The complete mitochondrial genome sequence of Sinopoppia nigroflagella Wei, 1997 (Hymenoptera: Tenthredinidae) reveals a new gene order

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ABSTRACT
The complete mitochondrial genome of Sinopoppia nigroflagella Wei, 1997 was sequenced and assembled. The circular genome is 15,940 bp long, with an A + T content of 80.33%, 37 genes, and a 658-bp control region. Specifically, trnL1 was translocated into the MQI gene cluster, and the other tRNA cluster was arranged as ARENS1F. The two gene clusters were thus arranged as ML1QI and ARENS1F. The phylogenetic results indicated that S. nigroflagella forms a sister group with Bleïnocampinae and Fenusinae.

Sinopoppia nigroflagella is a peculiar sawfly species and its systematic position remains uncertain (Wei 1997). Wei and Nie (1998) placed S. nigroflagella into Caliroinae of Heterarthridae. Taeger et al. (2010) treated it as a member of Heterarthridae of Tenthredinidae. Based on COI data S. nigroflagella seemed to be combined with the Dimorphopteryx species of Tenthredininae (Unpublished data). The phylogenetic position of S. nigroflagella remains to be determined. In this study, we sequenced the mitochondrial genome of S. nigroflagella to determine its phylogenetic position.

Specimens were collected from the Xinting, Jiulong, Lishui, Zhejiang, China (28.404 °N, 119.838 °E) on 31 March 2018 by Zejian Li, and identified by Meicai Wei. The specimen was deposited at the Asia Sawfly Museum, Nanchang (ASME) (Meicai Wei, weimc@126.com) under the voucher number CSCS-Hym-MC0073. Genomic DNA was sequenced using the high-throughput Illumina Hiseq 4000 platform, yielding a total of 90,672,018 raw reads (SRR13487075). DNA sequences were assembled using MitoZ (Meng et al. 2019) and Geneious Prime 2019.2.1 (https://www.geneious.com). Annotations were generated using the MITOS web server (Bernt et al. 2013) and revised where necessary.

Phylogenetic analysis was performed, including only hymenopteran taxa, to avoid possible effects of long-branch attraction. The nucleotide sequences of 13 protein-coding genes (PCGs) of 50 other Symphytan and two Apocritan species were aligned using the MAFFT method in the TranslatorX server (Abascal et al. 2010). The phylogenetic tree was constructed using iQTREE (Jana et al. 2016) with default parameters. Based on the previous experience (Malm and Nyman 2015), to avoid the long-branch attraction, the outer group was excluded. Thus, Xyelidae was used for rooting the tree.

The sequence yield by MitoZ was 16,730 bp in length and contained 37 genes with an incomplete control region. We used the sequence flanking the control region as a reference sequence. One of the flanking regions contained trnM (120 bp) and the other included part of the rnsS (110 bp) gene. The results of the two assemblies were consistently showing them as a control region 658 bp in length. We then verified the 15,940 bp long genome using Endemyolia tibialis (unpublished) as the reference sequence and the mean depth of coverage across the contig sequence was 1180.

The sequence analysis indicated that S. nigroflagella is a peculiar sawfly species and its systematic position remains uncertain (Wei 1997). Wei and Nie (1998) placed S. nigroflagella into Caliroinae of Heterarthridae. Taeger et al. (2010) treated it as a member of Heterarthridae of Tenthredinidae. Based on COI data S. nigroflagella seemed to be combined with the Dimorphopteryx species of Tenthredininae (Unpublished data). The phylogenetic position of S. nigroflagella remains to be determined. In this study, we sequenced the mitochondrial genome of S. nigroflagella to determine its phylogenetic position.

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Tenthredininae and Allantinae. This study further clarified the phylogenetic position of *Sinopoppia* in the Tenthredinidae. However, considering the complexity of Tenthredinidae, dense sampling is essential to obtain a robust phylogeny (Figure 1).

**Disclosure statement**

No potential conflict of interest was reported by the author(s).

**Funding**

This work was supported by the National Natural Science Foundation of China [31970447, 31501885].

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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 MW487927. The associated BioProject, SRA, and BioSample numbers are PRJNA692343, SRR13487075, and SAMN17320634, respectively. All related files had been uploaded to figshare ([https://figshare.com/account/home/#/projects/100472](https://figshare.com/account/home/#/projects/100472)).

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