



Mitochondrial DNA Part A

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MITOGENOME ANNOUNCEMENT

Characterization of the complete mitochondrial genome of the treehopper *Darthula hardwickii* (Hemiptera: Aetalionidae)

Ai-Ping Liang, Jie Gao, and Xing Zhao

Key Laboratory of Zoological Systematics and Evolution, Institute of Zoology, Chinese Academy of Sciences, Chaoyang District, Beijing, P.R. China

Abstract

The complete sequence of the mitochondrial genome of the treehopper *Darthula hardwickii* is presented. The circular genome is 15,359 bp long with 37 genes and 77.4% A+T content. Twenty-three genes are located on the J-strand, the remaining being oriented on the N-strand. Gene order is identical to that of the typical arrangement of other treehoppers. This genome is highly economized with 66 overlapped nucleotides between neighboring genes in 16 locations. All protein-coding genes initiate with ATN codons. All of the 22 tRNAs, ranging from 60 to 73 bp, have the clover-leaf structure, except the dihydrouridine (DHU) arm of tRNA^{Ser} (AGN) and tRNA^{Arg} forms a simple loop as seen in many other metazoans. The sizes of the large and small ribosomal RNA genes are 1198 and 737 bp, respectively. The control region is 1081 bp in length with 83.72% A+T content. The complete mitogenome sequence of *D. hardwickii* could provide fundamental data for the phylogenetic studies of the Aetalionidae and Membracoidea and the Hemiptera as well.

Keywords

Aetalionidae, *Darthula hardwickii*, Membracoidea, mitogenome, treehopper

History

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Species of Membracoidea occur wherever their vascular plant hosts are found and are among the numerically dominant herbivores in most temperate and tropical terrestrial ecosystems. As such, they comprise vital links in terrestrial food chains and play important roles in ecosystem function. Membracoidea includes Cicadellidae (leafhoppers) and three families of treehoppers — Membracidae, Melizoderidae, and Aetalionidae (Deitz & Dietrich, 1993). Together, these families comprises of 25,000 described species, currently grouped into over 50 subfamilies, 150 tribes and 3000 genera (Dietrich et al., 2001).

Complete or nearly complete mitochondrial genomes are only known in three species of Membracoidea [*Empoasca vitis*, No. NC_024838, *Leptobelus gazella*, No. NC_023219, and *Homalodisca vitripennis*, No. NC_006899 (Zhao & Liang, in press; Zhou et al., 2014)]. Mitogenome data from more treehopper or leafhopper species are needed to elucidate the phylogeny and origin of the Membracoidea.

Darthula hardwickii is a rare Oriental treehopper species in India, Burma, Nepal, Sikkim, Bengal, and southwest China (Yunnan). This paper presents the complete sequence of the

Table 1. Organization of the mitochondrial genome of *D. hardwickii*.

Gene	Strand	Start	End	Anticodon	Length (bp)	Start codon	Stop codon	Intergenic nucleotides ^a (bp)
tRNA-Ile	J	1	65	GAT	65	–	–	0
tRNA-Gln	N	133	63	TTG	71	–	–	–3
tRNA-Met	J	133	200	CAT	68	–	–	–1
ND2	J	201	1163	–	963	ATG	TAG	0
tRNA-Trp	J	1162	1226	TCA	65	–	–	–2
tRNA-Cys	N	1285	1219	GCA	67	–	–	–8
tRNA-Tyr	N	1352	1286	GTA	67	–	–	0
CO1	J	1351	2885	–	1535	ATG	T-tRNA	–2
tRNA-Leu(TAA)	J	2885	2950	TAA	66	–	–	–1
CO2	J	2951	3629	–	679	ATT	T-tRNA	0
tRNA-Lys	J	3630	3700	CTT	71	–	–	0
tRNA-Asp	J	3706	3778	GTC	73	–	–	5
ATPase8	J	3779	3928	–	150	ATG	TAA	0
ATPase6	J	3922	4569	–	648	ATG	TAA	–7

(continued)

