

## The complete mitochondrial genome of *Anax parthenope* (Odonata: Anisoptera) assembled from next-generation sequencing data

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### ABSTRACT

The complete mitochondrial genome of *Anax parthenope* was assembled from next-generation sequencing data. The circularized mitochondrial genome spans 15,306 bp with a high A + T content of 74.7% and consists of 13 protein-coding genes, 22 tRNA genes, and 2 rRNA genes. Its gene composition and order were similar to *Anax imperator*. The overall base composition is 36.6% for A, 34.8% for T, 16.8% for C, and 11.8% for G. A phylogeny of 31 dragonfly species clustered this species within Odonata.

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Aeshnidae; gene order; mitogenome; phylogeny

Odonata (Insecta: Pterygota) are a kind of ancient, medium and small winged insects, consisting of three suborders, namely Anisoptera, Zygoptera, and Anisozygoptera. It takes an important position in the evolution of winged insects and as sensitive indicator organisms for freshwater ecosystems. Currently, a total of 6322 species were recorded in the world (Schorr and Paulson 2020). However, in the recent 30 years, the increasing water pollution degraded the habitat quality and resulted in the loss of dragonfly biodiversity. Besides, species relationships within Odonata are poorly understood. *Anax* Leach in Brewster, 1815, a genus of family Aeshnidae, is a cosmopolitan genus of the 32 species which are distributed in the temperate and tropical zones (Schorr and Paulson 2020). To date, only a few mitochondrial and ribosomal sequences have been reported for Aeshnidae (NCBI Reference Sequence, accessed 2020 Apr 19). To explore its evolution in Odonata, we report the complete mitochondrial genome of *Anax parthenope julis* Brauer.

In this study, the voucher specimen of *A. parthenope* was collected from Nanjing, Jiangsu Province, China (31.580°N, 119.176°E; NCBI BioSample accession SAMN14733969; specimen voucher number 33m-3). Total genomic DNA was extracted from one leg of a single individual using the QIAamp DNA Micro Kit (Qiagen GmbH, Hilden, Germany) and sequenced by NovaSeq 6000. The voucher specimen and extracted DNA were preserved at –20 °C in the Nanjing Agricultural University, China. The mitogenome was assembled with NOVOPlasty v3.8.2 (Dierckxsens et al. 2017), annotated with MitoZ v2.4-alpha (Meng et al. 2019), and deposited in GenBank with the accession number MT408029.

The circularized mitochondrial genome spans 15,306 bp with a high A + T content of 74.7% and consists of 13 protein-coding genes, 22 tRNA genes, and two rRNA genes. Its gene composition and order were similar to *Anax imperator* (NC\_031821.1). The overall base composition is 36.6% for A, 34.8% for T, 16.8% for C, and 11.8% for G, and the G-C skew is –11.15. Nine PCGs and 14 tRNA genes are located on the positive strand, while four PCGs (ND1, ND4, ND4L, and ND5), eight tRNA genes (tRNA<sup>Leu</sup>, tRNA<sup>Val</sup>, tRNA<sup>Gln</sup>, tRNA<sup>Cys</sup>, tRNA<sup>Tyr</sup>, tRNA<sup>Phe</sup>, tRNA<sup>His</sup>, and tRNA<sup>Pro</sup>), and two rRNA genes (l-rRNA and s-rRNA) are located on the reverse strand. For the 13 PCGs, 12 of them are terminated with TAA stop codon, while ND5 is ended with the incomplete TA stop codon.

Amino acid sequences were aligned using MAFFT v7.407 (Kato and Standley 2013) and trimmed with trimAl v1.4.1 (Capella-Gutiérrez et al. 2009) with the heuristic method ‘automated1’. The phylogeny was reconstructed using IQ-TREE v2.0 (Nguyen et al. 2015) with the partitioning method. Monophyly of Aeshnidae was recovered because *A. parthenope* was clustered within Aeshnidae (Figure 1).

### Disclosure statement

No potential conflict of interest was reported by the author(s).

