

Complete mitochondrial genome of *Compsilura concinnata* (Meigen) (Diptera, Tachinidae)

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ABSTRACT

The complete mitochondrial genome of *Compsilura concinnata* (Meigen), was analyzed by next-generation sequencing approach. Its mitogenome is 15,841 bp totally, which consists of 13 protein-coding genes, 22 transfer RNA genes, two ribosomal RNA genes, and one non-coding control region. The nucleotide composition biases toward A and T, the overall A + T% was up to 80.9% of the entire mitogenome. Phylogenetic analysis supported the sister relationship between Goniini and Blondeliini. The result also suggested that the monophyly of the Exoristinae.

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Compsilura concinnata (Meigen), belongs to the tribe Blondeliini of subfamily Exoristinae in Tachinidae where there are more than 1520 valid genera and 8500 described species around the world (O'Hara and Henderson 2020). The host range of *C. concinnata* is wide, mainly parasitizes on agricultural and forestry pests such as Phoeniidae, Danaidae, Geometridae, Hesperidae, Lasiocampidae, Libytheidae, Lymantriidae, Noctuidae, Notodontidae, Nymphalidae, and Pyralidae (Chao et al. 2001; Shima 2006; Stireman et al. 2006).

Since the complete mitochondrial genome of *Exorista sorbillans* was reported in 2012, there are currently only seven complete mitochondrial genomes of Tachinidae have been published (Shao et al. 2012; Zhao et al. 2013; Li et al. 2017; Hou et al. 2018; Hou et al. 2019; Pei et al. 2019; Seo et al. 2019). Herein, we sequenced mitochondrial genome of *C. concinnata*, which provided sufficient molecular theoretical basis for further analysis of phylogenetic and evolutionary relationship of Tachinidae.

We describe the complete mitochondrial genome of *C. concinnata* collected from Leigong Mountain, Leishan County, Guizhou Province, China (26°46'24"N, 108°21'29"E, 2080 m) on 11 August 2020. The specimens were obtained by net catching and stored at the Key Laboratory of Medical Insects of Guizhou Medical University (accession number: CC200811). Total DNA was extracted from muscle tissues of the thorax using Rapid Animal Genomic DNA Isolation Kit (Sangon Biotech Co., Ltd., Shanghai, China). The genomic library is established and then used Illumina HiSeq PE150 platform for whole genome next-generation sequencing. The initial

annotation of the mitogenome, including gene prediction and non-coding RNA, were conducted using MITOS Web Server (<http://mitos2.bioinf.uni-leipzig.de/index.py>) (Bernt et al. 2013; Cameron 2014). Geneious Prime 2020.2.2 was used to compare the homologous gene annotations of other insects and then submitted to NCBI (Kearse et al. 2012).

The complete mitogenome of *C. concinnata* (GenBank accession number: MW136259) 15,841 bp with double circular strands, which contains 13 protein-coding genes (PCGs), two rRNA genes, 22 tRNA genes, and one non-coding region. Four PCGs, two rRNA genes, and eight tRNA genes are distributed in the light strand among the 38 sequence elements, while others are distributed in the heavy strand. The distribution order of all elements is no different from subfamily Exoristinae in the sequence.

The 13 PCGs accounted for 70.4% of the complete mitogenome of *C. concinnata* (11,152 bp). PCGs utilize a variety of start codons including the standard ATN, except for the non-standard TCG (*COI*). The most frequent start codon was ATG, which was covered six PCGs (*COII*, *ATP6*, *COIII*, *ND4*, *ND4L*, *CYTB*). The complete standard TAA stop codon covered 12 genes except *COII* (T) and *ND1* (TAG).

With the mitogenomic of *C. concinnata*, a phylogenetic tree was reconstructed by the maximum-likelihood method using MEGA7 with bootstrap set to 1000 (Kumar et al. 2016), the topology is shown in Figure 1. Tribe Blondeliini is sister to Goniini. High bootstrap support values of the phylogenetic tree support the monophyly of subfamily Exoristinae.

