the mitochondrial genome of the treehopper *Leptobelus gazella* (Membracoidea: Hemiptera)

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Abstract

The first complete DNA sequence of the mitochondrial genome (mitogenome) of *Leptobelus gazelle* (Membracoidea: Hemiptera) is determined in this study. The circular molecule is 16,007 bp in its full length, which encodes a set of 37 genes, including 13 proteins, 2 ribosomal RNAs, 22 transfer RNAs, and contains an A + T-rich region (CR). The gene numbers, content, and organization of *L. gazelle* are similar to other typical metazoan mitogenomes. Twelve of the 13 PCGs are initiated with ATR methionine or ATT isoleucine codons, except the *atp8* gene that uses the ATC isoleucine as start signal. Ten of the 13 PCGs have complete termination codons, either TAA (nine genes) or TAG (*cytb*). The remaining 3 PCGs (*cox1*, *cox2* and *nad5*) have incomplete termination codons T (AA). All of the 22 tRNAs can be folded in the form of a typical clover-leaf structure. The complete mitogenome sequence data of *L. gazelle* is useful for the phylogenetic and biogeographic studies of the Membracoidea and Hemiptera.

Keywords

Hemiptera, *Leptobelus gazelle*, Membracoidea, mitochondrial genome

History

Received 2 December 2014
Revised 13 January 2015
Accepted 24 January 2015
Published online 25 February 2015

Treehoppers in the family Membracidae (Insecta: Hemiptera) exhibit diversity in behavioral and life history traits, including maternal care (subsociality), ant mutualism, host-plant specialization, and plant-borne vibrational communication (Cocroft, 2005; Lin et al., 2004; Rodriguez et al., 2004). The association between plant-feeding bugs (Membracoidea) and their attendant ants is one of the best known mutualisms between animal species (Wood, 1977). The studies referred to above put forth significant data about the treehoppers, however, the mitochondrial genomes of treehoppers are less well known. In this study, the complete

mitochondrial genome of the treehopper *Leptobelus gazelle* was sequenced and annotated.

The circular genome of *L. gazelle* was 16,007 bp in full length and has 37 genes typical for insect mitogenomes, including: 13 protein-coding genes (PCGs), 22 transfer tRNA genes, 2 ribosomal RNA genes, and a 1750 bp major non-coding region (or A + T-rich region) between the 12s rRNA and the tRNA^{Ile} gene (Table 1). The gene location and numbers were same as in *G. distinctissima* (Song & Liang, 2009). 23 genes (9 PCGs and 14 tRNA) genes were located on the majority-coding strand

Table 1. Gene organization of *L. gazelle* mitochondrial genome.

Gene	Strand	Location/bp	Size/bp	Anticodon	Startcodon	Stopcodon
<i>tRNA^{Ile}</i>	J	1–63	63	GAT(30–32)		
<i>tRNA^{Gln}</i>	N	61–129	69	TTG(97–99)		
<i>tRNA^{Met}</i>	J	129–195	67	CAT(160–162)		
<i>nad2</i>	J	196–1155	960		ATG	TAA
<i>tRNA^{Trp}</i>	J	1157–1220	64	TCA(1187–1189)		
<i>tRNA^{Cys}</i>	N	1214–1278	65	GCA(1246–1248)		
<i>tRNA^{Tyr}</i>	N	1280–1344	65	GTA(1311–1313)		
<i>cox1</i>	J	1347–2883	1537		ATG	T(AA)
<i>tRNA^{Leu-UUR}</i>	J	2884–2949	66	TAA(2914–2916)		
<i>cox2</i>	J	2950–3628	679		ATA	T(AA)
<i>tRNA^{Lys}</i>	J	3632–3699	68	CTT(3659–3661)		
<i>tRNA^{Asp}</i>	J	3700–3761	62	GTC(3731–3733)		
<i>atp8</i>	J	3762–3914	153		ATC	TAA
<i>atp6</i>	J	3908–4558	651		ATG	TAA

(continued)

