Mitochondrial genome of one kind of giant Asian mantis, Hierodula formosana (Mantodea: Mantidae)

Xiaoxuan Tian, Jie Liu, Ying Cui, Pengzhi Dong & Yan Zhu

To cite this article: Xiaoxuan Tian, Jie Liu, Ying Cui, Pengzhi Dong & Yan Zhu (2015): Mitochondrial genome of one kind of giant Asian mantis, Hierodula formosana (Mantodea: Mantidae), Mitochondrial DNA

To link to this article: http://dx.doi.org/10.3109/19401736.2015.1106519

Published online: 07 Dec 2015.

Submit your article to this journal

View related articles

View Crossmark data
Mitochondrial genome of one kind of giant Asian mantis, *Hierodula formosana* (Mantodea: Mantidae)

Xiaoxuan Tian1,2, Jie Liu1,2, Ying Cui1,2, Pengzhi Dong1,2, and Yan Zhu1,2,3

1State Key Laboratory of Modern Chinese Medicine, Tianjin University of Traditional Chinese Medicine, Tianjin, China, 2Research and Development Center of TCM, Tianjin International Joint Academy of Biotechnology & Medicine, Tianjin, China, and 3Molecular Cardiology Research Institute, Tufts Medical Center, Boston, MA, USA

Abstract

The giant Asian mantis *Hierodula formosana* (Mantodea: Mantidae) is widely distributed in Taiwan. In the present study, we investigated the complete mitochondrial genome of *H. formosana* and the mitogenome is $16,266$ bp in length. The circular molecule consists of 13 protein-coding genes, 2 ribosomal RNA genes, 22 transfer RNA genes, and a non-coding control region, with an AT content of 75.8%. An extra non-coding region is inserted between trnM and ND2, similar to the other Mantidae species *T. tamolana*. A preliminary phylogenetic analysis has been carried out with 11 related species and the status of *Hierodula formosana* is further confirmed.

*Hierodula* is a genus of mantid comprising about 85 species, and widely distributed in Asia, Africa and Central America. The dry ootheca of *Hierodula* species are named as Hei Piaoxiao, and are traditionally used to treat seminal leakage and frequent micturition in China (Committee, 2010; Wen et al., 2013). On the other hand, many species within this genus are referred to by the common name giant Asian mantis because of their large size and raised as ornamental insects. Within them, *Hierodula formosana* Giglio-Tos, 1912, is commonly found in mid and low altitude mountainous region in Taiwan. Although similar in appearance to *Hierodula membranacea*, a dark dot in the inside of foreleg femur is this species’ distinctive mark. Nowadays, there is only one report of complete mitochondrial genome (*Tamolanica tamolana*) in Mantidae (Cameron et al., 2006), and still no information on *Hierodula* mitogenome.

In this study, the individual of *H. formosana* (voucher ID: jftl-1) came from a commercial supplier and collected in Taiwan. We used the high-throughput sequencing method to acquire the *H. formosana* complete mitochondrial genome sequences (GenBank accession no. KR703238). The complete mtDNA sequence of *H. formosana* ($16,266$ bp in length) has 13 protein-coding genes (PCGs), 2 ribosomal RNA genes, and 22 transfer RNA genes. The gene order is identical to that observed in the most insects (Cameron, 2014). The AT content was 75.8%. This kind of bias was in agreement with other two mantises with complete mitogenome reports (75.3% for *T. tamolana* and 73.7% for *Leptomantella albella*). In 13 PCGs, the longest one is the ND5 gene (1720 bp) and the shortest one is the ATP8 gene (159 bp). Five of 13 PCGs have ATG as the starts codon, while ATP6, COX3, ND3, and ND6 utilize ATA, ND2, COX1, and ND3 translate from ATT, and ATP8 start from ATC. Nine of 13 PCGs start from ATC. Nine of 13 PCGs start from ATC, while COX3, ND2, and ND5, and CytB stop with incomplete TA– or T–. Each typical tRNA cloverleaf secondary structure is predicted by MITOS Web Server (Bernt et al., 2013). The major non-coding region is in D-loop region which is 840 bp.

Interestingly, an extra non-coding region is inserted between trnM and ND2 (625 bp). Together with four regions of PCGs overlapping (between ATP8 and ATP6, ATP6 and COX3, ND4 and ND4l, and ND6 and CytB), this phenomenon is consistent with *T. tamolana* rather than *Leptomantella albella*, and whether they are the common gene arrangement features of Mantidae remains to be tested by more mitogenome reports.

As shown in Figure 1, phylogenetic analysis was performed as the methods mentioned by Price et al. (2010). The result further confirmed that *H. formosana* was closed to *T. tamolana*, the only mitochondrial genome of Mantidae reported so far. Besides that, the relationships of Blattodea (cockroaches and termites) reconstructed was in accordance with previous report (Inward et al., 2007), while the mantids were also shown to be the sister group to Blattodea.
Declaration of interest

The authors report no conflicts of interest. The authors alone are responsible for the content and writing of the manuscript. This work was supported by National Key Technology R&D Program (2012BAI29B01), National Science Foundation of China (81202874), and Specialized Research Fund for the Doctoral Program of Higher Education (20121210120006). The field sampling and tissue samples are preserved by Xiaoxuan Tian’s research group of Tianjin University of Traditional Chinese Medicine.

References


