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MITOGENOME ANNOUNCEMENT

Characterization of complete mitochondrial genome of the skipper butterfly, *Celaenorrhinus maculosus* (Lepidoptera: Hesperiidae)

Kai Wang[1], Jiasheng Hao[2], and Huabin Zhao[1]

[1]*Department of Zoology, College of Life Sciences, Wuhan University, Wuhan, China and* [2]*Laboratory of Molecular Evolution and Biodiversity, College of Life Sciences, Anhui Normal University, Wuhu, China*

Abstract

The skipper butterfly, *Celaenorrhinus maculosus* (Lepidoptera: Hesperiidae), is a small butterfly species that is widely distributed in Taiwan and mainland China. In this work, we sequenced and characterized the complete mitochondrial genome of the butterfly. The circular genome of 15,282 bp in length contains 13 protein-coding genes, 22 transfer RNA genes, 2 ribosomal RNA genes and a non-coding AT-rich region. Overall base composition of the complete mt genome was 33.97% A, 39.90% T, 12.38% C and 7.75% G, with an AT bias of 79.87%. All protein-coding genes start with an ATN codon, and terminate with the typical stop codon TAA or a single T. The non-coding AT-rich region is 331 bp in length, including a 18 bp poly-T stretch and a microsatellite-like $(TA)_7$ element. The genome sequence is useful for future studies of phylogenetics, molecular evolution, conservation genetics and agricultural control.

Keywords

Celaenorrhinus, Hesperiidae, Lepidoptera, mitochondrial genome, skipper

History

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The butterfly family Hesperiidae (>4000 species), commonly known as skippers or skipper butterflies, are recognized by their quick, darting flight habits. Because of their distinct morphology and behavior, skippers are assigned to a separate butterfly family within a monotypic superfamily Hesperioidea, a sister group to superfamily Papilionoidea (true butterflies) (Grimaldi & Engel, 2005; Kristensen, 1999). However, most skippers have a fairly drab coloration of browns and greys with remarkable uniformity, which introduced few morphological synapomorphies that can be used to characterize different groups within skippers (Warren et al., 2008). Hence, molecular data appear to be particularly helpful in determining the evolutionary history of skipper groups (Larsen, 2005; Warren et al., 2008). Within skippers, only one complete mitochondrial (mt) genome of *Ctenoptilum vasava* (Hesperiidae: Pyrginae) has been reported to date (Hao et al., 2012), which limits our understanding of skipper evolution. In this study, we present the first complete mt genome of *Celaenorrhinus maculosus* (Hesperiidae: Eudaminae) from an additional subfamily Eudaminae (>55 genera) (Warren et al., 2009), with the aim of providing more molecular data for understanding the evolutionary history of skippers.

We extracted the genomic DNA from thoracic muscle of an adult individual of *Celaenorrhinus maculosus* using DNeasy Blood & Tissue Kit (QIAGEN). The complete mitochondrial genome was amplified with one published primer pair (Wahlberg & Wheat, 2008) and nine primer pairs newly designed according to the recently released mt genome sequence of a skipper, *Ctenoptilum vasava* (Hao et al., 2012). PCR amplification and sequencing procedure were described in detail elsewhere (Hao et al., 2012).

Correspondence: Huabin Zhao, Department of Zoology, College of Life Sciences, Wuhan University, Wuhan 430072, China. Tel: +86-27-68753526. Fax: +86-27-68752397. E-mail: huabinzhao@whu.edu.cn

The complete mt genome of *Celaenorrhinus maculosus* is a circular double-stranded molecule of 15,282 bp in length. It contains 37 genes which are shared with the vast majority of animals: 13 protein-coding genes (PCGs), 2 ribosomal RNAs, 22 transfer RNAs and a non-coding AT-rich region (Table 1). Overall base composition of the complete mt genome was 33.97% A, 39.90% T, 12.38% C and 7.75% G, with an AT bias of 79.87%.

Table 1. Details of the complete mitochondrial genome in *Celaenorrhinus maculosus*.

