

First mitochondrial genome of a stonefly from the subfamily Microperlinae: *Microperla geei* (Plecoptera: Peltoperlidae)

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ABSTRACT

The stonefly *Microperla geei* is the fourth sequenced peltoperlid and the first entire mitochondrial genome of *M. geei* representing the subfamily Microperlinae. The nearly complete mitogenome of *M. geei* is 15,216bp in size, has 37 genes and one partial control region, which is the classical structure for insect mitogenome. All PCGs started with ATN, except *ND1* and *ND5* genes used TTG and GTG. Eleven PCGs used the termination codon TAA or TAG and the *COII* and *ND5* genes stopped with a single T. Our phylogenetic topology tree supported Peltoperlidae was monophyletic and *M. geei* was a sister-group to the clade (*Soliperla* sp. + (*Cryptoperla stilifera* + *Peltoperlopsis cebuano*)). This study could provide new information for the further phylogenetic studies.

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About 50 species in 10 genera from two subfamilies divided between the nearctic, palearctic, and oriental regions comprise the Peltoperlidae, which is one of the smallest families of Plecoptera. Compared to other Systellognathan stoneflies such as perlids, the adults are recognizable as having small heads (DeWalt et al. 2019). The genus *Microperla* was proposed by Chu (1928) based on a new stonefly species, *Microperla geei*, which is a unique genus

in subfamily Microperlinae and contains four species in the world till now (Chen and Du 2018; Chen et al., 2018; Chen and Song 2019; Stark and Sivec 2007). The species *M. brevicauda* distributed in Japan (Kawai 1958), the *M. geei* and *M. retroloba* (Yang and Li 2018) only distributed in China and the newly reported species *M. qinlinga* was discovered from Shaanxi Province of northwestern China (Chen and Song 2019).

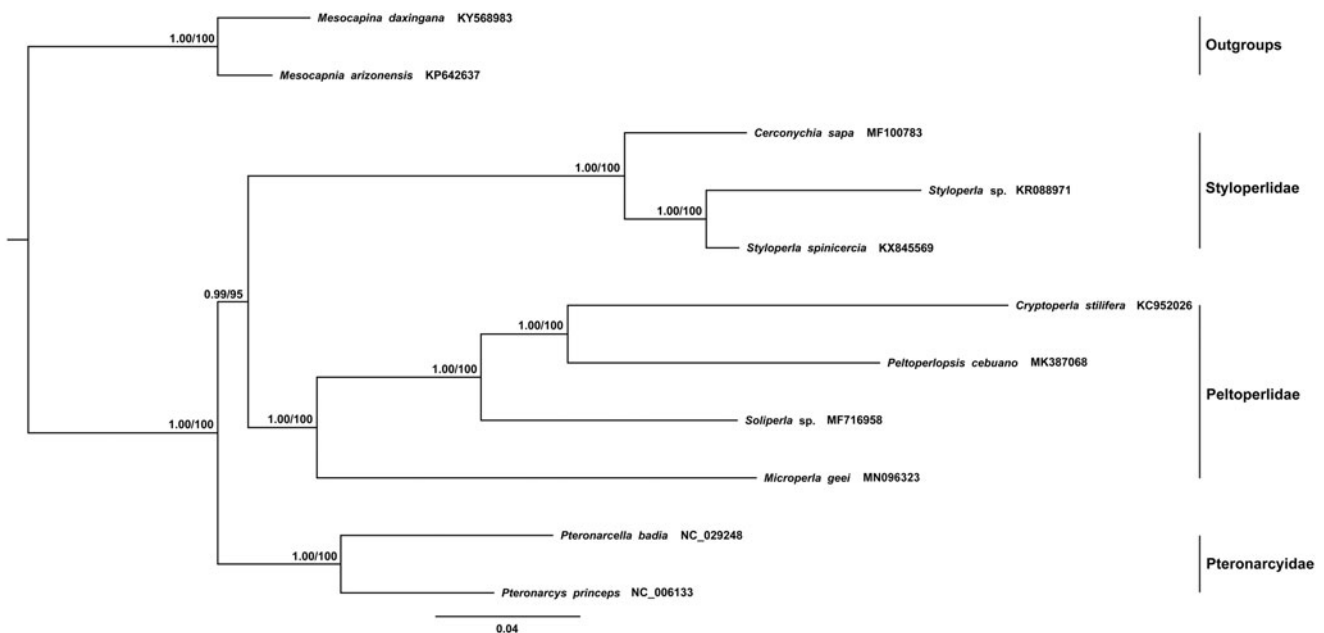


Figure 1. Phylogenetic analyses of *Microperla geei* based on the concatenated nucleotide sequences of the 13 PCGs and 2 rRNAs of 11 species. Numbers at nodes are bootstrap values. The NCBI accession number for each species is indicated after the scientific name.

There were only three peltoperlid that have been published previously (Cao et al. 2019; Chen et al. 2018; Wu et al. 2014). The *M. geei* is endemic to China where it is found in Henan and Zhejiang province. In this study, we report the first mitochondrial genome sequence of *M. geei* representing the subfamily Microperlinae by high-throughput sequencing for further research (GenBank accession No. MN096323). The tissue sample of *M. geei* was collected from Longquan gorge, Luoyang, Henan, China by Weihai Li in 2015 (coordinate as follows: 34.358°N, 111.351°E) and the voucher specimens (No. VHL-0018) were deposited in the insect specimen room of Henan institute of Science and Technology (HIST), China. Genetic DNA from the thorax muscle of male adult was individually extracted by using QIAamp DNA Mini Kit (QIAGEN, Hilden, Germany) following the manufacturer's protocol.

The nearly entire mitochondrial genome (except for partial control region) of *M. geei* was a linear molecule consisting of 15,216 bp, which possessed 22 transfer RNA genes (tRNAs), 13 protein-coding genes (PCGs), 2 ribosomal RNA genes (rRNAs), and 1 partial control region which were similar with other published stoneflies (Wang et al. 2017; Wang et al. 2018; Wu et al. 2014). Like other plecopteran, the nucleotide composition of *M. geei* mitochondrial genome was 37.0% of A, 31.3% of T, 19.5% of C, 12.2% of G, 68.3% of A + T content. Also, the A + T content of PCGs, tRNAs, and rRNAs was 68.1, 69.7, and 72.6%, respectively. The start codon ATG was shared with all PCGs except the *ND1* and *ND5* genes used TTG and GTG. Meanwhile, the stop codons for 11 PCGs used the termination codon TAA or TAG and the *COII* and *ND5* genes stopped with a single T. Based on the sequences of the 13 PCGs and 2 rRNAs among 11 species were used to conduct the same topology tree with the maximum likelihood (ML) and Bayesian (BI) method. As shown in Figure 1, the Peltoperlidae consisted of Peltoperlinae and Microperlinae was monophyletic and the *M. geei* was a sister-group to the clade (*Soliperla* sp. + (*Cryptoperla stilifera* + *Peltoperlopsis cebuano*)). Sequencing the mitogenome of *M. geei* could provide new information for further phylogenetic studies.

Disclosure statement

The authors report no conflict of interest.

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