

MITOGENOME ANNOUNCEMENT

The complete mitochondrial genome of *Hasora vitta* (Butler, 1870) (Lepidoptera: Hesperiiidae)

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Abstract

The complete mitochondrial genome (mitogenome) of *Hasora vitta* was sequenced and analyzed in the study. The mitogenome is 15 282 bp in size, including 37 genes and a putative control region. Thirteen protein-coding genes all start with a typical ATN codon, except that *COI* gene uses CGA as its initial codon. Majority of the 13 PCGs have a complete termination codon (TAA or TAG) except for *COII* and *ND4* have a single T residue. All tRNAs have typical clover-leaf secondary structure, except for *tRNA^{Ser}(AGN)*, in which the dihydrouridine (DHU) arm is a simple loop. In the sampled species of Hesperiiidae, *Hasora vitta*, *Choaspes benjaminii*, *Ampittia dioscorides*, the remaining sampled species, *Celaenorrhinus maculosus* (*Daimio tethys*, *Ctenoptilum vasava*), *Potanthus flavus* (*Polytremsis nascens*, *Ochlodes venata*), are recovered in phylogenetic analyses with high supports.

Keywords

Hasora vitta, Hesperiiidae, Lepidoptera, mitochondrial genome

History

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Hasora vitta (Butler, 1870) is a member of the genus *Hasora* Moore, 1881 of the subfamily Coeliadinae (Lepidoptera: Hesperiiidae). The species is distributed from India, Thailand, Burma, Malaysia, Vietnam, Southern China, Philippines, Indonesia to Papua New Guinea. At present, the research of *H. vitta* is not extensively studied except for its taxonomy and biological characters (Chou, 1994, 1998). Here, we present the complete mitogenome of *H. vitta*. Voucher specimen (No. W20120524008) was deposited at Shanxi Academy of Agriculture Science and the sequence data were deposited in GenBank under accession no. KR076553.

This mitogenome is 15 282 bp in size, containing 13 protein-coding genes, 22 tRNA genes, two rRNA genes, and a control region. Twenty-three genes are encoded on major strand (J-strand), the rest 14 genes are found in the minor strand (N-strand). The gene order and the orientation are identical to the completely sequenced lepidopteran mitogenomes (Chen et al., 2012; Wang et al., 2012, 2013; Zhang et al., 2012). By the translocation of *tRNA^{Met}* to a position 5' upstream of *tRNA^{Ile}*, the arrangement differs from that of *D. yakuba*, the hypothesized ancestral gene order of insects (Boore et al., 1998).

The A + T content is 79.9% with negative AT-skew (−0.01) and GC-skew (−0.22). The codon usage also exhibits a strong A + T-bias in the third codon positions and the five most abundant

codons are TTA (Leu), ATT (Ile), TTT (Phe), ATA (Met), and TAT (Tyr). All protein-coding genes initiate with typical ATN as the start codon (four with ATT, six with ATG, and two with ATA), except for *COI* gene, which starts at a CGA codon as observed in most lepidopteran insects (Cao et al., 2013; Kim et al., 2010; Yang et al., 2009). Eleven of the 13 PCGs harbor the usual complete stop codon TAA, and the remaining two genes (*COII* and *ND4*) possess the incomplete stop codons T.

This mitogenome contains all set 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^{Ser}(AGN)* cannot exhibit the classic cloverleaf secondary structure, due to the deficiency of the DHU arm which is typical feature of insect mitogenomes (Cameron, 2014; Li et al., 2012; Wang et al., 2013). The *lrRNA* is 1397 bp long with an A + T content of 84.4%, and the *srRNA* is 797 bp long with an A + T content of 85.2%. The control region is located between *srRNA* and *tRNA^{Met}* and is 255 bp long with a significant AT bias (A + T content of 94.1%).

