Mitochondrial DNA

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MITOGENOME ANNOUNCEMENT

The complete mitochondrial genome of *Carposina sasakii* (Lepidoptera: Carposinidae)

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Abstract

The peach fruit moth, *Carposina sasakii* belongs to Carposinidae in Lepidoptera. In this paper, we described the complete mitogenome of *C. sasakii*. It is 15,611 bp in length, including 13 PCGs, 2 rRNAs, 22 tRNAs and a major noncoding A + T-rich region, which revealed the typical gene content found in other metazoan mitogenomes. The overall base composition is 42.0% A, 39.5% T, 7.75% G and 10.75% C. The A + T-rich region is located between *rrnS* and *trnM*. There is a motif ATAGA in downstream of *rrnS* followed by a 19 bp Poly-T stretch. The Poly-A is not found in upstream of *trnM*, and the position of Poly-A is replaced by a stem-loop structure. There are eight mononucleotide repeat sequences (T_n/A_n) with the length of 7 bp-19bp, three dinucleotide repeat sequences $(TA)_n$/$(AT)_n$, and a longer repeat sequence $(AATATATA)_5$ in A + T-rich region. The mononucleotide repeat sequences occur repeatedly in A + T-rich reigion of *C. sasakii*, which is special in insects sequenced of Lepidoptera.

Keywords

Carposina sasakii, complete mitogenome, Lepidoptera

History

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The peach fruit moth, *Carposina sasakii* Matsumura (1900) belongs to Carposinidae, its junior synonym is *Carposina niponensis* Walsingham (1900). *Carposina sasakii* is widely distributed in North Korea, South Korea, Japan, the Russian Far East and China, which is harmful to apple, jujube, pear and other fruit trees. In this study, we described the complete mitogenome of *C. sasakii*, the first sequenced specie of Copromorphoidea, hoping it could provide useful genetic

Table 1. Organization of the *Carposina sasakii* Matsumura mitochondrial genome.

Gene	Direction	Location	Size (bp)	IN	Anticodon	Start codon	Stop codon
trnM	J	1–69	69		CAT		
trnI	J	70–133	64	0	GAT		
trnQ	N	131–199	69	−3	TTG		
nad2	J	253–1264	1012	53		ATT	T
trnW	J	1265–1331	67	0	TCA		
trnC	N	1324–1387	64	−8	GCA		
trnY	N	1388–1451	64	0	GTA		
cox1	J	1461–2991	1531	9		CGA	T
trnL2(TTR)	J	2992–3058	67	0	TTA		
cox2	J	3059–3740	682	0		ATC	T
trnK	J	3741–3811	71	0	CTT		
trnD	J	3813–3879	67	1	GTC		
atp8	J	3880–4047	168	0		ATC	TAA
atp6	J	4041–4715	675	−7		ATG	TAA
cox3	J	4715–5503	789	−1		ATG	TAA
trnG	J	5506–5571	66	2	TCC		
nad3	J	5572–5925	354	0		ATT	TAA
trnA	J	5934–5998	65	8	TGC		
trnR	J	6005–6065	65	6	TCG		
trnN	J	6071–6137	67	5	GTT		
trnS1(AGN)	J	6143–6207	65	5	GCT		
trnE	J	6217–6285	69	9	TTC		
trnF	N	6296–6360	65	10	GAA		
nad5	N	6361–8077	1717	0		ATT	T
trnH	N	8099–8165	67	21	GTG		
nad4	N	8172–9512	1341	6		ATG	TAA
nad4L	N	9514–9804	291	1		ATG	TAA
trnT	J	9807–9870	64	2	TGT		
trnP	N	9871–9937	67	0	TGG		
nad6	J	9940–10,470	531	2		ATT	TAA
cob	J	10,507–11,655	1149	36		ATG	T
trnS2(TCN)	J	11,662–11,726	65	6	TGA		
nad1	N	11,743–12,678	936	16		ATG	TAA
trnL1(CTN)	N	12,679–12,747	69	0	TAG		
rrnL	N	12,748–14,121	1374	0			
trnV	N	14,122–14,186	65	0	TAC		
rrnS	N	14,187–14,955	769	0			
A + T-rich region		14,956–15,611	656				

IN represents intergenic nucleotides. Negative numbers indicate overlapping nucleotides.

