The complete mitochondrial genome of *Tropidothorax sinensis* (Reuter, 1888) (Hemiptera: Lygaeidae)

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**ABSTRACT**

The complete mitochondrial genome (mitogenome) of *Tropidothorax sinensis* (Reuter, 1888) was determined in the present study by using high-throughput sequencing. This mitogenome is 15,422 bp in size and comprises 37 typical coding genes and a control region. All protein-coding genes are initiated with ATN, except for COX1 and ND4L use TTG as the start codon, and terminate with TAA or TAG with the exception of COX2, COX3 and ND1 which use a single T residue as the stop codon. Twenty-one of the 22 transfer RNA genes have the typical clover-leaf structure except for tRNA^Sm^ and tRNA^Gln^*. The monophyly of the family Lygaeidae and the sister relationship between *T. sinensis* and *T. cruciger* is supported by maximum likelihood analysis based on the protein-coding and ribosomal RNA gene sequences.

Lygaeoidea is the second largest superfamily in the Pentatomomorpha, which includes more than 4,290 described species classified into seventeen families (Henry 2017). Most Lygaeoidea species are phytophagous, whereas a few species are predators. *Tropidothorax sinensis* (Reuter, 1888) is an important agricultural and forest pest, mainly distributed in China mainland and Japan. In the present study, we describe the complete mitogenome of *T. sinensis*, which will be useful for the molecular identification of this important pest and phylogenetic study of the family Lygaeidae.

The sample was collected from Zunyi, Guizhou, China (28°23′27″N, 107°36′65″E). Voucher specimen is stored at the Entomological Museum of China Agricultural University (No. HEM-098, Weidong Huang, wdh6434@163.com). Genomic DNA extraction was performed using the DNeasy Blood and tissue kit (Qiagen, Germany) following the manufacturer’s protocol. An Illumina TruSeq library was prepared with an average insert size of 350 bp and sequenced using the Illumina Hiseq 2500 platform with 150 bp paired-end reads. Raw reads were trimmed of adapters using Trimmomatic (Bolger et al. 2014) and low quality and short reads were removed using Prinseq (Schmieder and Edwards 2011). High quality reads were then used to produce a *de novo* assembly using IDBA-UD (Peng et al. 2012) with minimum and maximum k values of 41 and 141 bp, respectively. The mitogenome sequence of *T. sinensis* was identified by Geneious 10.1.3 (http://www.geneious.com). Genomic annotations were performed using MITOS2 (Bernt et al. 2013) and tRNAscan-SE 2.0 (Lowe and Chan 2016), and the result was further confirmed using NCBI-BLAST (http://blast.ncbi.nlm.nih.gov).

The complete mitogenome of *T. sinensis* is 15,422 bp in size, including 13 protein-coding genes (PCGs), 22 transfer RNA genes (tRNAs), two ribosomal RNA genes (rRNAs) and a control region. The gene order and orientation is identical to the putative ancestral arrangement of insects (Cameron 2014). The A + T content of the mitogenome is 75.8% (A = 41.7%, T = 33.3%, C = 14.5%, G = 10.5%) which is significantly biased toward AT. Eleven PCGs initiate with ATN codons (2 with ATA, 5 with ATG, and 4 with ATT), whereas two genes, namely COX1 and ND4L, start with TTG. The stop codon TAA or TAG was assigned to 10 PCGs (2 with TAG, 8 with TAA). The remaining three PCGs (COX2, COX3 and ND1) use a single T residue as an incomplete stop codon, a phenomenon commonly observed in true bugs (Zhang et al. 2019). There are 22 tRNA genes, ranging from 60 to 75 bp in length. The secondary structure of 21 tRNAs were typical clover-leaf structure except for the tRNA^Sm^ and tRNA^Gln^*. The monophyly of the family Lygaeidae and the sister relationship between *T. sinensis* and *T. cruciger* is supported by maximum likelihood analysis based on the protein-coding and ribosomal RNA gene sequences.

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the sister relationship between *T. sinensis* and *T. cruciger* with high bootstrap value (100).

**Disclosure statement**

No potential conflict of interest was reported by the author(s).

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**Data availability statement**

The data that support the findings of this study will be available in GenBank at [https://www.ncbi.nlm.nih.gov/](https://www.ncbi.nlm.nih.gov/), accession number MW547017, SRR13712603.

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