

## MITOGENOME ANNOUNCEMENT

**The complete mitochondrial genome of *Hemiodoecus leai* (Hemiptera: Coleorrhyncha: Peloridiidae)**

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The mitochondrial genome of *Hemiodoecus leai* (Hemiptera: Coleorrhyncha: Peloridiidae) was determined and annotated. The entire genome was 15,949 bp in length, containing 37 genes of 13 protein-coding genes, 22 tRNA genes, 2 rRNA genes and an A+T-rich region. The genome has a gene arrangement identical to the inferred ancestral insects. Twelve of the 13 PCGs initiate with the standard start codons ATN, whereas *CO1* starts with CGA. The tRNAs have been folded into typical cloverleaf secondary structures, except that the stem of the DHU arm was absent in tRNA<sup>Ser(GCT)</sup>. The non-coding AT-rich region is 1414 bp long and is located between the *rrnS* and tRNA<sup>Ile</sup> genes. The complete mitogenome sequence of *H. leai* could provide fundamental data for the phylogenetic and biogeographic studies of the Peloridiidae as well as the Coleorrhyncha and Hemiptera.

**Keywords**Coleorrhyncha, complete mitochondrial genome, *Hemiodoecus leai*, peloridiidae**History**

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The suborder Coleorrhyncha (Hemiptera) is represented by only one extant family, the Peloridiidae, comprising 36 species in 17 genera (Burckhardt, 2009). Species of the group occur in South America (Chile, Argentina), New Zealand, New Caledonia and eastern Australia (from North Queensland to Tasmania) where they live in wet moss (Kuechler et al., 2013). Complete or nearly complete mitochondrial genomes are known in two species of Peloridiidae [*Xenophyes cascus*, No. JF323862 and *Hackeriella veitchi*, No. GQ884145, (Cui et al., 2013)], both are distributed in New Zealand. In this study the mitochondrial genome of *Hemiodoecus leai* was determined and annotated. The adult specimens of *H. leai* sequenced in this study were collected by Dr. G. Monteith from New South Wales of Australia in 2009 and are kept in authors' laboratory.

The circular genome of this species is 15,949 bp in length and contains a typical gene complement: 13 protein-coding genes (PCGs), 2 ribosomal RNA genes, 22 transfer RNA genes and a 1414 bp long non-coding AT-rich region that is usually present in animal mitogenomes (Table 1). The gene location is the same as in *X. cascus* and *H. veitchi* (Cui et al., 2013). Next to the putative control region, only very short intragenic spacers were found between neighboring genes. Short gene overlaps are observed between adjacent tRNA genes, PCGs, tRNA and PCGs as well as tRNA and rRNA genes. The majority-coding strand (J-strand) encodes 23 genes (9 PCGs and 14 tRNA genes) while the remaining 14 genes (4 PCGs, 8 tRNA genes and 2 rRNA genes) are encoded on the minority-coding strand (N-strand).

The nucleotide composition shows a remarkable bias toward A and T: in total the mitogenome contains 68.39% A and T.

Eleven of the 13 PCGs start with the standard start codons ATN, whereas *CO1* starts with CGA and *ND1* starts with TTG. In total, 5 PCGs terminate in the common stop codon TAA or TAG, except for the *CO2*, *CO3*, *ATP6*, *ATP8*, *ND1*, *ND4*, *ND5* and *CytB* which end with a single thymine stop codon (Table 1) as the cases found in some other insects (Kim et al., 2011; Liu & Liang, 2013).

The whole set of 22 tRNAs is present in *H. leai* (Table 1) and this is the typical arthropod mitogenome. Twenty of the 22 tRNAs were determined using RNAscan-SE (Lowe & Eddy, 1997). The tRNA<sup>Ser(GCT)</sup> and tRNA<sup>Gln</sup> genes were determined through comparison with previously published hemipteran mitogenomes (Cui et al., 2013). All tRNA sequences could be folded into typical cloverleaf secondary structures exposing appropriate anticodon triplets except for tRNA<sup>Ser(GCT)</sup>, in which the dihydrouracil (DHU) arm forms a simple loop. This feature is common to many arthropod mitogenomes (Sheffield et al., 2008). The lengths of tRNAs range from 61 to 71 bp. The aminoacyl (AA) stem (7 bp) and the AC loop (7 nucleotides) are invariable, and the DHU and TΨC (T) arms are often size-variable, within which the loop size (2–14 bp) is more variable than the stem size (2–5 bp).

