

## Characterization of the complete mitochondrial genome sequence of *Asiadodis yunnanensis* (Mantidae: Choeradodinae) and phylogenetic analysis

Yan Shi, Qin-Peng Liu, Lan Luo and Zhong-Lin Yuan

Key Lab of Integrated Crop Pest Management of Shandong Province, College of Plant Health and Medicine, Qingdao Agricultural University, Qingdao, China

### ABSTRACT

The complete mitochondrial genome of the praying mantises *Asiadodis yunnanensis* was characterized in this study. The circular molecule is 15,416 bp in length (GenBank accession no. MN037794), containing 13 protein-coding genes (PCGs), two ribosomal RNA (rRNA) genes, 22 transfer RNA (tRNA) genes. The nucleotide composition is asymmetric (39.5% A, 15.1% C, 9.6% G, 35.8% T), with an overall A + T content of 75.3%. The gene arrangement of *A. yunnanensis* is identical to that observed in other praying mantises. Seven PCGs are initiated with typical ATN start codons, Four genes (*cox1*, *nad3*, *nad4L*, and *nad6*) begin with TTN, *nad1* begin with GTT, and *nad5* use CTT, as initiation codon. Twelve PCGs stop with complete termination codon TAA and TAG, whereas *nad5* uses incomplete termination codon (T—). Twenty reading frame overlaps and seven intergenic regions are found in the mitogenome of *A. yunnanensis*. The phylogenetic relationships based on 13 PCGs show that *A. yunnanensis* clusters closest to the species of Mantidae.

### ARTICLE HISTORY

Received 12 July 2019  
Accepted 1 August 2019

### KEYWORDS

*Asiadodis yunnanensis*;  
praying man-  
tises; mitogenome

*Asiadodis* was established by Roy (2004) to distinguish from *Choeradodis*. *Asiadodis* have only been found in Southeast Asia and South Asia. There are two species involved in: *A. yunnanensis* and *A. squilla*. *A. yunnanensis* (Wang and Liang 1995) is a type of praying mantises belonging to the order Mantodea, family Mantidae, subfamily Choeradodinae, genus *Asiadodis*, distributing in China, Yunnan. *Asiadodis yunnanensis* captures insect pests as food and is recognized as an important natural enemy for biological control. In this study, samples of *A. yunnanensis* were collected from China, Mengla, Xishuangbanna, Yunnan (21.47°N, 101.54°E) and stored in the praying mantises specimen room of College of Plant Medicine, Qingdao Agricultural University with an accession number 01-XXBNJH.

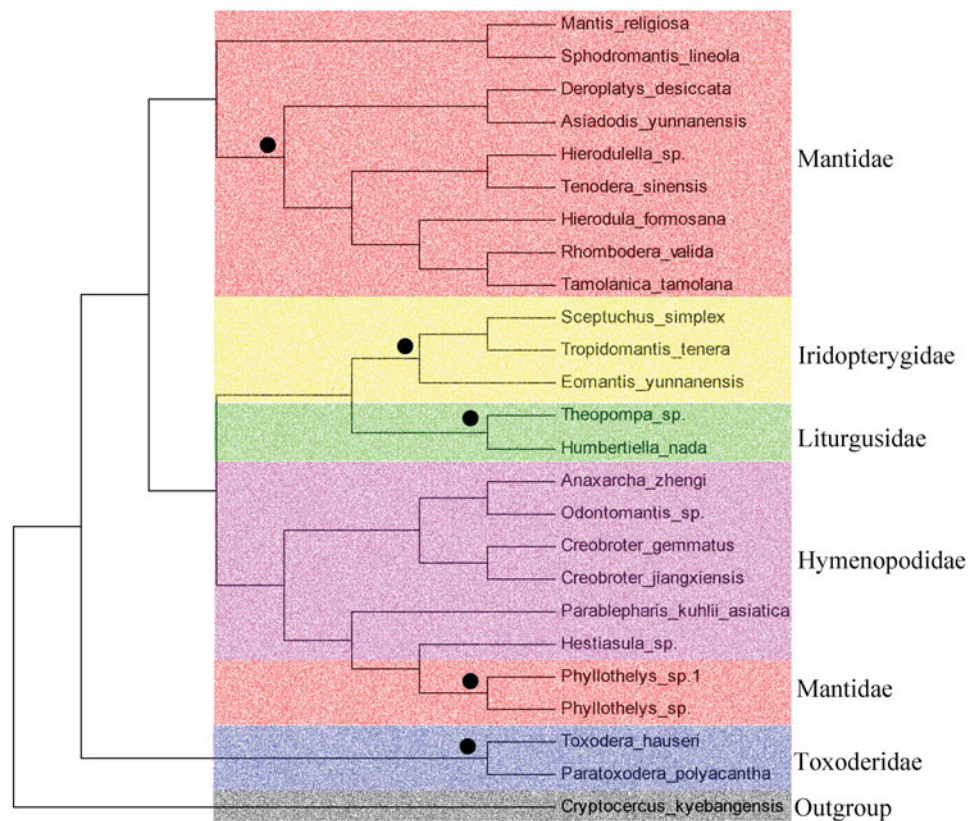
The complete mitogenome of *A. yunnanensis* is a circular molecule of 15,416 bp in length (GenBank under accession no. MN037794) and contains 13 protein-coding genes (PCGs), 22 transfer RNA genes (tRNAs), two ribosomal RNA genes (*rrnL* and *rrnS*). The nucleotide composition of *A. yunnanensis* mitogenome is asymmetric (39.5% A, 15.1% C, 9.6% G, 35.8% T), with an overall A + T content of 75.3%. The AT-skew and GC-skew of this genome were 0.049 and -0.223, respectively. The gene organization of *A. yunnanensis* is similar to that observed in other praying mantises (Ye et al. 2016; Zhang et al. 2018). Twenty-one genes were encoded on the major strand (J-strand), whereas the others were encoded on the minor strand (N-strand).

