

MITOGENOME ANNOUNCEMENT

Mitochondrial genome of a flashwing demoiselle, *Vestalis melania* from the Philippine ArchipelagoMing-Yu Chen¹, Shu-Miaw Chaw², Jo-Fan Wang^{1,3}, Reagan Joseph T. Villanueva⁴, Olga M. Nuñez⁵, and Chung-Ping Lin^{1,3}¹Department of Life Science & Center for Tropical Ecology and Biodiversity, Tunghai University, Taichung, Taiwan, ²Biodiversity Research Center, Academia Sinica, Taipei, Taiwan, ³Department of Life Science, National Taiwan Normal University, Taipei, Taiwan, ⁴Forestal Healing Homes and Therapeutic Milieu, Davao City, Philippines, and ⁵Department of Biological Sciences, Iligan Institute of Technology, Mindanao State University, Tibanga, Iligan City, Philippines

Abstract

This study determined the first complete mitochondrial genome of a demoiselle, *Vestalis melania* (Odonata, Zygoptera, Calopterygidae) using long-range PCR and a primer walking approach. This mitogenome is 16,685 bp long and contains the entire set of 37 genes and an A+T-rich control region typically found in insects. Presently, this mitogenome is the largest mitogenome of all available odonates, mainly because of its long A+T-rich region (2036 bp). The gene arrangement of the *V. melania* mitogenome is identical to that of other known odonates. The inter-genic spacer s5 shared by the Anisoptera is absent in *V. melania*, which supports the view that the absence of the s5 spacer is a synapomorphy of the Zygoptera.

Keywords

Calopterygidae, damselfly, inter-genic spacer, Odonata, synapomorphy, Zygoptera

History

Received 29 August 2013
Revised 9 September 2013
Accepted 14 September 2013
Published online 24 January 2014

Mitochondrial DNA has continued to provide useful genetic markers for phylogenetic studies of numerous dragonflies and damselflies (Insecta, Odonata) (Ballare & Ware, 2011). However, the complete or nearly complete mitochondrial genomes are only known for six species and families in two suborders, Anisoptera (Libellulidae, *Orthetrum triangulare melania*, AB126005, incomplete, Yamauchi et al., 2004; Gomphidae, *Davidius lunatus*, EU591677, Lee et al., 2009; Corduliidae, *Cordulia aenea*, JX963627, Simon & Hadrys, 2013) and Zygoptera (Euphaeidae, *Euphaea formosa*, HM126547, Lin et al., 2010; Coenagrionidae, *Ischnura pumilio*, KC878732, Lorenzo-Carballa et al., 2013; Pseudolestidae, *Pseudolestes mirabilis*, FJ606784). The demoiselle (Calopterygidae) contains numerous large damselflies with conspicuous reproductive behaviors, which are consequently one of the most common research subjects in mating system studies (Córdoba-Aguilar, 2008). In this study, we elucidated the first complete mitogenome of a flashwing demoiselle, *Vestalis melania* from the Philippine Archipelago, to investigate the mitochondrial phylogenomic properties of the odonates.

We extracted genomic DNA from the thorax muscle of a single *V. melania* (specimen Vm0501, Oras, Samar, Philippines, 12° 08' 53" N, 125° 25' 53" E, 2009 September 9) following standard CTAB protocol, amplified the mitogenome using long PCRs

(Yamauchi et al., 2004), and conducted DNA sequencing by using primer walking (supplementary materials: http://sysnevo.thu.edu.tw/lib/publications_lib_pdf/sm_chen_et_al_2013.pdf). The sequences were edited and assembled using SegMan (v. 7.1, DNASTar, Madison, WI). Gene identity and open-reading frames were confirmed using BLAST searches in GenBank and by comparing with available odonate mitogenomes. Transfer RNA genes and the predicted secondary folding were identified using DOGMA (Wyman et al., 2004).

The complete *V. melania* mitogenome (GenBank accession no. JX050224) is 16,685 bp and the largest among the available odonates (15,122 bp in *P. mirabilis*, 15,250 bp in *I. pumilio*, 15,700 bp in *E. formosa* and 15,913 bp in *D. lunatus*), because it possesses a long A+T-rich control region (2036 bp). This mitogenome contains 37 genes (13 protein-coding genes, 22 tRNA genes and 2 rRNA genes) and an A+T-rich region, and the gene arrangement is identical to that of all known odonates (Figure 1). The base frequency of the entire *V. melania* mitogenome has a typically high A+T content of 64.2% (A = 37.6%; T = 26.5%; C = 21.1%; G = 14.7%), which is within the range of values observed in all known odonates. All 22 tRNA-coding sequences can be folded into the characteristic clover-leaf secondary structures (Supplementary materials: http://sysnevo.thu.edu.tw/lib/publications_lib_pdf/sm_chen_et_al_2013.pdf). This mitogenome contains three non-coding inter-genic spacers (s1–s3), which are shared in all known odonate mitogenomes. The inter-genic spacer s5 located between *nad1* and *trnL2* is absent in *V. melania* (and *E. formosa*, *I. pumilio* and *P. mirabilis* of the Zygoptera). The s5 spacer is shared only by *O. triangulare melania* and *D. lunatus* of the Anisoptera, which supports the hypothesis that the absence of s5 spacer is a synapomorphy of the Zygoptera (Lin et al., 2010).

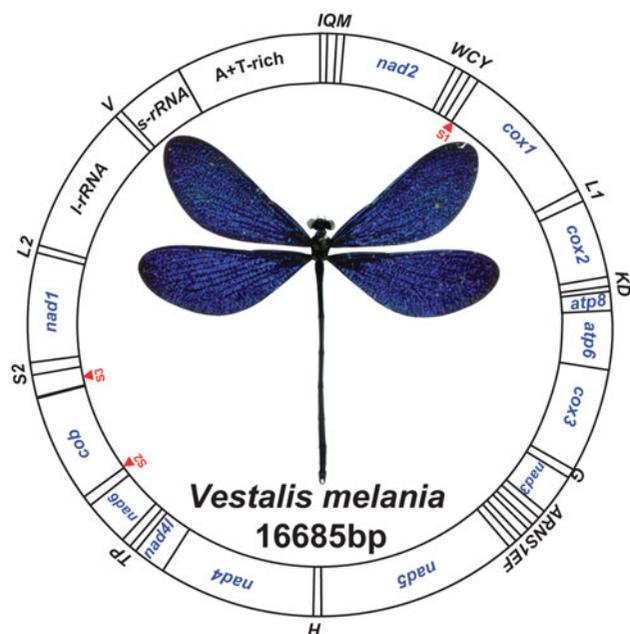


Figure 1. Gene map and organization of the mitochondrial genome of *V. melania*. Protein-coding genes are color-coded in blue. Transfer RNA genes are labeled by the one-letter amino acid code. s1–s3, inter-genic spacers coded in red.

Acknowledgements

The authors thank Hilario Cahilog and Arnulito Viojan for collecting damselflies, and the Department of Environment and Natural Resources (DENR) of the Philippines for research permits (DENR-GP No. RO8 2010-02).

Declaration of interest

The authors report no conflicts of interest. The authors alone are responsible for the content and writing of the article. This study was supported by research grants from the National Science Council of Taiwan (NSC 97-2621-B-029-001-MY3 & 99-2621-M-029-001 to CPL; NSC 97-2621-B-001-003-MY3 to SMC) and Biodiversity Research Center of Academia Sinica (BRC PI grant to SMC).

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