Complete mitochondrial genome of *Cylindromyia* (Calocyptera) intermedia from Guiyang, China, and phylogeny of Phasiinae (Diptera: Tachinidae)

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**ABSTRACT**

The mitochondrial genome of *Cylindromyia* (Calocyptera) intermedia (Meigen, 1824) was sequenced and assembled through high-throughput sequencing techniques and reference-based assembly methods. The mitochondrial genome is 15,114 bp in total, consisting of 13 protein-coding genes, 22 transfer RNA genes, 2 ribosomal RNA genes, and 1 noncoding control region. The nucleotide composition biases toward A and T; the overall A + T content are up to 76.9% of the entire mitogenome. The result of phylogenetic analysis suggested a close relationship between *C. intermedia* and subfamily Dexiniae.

**Keywords**

*Complete mitochondrial genome; phylogenetic analysis; Tachinidae; Phasiinae*
Macquart, 1839 from Sarcophagidae were set as outgroups. The subfamily Phasiinae received a molecular phylogenetic treatment by Stireman et al. (2019, Fig. 4), the clade tribe Cylindromyiini of Phasiinae sometimes joins the subfamily Dexiinae in individual gene-trees. Our phylogenetic analysis showed a close relationship between *C. intermedia* of Phasiinae and *Rutilia goerlingiana* of Dexiinae (Figure 1), which was partially consistent with the previous work of Stireman et al. (2019). The complete mitogenome of *C. intermedia* will contribute to the further studies on molecular bases for the classification and phylogeny of between Phasiinae and other three subfamilies within Tachinidae.

**Ethical approval statement**

The ethical approval (No. 1900074) was granted by the Animal Care Welfare Committee of Guizhou Medical University for the study.

**Author contributions**

Ming Yang and Jiayu Liu were involved in the conception and design; Rong Wang and Jiayu Liu analyzed and interpreted the data; Rong Wang drafted the article; Yan Zhi and Chuntian Zhang revised it critically for intellectual content. All authors approved the final version to be published and agreed to be accountable for all aspects of the work.

**Disclosure statement**

The authors report in this article without any conflict of interest. All authors agree to be accountable for all aspects of the work.

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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 under the accession no. OLS39555. The associated BioProject, SRA, and Bio-Sample numbers are PRJNA781126, SRR16980901, and SAMN23239677, respectively.

**References**

Bernt M, Donath A, Jühling 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): 1008–319.
Kearse M, Moir R, Wilson A, Stones-Havas S, Cheung M, Sturrock S, Buxton S, Cooper A, Markowitz S, Duran C, Thierer T, Ashton B, Meintjes P, Drummond A. 2012. Geneious Basic: an integrated and extendable desktop software platform for the organization and analysis of sequence data. Bioinformatics. 28(12):1647–1649.

Kumar S, Stecher G, Li M, Knyaz C, Tamura K. 2018. MEGA X: molecular evolutionary genetics analysis across computing platforms. Mol Biol Evol. 35(6):1547–1549.

Li X, Ding SM, Hou P, Liu XY, Zhang CT, Yang D. 2017. Mitochondrial genome analysis of Ectophasia roundiventris (Diptera, Tachinidae). Mitochondrial DNA B Resour. 2(2):457–458.

O’Hara JE, Henderson SJ, Wood DM. 2020. Preliminary checklist of the Tachinidae (Diptera) of the world. Version 2.1. PDF document, 1039 pp.; [accessed 14 March 2022]. http://www.nadsdiptera.org/Tach/WorldTachs/Checklist/Tachchlist_ver2.1.pdf.

Pei WY, Yan LP, Yang N, Zhang CT, Zheng CY, Yang J, Zhang D. 2019. First report of mitogenome of Subclytia rotundiventris (Diptera, Tachinidae) yielded by next-generation sequencing. Mitochondrial DNA B Resour. 4(2):2910–2911.

Stireman JO, Cerretti P, O’Hara JE, Blaschke JD, Moulton JK. 2019. Molecular phylogeny and evolution of world Tachinidae (Diptera). Mol Phylogenet Evol. 139:106358.