Gene	Direction	Position	Size (bp)	Intergenic length[a]	Start codon	Stop codon
$tRNA^{Met}$	F	1–68	68	0		
$tRNA^{Ile}$	F	71–134	64	2		
$tRNA^{Gln}$	R	200–132	69	−3		
ND2	F	260–1271	1012	59	ATT	T + tRNA
$tRNA^{Trp}$	F	1272–1339	68	0		
$tRNA^{Cys}$	R	1396–1332	65	−8		
$tRNA^{Tyr}$	R	1470–1405	66	8		
COI	F	1468–3010	1543	−3	ATT	T + tRNA
$tRNA^{Leu}(UUR)$	F	3011–3078	68	0		
COII	F	3079–3754	676	0	ATG	T + tRNA
$tRNA^{Lys}$	F	3755–3825	71	0		
$tRNA^{Asp}$	F	3829–3899	71	0		
ATP8	F	3900–4061	162	0	ATT	TAA
ATP6	F	4055–4732	678	−7	ATG	TAA
COIII	F	4732–5517	786	−1	ATG	TAA
$tRNA^{Gly}$	F	5520–5585	66	2		
ND3	F	5586–5937	352	0	ATT	T + tRNA
$tRNA^{Ala}$	F	5938–6004	67	0		
$tRNA^{Arg}$	F	6004–6066	63	−1		
$tRNA^{Asn}$	F	6067–6131	65	0		
$tRNA^{Ser}(AGN)$	F	6135–6195	61	3		
$tRNA^{Glu}$	F	6205–6271	67	9		
$tRNA^{Phe}$	R	6335–6270	66	−2		
ND5	R	8076–6336	1741	0	ATT	T + tRNA

(*continued*)

Table 1. Continued.

Gene	Direction	Position	Size (bp)	Intergenic length[a]	Start codon	Stop codon
tRNA^{His}	R	8145–8077	69	0		
ND4	R	8146–9484	1339	0	ATG	T + tRNA
ND4L	R	9772–9488	285	3	ATG	TAA
tRNA^{Thr}	F	9786–9848	63	13		
tRNA^{Pro}	R	9914–9849	66	0		
ND6	F	9917–10,447	531	2	ATT	TAA
CYTB	F	10,454–11,605	1152	6	ATG	TAA
tRNA^{Ser}(UCN)	F	11,611–11,674	64	5		
ND1	R	12,627–11,692	936	17	ATA	TAA
tRNA^{Leu}(CUN)	R	12,698–12,631	68	3		
16SrRNA	R	14,111–12,699	1413	0		
tRNA^{Val}	R	14,175–14,112	64	0		
12SrRNA	R	14,176–14,951	776	0		
A + Trich region		14,952–15,282	331			

[a]The positive number indicates interval base pairs between genes, while the negative number indicates the overlapping base pairs between genes.

The open-reading frames of the 13 PCGs were determined based on sequence alignments of published mt genome sequences of lepidopteran insects. All PCGs use standard ATN (ATT, ATG or ATA) as the start codon. Seven PCGs (*ATP8*, *ATP6*, *COIII*, *ND4L*, *ND6*, *CYTB*, *ND1*) employ the typical stop codon TAA, while the remaining six PCGs terminate with a single T. The non-coding AT-rich region is 331 bp long located between *12S rRNA* and *tRNA^{Met}*, containing a 18 bp poly-T stretch, a microsatellite-like $(TA)_7$ element.

The mt genome of *Celaenorrhinus maculosus* contains 22 transfer RNA genes (tRNAs): 2 isotypes for Ser (AGN and UCN) and Leu (UUR and CUN), 1 type for the other 18 types of amino acids. All 22 tRNAs could be folded into classic clover-leaf secondary structure except for *tRNA^{Ser} (AGN)* which lacks the dihydrouridine (DHU) arm, a tRNA component commonly found in metazoan mt genomes (Wolstenholme, 1992). Similar to other lepidopterans, the arrangement of all tRNAs of the skipper is identical to most insects except for *tRNA^{Met}* located between the AT-rich region and *tRNA^{Ile}* (Cameron & Whiting, 2008; Chandra et al., 2006).

Nucleotide sequence accession number

The complete genome sequence of *Celaenorrhinus maculosus* has been deposited into the GenBank under accession number KF543077.

Declaration of interest

This work was supported by a start-up fund from Wuhan University to H. Z. The authors report no conflict of interest. The authors alone are responsible for the content and writing of the article.

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