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MITOGENOME ANNOUNCEMENT

The complete mitochondrial genome of *Cosmoscarata bispecularis* (Hemiptera, Cicadomorpha, Cercopoidea, Cercopidae)

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*Key Laboratory of Zoological Systematics and Evolution, Institute of Zoology, Chinese Academy of Sciences, 1 Beichen West Road, Chaoyang District, Beijing, China***Abstract**

To characterize froghopper mitochondrial genome (mitogenome) features, in this study, the mitochondrial genome of *Cosmoscarata bispecularis* (Hemiptera, Cicadomorpha, Cercopoidea, Cercopidae) was sequenced and annotated. The complete genome is 15,426 bp in length. It contains 13 protein-coding genes (PCGs), 22 tRNA genes, 2 rRNA genes and a control region (A + T-rich region). All the PCGs initiate with the standard start codons ATN and all the tRNAs can be folded into typical cloverleaf secondary structures except *tRNA^{Ser}*(GCT), which only formed a simple loop. The control region is consisted of 861 bp bases located between the *srRNA* gene and the *tRNA^{Ile}-tRNA^{Gln}-tRNA^{Met}*(IQM) gene cluster. The measure of complete mitogenome sequence of *C. bispecularis* will provide fundamental data for the phylogenetic and biogeographic studies of the Cercopoidea and Hemiptera.

KeywordsCercopoidea, complete mitochondrial genome, *Cosmoscarata bispecularis***History**Received 4 November 2014
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Cercopidae (Hemiptera, Cicadomorpha, Cercopoidea) is a large hemipteran family with about 1500 described species in 150 genera (Liang & Webb, 2002). According to GenBank, only three complete mitochondrial genomes were founded in this family (*Paphnutius ruficeps*, No. NC_021100.1; *Abidama producta*, No. NC_015799.1 and *Callitettix versicolor*, No. NC_020031.1). Thus, in this study, we determined and annotated the mitochondrial genome sequence of *Cosmoscarata bispecularis*, one of the respective species of the genus *Cosmoscarata* in Cercopidae.

The complete mt genome of *C. bispecularis* is a double-stranded circular molecule of 15,426 bp in size with a typical A + T biased (78.60%). It contains 13 standard complement PCGs, 22 tRNA genes, 2 rRNA genes and a control region. The majority coding strand (J strand) encoded 23 genes (9 PCGs and 14 tRNA genes), while the minority coding strand (N strand) encoded the left 14 genes (4 PCGs, 8 tRNA genes and 2 rRNA genes) (Table 1). These are the same as in the relative species (Liu & Liang, 2013; Wang et al., 2014). A total of 54 bp overlaps had been found in 11 gene junctions and the longest overlap existed between *ND4* and *ND4L* is 16 bp (Table 1).

All the 13 PCGs start strictly with the standard initiation codons ATN (5 with ATG, 2 with ATT and 6 with ATA). Conventional stop codons TAA and TAG had been assigned to the majority of PCGs, except for the *COII*, *COI*, *ND4* and *ND5*, which

end up with a single thymine (T). Nine PCGs genes were encoded in the J strand, while *ND1*, *ND4*, *ND5* and *ND4L* were encoded in the N strand (Table 1).

The complete set of 22 tRNA genes of *C. bispecularis* are typical tRNA genes in metazoan mitogenome. Seventeen of them were determined by tRNAscan-SE(US) (Lowe & Eddy, 1997), while the other 5 (*tRNA^{Ile}*, *tRNA^{Tyr}*, *tRNA^{Arg}*, *tRNA^{Ser}*(GCT) and *tRNA^{His}*) that could not be detected by software had been described through comparison with previous patterns. These tRNAs ranged in size from 61 bp (*tRNA^{Gly}*) to 73 bp (*tRNA^{Ile}* and *tRNA^{Val}*) with differences mainly in stem and loop sizes of dihydrouridine (DHU) arms and TΨC arms. Fourteen tRNA genes were encoded in the J strand and the others in the N strand. Most tRNA genes could be folded into a perfect classic clover leaf structure with the exception of *tRNA^{Ser}*(GCT), of which its DHU arm simply formed a loop that is the same in many other insect mitogenomes (Cameron et al., 2008; Wan et al., 2012).