Maximum-likelihood (ML) and Bayesian analyses based on 12 Hesperiiidae mitogenome sequences highly support the monophyly of Hesperiiidae (BP = 100; PP = 1.0). Phylogenetic analyses showed the following clades were highly supported within Hesperiiidae species (Figure 1): (1) *Hasora vitta*, *Choaspes benjaminii*; (2) *Ampittia dioscorides*, the remaining sampled species; (3) *Celaenorrhinus maculosus* (*Daimio tethys*, *Ctenoptilum vasava*); and (4) *Potanthus flavus* (*Polytremsis nascens*, *Ochlodes venata*). The newly sequenced species *H. vitta* is placed sister to *Choaspes benjaminii* within Hesperiiidae (BP = 100; PP = 1.0).

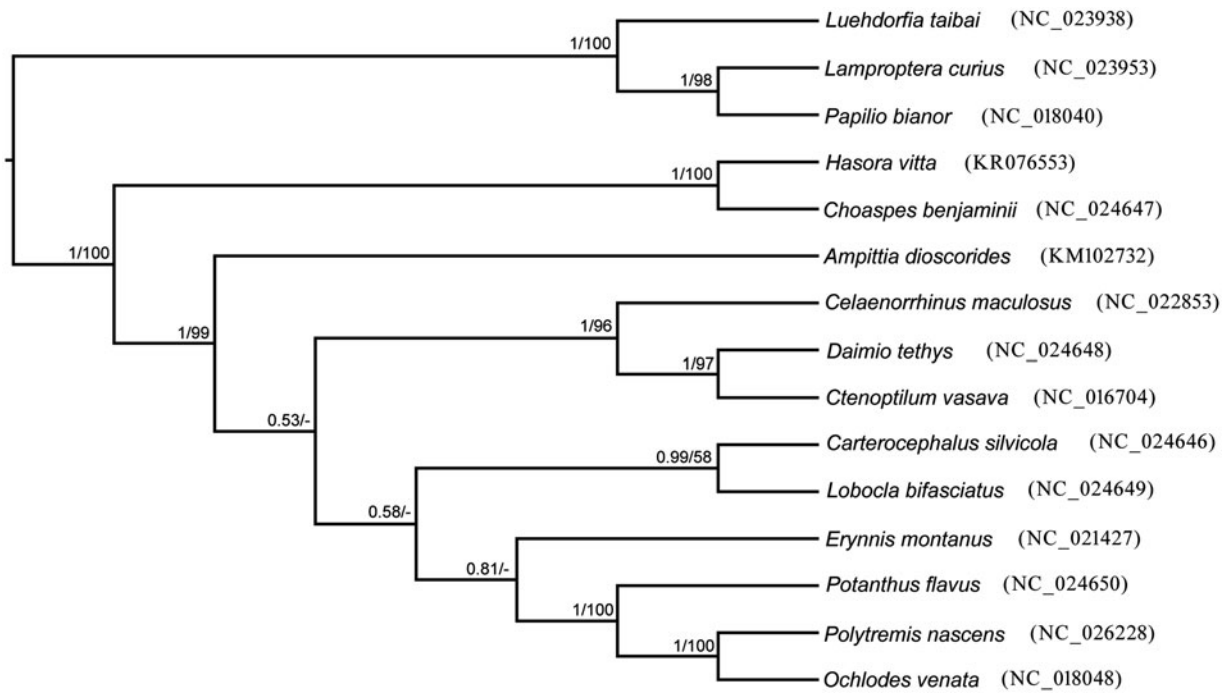


Figure 1. Phylogenetic relationships of Hesperiidae inferred from mitochondrial sequences of 13 protein-coding genes (10 971 bp). Phylogenetic trees were generated from Bayesian inference (MrBayes, Tallahassee, FL; Ronquist & Huelsenbeck, 2003) under the GTR+I+G model and maximum likelihood analysis (RAxML, München, Germany; Stamatakis, 2006) under the GTR+G model. Dataset was partitioned by gene. The nodal values indicated the Bayesian posterior probabilities (PP, in left) estimated by 2 000 000 generations (nrns = 2, nchains = 4, samplefreq = 1000) with the initial 25% trees discarded as burn-in and RAxML bootstrap percentages (BP, in right) obtained with 1000 replicates. The GenBank accession number of the species is shown in the bracket behind the species name.

Declaration of interest

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