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The complete mitochondrial genome of *Mantis religiosa* (Mantodea: Mantidae) from Canada and its phylogeny

Yi-Yang Jia^a, Le-Ping Zhang^a, Xiao-Dong Xu^a, Xin-Yi Dai^a, Dan-Na Yu^{a,b} , Kenneth B. Storey^c  and Jia-Yong Zhang^{a,b} 

^aCollege of Chemistry and Life Science, Zhejiang Normal University, Jinhua, Zhejiang Province, China; ^bKey Lab of Wildlife Biotechnology, Conservation and Utilization of Zhejiang Province, Zhejiang Normal University, Jinhua, Zhejiang Province, China; ^cDepartment of Biology, Carleton University, Ottawa, Canada

ABSTRACT

The complete mitochondrial genome of *Mantis religiosa* (Mantodea: Mantidae) from Canada was successfully sequenced. The mitochondrial genome was a circular molecule of 15,521 bp in length, containing 13 protein-coding genes, two rRNA genes, 23 tRNA genes (including an extra tRNA^{Arg} gene), and the control region. The AT content of the whole genome was 76.9% and the length of the control region was 636 bp with 81.9% AT content. The structure of the *M. religiosa* mitochondrial genome from Canada was almost identical to *M. religiosa* from China and their genetic distance was just 0.017. In Bayesian inference (BI) and maximum likelihood (ML) analyses, we found that *M. religiosa* was a sister clade to *Statilia* sp. and the monophyly of the genera Hierodula and Rhombodera was not supported.

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Mantidae; mitogenome; phylogeny; *Mantis religiosa*

Mantis religiosa (Mantodea: Mantidae), the European Mantis, is widely distributed across the world. The species occurs in China where it is characterized by an additional tRNA-Arg gene in the mitochondrial genome (Ye et al. 2016). It is listed as an introduced species in Canada (Kevan 1979; Miskelly and Paiero 2019). In this study, we sequenced the mitochondrial genome of *M. religiosa* from Canada to compare the gene structure with the Chinese counterpart and provide more molecular data to discuss the phylogenetic relationship within Mantidae.

The sample of *M. religiosa* was collected from Upper Canada Village (N 45°3'55", E 74°56'34"), Morrisburg, Ontario, Canada. The sample (CA20170830-1) was identified and stored at -40°C in the Animal Specimen Museum, College of Life Sciences and Chemistry, Zhejiang Normal University, China. Total genomic DNA was extracted from leg muscle using an Ezup Column Animal Genomic DNA Purification Kit (Sangon Biotech Company, Shanghai, China) and stored in the Zhang laboratory. A set of modified universal primers (Zhang et al. 2008; Zhang, Yu, et al. 2018) were designed for polymerase chain reaction (PCR) amplification. All PCR products were sequenced in both directions by the Sangon Biotech Company (Shanghai, China). The mitochondrial genome is deposited in GenBank with accession number MN356097.

The phylogenetic relationship was constructed using the Bayesian Inference (BI) (Ronquist et al. 2012) and RAxML 8.2.0 (Stamatakis 2014) softwares. To select conserved regions of the putative nucleotide sequences, each alignment was analyzed with Gblocks 0.91 b (Castresana 2000) using default settings. BI and ML trees were constructed using the 13 protein-coding genes of 21 species, which included 18 Mantidae species (Cameron et al. 2006; Song et al. 2016; Ye et al. 2016; Tian et al. 2017; Zhang and Ye 2017; Zhang, Yu et al. 2018; Zhang et al. 2018a, 2018b) and three Blattaria species as the outgroups (Cameron and Whiting 2007; Dietrich and Brune 2016).

The complete mitogenome of *M. religiosa* from Canada was circular and 15,521 bp in length, containing the 38 mitochondrial genes including 13 protein-coding genes, 23 transfer RNA genes (including an additional tRNA^{Arg} gene), 2 ribosomal RNA genes. The same situation is typically found in the mitogenomes of other mantises (Ye et al. 2016; Zhang et al. 2019). The AT content of the complete mtDNA was 76.9% and the length of the control region was 636 bp with 81.9% AT content. Most protein-coding genes began with ATN (N represents A, T, C, G) as the start codons whereas the *CO1* gene began with TTG. *COX2* and *ND5* genes ended with an incomplete stop codon (T-) whereas the remaining 11 protein-coding genes ended with TAA. The structure of the mitochondrial genome of the specimen from Canada was