The two rRNA genes of *C. bispecularis* were determined by sequence alignment with other species. The *lrRNA* is located between the *tRNA^{Leu}* (TAG) and *tRNA^{Val}* with a 1245 bp in length and 80.50% AT contents, while the *srRNA* is located between the *tRNA^{Val}* and the control region with a 819 bp in length and 80.88% AT contents. The 861 bp control region is located between the *srRNA* gene and the IQM gene cluster with the AT content of 84.24%.

Table 1. Organization of the *C. bispecularis* mitochondrial genome.

Gene	Strand	Start	End	Anticodon	Length (bp)	Start codon	Stop codon	Intergenic nucleotides (bp)
<i>tRNA^{Ile}</i>	J	1	73	GAT	73	–	–	–
<i>tRNA^{Gln}</i>	N	71	140	TTG	70	–	–	–3
<i>tRNA^{Met}</i>	J	140	210	CAT	71	–	–	–1
<i>ND2</i>	J	217	1200	–	984	ATA	TAG	8
<i>tRNA^{Trp}</i>	J	1201	1266	TCA	66	–	–	0
<i>tRNA^{Cys}</i>	N	1259	1322	GCA	64	–	–	–8
<i>tRNA^{Tyr}</i>	N	1323	1387	GTA	65	–	–	0
<i>COI</i>	J	1400	2921	–	1522	ATA	T–	14
<i>tRNA^{Leu}(TAA)</i>	J	2922	2987	TAA	66	–	–	0
<i>COII</i>	J	2988	3660	–	673	ATG	T–	0
<i>tRNA^{Lys}</i>	J	3661	3732	CTT	72	–	–	0
<i>tRNA^{Asp}</i>	J	3733	3797	GTC	65	–	–	0
<i>ATPase8</i>	J	3798	3953	–	156	ATA	TAA	0
<i>ATPase6</i>	J	3947	4612	–	666	ATG	TAA	–7
<i>COII</i>	J	4617	5399	–	783	ATG	TAA	6
<i>tRNA^{Gly}</i>	J	5402	5462	TCC	61	–	–	4
<i>ND3</i>	J	5451	5816	–	366	ATA	TAG	–12
<i>tRNA^{Ala}</i>	J	5815	5877	TGC	63	–	–	–2
<i>tRNA^{Arg}</i>	J	5878	5940	TCG	63	–	–	0
<i>tRNA^{Asn}</i>	J	5943	6006	GTT	64	–	–	4
<i>tRNA^{Ser}(GCT)</i>	J	6006	6073	GCT	68	–	–	–1
<i>tRNA^{Glu}</i>	J	6074	6139	TTC	66	–	–	0
<i>tRNA^{Phe}</i>	N	6138	6205	GAA	68	–	–	–2
<i>ND5</i>	N	6206	7892	–	1687	ATT	T–	0
<i>tRNA^{His}</i>	N	7909	7971	GTG	63	–	–	18
<i>ND4</i>	N	7971	9301	–	1331	ATT	T–	–1
<i>ND4L</i>	N	9286	9573	–	288	ATG	TAA	–16
<i>tRNA^{Thr}</i>	J	9576	9639	TGT	64	–	–	4
<i>tRNA^{Pro}</i>	N	9640	9705	TGG	66	–	–	0
<i>ND6</i>	J	9707	10,219	–	513	ATA	TAA	3
<i>CytB</i>	J	10,219	11,352	–	1134	ATG	TAA	–1
<i>tRNA^{Ser}(TGA)</i>	J	11,355	11,423	TGA	69	–	–	2
<i>NDI</i>	N	11,445	12,356	–	912	ATA	TAA	23
<i>tRNA^{Leu}(TAG)</i>	N	12,363	12,427	TAG	65	–	–	8
<i>lrRNA</i>	N	12,428	13,672	–	1245	–	–	0
<i>tRNA^{Val}</i>	N	13,673	13,745	TAC	73	–	–	0
<i>srRNA</i>	N	13,746	14,564	–	819	–	–	0
Control	J	14,565	15,425	–	861	–	–	0

Nucleotide sequence accession number

The complete mitogenome of *Cosmoscarata bispecularis* sequenced in this work is now available in GenBank under accession No. KP064511.

Declaration of interest

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