

Characterization of the complete mitochondrial genome of *Nemoura meniscata* Li & yang (Plecoptera: Nemouridae) from China

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ABSTRACT

We sequenced the third complete mitochondrial genome of *Nemoura meniscata* by using the high-throughput sequencing method. The mitochondrial genome harbored 37 typical code genes and a control region with 15,895 bp in length was a double-stranded and circular genome. The nucleotide composition is partial to A and T. Seventy-eight nucleotides were dispersed in 10 intergenic spacers and gene overlaps were also found at 13 gene junctions with 48 nucleotides. In phylogenetic trees, the 13 Nemouridae species form a clade diverged from the outgroup clade. The genus *Nemoura* and *Amphinemura* were sister groups which is consistent with the previous study.

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So far as we know, there are approximately 700 species in the big family Nemouridae of Plecoptera (DeWalt and Ower 2019; DeWalt et al. 2020). The genus *Nemoura* Latreille which belongs to the family Nemouridae and has more than 190 known species from the Holarctic and Oriental Regions (DeWalt et al. 2020). And over 25 species are known to occur from China, and the species of *Nemoura meniscata* are distributed in Henan and Shaanxi provinces of China (Li and Yang 2007; Yang and Li 2018; DeWalt et al. 2020). The phylogenetic position of the family Nemouridae has been performed based on morphological or mitochondrial genome data previously, while there are still many different viewpoints to date (Zwick 2000; Chen and Du 2017, 2018; Cao, Wang, and Li 2019; Cao, Wang, Ma, et al. 2019; Wang et al. 2019). Two mitochondrial genomes of genus *Nemoura* have been reported previously (Chen and Du 2017; Cao, Wang, Ma, et al. 2019), we sequenced and assembled the complete mitochondrial genome of *N. meniscata* from Longyuwan, Henan Province, China (33.699°N, 111.809°E) with the GenBank accession number MN944386 by using the high-throughput sequencing method in this study. The male specimen with the number VHL-0042 was collected on 15 May 2016 by Weihai Li and Junchao Wang. The voucher specimen was preserved in 100% ethanol and stored in the Entomological Museum of the Henan Institute of Science and Technology (HIST), China. The genomic DNA was extracted from the male adult's chest muscle of *N. meniscata* by the QIAamp DNA Blood Mini Kit (QIAGEN, Hilden, Germany). We annotated the mitochondrial genome by the MITOS WebServer and checked manually (Bernt et al. 2013).

The mitochondrial genome of *N. meniscata* harbored 37 typical code genes and a control region with 15,895 bp in length was a double-stranded and circular genome as well as most other stoneflies. The nucleotide composition is partial to A and T, with 70.8% of A+T content (A = 37.0%, T = 33.8%, C = 17.4%, G = 11.8%) and the AT Skew and GC Skew were 0.044 and -0.189. There were 78 nucleotides dispersed in 10 intergenic spacers ranging from 1 to 43 bp and gene overlaps were also found at 13 gene junctions ranging from 1 to 8 bp with 48 nucleotides. 12 protein-coding genes (PCGs) used ATN as start codon; with the exception of *ND1*, which used TTG as a start codon. Most PCGs used the typical stop codon TAA/TAG, while *COII* and *ND5* stopped with the signal T.

We reconstructed phylogenetic trees based on 'PCG matrix' (including 13 PCGs) and 'PCG12R matrix' (containing PCGs first and second codons and two ribosomal RNA genes) data sets with Bayesian (BI) and maximum-likelihood (ML) methods from 14 published genera and *N. meniscata* mitochondrial genomes (Figure 1). Two species in Taeniopterygidae, *Doddsia occidentalis* and *Taeniopteryx ugoly*, were used as outgroups. From the consensus phylogenetic trees, the result showed that the clade ((*N. meniscata* + *Nemoura nankinensis*) + *Nemoura papilla*) and (*Amphinemura longispina* + *Amphinemura yao*) were sister groups which are consistent with the previous study (Cao, Wang, and Li 2019).

Disclosure statement

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

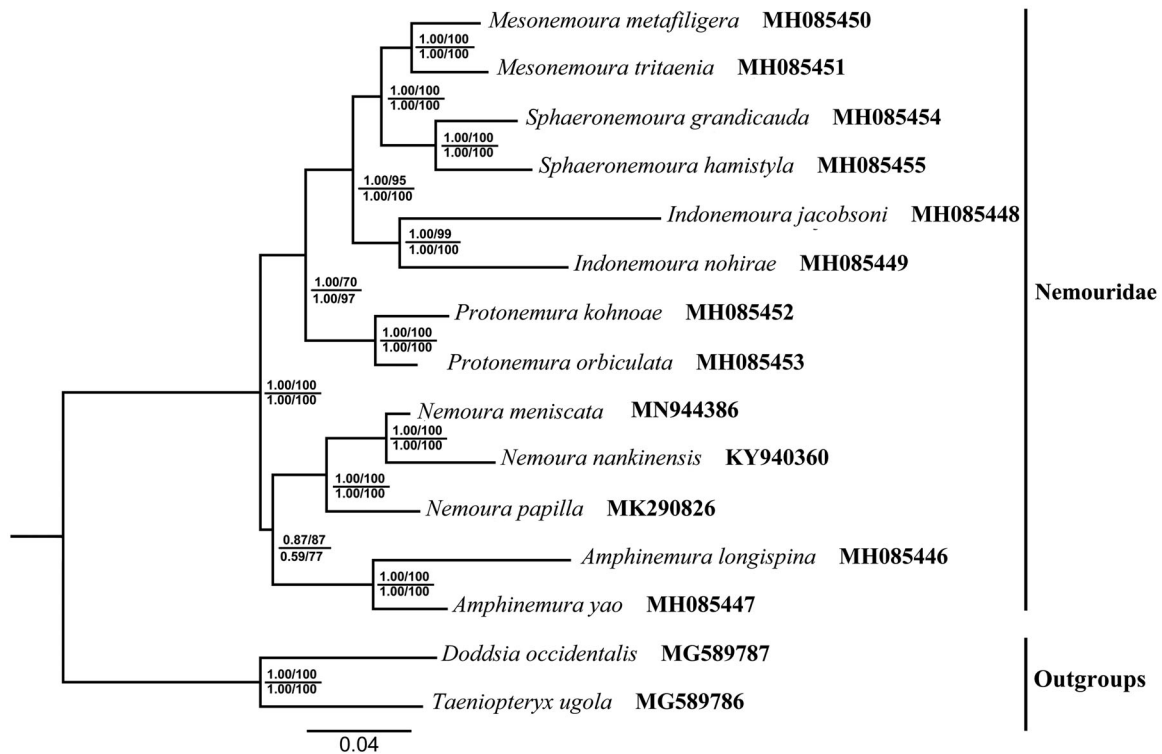


Figure 1. The consensus phylogenetic trees based on the concatenated nucleotide sequences of two data sets by using Bayesian inference (BI) and maximum-likelihood (ML) methods. The complete mitochondrial genomes of *Nemoura meniscata* and 14 other species are available from GenBank and the scientific name is followed by the accession number for each species.

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