Table 1. Continued

Gene	Strand	Start	End	Anticodon	Length (bp)	Start codon	Stop codon	Intergenic nucleotides ^a (bp)
<i>CO3</i>	J	4571	5350	–	780	ATG	T-tRNA	1
tRNA-Gly	J	5350	5411	TCC	62	–	–	–1
<i>ND3</i>	J	5409	5765	–	357	ATA	TAG	–3
tRNA-Ala	J	5764	5823	TGC	60	–	–	–2
tRNA-Arg	J	5826	5887	TCG	62	–	–	2
tRNA-Asn	J	5888	5957	GTT	70	–	–	0
tRNA-Ser(GCT)	J	5962	6030	GCT	69	–	–	4
tRNA-Glu	J	6022	6083	TTC	62	–	–	–9
tRNA-Phe	N	6149	6085	GAA	65	–	–	1
<i>ND5</i>	N	7819	6152	–	1668	ATG	TAA	2
tRNA-His	N	7890	7821	GTG	70	–	–	1
<i>ND4</i>	N	9203	7890	–	1314	ATG	TAA	–1
<i>ND4L</i>	N	9472	9197	–	276	ATG	TAA	–7
tRNA-Thr	J	9475	9537	TGT	63	–	–	2
tRNA-Pro	N	9602	9538	TGG	65	–	–	0
<i>ND6</i>	J	9605	10,087	–	483	ATT	TAA	2
<i>CytB</i>	J	10,080	11,213	–	1134	ATG	TAG	–8
tRNA-Ser(TGA)	J	11,220	11,283	TGA	64	–	–	–4
<i>ND1</i>	N	11,277	12,206	–	930	ATA	TAA	–7
tRNA-Leu(TAG)	N	12,280	12,213	TAG	68	–	–	6
<i>lrRNA</i>	N	12,281	13,478	–	1198	–	–	0
tRNA-Val	N	13,541	13,479	TAC	63	–	–	0
<i>srRNA</i>	N	13,542	14,278	–	737	–	–	0
Control	–	14,279	15,359	–	1081	–	–	0

^aNumbers correspond to nucleotides separating a gene from an upstream one; the negative numbers refer to overlaps between the adjacent genes.

mitochondrial genome of this species. The mitochondrial genome of *D. hardwickii* is 15,359 bp long. It includes the entire set of 37 genes (i.e. 13 protein-coding genes, 22 tRNA genes and 2 rRNA genes) and a control region which are usually present in animal mitochondrial genomes (Table 1). Gene order is identical to that of the putative ancestral arrangement of insects and other treehoppers (Zhao & Liang, in press; Zhou et al., 2014). There are a total of 66 overlapped nucleotides between genes in 16 locations, ranging from 1 to 9 bp in size. The orientation and gene order is the same as that in *Drosophila yakuba*, which has been hypothesized to be the ancestral arrangement for insects (Boore, 1999). The majority-coding strand (J-strand) encodes 23 genes, and the other 14 genes are oriented on the minority-coding strand (N-strand). In addition, this mitogenome harbors 26 bp of intergenic spacer sequences, which are spread over 10 regions, ranging in the size from 1–6 bp.

The total length of all 13 PCGs is 10,917 bp, accounting for 71.1% of the entire length of *D. hardwickii*. The overall AT content of PCGs is 76.7%. Start codons of all PCGs are ATN. The majority of PCGs has a complete termination codon of TAA (ATP8, ATP6, ND5, ND4, ND4L, ND6 and ND1) and TAG (ND2, ND3, and CytB), while the remaining three PCGs use the incomplete termination codons, T (COI, COII and COIII; Table 1). The incomplete stop codons are presumably completed by post-transcriptional polyadenylation (Ojala et al., 1981).

Twenty-two tRNAs are found in *D. hardwickii*, ranging in size from 60 to 73 bp. All tRNAs can be folded into the typical cloverleaf structure, with the exception of tRNA^{Ser}(AGN) and tRNA^{Arg}, in which the dihydrouridine (DHU) arm forms a simple loop. This phenomenon is common in the mitogenomes of Hemiptera (Gao & Liang, 2014; Zhao & Liang, in press), and is also considered as a typical feature in metazoan mtDNAs (Sheffield et al., 2008).

The A + T region is located between *srRNA* and tRNA^{Leu} with a length of 1081 bp. The A + T content of this region is 83.72% and this region is believed to be involved in the regulation of transcription and control of DNA replication. No repeat sequence is present on the downstream of the A + T-rich region.

Nucleotide sequence accession number

The complete mtDNA sequence of *D. hardwickii* is available from GenBank (<http://www.ncbi.nlm.nih.gov/genbank/>) with the accession number KP316404.

Declaration of interest

The authors have declared that no competing interests. This study was supported by the National Basic Research Program of China (973 Program) (grant number 2011CB302102), the National Natural Science Foundation of China (grant nos. 31172128, 31372249, 3141101191) and a grant from the Ministry of Science and Technology of the People's Republic of China (MOST grant no. 2011FY120200).

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