The complete mitochondrial genome of *Eriocampa ovata* Linné, 1760 (Hymenoptera: Tenthredinidae) and phylogenetic analysis

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**ABSTRACT**

*Eriocampa* Hartig, 1837 is a small Holarctic genus of Tenthredinidae and its systematic position has never been fully assessed. The complete mitochondrial genome of *Eriocampa ovata* Linné, 1760 was described. The circular genome is 16,293 bp in length with an A+T content of 80.6%. It contains 37 genes and a 1254 bp control region with a 405 bp repetitive sequence. All the 13 protein-coding genes initiate with a typical ATN. The CR - trnI (+) - trnQ (-) - trnM(+) cluster rearranges to trnQ (-) - trnM (+) - CR -trnI(+). Phylogenetic analysis demonstrates that *E. ovata* and *Conaspidia wangi* Wei, 2015 are closely related within the subfamily of Tenthredinidae.

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*Eriocampa* Hartig, 1837 is a small Holarctic genus of Tenthredinidae and mainly occurs in eastern Asia. Its systematic position has never been fully assessed. Ashmead (1898) placed *Eriocampa* into the subfamily Selandriinae of his Selandriidae and thought *Eriocampa* is close to *Calirhoa* Costa, and the genus now is a member of Heterarthrini (Abe and Smith 1991; Taeger et al. 2010) or Blennocampinae (Benson 1952) of Tenthredinidae, or Caliroinae of Heterarthridae (Wei and Nie, 1998), etc. Rohwer (1911) erected Eriocampini for the genus only under Allantinae of Tenthredinidae. Ross (1937) placed *Eriocampa* with *Pseudosiobla* and Dimorphopteryx together into Eriocampini of Allantinae within the family Tenthredinidae, but he stated that the three genera were grouped together chiefly on the rugose mesopleurae, but they differ radically from each other in mandibular, antennal structure, and genitalia. Benson (1952) thought that Eriocampini included only *Eriocampa* and placed the tribe into its complicated Blennocampinae, which also includes Athaliini, Allantini, Empriini, Fenusini, and Blennocampini. Takeuchi (1952) placed *Eriocampa* with *Eriocampopsis* into Eriocampini under the subfamily Allantinae, which includes Athaliini, Belesini, Empriini, and Allantini; besides Eriocampini. Zombori (1981) placed *Eriocampa* into Eriocampini under a heterogenous subfamily Sellandriinae, which includes 13 tribes, such as Aneugeminini, Athaliini, Empriini, Heptamelinini, Heterarthrini, Hoplocampini, etc. Abe and Smith (1991) and Taeger et al. (2010) placed *Eriocampa* into Allantinae without tribal arrangement. Wei and Nie (1998) grouped *Eriocampa* with *Pseudosiobla*, *Eriocampopsis*, *Dimorphopteryx*, and *Armitarsus* into Eriocampini and placed the tribe into Tenthredininae.

Comparing the above systems concerning *Eriocampa*, most of them regarded *Eriocampa* to be a member of Eriocampini and thought that it was close to Allantinae or even placing the genus directly into Allantinae, except for Wei and Nie (1998) thought that *Eriocampa* was not close to Allantinae but a member of Tenthredininae. In this study, we sequenced the mitochondrial genome of *Eriocampa ovata* Linné, 1760 to determine the phylogenetic position of *Eriocampa*.

Specimens of *E. ovata* were collected from Villa Luganese (46.061 N, 9.025 E), Switzerland. Samples were identified by Wei Meicai (weimc@126.com) at the Asia Sawfly Museum, Nanchang (ASMN), where a voucher specimen (CSCS-Hym-MC0143) is kept. Genomic DNA was extracted from a female and sequenced using Illumina Hiseq 4000 platform by following the standard protocols. A total of 12.92 Gb raw data was yielded and used for subsequent genome assembly by MitoZ (Meng et al., 2019) and Geneious Prime 2019.2.1 (http://www.geneious.com). Genome annotation referred to the results produced by MITOS (Bernt et al. 2013), in which the starting and ending of PCGs were determined according to the results of comparative genomics. Each PCG was aligned individually with the MAFFT algorithm in the TranslatorX server (Abascal et al. 2010). The maximum likelihood method was constructed by IQTREE (Nguyen et al. 2015) with the GTR + CAT model and Bayesian inference conducted by PhyloBayes MPI on XSEDE (Lartillot et al. 2009) was used for 13 PCGs and nine unsaturated PCGs, respectively. The sequence yield by MitoZ was 12,065 bp long. We thoroughly checked the obtained whole sequence by assembling...
using *Dimorphopteryx* sp. (new species, unpublished) as reference sequences (mean coverage was 18,525). The 1254-length control region (CR) was identified by extending both ends of the above sequence. The circular genome is 16,293 bp long and the overall A+T content is 80.60%. Compared with the ancestral insect mitochondrial genome (Boore 1999), CR-trnI (+) -trnQ (-) -trnM (+) is rearranged to trnQ (-) - trnM (+) -CR-trnI(-). However, within this region, there is only a 9-bp intergenic sequence between trnI and nad2. The other 192 intergenic nucleotides are distributed between 19 gene pairs, with the longest being up to 41 bp between cob and trnS. All 13 PCGs utilize ATN as the start codon, while 9 PCGs end with the canonical triplet stop codon. cob and nad4l use TAG, while nad1 and nad4 end with a single T.

