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MITOGENOME ANNOUNCEMENT

The characteristics and phylogenetic relationship of two complete mitochondrial genomes of *Matrona basilaris* (Odonata: Zygoptera: Calopterygidae)

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ABSTRACT

The relationship of *Matrona* and *Atrocalopteryx* (Odonata: Calopterygidae) is still unclear. To better understand the phylogenetic relationship of *Matrona* and *Atrocalopteryx*, we sequenced and annotated two complete mitochondrial genomes of *Matrona basilaris* sampled from two different locations. The length of the two complete mitochondrial genomes of *M. basilaris* is 16,149 bp and 15,893 bp for the specimens collected in Jinhua, Zhejiang Province and Tianmushan, Zhejiang Province, China, respectively. The two mitochondrial genomes include the typical invertebrate set of 37 genes: 13 protein-coding genes (PGCs), 22 tRNA genes, and 2 rRNA genes. The nucleotide composition of the mitogenome is similar to other odonates with high content of A + T (68.9%) and all PCGs use ATN as the start codon. Tandem repeats were detected in the control regions of the two *M. basilaris* samples that accounted for the different sequence lengths of the mitochondrial genomes from the two locations. Finally, BI and ML phylogenetic analysis based on the concatenated nucleotide sequences of the 13 PCGs supported the conclusion that *M. basilaris* is a sister clade to *Atrocalopteryx melli*.

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The relationship between *Matrona* and *Atrocalopteryx* (Odonata: Calopterygidae) is unclear (Dumont et al. 2007; Guan et al. 2012). To help resolve this, we sequenced the mitochondrial genome of two specimens of *Matrona basilaris* (Zygoptera: Calopterygidae) to better determine their phylogenetic relationship within Odonata. Two samples of *M. basilaris* were collected from Jinhua (JH), Zhejiang province and Tianmushan (TMS), Zhejiang province, China, respectively. Using an Ezup Column Animal Genomic DNA Purification Kit (Sangon Biotech Company, Shanghai, China), the total genomic DNA was isolated from the thorax muscle of the two samples. Remaining samples and DNA extracts were stored in the lab of Dr. Zhang, College of Chemistry and Life Science, Zhejiang Normal University. A set of conserved and modified primers (Simon et al. 2006; Zhang et al. 2008; Zhang, Cai, et al. 2018; Zhang, Yu, et al. 2018) and six specific primers were designed for polymerase chain reaction (PCR) amplification. The sequences of the two mitogenomes are deposited in GenBank with accession numbers MK722304 and MK722305 for JH and TMS, respectively.

The two complete mitochondrial genomes of *M. basilaris* are 16,149 bp (JH) and 15,893 bp (TMS) in length, respectively. All protein-coding genes of the two samples are AT-biased (68.9%), with *atp8* showing the highest A + T content (76.8% and 76.1%) whereas *cox1* has the lowest A + T content (both samples are 63%); these results are similar to other odonates (Lin et al. 2010; Lorenzo-Carballa et al. 2014; Feindt et al. 2016). All protein-coding genes of *M. basilaris* employ the characteristic invertebrate specific mitochondrial start codons: *cox2*, *cox3*, *atp6*, *nad4*, *nad4L*, *cytb* and *nad1* start with ATG; *cox1* and *nad3* with ATA; *atp8* and *nad5* with ATT; and *nad2* and *nad6* with ATC. Eight protein-coding genes have the standard stop codons TAA (*cytb*, *nad2*, *nad6*, *nad4L*, *atp6*, *atp8* and *cox1*) and TAG (*nad1*) whereas *cox2*, *cox3*, *nad3* and *nad5* have incomplete stop codons of a single T, and *nad4* has an incomplete TA stop codon. Tandem repeats occured in the control region and were responsible for the different full lengths of the *M. basilaris* from the JH and TMS locations.

We constructed Bayesian inference (BI) and maximum likelihood (ML) trees from the 13 PCGs of *M. basilaris* and 28 other Odonata species (Yamauchi et al. 2004; Lin et al. 2010; Lorenzo-Carballa et al. 2014; Tang et al. 2014; Feindt et al. 2016; Yong et al. 2016; Yu et al. 2016; Zhang et al. 2017) and using four outgroups: *Isonychia kiangsinensis* (Ye et al. 2018), *Epeorus herklotsi* (Gao et al. 2018), *Siphluriscus chinensis* (Li et al. 2014) and *Caenis* sp. (Cai et al. 2018) (Figure 1). In order to select conserved regions of the nucleotide sequences, each alignment was performed by Gblock 0.91b (Castresana 2000) using default settings. BI and ML analyses were performed by MrBayes 3.1.2 (Huelsenbeck and Ronquist

