The complete mitochondrial genome of *Leptomantella tonkinae* (Hebard, 1920) (Mantodea: Leptomantellidae) and its phylogeny

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**ABSTRACT**

The complete mitochondrial (mt) genome of *Leptomantella tonkinae* (Hebard, 1920) was 15,527 bp in length and contained 13 protein-coding genes, 22 transfer RNAs, two ribosomal RNAs, and one control region. The gene arrangement of mt genome of *L. tonkinae* was identical to the primitive mantis. The overall AT content of the mt genome was 74%. In ML and BI phylogenetic analyses, the monophyly of Leptomantellidae was robustly supported and the clade of Leptomantellidae is a sister clade to the group of (Gonypterae+(Leptomantellidae+(Amoroscelidae+Nanomantidae))).
To discuss the phylogenetic position of *L. tonkinae*, one newly sequenced mantis mt genome as well as 68 previously sequenced mantis mt genomes were used in phylogenetic analyses (Cameron et al. 2006; Song et al. 2016; Wang, Yu, et al. 2016a; Wang, Hou, et al. 2016b; Ye et al. 2016; Tian et al. 2017; Zhang and Ye 2017; Zhang et al. 2018a, 2018b, 2018c, 2018d, 2019; Jia et al. 2019; Shi et al. 2019; Yan and Lin 2019; Zhang et al. 2019; Guan et al. 2020; Wang et al. 2020; Xu et al. 2021). In addition, two cockroach species (*Eupolyphaga sinensis, Cryptocercus kyebangensis*), and two termite (*Termes hospes, Macrotermes barneyi*) species chosen as outgroups. The GenBank accession numbers of all species are shown in the figure.

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explore these discrepancies, more mt genomes should be sequenced in the future.

**Author contributions**

All authors were involved in the conception and design, or analysis and interpretation of the data; Lin YJ, Zhao YY, Yang YM, Jin WT, and Cai LN were involved in the drafting of the paper; Storey KB, Zhang JY, and Yu DN were involved in revising it critically for intellectual content; and all authors were involved in the final approval of the version to be published; and that all authors agree to be accountable for all aspects of the work.

**Disclosure statement**

The authors report no conflict of interest. The authors alone are responsible for the content and writing of the article.

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**Data availability statement**

The mitochondrial genome data that support the findings of this study are openly available in GenBank of NCBI at [https://www.ncbi.nlm.nih.gov/nuccore/OK480879 under the accession no. OK480879. The mt genome was obtained by the Sanger method, so no associated Bio-Sample numbers should be shown.

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