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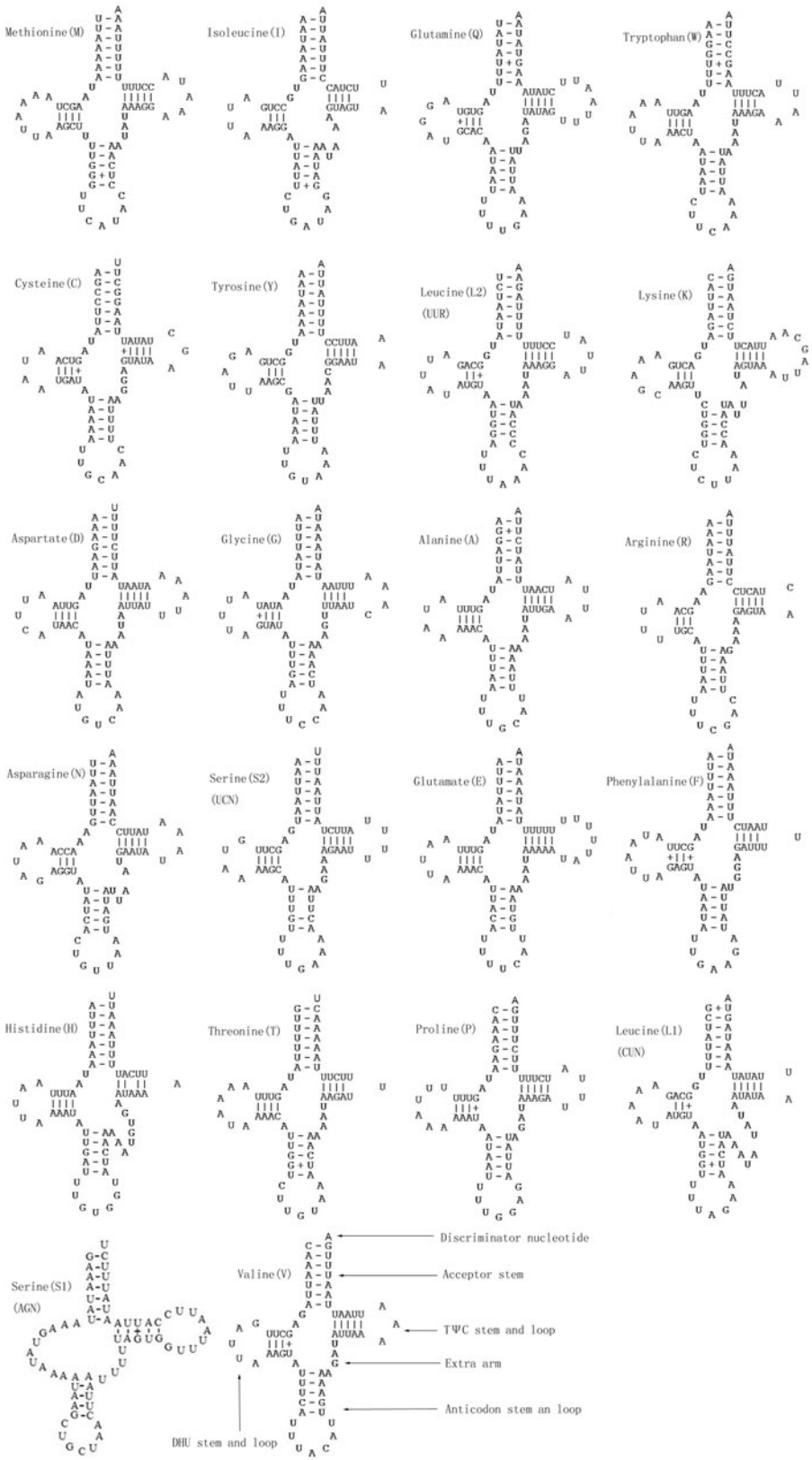

Figure 1. Putative secondary structures for the tRNA genes of *Carposina sasakii* mitogenome.

information for resource conservation, species identification and phylogenetic analysis.