The boundaries of the rRNA genes were determined by sequence alignment with that of other peloridiid species. Similar to other insects, the *lrRNA* of *H. leai* is located between the tRNA<sup>Leu(TAG)</sup> and tRNA<sup>Val</sup>, and the *srRNA* is located between the tRNA<sup>Val</sup> and the A+T-rich region. The lengths of the *lrRNA* and *srRNA* in *H. leai* mitogenome are 1259 bp and 783 bp, respectively; and the A+T contents are 68.15% and 68.84%, respectively. The 1414 bp long non-coding AT-rich region is located between the *srRNA* gene and the tRNA<sup>Ile</sup>-tRNA<sup>Gln</sup>-tRNA<sup>Met</sup> (IQM) gene cluster, with the AT content of 70.27%.

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Table 1. Organization of the mitochondrial genome of *Hemiodoecus leai*.

Gene	Strand	Start	End	Anticodon	Length (bp)	Start codon	Stop codon	Intergenic nucleotides (bp)
tRNA <sup>Ile</sup>	J	1	67	GAT	67	–	–	–
tRNA <sup>Gln</sup>	N	66	137	TTG	71	–	–	–2
tRNA <sup>Met</sup>	J	141	206	CAT	66	–	–	3
ND2	J	186	1199	–	1014	ATC	TAA	–21
tRNA <sup>Trp</sup>	J	1198	1260	TCA	63	–	–	–1
tRNA <sup>Cys</sup>	N	1253	1313	GCA	61	–	–	–8
tRNA <sup>Tyr</sup>	N	1314	1377	GTA	64	–	–	0
CO1	J	1379	2914	–	1536	CGA	TAG	1
tRNA <sup>Leu</sup> (TAA)	J	2910	2973	TAA	64	–	–	–4
CO2	J	2974	3663	–	690	ATA	T-tRNA	0
tRNA <sup>Lys</sup>	J	3659	3722	CTT	64	–	–	–5
tRNA <sup>Asp</sup>	J	3721	3784	GTC	64	–	–	–2
ATPase8	J	3785	3934	–	150	ATA	T-tRNA	0
ATPase6	J	3928	4593	–	666	ATG	T-tRNA	–7
CO3	J	4598	5386	–	789	ATG	T-tRNA	4
tRNA <sup>Gly</sup>	J	5385	5447	TCC	63	–	–	–1
ND3	J	5472	5801	–	330	ATT	TAG	25
tRNA <sup>Ala</sup>	J	5800	5860	TGC	61	–	–	–2
tRNA <sup>Arg</sup>	J	5859	5923	TCG	65	–	–	–2
tRNA <sup>Asn</sup>	J	5924	5994	GTT	71	–	–	0
tRNA <sup>Ser</sup> (GCT)	J	5992	6054	GCT	63	–	–	–3
tRNA <sup>Glu</sup>	J	6054	6120	TTC	67	–	–	–1
tRNA <sup>Phe</sup>	N	6124	6195	GAA	72	–	–	3
ND5	N	6182	7918	–	1737	ATT	T-tRNA	–13
tRNA <sup>His</sup>	N	7898	7960	GTG	63	–	–	–20
ND4	N	7950	9287	–	1338	ATA	T-tRNA	–10
ND4L	N	9281	9568	–	288	ATA	TAA	–6
tRNA <sup>Thr</sup>	J	9574	9635	TGT	62	–	–	6
tRNA <sup>Pro</sup>	N	9636	9701	TGG	66	–	–	0
ND6	J	9707	10,214	–	508	ATT	TAA	6
CytB	J	10,214	11,350	–	1137	ATG	T-tRNA	–1
tRNA <sup>Ser</sup> (TGA)	J	11,349	11,417	TGA	69	–	–	–3
ND1	N	11,422	12,351	–	930	TTG	T-tRNA	5
tRNA <sup>Leu</sup> (TAG)	N	12,352	12,421	TAG	70	–	–	0
lrRNA	N	12,423	13,681	–	1259	–	–	1
tRNA <sup>Val</sup>	N	13,684	13,749	TAC	66	–	–	2
srRNA	N	13,753	14,535	–	783	–	–	3
Control	–	14,536	15,949	–	1414	–	–	0

### Nucleotide sequence accession number

The complete mitogenome of *H. leai* sequenced in this work is now available in Genbank under accession No. KM035420.

### Declaration of interest

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