

## Characterization of the complete mitochondrial genome of a stonefly, *Perlesta teaysia* (Plecoptera: Perlidae)

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### ABSTRACT

In this study, we sequenced the mitochondrial genome of *Perlesta teaysia*. The complete mitochondrial genome was 16,023 bp in length, including 37 typical genes and a control region. The overall nucleotide composition was biased toward the A/T nucleotides. All the protein-coding genes (PCGs) started with typical ATN codon as the start codon except for *ND1* and *ND5*, which started with TTG and GTG, respectively. In addition, 11 of 13 PCGs possessed the typical stop codon TAA/TAG, whereas *ND4* and *ND5* terminated with an incomplete stop codon. Phylogenetic analysis suggested that *P. teaysia* was a sister group to *Calineuria stigmatica*.

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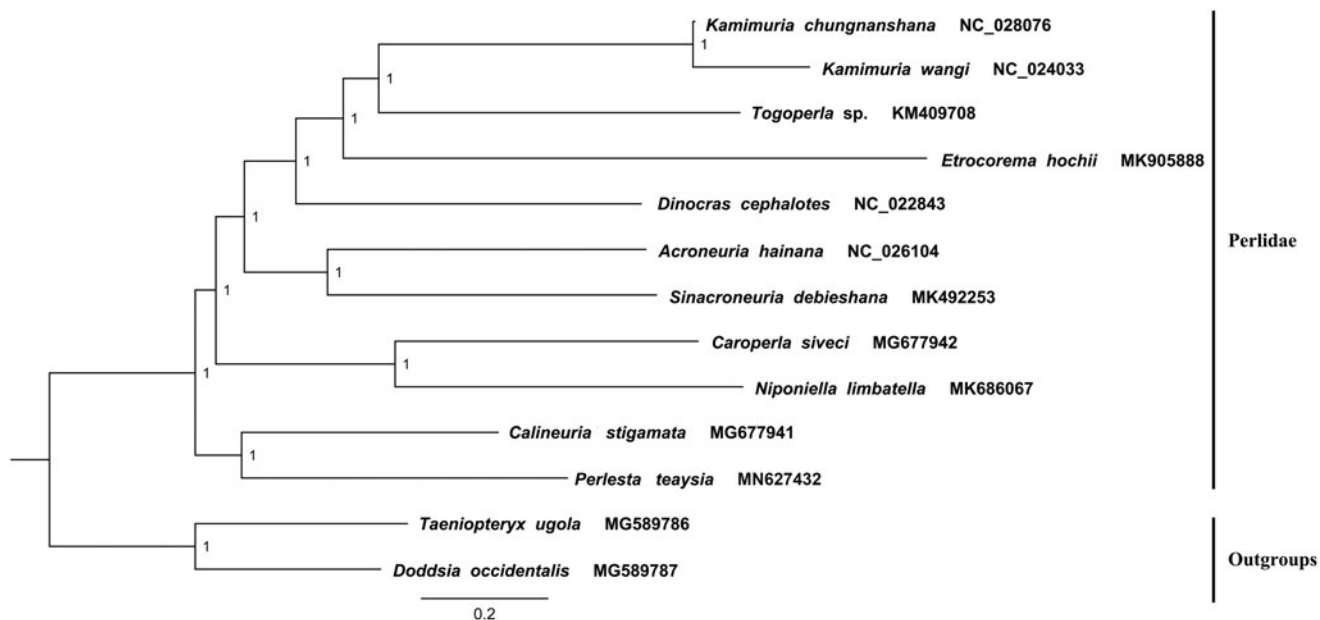
The Perlidae Latreille, 1802 is one of the largest families of Plecoptera with more than 1110 species recognized in the World (DeWalt et al. 2019). The genus *Perlesta* Banks, 1906 of the subfamily Acroneuriinae Klapálek, 1914 of Perlidae includes 33 species currently, of which only two are known from China (Wu 1938, 1948; Murányi and Li 2016; DeWalt et al. 2019). Although a few mitochondrial genomes of the Acroneuriinae have been previously published (Huang et al. 2015; Cao, Li, et al. 2019; Cao, Wang, Li, et al. 2019; Cao, Wang, Zhang, et al. 2019; Li et al. 2019; Wang et al. 2019) and listed in GenBank database, the mitochondrial genome of *Perlesta* is unavailable. Herein, we sequenced and annotated the complete mitochondrial genome sequence of the Nearctic *P. teaysia* Kirchner & Kondratieff, 1997 (GenBank accession number MN627432) by Illumina sequencing for the first time.

The *P. teaysia* specimen we used in this study was collected and identified by Boris C. Kondratieff from Wolf Creek, Co. Road 614 (Grapefield Road), Bland Co., Virginia, USA. (N 37.14702, W -81.26314) on 4 June 2016. The voucher specimen (No. VHL-0158) is now deposited in Henan Institute of Science and Technology (HIST), Henan Province, China. The sternal muscle of the adult was used to extract the total DNA by QIAamp DNA Mini Kit (QIAGEN, Hilden, Germany) and the sequencing sequences were assembled into contigs by BioEdit version 7.0.5.3 (Hall 1999). The relative synonymous codon (RSCU) was calculated by using the nucleotide from

13 protein-coding genes (PCGs) with MEGA 5.1 (Tamura et al. 2011).

The complete mitochondrial genome of *P. teaysia* was 16,023 bp long and contains the normal 37 genes (23 in J strand and 14 in N strand) and a control region. Like other reported Plecoptera species, *P. teaysia* obviously preferred A/T nucleotides (A = 34.7%, T = 30.0%, G = 12.4%, C = 22.9%) through the data analysis. All PCGs used ATN as start codon except *ND5* (GTG) and *ND1* (TTG) genes. Among them, the initial codon of *COI* and *ND3* genes was ATC, and the rest was ATG. *ND5* and *ND4* used incomplete T as the termination signal and the remaining 11 protein genes used TAG or TAA. The total lengths of all PCGs tRNAs, rRNAs, and the control region were 11,247, 1473, 2122, and 1188 bp and their A + T content was 63.0, 67.1, 68.6, and 71.0%, respectively. The control region located between *srRNA* and *tRNA<sup>Leu</sup>* made up the highest content of A + T.

The Bayesian (BI) method was used for phylogenetic analysis by the sequences of 13 PCGs and two rRNAs from eleven species of Perlidae and two species of Taeniopterygidae (*Taeniopteryx ugola* Ricker & Ross, 1968 and *Doddsia occidentalis* Banks, 1900) as outgroups. From the phylogenetic tree (Figure 1), the *P. teaysia* and another Acroneuriinae species, the Japanese *Calineuria stigmatica* Klapálek, 1907 were the most closely related and all the 11 species were clustered in a clade. We hope that the results of this study can help future studies in the genus *Perlesta* and Perlidae in general.



**Figure 1.** Phylogenetic analyses of *Perlesta teaysia* based on the 13 protein-coding genes by Bayesian (BI) methods. The NCBI accession number for each species is indicated after the scientific name.

## Disclosure statement

The authors report no conflict of interest.

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