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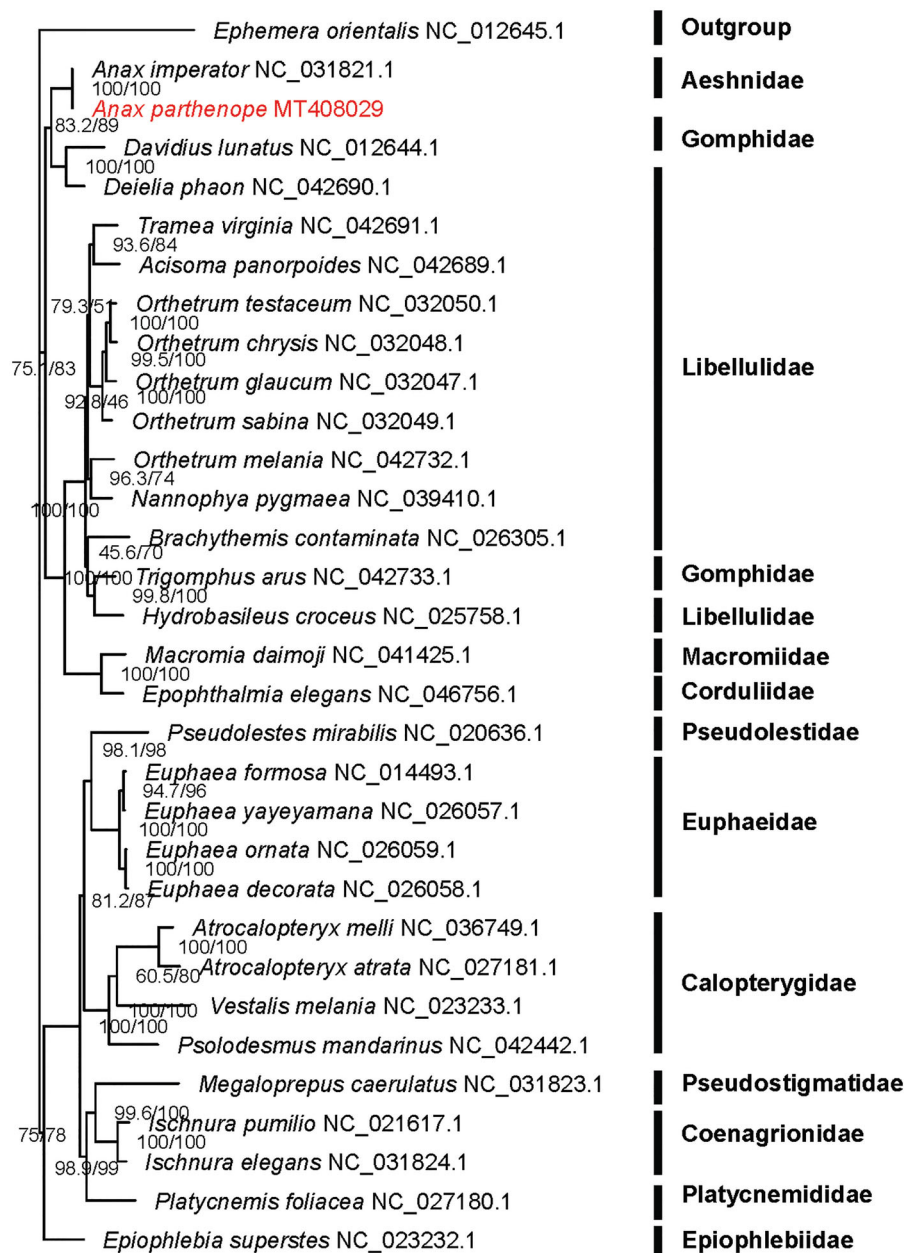


Figure 1. Maximum-likelihood phylogenetic tree inferred from 13 PCGs. SH-aLRT and UFBoot support values are given on nodes.

## Data availability

The data that support the findings of this study are openly available in NCBI GenBank database at <https://www.ncbi.nlm.nih.gov> with the accession number MT408029, which permits unrestricted use, distribution, and reproduction in any medium, provided the original work is properly cited.

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