

The mitochondrial genome analysis of *Sphaeronemoura elephas* (Plecoptera: Nemouridae) from Jiangxi Province of southeastern China

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ABSTRACT

We sequenced and annotated the species of *Sphaeronemoura elephas* which represents the first record for continental China from Jiangxi Province in this study to provide mitochondrial genome data for future studies. The entire mitochondrial genome of *S. elephas* harbored 37 typical code genes and one control region with 15,846 bp in length. The A+T account of total nucleotide, PCGs, tRNAs, rRNAs and control region were 67.1, 64.5, 70.5, 71.0, 82.4%, respectively and the A+T content was the highest in control region. The start codon of all PCGs used ATN except *ND5* and *ND1* started with GTG and TTG. Eleven PCGs used typical terminal codon TAA or TAG while the *COII* and *ND5* stopped with the single T. Based on 13 PCGs by using Bayesian (BI) and maximum-likelihood (ML) methods, we found that the genus *Sphaeronemoura* and *Mesonemoura* were sister groups and the species of Amphinemurinae was monophyletic group.

ARTICLE HISTORY

Received 19 January 2020
Accepted 1 February 2020

KEYWORDS

Mitochondrial genome;
phylogenetics;
Sphaeronemoura elephas

Till now, there are 19 valid species in genus *Sphaeronemoura* Shimizu and Sivec over the world (Sivec and Stark 2010; Qian et al. 2019; DeWalt et al. 2020; Li et al. 2020), 12 species are distributed in China mainland while the rest seven species occur in other countries of Asia (Wu 1973; Li et al. 2014, 2016; Qian et al. 2019; Li et al. 2020). Two mitochondrial genomes of genus *Sphaeronemoura* have been reported previously and we sequenced and annotated the species of *S. elephas* which was reported from Jiangxi Province and it also represents the first record for continental China in this study to provide mitochondrial genome data for future studies of the stoneflies (Cao et al. 2019; Li et al. 2020). The male specimen with the number VHL 0119 is deposited in the Department of Plant Protection, Henan Institute of Science and Technology (HIST) and tissue sample was from Yongxiu County, Jiangxi Province, China (N29°50', E 115°35') and was collected in April 2016 by Rongfeng Wang and Weihai Li. We extracted the genetic DNA from the adult's chest of *S. elephas* and was extracted by QIAamp DNA Mini Kit (QIAGEN, Germany) following the manufacturer's protocol.

The complete mitochondrial genome of *S. elephas* possessed a closed circular molecule with 15,846 bp in length and deposited in the GenBank under the accession number MN944385. Annotation of the complete mitochondrial genome was performed with MITOS WebServer and checked manually (Bernt et al. 2013). The mitogenome sequenced harbored 37 typical code genes and one control region (D-loop). The total nucleotide composition was A = 35.9%, T = 31.2%,

C = 20.3%, G = 12.6%, and the AT Skew and GC Skew were 0.070 and -0.236, suggesting that the content of A+T accounts for 67.1% was higher than G+C (32.9%), which is similar to other Plecopterid species. The A+T account of PCGs, tRNAs, rRNAs, and control region were 64.5, 70.5, 71.0, 82.4%, respectively and the A+T content was the highest occurring in control area. The initial codon of all PCGs was ATN except *ND5* and *ND1* are excluded, starting with GTG and TTG. Eleven PCGs used conservative TAA or TAG as terminal codon while the *COII* and *ND5* stopped with the single T. Among the 22 tRNAs, only the *tRNA^{Ser(AGN)}* DHU arm forms a ring, the secondary structures of other tRNAs all have the normal clover structure.