CONTACT Jia-Yong Zhang  zhang3599533@163.com, zhangjiayong@zjnu.cn  College of Chemistry and Life Science, Zhejiang Normal University, Jinhua, Zhejiang Province, China

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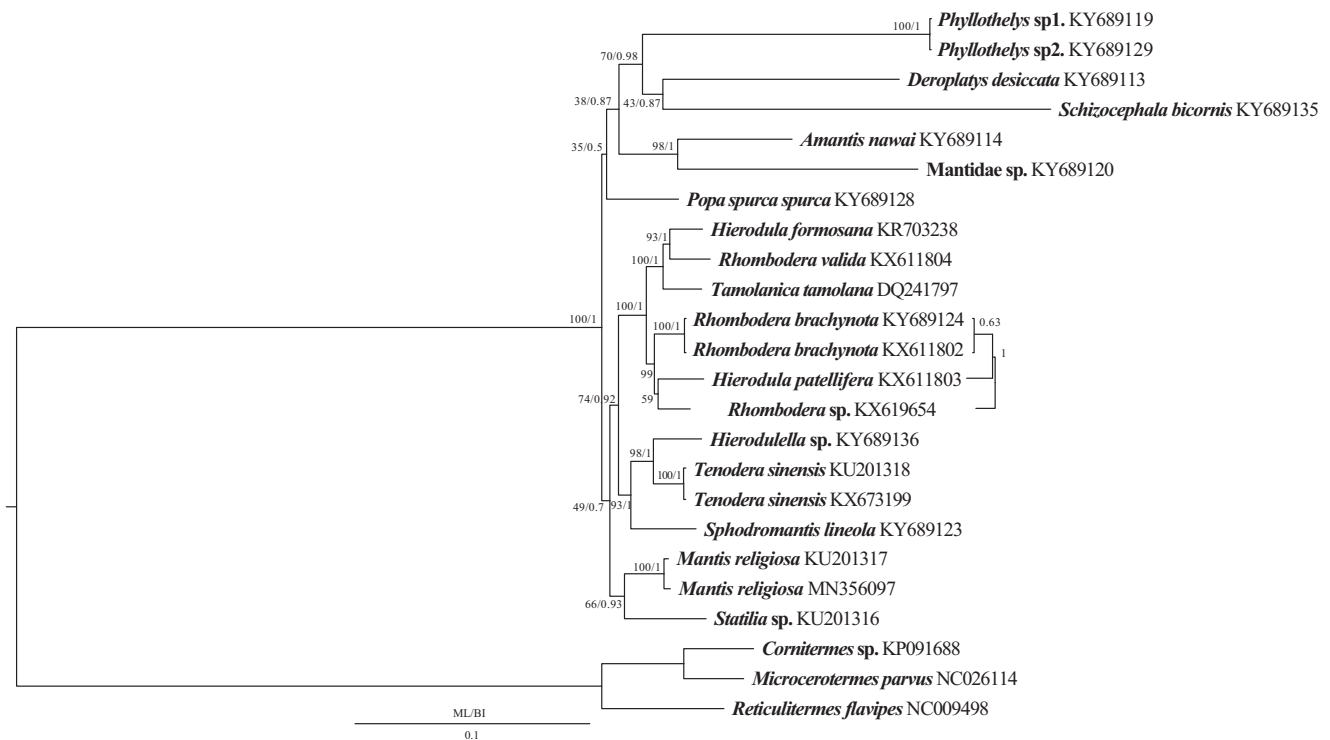


Figure 1. Phylogenetic tree of the relationships among 18 species of Mantodea based on the first and the second codon positions of the 13 mitochondrial protein-coding genes of 7338 nucleotides. Three termite species were included as the outgroups (*Cornitermes* sp., *M. parvus*, *R. flavipes*). Numbers around the nodes are the bootstrap values of ML on top and the posterior probabilities of BI on the bottom. The GenBank numbers of all species are shown in the figure.

very similar to *M. religiosa* from China and their genetic distance was 0.017. The phylogenetic relationships inferred from the BI and ML analyses shared almost similar topologies (Figure 1). *Mantis religiosa* was a sister clade to *Statilia* sp. and the monophyly of the genera *Hierodula* and *Rhombodera* were not supported, which agrees with the previous results of Zhang and Ye (2017) (Figure 1).

Disclosure statement

No potential conflict of interest was reported by the authors.

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ORCID

Dan-Na Yu  <http://orcid.org/0000-0002-9870-1926>
 Kenneth B. Storey  <http://orcid.org/0000-0002-7363-1853>
 Jia-Yong Zhang  <http://orcid.org/0000-0002-7679-2548>

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