The complete mitochondrial genome of *Tenomerga trabecula* (Coleoptera: Archostemata: Cupedidae) and phylogenetic analysis among Coleoptera

Lijie Jin, Yujie Li, and Ming Bai

*Key Laboratory of Zoological Systematics and Evolution, Institute of Zoology, Chinese Academy of Sciences, Beijing, China; Jiangsu Key Laboratory for Biodiversity and Biotechnology, College of Life Sciences, Nanjing Normal University, Nanjing, China*

**ABSTRACT**

*Tenomerga trabecula* belongs to the Cupedidae family of Coleoptera. The first complete mitogenome of Cupedidae is reported in this paper. The genome is 16,741 bp in length and contains the typical 37 genes with 22 transfer RNA genes, 13 protein-coding genes, and 2 ribosomal RNA genes, which are arranged in the same order as the putative ancestor of beetles. The average base composition of the mitogenome is 42.9% for A, 14.5% for C, 8.7% for G, and 33.9% for T. The percentage of A + T is 76.8%. The genome organization, nucleotide composition, and codon usage are similar to other beetles. Phylogenetic analysis shows that Archostemata is monophyletic. Myxophaga, Adephaga, and Polyphaga are also monophyletic.
Acknowledgments

The authors thank Kinfung Chan, Yin Yip, Kahong Cheung, Yingming Lee, Manhin Leung, and the fellows of the Beetle Working Group of AFCD for the field work in Hong Kong; Yandong Chen and Xu He from Institute of Zoology, Chinese Academy of Sciences, for specimens sorting and identification; and ReiÈŒ Nie from Institute of Zoology, Chinese Academy of Sciences, for data analysis.

Disclosure statement

No potential conflict of interest was reported by the authors.

Funding

This work was supported by the National Science & Technology Fundamental Resources Investigation Program of China (Grant Nos. 2019FY100400, 2019FY101800), the National Natural Science Foundation of China (No. 31961143002), the Bureau of International Cooperation, Chinese Academy of Sciences, GDAS Special Project of Science and Technology Development (Nos. 2020GDASYL-20200102021, 2020GDASYL-20200301003), the Second Tibetan Plateau Scientific Expedition and Research Program (STEP), Grant No. 2019QZKK05010101.

Data availability statement

The genome sequence data supporting the findings of this study are openly available in the NCBI GenBank at https://www.ncbi.nlm.nih.gov/ under accession number MW820160. The associated BioProject, SRA, and Bio-Sample numbers are PRJNA750629, SRR15293804, and SAMN20448115, respectively.

References

Bernt M, Donath A, Juhlving F, Externbrink F, Florentz C, Fritzsch G, Pütz J, Middendorf M, Stadler PF. 2013. MITOS: improved de novo metazoan mitochondrial genome annotation. Mol Phylogenet Evol. 69(2): 313–319.

Bolger AM, Lohse M, Usadel B. 2014. Trimmomatic: a flexible trimmer for Illumina sequence data. Bioinformatics. 30(15):2114–2120.

Dierckxsens N, Mardulyn P, Smits G. 2017. NOVOPlasty: de novo assembly of organelle genomes from whole genome data. Nucleic Acids Res. 45(4):e18.

Kearse M, Moir R, Wilson A, Stones-Havas S, Cheung M, Sturrock S, Buxton S, Cooper A, Markowitz S, Duran C, et al. 2012. Geneious Basic: an integrated and extendable desktop software platform for the organization and analysis of sequence data. Bioinformatics. 28(12): 1647–1649. doi:10.1093/bioinformatics/bts199. 22543367

Meng G, Li Y, Yang C, Liu S. 2019. MitoZ: a toolkit for animal mitochondrial genome assembly, annotation and visualization. Nucleic Acids Res. 47(11):e63.

Neboiss A. 1984. Reclassification of Cuper Fabricius (S Lat), with descriptions of new genera and species (Cupedidae, Coleoptera). System Entomol. 9(4):443–477.

Nguyen LT, Schmidt HA, von Haeseler A, Minh BQ. 2015. IQ-TREE: a fast and effective stochastic algorithm for estimating maximum-likelihood phylogenies. Mol Biol Evol. 32(1):268–274.

Rodriguez-Miron GM, Lopez-Perez S. 2019. A new reticulated beetle (Coleoptera: Cupedidae) from Mexico with a catalogue of Cupedidae species of the world. Zootaxa. 1:4567.
Sheffield NC, Song H, Cameron SL, Whiting MF. 2008. A comparative analysis of mitochondrial genomes in Coleoptera (Arthropoda: Insecta) and genome descriptions of six new beetles. Mol Biol Evol. 25(11): 2499–2509.

Zhang D, Gao F, Jakovlic I, Zou H, Zhang J, Li WX, Wang GT. 2020. PhyloSuite: An integrated and scalable desktop platform for streamlined molecular sequence data management and evolutionary phylogenetics studies. Mol Ecol Resour. 20(1): 348–355.

Zhang H, Liu N, Han Z, Liu J. 2016. Phylogenetic analyses and evolutionary timescale of Coleoptera based on mitochondrial sequence. Biochem Syst Ecol. 66:229–238.