In order to understand the phylogenetic relationships of the genus *Sphaeronemoura* with other closely related species, the sequences of 13 PCGs among 12 Amphinemurinae species and two species in Perlidae (*Kamimuria chungnanshana* and *Kamimuria wangi* as outgroups) were used to conduct a phylogenetic analysis by Bayesian (BI) and maximum likelihood (ML) methods. The consensus tree topology (Figure 1) showed that the relationships among Amphinemurinae in genus level is (*Amphinemura* + (*Protonemura* + (*Indonemoura* + (*Mesonemoura* + *Sphaeronemoura*))))). The genus *Sphaeronemoura* and *Mesonemoura* were sister groups and the species of Amphinemurinae were clustered in one clade indicated that subfamily Amphinemurinae is monophyletic, this result support the previous assumptions about subfamily-level relationships.

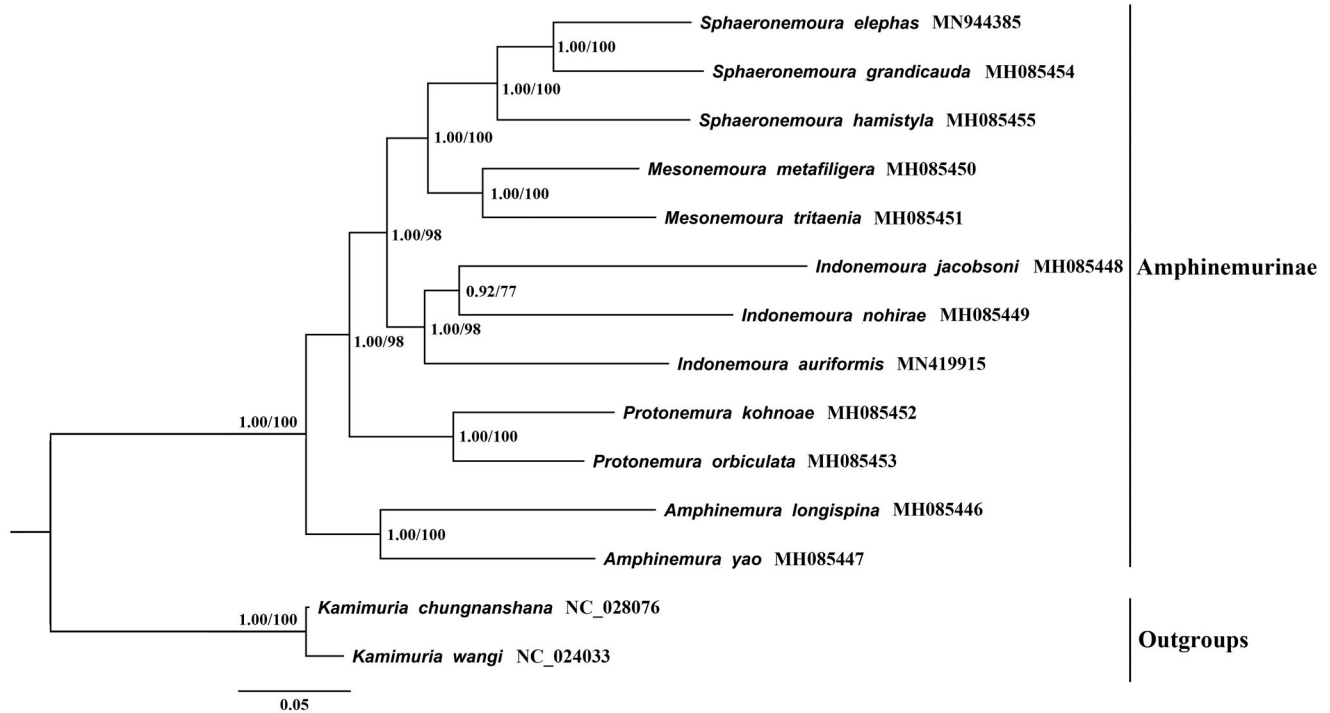


Figure 1. The phylogenetic trees based on the concatenated nucleotide sequences of 13 PCGs by using Bayesian inference (BI) and maximum-likelihood (ML). The complete mitochondrial genomes of other species are available from GenBank and the scientific name is followed by the accession number for each species.

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 [No. 31801999].

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