

MITOGENOME ANNOUNCEMENT

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The complete mitochondrial genome of a stonefly species, *Neoperlops gressitti* (Plecoptera: Pelidae)

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ABSTRACT

The small genus *Neoperlops* only contains four species over the whole world now, and the mitochondrial genome of the genus *Neoperlops* is still a gap. Here, we report the complete mitochondrial genome of *Neoperlops gressitti* representing the rare perlid stonefly genus *Neoperlops*. The circular mitochondrial genome is 15,699 bp in length, which consisting of A (33.30%), G (12.5%), T (29.7%), and C (24.6%), and it is composed of 22 tRNA genes, 13 protein-coding genes (PCGs), two rRNA genes, and a control region like the other published stonefly. In all PCGs, eleven genes initial with the typical start codon ATN, the rest of the two genes (ND1, ND2) with TTG. All PCGs stop with TAG/TAA, except COIII, ND5 use incomplete T—as stop codon. Besides, the phylogenetic result based on the nucleotide of the 13 PCGs and two rRNA genes by using Bayesian (BI) method supports the sister relationship between *N. gressitti* and *Dinocras cephalotes*. The complete mitogenome of *N. gressitti* can provide genetics data to further explore the taxonomic status of Pelidae.

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A rare perlid stonefly genus *Neoperlops* (Plecoptera: Pelidae) was initially established by Banks (1939) and included three species (*N. cheni*, *N. gressitti* and *N. obscuripennis*) which only distributed in Guangdong and Guangxi Provinces, China (Du et al. 1999; Stark and Sivec 2008; Chen and Du 2018; Yang and Li 2018). The genus remained in obscurity until Zwick (1984) and Sivec et al. (1988) emended the group as a valid genus and removed it from the synonymy of *Neoperla* where it had been placed by Illies (1966). Cao and Bae (2008) reported the fourth species *N. vietnamellus* restrictively distributed in Vietnam. In general, the small genus *Neoperlops* contains four species regionally in China and Vietnam over the whole world (DeWalt et al. 2019). Though there are about ten mitochondrial genomes in Perlidae has been published to date, the genus *Neoperlops* is still a gap. Therefore, urgent research has become necessary for these scarce species. We sequenced and assembled the mitochondrial genome of *N. gressitti* by next-generation sequencing method for the first time representing the genus *Neoperlops* in this study. The specimen of *N. gressitti* was collected by Li Weihai from Wuyi Mountain (coordinate as follows: 27.754°N, 117.688°E), Fujian Province, China in 2016. Samples and voucher specimens (No. Voh-0055) were deposited in Henan institute of Science and Technology (HIST), China. The total DNA was extracted by QIAamp DNA Mini Kit (QIAGEN, Hilden, Germany) and we assembled the sequence reads into contigs with BioEdit version 7.0.5.3 (Hall 1999).

The annotated mitogenome of *N. gressitti* has been deposited into GenBank with the accession number MN400756. The complete mitogenome of *N. gressitti* is 15,699 bp in length which contains 13 protein-coding genes (PCGs), 22 transfer RNA (tRNA) genes, 2 ribosomal RNA (rRNA) genes and one control region. The total nucleotide composition was included: A 33.30%, G 12.5%, T 29.7%, and C 24.6%. The protein-coding genes use the start codon as follow: ATG (ATP6, COII, COIII, CYTB, ND4, ND4L, ND5), ATT (ATP8), TTG (ND1, ND2) and ATC (COI, ND3, ND6). Two genes (COIII, ND5) use single-nucleotide (T—) as stop codons, four (CYTB, ND1, ND3, ND4) with TAG and the remaining ended with TAA. The total length of all PCGs was 11,247 bp with 60.6% A + T content. The A + T content of tRNAs, rRNAs and the control region was 66.4%, 68.0% and 74.5, respectively. The length of 12S rRNA and 16S rRNA was 804 bp and 1349 bp with A + T content as 64.7% and 70.1% slightly below the highest AT enrichment region i.e. the control region.

The phylogenetic result based on the nucleotide of the 13 PCGs and two rRNA genes was constructed by using Bayesian (BI) method from 11 species in Pelidae and two species (as outgroups) in Nemouridae highly supports the sister relationship between *N. gressitti* and *Dinocras cephalotes* (Figure 1). The monophyly of Acroneuriinae and Perlinae are recovered, which is similar to the results of previous studies and the phylogenetic tree provides a reference for understanding the taxonomic status.

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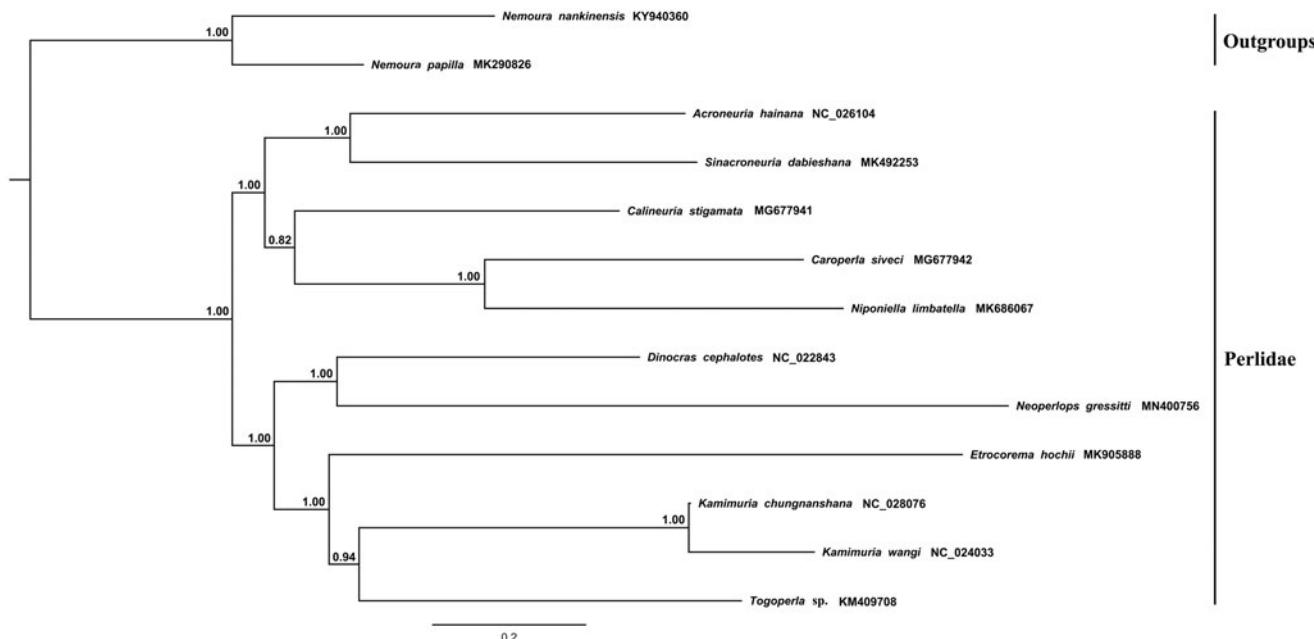


Figure 1. Phylogenetic tree inferred from ML analysis of the nucleotide of the 13 PCGs and two rRNA genes (13,055 bp). GenBank accession numbers for the sequences are indicated behind the species name.

Disclosure statement

No potential conflict of interest was reported by the authors.

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