

## MITOGENOME ANNOUNCEMENT

**The complete mitochondrial genome of *Acleris fimbriana* (Lepidoptera: Tortricidae)**Jin-Liang Zhao<sup>1,2</sup>, Yu-Peng Wu<sup>1,3</sup>, Tian-Juan Su<sup>1,4</sup>, Guo-Fang Jiang<sup>2</sup>, Chun-Sheng Wu<sup>1</sup>, and Chao-Dong Zhu<sup>1</sup><sup>1</sup>Key Laboratory of Zoological Systematics and Evolution (CAS), Institute of Zoology, Chinese Academy of Sciences, Beijing, China, <sup>2</sup>Jiangsu Key Laboratory for Bioresource Technology, College of Life Sciences, Nanjing Normal University, Nanjing, P.R. China, <sup>3</sup>College of Environment and Safety, Taiyuan University of Science and Technology, Taiyuan, China, and <sup>4</sup>Forestry and Environmental Institute, Jiangxi Environmental Engineering Vocational College, Ganzhou, China**Abstract**

The yellow tortrix, *Acleris fimbriana* belongs to Tortricidae in Lepidoptera. We described the complete mitogenome of *A. fimbriana*, which is typical circular duplex molecules and 15,933 bp in length containing the standard metazoan set of 13 protein-coding genes, 22 transfer RNA genes, 2 ribosomal RNA genes and an A + T-rich region with macro-repeat sequences. All the inferred tRNA secondary structures show the common cloverleaf pattern, with the exception of *trnS1*(AGN) which lacks the DHU arm. The *A. fimbriana* mitochondrial genome has the same gene order with other lepidopterans.

**Keywords***Acleris fimbriana*, complete mitogenome, Lepidoptera**History**

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The yellow tortrix, *Acleris fimbriana* (Thunberg & Becklin, 1791) is an economically important orchard insect. It belongs to Tortricidae (Lepidoptera). It is widely distributed in Japan, Russian, China and Europe (Liu & Li, 2002). In this study, Zhao reared the moths from an apple orchard in Changping, Beijing. We sequenced and described the complete mitogenome of *A. fimbriana* to provide useful genetic information

for species identification and phylogenetic analysis (Lu et al., 2013).

The complete mitogenome sequence of *A. fimbriana* is 15,933 bp (GenBank accession number: HQ662522). As with other insect mitogenomes, the major strand encodes a larger number of genes (9 PCGs and 14 tRNAs) than the minor strand (4 PCGs, 8 tRNAs and 2 rRNA genes). A large non-coding,

Table 1. Organization of the *A. fimbriana* mitogenome.

Gene	Direction	Location	Size (bp)	IN	Anticodon	Start codon	Stop codon
<i>trnM</i>	J	1–68	68				
<i>trnI</i>	J	69–133	65	0	GAU		
<i>trnQ</i>	N	131–199	69	–3	UUG		
<i>nad2</i>	J	277–1275	999	77		ATG	TAA
<i>trnW</i>	J	1274–1342	69	–2	TCA		
<i>trnC</i>	N	1335–1398	64	–8	GCA		
<i>trnY</i>	N	1437–1501	65	38	GTA		
<i>cox1</i>	J	1506–3036	1536	4		CGA	TAA
<i>trnL2(UUR)</i>	J	3037–3103	67	0	TAA		
<i>cox2</i>	J	3104–3785	682	0		ATG	T–
<i>trnK</i>	J	3786–3856	71	0	CTT		
<i>trnD</i>	J	3867–3932	66	10	GTC		
<i>atp8</i>	J	3933–4094	162	0		ATC	TAA
<i>atp6</i>	J	4088–4765	678	–7		ATG	TAA
<i>cox3</i>	J	4765–5553	789	–1		ATG	TAA
<i>trnG</i>	J	5556–5620	65	2	TCC		
<i>nad3</i>	J	5621–5974	354	0		ATT	TAA

(continued)

