

## Mitochondrial DNA

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## MITOGENOME ANNOUNCEMENT

# The complete mitochondrial genome of the butterfly *Hasora anura* (Lepidoptera: Hesperiiidae)

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**Abstract**

The complete mitochondrial genome (mitogenome) of *Hasora anura* was sequenced and analyzed in the study. The mitogenome is a typical circular DNA molecule of 15 290 bp, including 37 genes and a putative control region. All protein-coding genes, except for *COI* begins with the CGA codon as observed in other lepidopterans, start with a typical ATN initiation codon. Eleven genes terminate with TAA or TAG codons, and two genes use a single T residue as the termination codon. All tRNAs have the typical clover-leaf structure, except that the dihydrouridine (DHU) arm of *tRNA<sup>Ser(AGN)</sup>* forms a simple loop. In the sampled species of Hesperiiidae, *Lobocla bifasciatus* (*Celaenorrhinus maculosus* (*Daimio Tethys*, *Ctenoptilum vasava*)), *Erynnis montanus*, *Carterocephalus silvicola*, *Ampittia dioscorides* (*Potanthus flavus* (*Ochlodes venata*, *Polytremis nascens*)), *Choaspes benjaminii* (*Hasora vitta*, *Hasora anura*), are recovered in phylogenetic analyses with high supports.

**Keywords**

*Hasora anura*, Hesperiiidae, lepidoptera, mitochondrial genome

**History**

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*Hasora anura* is a member of the *Hasora* genus of the subfamily Coediadinae (Lepidoptera: Hesperiiidae). The species is distributed over Northeast India, Northern Thailand, Burma and Southern China. At present, the research of *H. anura* is less except for its taxonomy and biological characters (Chou, 1994, 1998). Here, we present the complete mitogenome of *H. anura*. Voucher specimen (No. W20120505001) was deposited at Shanxi Academy of Agricultural Sciences and the sequence data was deposited in GenBank under the accession number NC\_027263.

This mitogenome is 15 290 bp in size, containing 13 protein-coding genes, 22 tRNA genes, 2 rRNA genes and a control region. Among 37 genes, 23 are encoded on major strand (J-strand) while the rest are found in the minor strand (N-strand). The gene order and orientation are identical to the completely sequenced lepidopteran mitogenomes (Cao et al., 2013; Wang et al., 2012, 2013; Zhang et al., 2012). By the translocation of *tRNA<sup>Met</sup>* to a position 5' upstream of *tRNA<sup>Ile</sup>*, the arrangement differs from that of *Drosophila yakuba*, the hypothesized ancestral gene order of insects (Boore et al., 1998).

All protein-coding genes initiate with typical ATN as the start codon (three with ATT, seven with ATG, one with ATA, one with ATC), except for *COI* gene, which starts at a CGA codon as

observed in most lepidopteran insects (Chen et al., 2012; Yang et al., 2009; Wang et al., 2015). Eleven of 13 PCGs harbor the usual complete stop codon TAA, the rest genes (*COII* and *ND4*) possess the incomplete stop codons T—. The genome composition is highly A + T biased (79.5%) and exhibits negative AT-skew (−0.16) and positive GC-skew (0.01). The codon usage also exhibits a strong A + T-bias in the third codon position and the five most abundant codons are TTA (Leu), ATT (Ile), TTT (Phe), ATA (Met) and AAT (Asn).

This mitogenome contains all sets of 22 tRNA genes, ranging from 61 to 71 bp in size, that are present in most metazoan mitogenomes. Among all tRNA genes, only *tRNA<sup>Ser(AGN)</sup>* cannot exhibit the classic cloverleaf secondary structure due to the deficiency of the DHU arm, which is a typical feature of insect mitogenomes (Cameron, 2014; Liao et al., 2010; Wang et al., 2015). The *lrRNA* is 1387 bp long with an A + T content of 83.5%, and the *srRNA* is 799 bp long with an A + T content of 85.4%. The control region is located between *srRNA* and *tRNA<sup>Met</sup>* and is 234 bp long with a significant AT bias (A + T content of 95.8%).