The *A. yunnanensis* mitogenome harbours a total of 32 bp intergenic spacer sequences, which is made up of 5 regions in the range from 5 to 10 bp. Gene overlaps were found at nine gene junctions and involved a total of 223 bp, the longest 39 bp overlapping located between *nad3* and *trnL2*. The A + T content of the *A. yunnanensis* mitogenome was 75.3%. The higher A + T content of *A. yunnanensis* was present in all regions, both genes and noncoding regions. Gln (Q), Glu (E), and Trp (W) are most frequently used. Moreover, the A + T content were also reflected further in the codon usage: the relative synonymous codon usages showed that *A. yunnanensis* used more NNA and NNT codon. The *rrnL* was 1313 bp in length with A + T content of 79.3%, and *rrnS* was 767 bp in length with A + T content of 74.9%.

Seven PCGs in *A. yunnanensis* mitogenome start with a typical ATN (ATA and ATG) codon, four genes begin with TTN (TTG, ATC, and TTA), *nad1* uses GTT and *nad5* use CTT as initiation codon. Twelve PCGs stop with complete termination codon (TAA and TAG), whereas *nad5* uses incomplete codon (T—) as termination codon. Based on the Maximum-likelihood analyses, we constructed the phylogenetic relationships of *A. yunnanensis* and 23 other praying mantises based on the 13 PCGs amino acids using RAXML. *Cryptocercus kyebangensis* was used as an outgroup. The results have shown that *A. yunnanensis* is closely clustered with other species in family Mantidae (Figure 1), which agree with the morphology classifications.

**CONTACT** Zhong-Lin Yuan  [zhongliny@163.com](mailto:zhongliny@163.com); Yan Shi  [shiyanyuanyi@qau.edu.cn](mailto:shiyanyuanyi@qau.edu.cn) 

© 2019 The Author(s). Published by Informa UK Limited, trading as Taylor & Francis Group.  
This is an Open Access article distributed under the terms of the Creative Commons Attribution License (<http://creativecommons.org/licenses/by/4.0/>), which permits unrestricted use, distribution, and reproduction in any medium, provided the original work is properly cited.



**Figure 1.** Phylogenetic tree showing the relationship between *A. yunnanensis* (MN037794) and 23 other praying mantises. *Cryptocercus kyebangensis* (KP872847.1) was used as an outgroup. The black circle indicates popularity >90. GenBank accession numbers used in the study are the following: *Rhombodera valida* (KX611804.1), *Hierodula formosana* (KR703238.1), *Tamolonica tamolana* (DQ241797.1), *Sphodromantis lineola* (KY689123.1), *Tenodera sinensis* (KY689132.1), *Hierodulella sp.* (KY689136.1), *Deroplatys desiccata* (KY689113.1), *Mantis religiosa* (KU201317.1), *Sceptuchus simplex* (KY689133.1), *Tropidomantis tenera* (KY689127.1), *Eomantis yunnanensis* (KY689138.1), *Theopompa sp.* (KU201314.1), *Humbertiella nada* (KU201315.1), *Anaxarcha zhengi* (KU201320.1), *Odontomantis sp.* (KY689121.1), *Creobroter gemmatus* (KU201319.1), *Creobroter jiangxiensis* (KY689134.1), *Parablepharis kuhlii asiatica* (KY689117.1), *Hestiasula sp.* (KY689115.1), *Phyllothelys sp.1* (KY689119.1), *Phyllothelys sp.* (KY689129.1), *Toxodera hauseri* (KX434837.1), and *Paratoxodera polyacantha* (MG049920.1). Mantis determined in this study was underlined.

## Disclosure statement

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

## Funding

This study was supported in part by the Qingdao Agricultural University High-level Talent Fund [665-1117002; 663-1119002]. Establishment of Technical Model for Reduction of Pesticides in Chinese Cabbage in the Open Field of Northern Jiaodong Peninsula [2018YFD0201206-06].

## References

- Roy R. 2004. Révision et phylogénie des Choeradodini Kirby, 1904 (Dictyoptera, Mantidae). Bulletin de la Société Entomologique de France. 109:113–128.
- Wang TQ, Liang GQ. 1995. New Record of Choeradodis and One New Species of Mantodea from China. Acta Scientiarum Naturalium Universitatis SunYatsen. 2:1–34.
- Ye F, Lan XE, Zhu WB, You P. 2016. Mitochondrial genomes of praying mantises (dictyoptera, mantodea): rearrangement, duplication, and reassignment of trna genes. Sci Rep. 6:25634.
- Zhang LP, Yu DN, Storey KB, Cheng HY, Zhang JY. 2018. Higher tRNA gene duplication in mitogenomes of praying mantises (Dictyoptera, Mantodea) and the phylogeny within Mantodea. Int J Biol Macromol. 111:787–795.