Table 1. Continued

Gene	Direction	Location	Size (bp)	IN	Anticodon	Start codon	Stop codon
<i>trnA</i>	J	6041–6104	64	66	TGC		
<i>trnR</i>	J	6129–6193	65	24	TCG		
<i>trnN</i>	J	6195–6261	67	1	GTT		
<i>trnS1(AGN)</i>	J	6273–6335	63	11	GCT		
<i>trnE</i>	J	6344–6411	68	8	TTC		
<i>trnF</i>	N	6416–6482	67	4	GAA		
<i>nad5</i>	N	6483–8199	1734	0		ATT	TAA
<i>trnH</i>	N	8221–8285	65	21	GTG		
<i>nad4</i>	N	8290–9624	1401	4		ATG	TAA
<i>nad4L</i>	N	9624–9914	291	–1		ATG	TAA
<i>trnT</i>	J	9933–9996	64	18	TGT		
<i>trnP</i>	N	9997–10,062	66	0	TGG		
<i>nad6</i>	J	10,065–10,592	528	2		ATA	TAA
<i>cob</i>	J	10,604–11,755	1152	11		ATG	TAA
<i>trnS2(UCN)</i>	J	11,762–11,824	63	6			
<i>nad1</i>	N	11,841–12,799	939	16		ATG	TAA
<i>trnL1(CUN)</i>	N	12,781–12,849	69	–19	TAG		
<i>rrnL</i>	J	12,850–14,270	1421	0			
<i>trnV</i>	N	14,271–14,336	66	0	TAC		
<i>rrnS</i>	J	14,337–15,121	785	0			
A + T-rich region		15,122–15,933	812				

IN represents intergenic nucleotides, negative numbers indicate overlapping nucleotides.

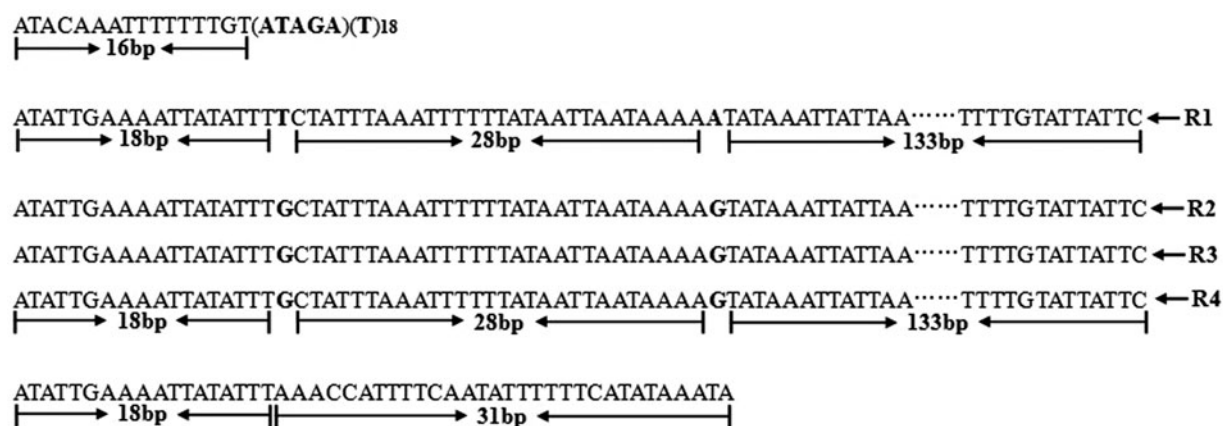


Figure 1. The macro-repeat sequences of the A + T-rich region in *Acleris fimbriana* mitogenome.

A + T-rich region in insects is present between *rrnS* and *trnM* (Table 1). The mitochondrial gene order of *A. fimbriana* is identical to those of all other sequenced lepidopterans (Hu et al., 2010; Kim et al., 2006; Lee et al., 2006).

Twelve PCGs have the usual start codon ATN, but the *cox1* gene commences with exceptional codon CGA, which was found in another tortricid species (*Spilonota lechriaspis*) as the initial codon (Zhao et al. 2011). The feature is common across insects (Liao et al., 2010; Wu et al., 2012a,b; Yang et al., 2009). Twelve PCGs have the common stop codon TAA, except for *cox2* having an in-complete stop codon T.

The *A. fimbriana* mitogenome is biased toward A + T (80.95%). The overall base composition is 39.98% A, 40.97% T, 7.91% G and 11.13% C. 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. The secondary structure of *trnS1(AGN)* is incomplete, lacking the DHU arm. The *rrnL* gene (1421 bp) is located between *trnL(CUN)* and *trnV*, and the *rrnS* (785 bp) between *trnV* and the A + T-rich region.

The *A. fimbriana* mitogenome includes 6 overlapping regions ranging from 1 bp to 19 bp and 17 intergenic spacers ranging from 1 bp to 77 bp, with the exception of the A + T-rich region (the largest non-coding region).

The A + T-rich region (812 bp) is known for regulating transcription and replication of the mitogenome (Clayton, 1992). This region is the longest among the lepidopterans so far. There is a motif ATAGA in downstream of *rrnS* followed by an 18 bp poly-T stretch, the poly-A is not found in upstream of *trnM*. There are several macrosatellite regions in the A + T-rich region (Figure 1). There are four similar tandem macro-repeat sequences (R1, R2, R3, and R4) with each 181 bp long, except for R1 with 2 bp substitution mutations (marked in bold). In addition, an 18 bp repeat region and a 31 bp common region follow the R4-macro-repeat.

#### Declaration of interest

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