Bayesian analyses based on 13 Hesperiiidae mitogenome sequences highly support the monophyly of Hesperiiidae (PP=1.0). Phylogenetic analyses showed the following clades were highly supported within Hesperiiidae species (Figure 1): (1) *Lobocla bifasciatus* (*Celaenorrhinus maculosus* (*Daimio Tethys*, *Ctenoptilum vasava*)); (2) *Erynnis montanus*, *Carterocephalus silvicola*; (3) *Ampittia dioscorides* (*Potanthus flavus* (*Ochlodes venata*, *Polytremis nascens*)); and (4) *Choaspes benjaminii* (*Hasora vitta*, *Hasora anura*). The newly sequenced species *H. anura* is considered sister to *Hasora vitta* within Hesperiiidae (PP=1.0).

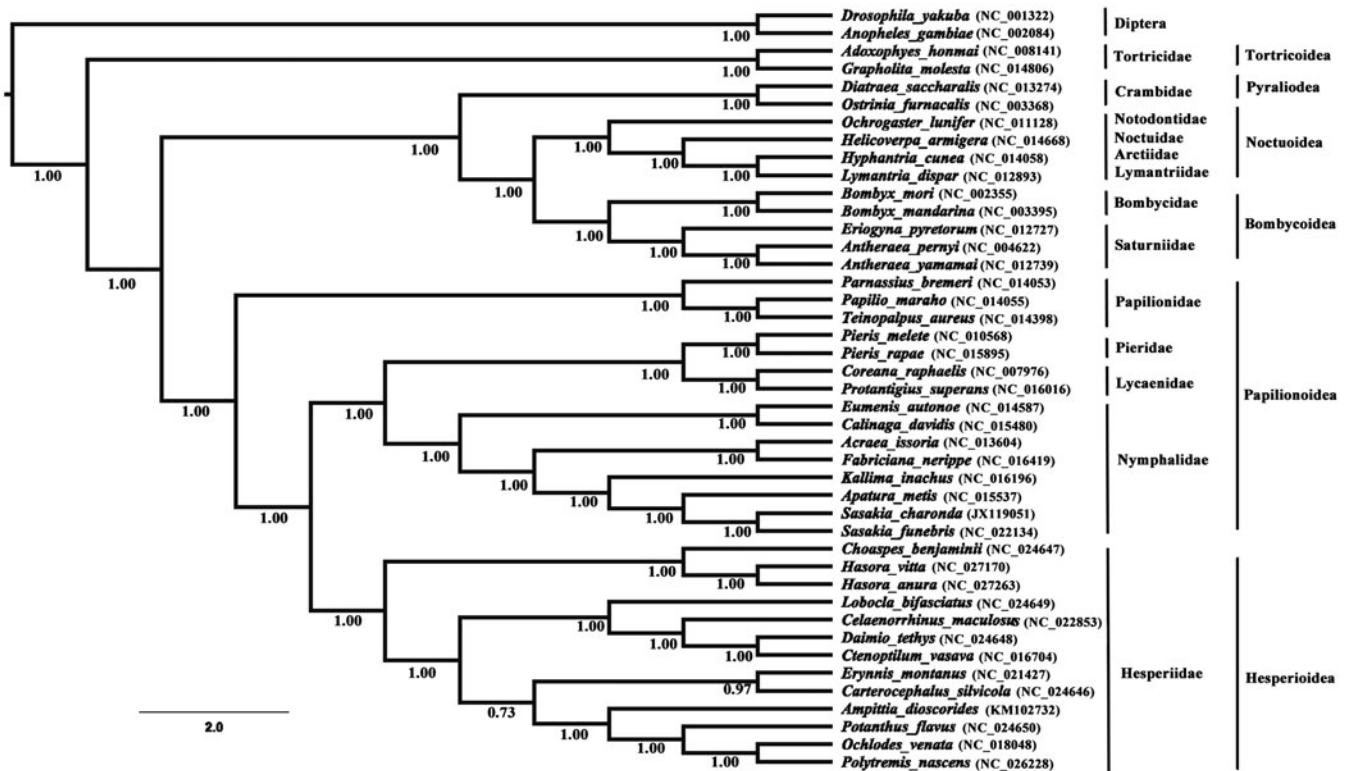


Figure 1. Phylogenetic relationships of Hesperidae inferred from mitochondrial sequences of the first and the second codon positions of 13 protein-coding genes and two rRNAs (9936 bp). Phylogenetic trees were generated from Bayesian inference (MrBayes; Ronquist & Huelsenbeck, 2003) under the GTR + I+G model. Dataset was partitioned by gene. The nodal values indicated the Bayesian posterior probabilities (PP) estimated by 2 000 000 generations ( $n$ -runs = 2,  $n$ -chains = 4, sample frequency = 1000) with the initial 25% trees discarded as burn-in.

## Declaration of interest

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