

## 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.

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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; Kubáň 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; Kubáň 2016) with adults feeding on flowers of various trees (Utsiann and Takaharu 2019). Some specimens of *A. chinensis* was collected from Sanming 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](mailto: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.

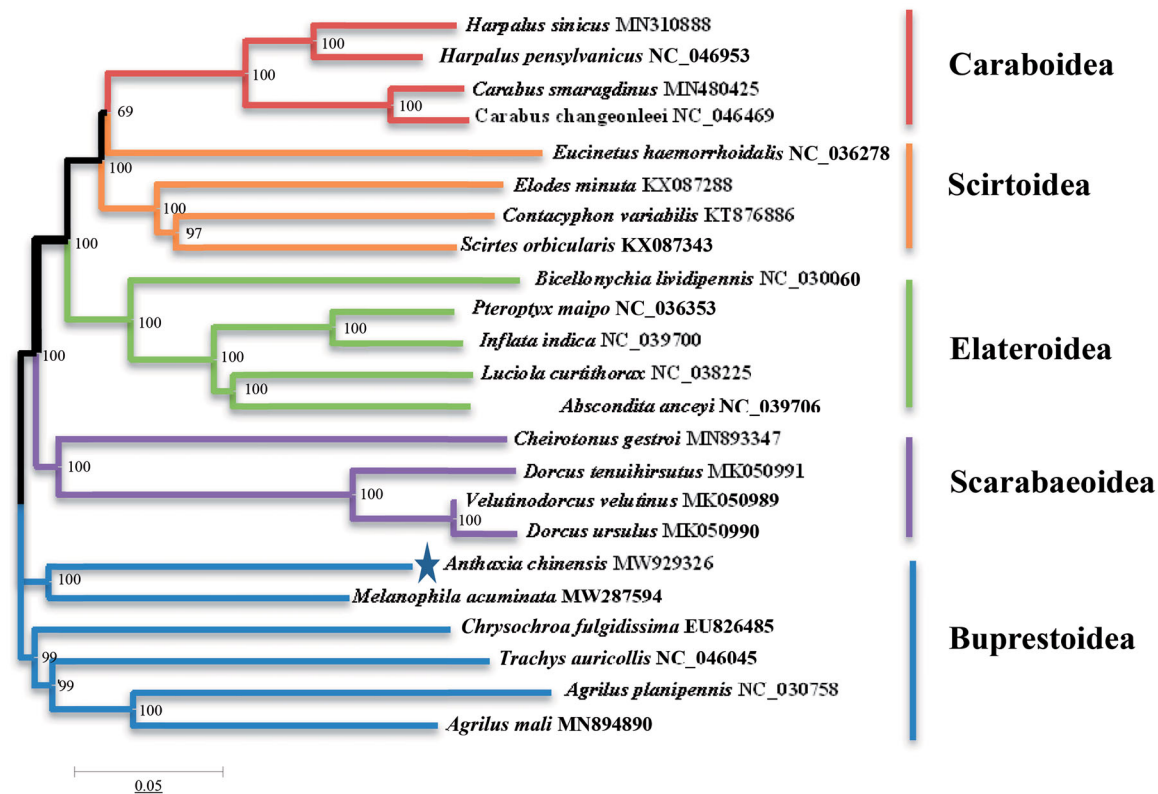
Complete mitogenome of 22 Coleoptera species was downloaded from GenBank in order to ensure the phylogenetic position of *A. chinensis*. The phylogenetic tree (Figure 1) shows that *A. chinensis* and *Melanophila acuminata* were closely related. In the meantime, the result indicates that Buprestoidea 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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**Figure 1.** Phylogenetic relationship of the *Anthaxia chinensis* and 22 Polyphaga species. Neighbor-joining phylogeny tree by MEGA version 7.0.14.

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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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