The complete mitochondrial genome of Psychomantis borneensis (Mantodea: Hymenopodidae)

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Psomantis borneensis is currently assigned to the Acromantinae subfamily of Hymenopodidae. The phylogenetic relationships and classifications of Hymenopodidae species have not been studied extensively and up to date, only two Hymenopodidae species mitogenomes are published (Ye et al. 2016). Without extensive taxonomic sampling of DNA sequences, understanding the phylogenetic relationship between these species becomes virtually impossible (Svenson et al. 2015). In this study, we sequenced the complete mitochondrial genome of Psychomantis borneensis (MG520077) to provide more molecular data that enables researchers to discuss the phylogenetic relationships of Hymenopodidae.

The sample of P. borneensis was collected from Borneo island, Indonesia in 2016, identified and stored at −40°C in Zhang’s laboratory, College of Life Sciences and Chemistry, Zhejiang Normal University, China. Total DNA was extracted from leg muscle using DNeasy Blood and Tissue Kit (Qiagen, Germany). The universal primers used were the same as that used in the study by Simon et al. (2006) and Wang et al. (2016) with modifications. PCR products were sequenced in both directions by the primer-walking method by the Sangon Biotech Company (Shanghai, China).

The mitogenome of P. borneensis was found to be a circular 15,493 bp long molecule containing 37 genes (13 protein-coding genes, 22 tRNAs, and 2 rRNAs) and an A+T-rich region typically found in other mantis mitochondrial genomes. The AT content of the whole genome was 72.4% and the length of the control region was 697 bp with 79.9% AT content. The phylogenetic tree was constructed based on the BI and ML analysis of 16 species of Mantodea. The results showed that P. borneensis was a sister clade to (Anaxarcha zhengi + Creobroter gemmata) (Hymenopodidae). The monophyly of the family Mantidae and the genus Theopompa, Hierodula, and Rhombodera were not supported. The outcome of this study will provide a useful data for population genetics studies as well as serve as a tool for better characterizing phylogenetic analysis of Mantodea.

The phylogenetic relationships inferred from the BI and ML analyses shared the similar topologies (Figure 1). P. borneensis was a sister clade to (Anaxarcha zhengi + Creobroter gemmata) (Hymenopodidae), hence, the monophyly of the family Hymenopodidae was supported in this study. Three Liturgusidae species clustered together and were sister to the remaining mantises while the topology ((Humertiella nana + Theopompa sp.-YN) + Theopompa sp.-HN) indicated that Theopompa was a paraphyletic group. Mantidae was a polyphyletic assemblage which split into three clades. Tenodera sinensis (Mantidae) was a sister clade to the remaining Mantidae and Hymenopodidae species. Statilia sp. was a
sister clade to *Mantis religiosa* and a total of six Paramantini species formed a clade. The monophyly of the genus *Hierodula* and *Rhombobera* were not supported.

**Nucleotide sequence accession number**

The complete mitochondrial genome of *P. borneensis* has been assigned and deposited to GenBank with the following accession number MG520077.

**Disclosure statement**

The authors declare that the research was conducted in the absence of any commercial or financial relationships that could be construed as a potential conflict of interest.

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