Complete mitochondrial genome sequence of Bekko Tombo *Libellula angelina* Selys, 1883 (Odonata: Libellulidae)

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**ABSTRACT**

The dragonfly *Libellula angelina* Selys, 1883 (Odonata: Libellulidae) has been listed as a critically endangered species by the International Union for Conservation of Nature (IUCN) and is also an endangered insect in South Korea. We sequenced the whole genome (15,233 bp) of *L. angelina* species, which included a set of typical genes and one major non-coding AT-rich region with an arrangement identical to that observed in most insect genomes. The A+T-rich region harbored one identical repeat composed of 65 bp and two tRNA-like structures (trnF and trnK-like sequences) with proper anticodon and clover-leaf structures. Phylogenetic reconstruction using the concatenated sequences of 13 protein-coding genes (PCGs) and two rRNAs of the representative odonate mitogenomes utilizing both Bayesian inference and maximum-likelihood methods revealed a strong support for the monophyletic Zygoptera and a moderate to high support for the monophyletic Anisoptera suborders. Unlike that in conventional phylogenetic analysis, a relatively strong sister relationship was revealed between the suborders of Anisozygoptera and Zygoptera.

*Libellula angelina* Selys, 1883 (Odonata: Libellulidae), also known as Bekko Tombo is distributed throughout northern China, Japan, and Korea (Inoue 2006; Jung 2012), which is known as Bekko Tombo is distributed throughout northern China, Japan, and Korea (Inoue 2006; Jung 2012), which is an endangered species by the International Union for Conservation of Nature (IUCN), and is also an endangered species in Korea.

An *L. angelina* adult male was collected at Seoun-myeon, Gyeonggi-do, Korea (36°56′17″ N, 127°15′44″ E) on June 2015 after obtaining the necessary approvals. This voucher specimen was deposited at National Institute of Biological Resources, Incheon, Korea, with the accession number GEIBIN0000339512. DNA was extracted from the hind legs of *L. angelina* species using a Wizard Genomic DNA Purification Kit (Promega, Madison, WI, USA), and four long overlapping fragments (LFs; COI-ND5, ND5-CytB, CytB-srRNA, and srRNA-COI) were amplified using four sets of primers designed from the available mitogenomes of Odonata (Lee et al. 2009; Lin et al. 2010; Wang et al. 2015); these were then used as templates for primer walking. The *L. angelina* sequence was deposited in GenBank with the accession number MG189907.

We reconstructed the odonate phylogenetic tree using the Bayesian inference (BI) and maximum-likelihood (ML) methods based on the concatenated nucleotide sequences of 13 protein-coding genes (PCGs) and two rRNA genes. The optimal partitioning scheme (6 partitions) and substitution model (GTR + Gamma + I) were determined using the PartitionFinder 2 and the Greedy algorithm (Lanfear et al. 2012, 2014, 2016). Both the BI and ML methods were implemented in CIPRES Portal v. 3.1 (Miller et al. 2010).

The 15,233 bp complete mitogenome of *L. angelina* consisted of two rRNAs, 22 tRNAs, 13 PCGs, and one A+T-rich region. Twelve PCGs had the typical ATN start codon, whereas ND1 had the atypical TTG codon. Nine of the 13 PCGs had a complete stop codon; however, COI, COII, COIII, and ND5 had incomplete stop codons, i.e. T or TA. The arrangement of this genome was identical to that typically observed in other insects (Cameron 2014). The A+T-rich region of *L. angelina* was 529 bp. It harboured two identical 55 bp copies, separated by a 57 bp sequence. Additionally, the A+T-rich region of *L. angelina* had two tRNA-like structures: one trnF-like structure encoded in the major strand and another trnK-like structure, encoded in the minor strand.

Both the BI and ML methods exhibited identical topology. Both the Anisoptera and Zygoptera suborders were monophyletic (Figure 1) although the Anisoptera monophyly was poorly supported by ML [bootstrap (BS) = 37%], whereas it was strongly supported by BI [Bayesian posterior probabilities (BPP) = 0.89]. In addition, all the superfamilies (Calopterygidae and Coenagrionioidea in Zygoptera; and Libelluloidae and Gomphoidea in Anisoptera) and families (Euphaeidae and Calopterygidae in Calopterygidae; Coenagrionidae in Coenagrionioidea; Libellulidae in Libellulidae; and Gomphidae in Gomphoidea) were consistently and strongly supported as
monophyletic groups. All the analyses consistently supported the sister relationship between the Anisozygoptera and Zygoptera suborders, with moderate to high nodal supports (BPP = 1; BS = 75). The sister relationship between the Zygoptera and Anisozygoptera suborders was unconventional (Rehn 2003; Davis et al. 2011; Kim et al. 2014); however, recent mitogenome-based phylogenetic results consistently supported the sister relationship between these two suborders (Yong et al. 2016; Jeong et al. 2018). Thus, more diverse taxonomic groups might be helpful to correctly infer the odonate phylogeny.

Disclosure statement
No potential conflict of interest was reported by the authors.

Funding
This work was supported by a grant from the National Institute of Biological Resources (NIBR), funded by the Ministry of Environment (MOE) of the Republic of Korea [NIBR201503204].

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