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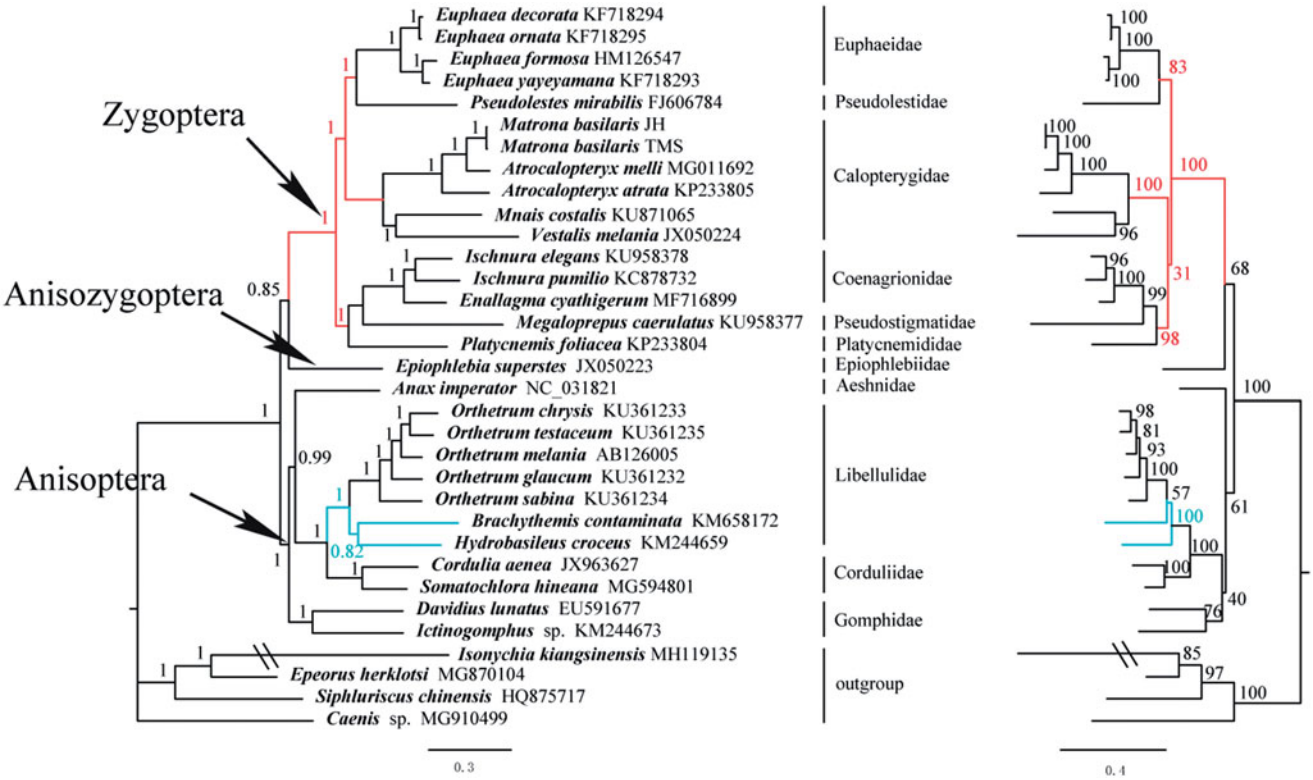

Figure 1. Phylogenetic tree of the relationships among 29 species of Odonata including *Matrona basilaris*, based on the nucleotide dataset of the 13 mitochondrial protein-coding genes. Four outgroups (*Isonychia kiangsinensis*, *Epeorus herklotsi*, *Siphluriscus chinensis* and *Caenis* sp.) were used. Numbers above branches specify posterior probabilities from Bayesian inference (BI) (left) and bootstrap percentages from maximum likelihood (ML) (right) analyses. The red and blue lines indicate a different topology between BI and ML analyses. GenBank accession numbers of all species are also shown.

2001) and RAxML 8.2.0 (Stamatakis 2014), respectively. Both BI and ML phylogenetic trees showed that *M. basilaris* is a sister clade to *Atrocalopteryx melli*. However, the monophyly of *Atrocalopteryx* failed because *M. basilaris* is clustered into *Atrocalopteryx*.

Disclosure statement

The authors report no conflicts of interest and are responsible for the content and writing of the paper.

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