Specimens of *C. sasakii* were collected from an orchard in Beijing, China. Total DNA was extracted from a single specimen using the DNeasy Tissue kit (QIAGEN, Shanghai, China) according to the manufacturer's instructions.

The *C. sasakii* mitogenome (HQ840719) is 15,611 bp in length, containing 13 PCGs, 2 rRNAs, 22 tRNAs and a major noncoding region, which showed the typical metazoan gene content (Table 1). The *C. sasakii* mitogenome is biased toward A + T (81.5%). The overall base composition is 42.0% A, 39.5% T, 7.75% G and 10.75% C. The A + T content is 79.77% in PCGs,

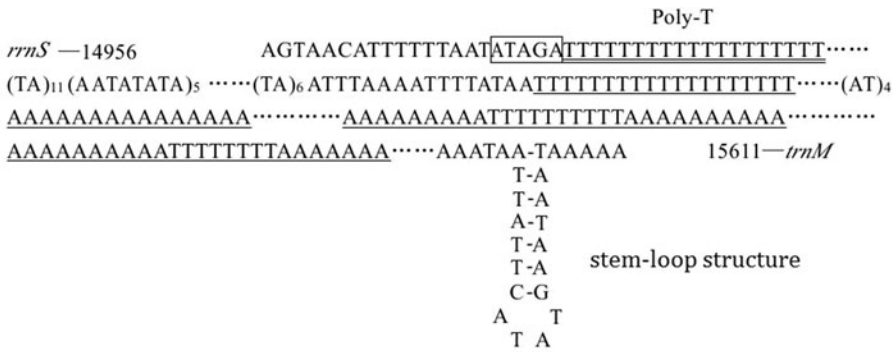

Figure 2. The structure of the A + T-rich region of *Carposina sasakii* mitogenome. Marked box is motif ATAGA; double underline is the Poly-T; single underline, $(TA)_n/(AT)_n$ and $(AATATATA)_5$ are tandem repeat sequences; the stem-loop structure in upstream of *trnM*.

84.64% in *rrnL* genes, 86.35% in *rrnS* genes, and 92.84% in the A + T-rich region. Twelve PCGs start with a typical ATN codon, except for the *cox1* gene, which uses CGA as the start codon. The feature is common across insects (Kim et al., 2009, 2010; Liao et al., 2010; Yang et al., 2009). Eight PCGs have the common stop codon TAA, other five PCGs have the in-complete stop codon T.

The 22 tRNA genes ranged from 64 to 71 nucleotides. Fourteen tRNAs are coded on the J-strand and others on the N-strand. Complete cloverleaf secondary structures could be inferred for 21 of the 22 tRNAs (Figure 1). The secondary structure of *trnS1*(AGN) is incomplete, lacking the DHU arm. The *rrnL* gene (1374 bp) is located between *trnL(CUN)* and *trnV*, and the *rrnS* (769 bp) between *trnV* and the A + T-rich region.

The A + T-rich region (656 bp) is located between *rrnS* and *trnM*. There is a motif ATAGA in downstream of *rrnS* followed by a 19 bp Poly-T stretch, but the Poly-A is not found in upstream of *trnM,* and the position is replaced by a stem-loop structure (Figure 2). The stem-loop structure in the A + T-rich region was also observed in other insect orders (Brehm et al., 2001; Cameron et al., 2007; Cha et al., 2007; Schultheis et al., 2002; Ye et al., 2008), but with the difference that the position replaced by stem loop structure in *C. sasakii* is Poly-A rather than Poly-T. Some researchers suggested that the stem-loop structure in A + T-rich region maybe play an important role in recognition of the light strand replication origin, and have the same function as the poly-(A)/poly-(T) stretch (Ye et al., 2008). There are several microsatellite regions in A + T-rich region, including three dinucleotide repeat sequences $(TA)_{11}$, $(TA)_6$ and $(AT)_4$, and a longer repeat sequence $(AATATATA)_5$. In addition to eight mononucleotide repeat sequences (T_n/A_n) in length of 7 bp–19bp except for the Poly-T, the mononucleotide repeat sequences occur repeatedly in A + T-rich region of *C. sasakii*, which is special in insects sequenced of Lepidoptera.

Declaration of interest

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