Table 1. Continued

Gene	Strand	Location/bp	Size/bp	Anticodon	Startcodon	Stopcodon
<i>cox3</i>	J	4559–5338	780		ATG	TAA
<i>tRNA^{Gly}</i>	J	5338–5400	63	TCC(5368–5370)		
<i>nad3</i>	J	5404–5754	351		ATA	TAA
<i>tRNA^{Ala}</i>	J	5753–5814	62	TGC(5782–5784)		
<i>tRNA^{Arg}</i>	J	5819–5886	68	TCG(5848–5850)		
<i>tRNA^{Asn}</i>	J	5887–5950	64	GTT(5918–5920)		
<i>tRNA^{Ser-AGN}</i>	J	5951–6015	65	ACT(5983–5985)		
<i>tRNA^{Glu}</i>	J	6016–6076	61	TTC(6046–6048)		
<i>tRNA^{Phe}</i>	N	6079–6144	66	GAA(6113–6115)		
<i>nad5</i>	N	6145–7807	1662		ATT	T(AA)
<i>tRNA^{His}</i>	N	7811–7873	63	GTG(7840–7842)		
<i>nad4</i>	N	7876–9186	1311		ATG	TAA
<i>nad4l</i>	N	9180–9455	276		ATG	TAA
<i>tRNA^{Thr}</i>	J	9458–9520	63	TGT(9489–9491)		
<i>tRNA^{Pro}</i>	N	9521–9587	67	TGG(9555–9557)		
<i>nad6</i>	J	9590–10,075	486	ATA TAA		
<i>cytb</i>	J	10,068–11,204	1137	ATG TAG		
<i>tRNA^{Ser-UCN}</i>	J	11,203–11,268	66	TGA(11,235–11,237)		
<i>nad1</i>	N	11,268–12,203	936	ATT	TAA	
<i>tRNA^{Leu-CUN}</i>	N	12,201–12,266	66	TAG(12,234–12,236)		
<i>lrRNA</i>	N	12,267–13,454	1188			
<i>tRNA^{Val}</i>	N	13452–13,520	69	TAC(13,486–13,488)		
<i>srRNA</i>	N	13,522–14,257	736			
A + T-rich region		14,258–16,007	1750			
repeat region1		14,361–14,872	512			
repeat region2		15,137–15,923	787			

(J-strand), however, other genes (4 PCGs, 8 tRNA genes and 2 rRNA genes) were encoded by the minority-coding strand (N-strand). The mitogenome sequence was A + T-rich, at 78.8% in total genome.

Twelve to 13 PCGs were initiated with ATR methionine or ATT isoleucine codons except *atp8* gene that using ATC isoleucine as start signals. In total, 10 PCGs have complete termination codons, either TAA (nine genes) or TAG (*cytb*). However, 3 PCGs (*cox1*, *cox2* and *nad5*) have incomplete termination codons T (AA; Table 1) as often found in some invertebrate and mammalian mitogenomes (Bibb et al., 1981; Crozier & Crozier 1993; Lessinger, 2000).

All of 22 tRNAs are presented in Table 1 and they are the typical arthropod mitogenome. Nineteen of the 22 tRNA genes were determined by tRNAscan-SE version 1.21 (Lowe & Eddy, 1997) except for tRNA^{Lys}, tRNA^{Arg}, and tRNA^{Ser} (ANG), which were identified by the sequence comparison of *L. gazella* and other previously published hemipteran mitogenomes. The sizes of tRNA genes are 61 to 69 bp, and they have similar secondary structures, including the amino acid acceptor (7 bp), the anticodon arms (5 bp), and the anticodon loop (7 bp), while the DHU arms and T ψ C arms are more variable.

rRNA genes boundaries were determined by the neighboring tRNAs location and the sequence comparison with other hemipteran insects. The 16s rRNA gene was 1188 bp and was located between tRNA^{Leu(CUN)} and tRNA^{Val}, and the 12s rRNA gene was 736 bp and was located between tRNA^{Val} and A + T rich region, which were similar to other insects. The A + T-rich region of *L. gazella* was located between 12s rRNA and tRNA^{Ile} genes with 1750 bp in size. There were two repeat regions in A + T-rich region (Table 1) and has an A + T content at 88.4%.

Nucleotide sequence accession number

The complete mtDNA sequence of *L. gazella* is available from GenBank (<http://www.ncbi.nlm.nih.gov/genbank/>) with the accession number: JF801955.

Declaration of interest

The authors have declared that no competing interests exist.

This work was supported by a grant from the National Basic Research Program of China (973 Program) (grant no. 2011CB302102), a grant from the Ministry of Science and Technology of the People's Republic of China (MOST Grant No. 2011FY120200) and the National Natural Science Foundation of China (grant nos. 31172128, 31372249), all awarded to APL.

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