Phylogenetic trees constructed under four strategies constantly support the sister group relationship between *E. ovata* and *Conaspedia wangi* Wei, 2015 (Qi et al., 2015). None of the results support *E. ovata* and *Dimorphopteryx* sp. originating from the same subfamily clade. It confirms the suspicion based on morphological evidence (Ross, 1937). Three results support Selandriinae, rather than Nematinae, as the sister group of *E. ovata* + *C. wangi*. However, Selandriinae, as the most basal branch, is supported by three of the four trees. However, these unconfirmed phylogenetic relationships all indicate that the current sampling is far from enough to solve the internal relations in Tenthredinidae (Figure 1).

**Ethics statement**

The collection of specimen conformed to the requirement of International ethics, which are unrestricted species. And the collection were approved by the local authorities. The process and purpose of this experimental research were in line with the rules and regulations of our institute. There are no ethical issues and other conflicts of interest in this study.

**Author contributions**

Zejian Li and Meicai Wei conceived the idea and designed the research, and the final approval of the version to be published; Mengmeng Liu and Min Li analyzed the data and wrote the manuscript; Mengmeng Liu revised the manuscript. All authors agree to be accountable for all aspects of the work.

**Disclosure statement**

No potential conflict of interest was reported by the authors. The authors alone are responsible for the content and writing of the article.

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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]
(https://www.ncbi.nlm.nih.gov/) under the accession number OK287350. The associated BioProject, SRA, and Bio-Sample numbers are PRJNA764375, SRR15990418, and SAMN21501672, respectively. All related files are publicly available in figshare (https://figshare.com/account/home/#/projects/123754).

**References**

Abascal F, Zardoya R, Telford MJ. 2010. TranslatorX: multiple alignment of nucleotide sequences guided by amino acid translations. Nucleic Acids Res. 38(Web Server issue):W7–13.

Abe M, Smith DR. 1991. The genus-group names of Symphyta (Hymenoptera) and their type species. Esakia, Fukuoka. 31:1–115.

Ashmead WH. 1898. Classification of the horntails and sawflies, or the sub-order Phytophaga (Paper No. 5). Can Entomol. 30(10):249–257.

Benson R. B. 1952. Hymenoptera, Symphyta. In: Handbooks for the identification of British insects. Vol. 6b(2). London: pp. 51–137.

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):313–319.

Boore JL. 1999. Animal mitochondrial genomes. Nucleic Acids Res. 27(8):1767–1780.

Hartig T. 1837. Die Aderflügler Deutschlands mit besonderer Berücksichtigung ihres Larvenzustandes und ihres Wirkens in Wäldern und Garten für Entomologen, Wald- und Gartenbesitzer. Die Familien der Blattwespen und Holzwespen nebst einer allgemeinen Einleitung zur Naturgeschichte der Hymenopteren. Erster Band. Haude und Spener, Berlin, pp. i–xiv + 1–416.

Lartillot N, Lepage T, Blanquart S. 2009. Phylobayes 3: a Bayesian software package for phylogenetic reconstruction and molecular dating. Bioinformatics. 25(17):2286–2288.

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.

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.

Qi L, Niu G, Liu T, Wei M. 2015. New species and new synonyms of Conaspidea Konow (Hymenoptera: Tenthredinidae) with keys to species of the Conaspidea bicuspis group and Japanese species. Entomotaxonomia. 37(3):1–13.

Rohwer SA. 1911. A classification of the suborder Chalastogastra of the Hymenoptera. Proceedings of the Entomological Society of Washington. Vol. 13(4). Washington: pp. 215–226.

Ross HH. 1937. A generic classification of the Nearctic sawflies (Hymenoptera, Symphyta). Illinois biological monographs. Urbana: University of Illinois. Vol. 15, no. 2.

Taeger A, Blank SM, Liston AD. 2010. World Catalog of Symphyta (Hymenoptera). Zootaxa. 2580:1–1064.

Takeuchi K. 1952. A Generic Classification of the Japanese Tenthredinidae (Hymenoptera: Symphyta). Kyoto . p. 1–90.

Wei M, Nie H. 1998. Generic list of Tenthredinoidea s. str. in new systematic arrangement with synonyms and distribution data. J. Central South Forestry University, Zhuzhou. 18(3):23–31.

Zombori L. 1981. The European genera of Selandriinae and Dolerinae (Hymenoptera: Symphyta, Tenthredinidae). Acta Zool Acad Scientiarum Hungaricae, Budapest. 27(3–4):443–450.