

MITOGENOME ANNOUNCEMENT

Complete mitochondrial genome of an enigmatic dragonfly, *Epiophlebia superstes* (Odonata, Epiophlebiidae)Jo-Fan Wang^{1,2}, Ming-Yu Chen¹, Shu-Miaw Chaw³, Yuta Morii⁴, Mayumi Yoshimura⁵, Teiji Sota⁶, and Chung-Ping Lin^{1,2}¹Department of Life Science & Center for Tropical Ecology and Biodiversity, Tunghai University, Taichung, Taiwan, ²Department of Life Science, National Taiwan Normal University, Taipei, Taiwan, ³Biodiversity Research Center, Academia Sinica, Taipei, Taiwan, ⁴Division of Ecology and Evolutionary Biology, Graduate School of Life Sciences, Tohoku University, Aobayama, Sendai, Japan, ⁵Kansai Research Center, Forestry and Forest Products Research Institute, Fushimi, Kyoto, Japan, and ⁶Department of Zoology, Graduate School of Science, Kyoto University, Sakyo, Kyoto, Japan

Abstract

This study reported the 15,435 bp-long complete mitochondrial genome of the relict *Epiophlebia superstes* (Odonata, Epiophlebiidae), an enigmatic dragonfly of the paraphyletic 'Anisozygoptera' possessing characteristics similar to members of both extant odonate suborders, the Zygoptera and the Anisoptera. This mitogenome comprises the common set of 37 genes and an A + T-rich control region, and has a gene arrangement identical to those of all available odonates. The genome contains three non-coding inter-genic spacers (s1–s3), which occurs in all of other known odonates, but it lacks the inter-genic spacer s5 typically found in the Anisoptera. This result suggests that *E. superstes* possesses a mitogenomic organization more closely related to that of the Zygoptera than that of the Anisoptera.

Keywords

Anisoptera, Anisozygoptera, living fossil, inter-genic spacer, synapomorphy, Zygoptera

History

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The extant dragonflies include approximately 6500 species, which are divided into three suborders: Zygoptera (damselflies), Anisoptera (true dragonflies) and paraphyletic 'Anisozygoptera' (ancient dragonflies) (Silsby, 2001). The two suborders, Zygoptera and Anisoptera encompass the majority of species diversity (28 families), whereas the Anisozygoptera comprise primarily Jurassic fossils, and are represented by only four surviving species of the Epiophlebiidae: *Epiophlebia superstes* from Japan, *E. laidlawi* from Nepal, and the recently discovered *E. sinensis* and *E. diana* from China (Carle, 2012; Li et al., 2012). *Epiophlebia* dragonflies are generally recognized as 'living fossils', and possess morphological and ecological characteristics similar to both Zygoptera and Anisoptera, which renders their phylogenetic positions within the extant odonates to be debatable (Carle, 2012). Complete or nearly complete mitochondrial genomes are known in six species of the 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). Therefore, a complete mitogenome of the enigmatic *Epiophlebia* is necessary for its robust phylogenomic placement within extant odonates.

This article reports the first complete mitogenome of a relict dragonfly, *E. superstes*.

Total genomic DNA was extracted from the thorax muscle of a single *E. superstes* (specimen Es2-1, Kibune, Kyoto, 35° 0' 41.9" N, 135° 46' 4.9" E, 2010 July 23) by using standard CTAB protocol. The mitogenome was amplified by two long PCRs (Yamauchi et al., 2004) and sequenced with a primer walking procedure (Supplementary materials: http://sysnevo.thu.edu.tw/lib/publications_lib_pdf/sm_wang_et_al_2013.pdf). The DNA sequences were edited and assembled using SegMan (v. 7.1, DNASTar, Madison, WI). Gene identity and open-reading frames were confirmed by 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 15,435 bp-long complete *E. superstes* mitogenome (GenBank accession no. JX050223) is within the size range of the other four 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*). This mitogenome contains the common odonate organization of 13 protein-coding genes, 22 tRNA genes, 2 rRNA genes and an A + T-rich control region (Figure 1). All tRNA sequences fold into the characteristic clover-leaf secondary structures, except *trnD* and *trnE* lack the TΨC loop (Supplementary materials: http://sysnevo.thu.edu.tw/lib/publications_lib_pdf/sm_wang_et_al_2013.pdf). This mitogenome comprises three non-coding inter-genic spacers (s1–s3) that occur in all known odonates, but it lacks inter-genic spacer s5 between *nad1* and *trnL2*. The absence of inter-genic spacer s5 is a putative synapomorphy shared by members of the Zygoptera (*E. formosa*, *I. pumilio* and *P. mirabilis*), which suggests that the relict *E. superstes* possesses a mitogenomic organization more similar to that of the Zygoptera than to that of the Anisoptera.

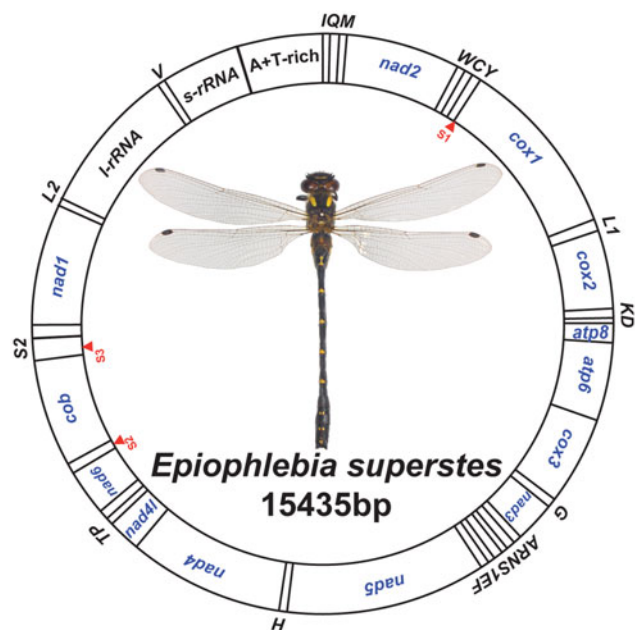


Figure 1. Organization of the mitochondrial genome of *Epiophlebia superstes*. Protein-coding genes are color-coded in blue. Transfer RNA genes are labeled by the one-letter amino acid code. s1–s3, inter-genic spacers coded in red.

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 C. P. L.; NSC 97-2621-B-001-003-MY3

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