The complete mitochondrial genome of the jewel beetle, *Anthaxia chinensis* (Coleoptera: Buprestidae)

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**ABSTRACT**

The mitogenome of *Anthaxia chinensis* is a typical circular DNA molecule of 15,881 bp. All protein-coding genes use ATN codons as the start codon except for ATP8 and COI. The stop codon TAA and TAG are assigned to all protein-coding genes. Most of tRNAs have the typical secondary clover-leaf structure except for tRNA-Ala, tRNA-Phe, tRNA-His, and tRNA-Ser ( AGN). The length of tRNAs ranged from 63 bp to 70 bp. Genome organization and nucleotide composition of the mitogenome were also noted.

The genus *Anthaxia* Eschscholtz, 1829 (Coleoptera: Buprestidae) is a diversified population with wide distribution. Six hundred and ninety-seven species of this genus have been recorded around the world and 63 species recorded in China (Bellamy 2008; Kubán 2016). *Anthaxia chinensis* Kerremans, 1898 is a medium sized beetle in this genus and widespread in most of the areas of the South China (Bellamy 2008; Kubán 2016) with adults feeding on flowers of various trees (Uitsiann and Takaharu 2019). Some specimens of *A. chinensis* was collected from Sannng City, Fujian Province, China (26°15′54.1″N, 117°38′6.036″E). One specimen was sequenced by next-generation sequencing on Illumina on NovaSeq 6000 platform (Illumina, Nanjing, China). The voucher specimen and isolated DNA were deposited at the College of Life Science, China West Normal University (https://life.cwnu.edu.cn, Aimin Shi and aiminshi2003@126.com) under the voucher number CWNU2021003. The complete mitogenome was annotated using the MITOS web server (Bernt et al. 2013).

The mitogenome extraction of *A. chinensis* was constructed into a circular DNA molecule with 15,881 bp, including 37 genes (13 CDSs, 22 tRNA genes, and two rRNA genes) and a long non-coding region called control region. Twenty-three genes (nine CDSs and 14 tRNAs) are located on the major strand (N-strand) and 14 genes (four CDSs, eight tRNAs, and two rRNAs) on the minor strand (J-strand).

The nucleotide composition of the whole mitogenome is significantly biased toward to A and T. The A + T content is 73.61% with positive A-T skew (0.09) and negative G-C skew (−0.29). All protein-coding genes use ATN codons as the start codon except for ATP8 and COI. ATP8 initiates with TTG and start codon of COI is quite unusual that they could not be determined (Sheffield et al. 2008). The stop codon TAA and TAG are assigned to all protein-coding genes.

This mitogenome contains all sets of typical 22 tRNA genes and the length ranges from 63 bp to 70 bp. Among them, only four tRNA (tRNA-Ala, tRNA-Phe, tRNA-His, and tRNA-Ser(AGN)) have a typical structure with reduced T- or D-arms and others can be folded into the typical clover-leaf secondary structure. The tRNA with reduced T- or D-arms is also founded in other insect (Li et al. 2012; Song et al. 2016). The 16S rRNA is 1303 bp long with a high A + T content (79.13%), and the 12S rRNA is 748 bp long with an A + T content of 76.07%. The control region is located between 12S rRNA and tRNA-Ile with 1227 bp in length.

Complete mitogenome of 22 Coleoptera species was downloaded from GenBank in order to ensure the phylogenetic position of *A. chinensis*. The phylogenetic tree (Figure 1) shows that *A. chinensis* and *Melanophila acuminata* were closely related. In the meantime, the result indicates that Buprestoidea is tend to place at the basal position of the tree and is sister group to (Caraboidea + Scirtoidea + Elateroidea + Scarabaeoidea). The present study will provide valuable information for understanding the complete mitochondrial genome of jewel beetle and for further phylogenetic analyses of Polyphaga.

**Disclosure statement**

No potential conflict of interest was reported by all the authors.

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Data availability statement

The genome sequence data that support the findings of this study are openly available in GenBank of NCBI at https://www.ncbi.nlm.nih.gov, reference number MW929326. The associated BioProject, SRA, and Bio-Sample numbers are PRJNA745331, SRX11427895, and SAMN20163532, respectively.

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