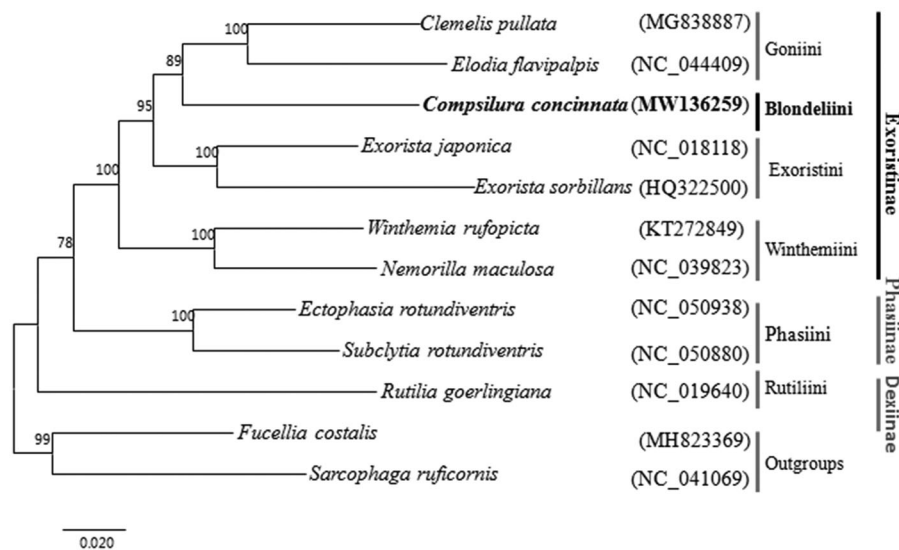


Figure 1. The maximum-likelihood tree was constructed based on the 13 PCGs sequence in the mitochondrial genome sequence.

Disclosure statement

The authors report in this article without any conflict of interest.

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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/> under the accession no. MW136259. The associated BioProject, SRA, and Bio-Sample numbers are PRJNA693049, SRR13480461, and SAMN17376814, respectively.

References

- Bernt M, Donath A, Jühling F, Externbrink F, Florentz C, Fritzsche G, Pütz J, Middendorf M, Stadler PF. 2013. MITOS: improved de novo metazoan mitochondrial genome annotation. *Mol Phylogenet Evol.* 69(2): 313–319.
- Cameron SL. 2014. How to sequence and annotate insect mitochondrial genomes for systematic and comparative genomics research. *Syst Entomol.* 39(3):400–411.
- Chao CM, Liang Ey, Shi YS, Zhou SX. 2001. *Fauna sinica. Insecta. Vol. 23. Diptera. Tachinidae (1).* Beijing: Science Press; p. 296.
- Hou P, Ding SM, Li X, Yang D, Zhang CT, Wang Q. 2018. The mitochondrial genome of *Drino* sp. (Diptera, Tachinidae). *Mitochondrial DNA B Resour.* 3(2):886–887.
- Hou P, Gao S, Li X, Yang D, Zhang CT. 2019. The mitochondrial genome of *Janthicuomyia* sp. (Diptera, Tachinidae). *Mitochondrial DNA Part B.* 4(1):1601–1602.
- 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.
- Kumar S, Stecher G, Tamura K. 2016. MEGA7: molecular evolutionary genetics analysis version 7.0 for bigger datasets. *Mol Biol Evol.* 33(7): 1870–1874.
- Li X, Ding SM, Hou P, Liu XY, Zhang CT, Yang D. 2017. Mitochondrial genome analysis of *Ectophasia rotundiventris* (Diptera, Tachinidae). *Mitochondrial DNA B.* 22:457–458.
- O'Hara JE, Henderson SJ. 2020. World genera of the Tachinidae (Diptera) and their regional occurrence. Version 11.0. PDF document, 90 pp. Available from: http://www.nadsdiptera.org/Tach/WorldTachs/Genera/Gentach_ver11.pdf ([accessed 2020 Dec 27]).
- 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 Part B.* 4(2):2910–2911.
- Seo BY, Cho J, Lee GS, Park J, Park J. 2019. The complete mitochondrial genome of *Exorista japonica* (Townsend, 1909) (Diptera: Tachinidae). *Mitochondrial DNA Part B.* 4(2):2244–2245.
- Shao YJ, Hu XQ, Peng GD, Wang RX, Gao RN, Lin C, Shen WD, Li R, Li B. 2012. Structure and evolution of the mitochondrial genome of *Exorista sorbillans*: the Tachinidae (Diptera: Calyptratae) perspective. *Mol Biol Rep.* 39(12):11023–11030.
- Shima H. 2006. A host-parasite catalog of Tachinidae (Diptera) of Japan. *Makunagi Acta Dipterol Suppl.* 2:171.
- Stireman JO, O'Hara JE, Wood DM. 2006. Tachinidae: evolution, behavior, and ecology. *Annu Rev Entomol.* 51:525–555.
- Zhao Z, Su TJ, Chesters D, Wang SD, Ho SYW, Zhu CD, Chen XL, Zhang CT. 2013. The mitochondrial genome of *Elodia flavipalpis* Aldrich (Diptera: Tachinidae) and the evolutionary timescale of Tachinid flies. *PLOS One.* 8(4):e61814.