

The mitochondrial genome from the stonefly: *Claassenia* sp. (Plecoptera: Perlidae)

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ABSTRACT

Claasseniini is the apparent sister group to all the other groups of Perlidae, and the small tribe Claasseniini has only one genus includes 12 species in the world. Only five mitochondrial genomes in the Perlinae have previously been reported. In this study, we sequenced the mitochondrial genome of *Claassenia* sp. Wu in genus *Claassenia* for the first time. The total length of the mitochondrial genome is 15,774 bp, and the DNA base composition is 34.0% A, 27.4% T, 25.6% C and 13.0% G. The whole genome contains 37 genes and one control region, which is similar to other published stoneflies. All PCG started with ATN except CCG for COI gene, TTG for ND1 gene, GTG for ND4 and ND5 genes. The termination codon of 11 PCGs used the normal complete codon TAA or TAG, and the COII and ND5 genes were terminated by a single T. All tRNAs except *tRNA^{Ser(AGN)}* fold into a classic clover structure. The phylogenetic tree by Maximum likelihood (ML) and Bayesian (BI) methods supported that *Claassenia* sp. was the basal taxa of the Perlidae clade. This study provides new data for further mitochondrial genome study on the Perlidae.

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Currently, we know more than 1100 species of Perlidae in the world, most of which are distributed in the north of the earth, and a few extend to southern Africa and South America (DeWalt et al. 2019). Claasseniini is a small tribe in Perlidae with only one genus including 12 species in the world (DeWalt et al. 2019), and the Claasseniini is the apparent sister group to all the other groups of Perlidae (Sivec et al. 1988). However, only five mitochondrial genomes in the Perlinae have previously been reported worldwide (Qian et al. 2014; Elbrecht et al. 2015; Wang, Ding, et al. 2016; Wang, Wang, et al. 2016; Liu et al. 2019). Therefore, urgent molecular research has become necessary for these species. In this study, we sequenced and determined the mitochondrial genome of *Claassenia* sp. in the genus *Claassenia* by Illumina sequencing technology for the first time. The specimen of *Claassenia* sp. was obtained in Wuyi Mountain, Fujian Province, southeast China in 2016 (27.754°N, 117.688°E) by Li Weihai and Wang Rongfeng. The samples and voucher specimens (No. Voh-0044) were stored in Henan institute of Science and Technology (HIST), Henan Province, China. Total mitochondrial genomic DNA from the adult muscle tissues was extracted using QIAamp DNA Mini Kit (QIAGEN, Hilden, Germany). The tRNA secondary structures were predicted using MITOS (Bernt et al. 2013).

The complete mitochondrial genome of *Claassenia* sp. with the length of 15,774 bp has been deposited into GenBank with the accession number MN419914. It contains

22 transfer RNA genes (tRNAs), 13 protein-coding genes (PCGs), 2 ribosomal RNA genes (rRNAs), and a control region, which is similar to other published stoneflies. The overall base composition showed significant bias toward A/T nucleotides: A (34.0%), T (27.4%), C (25.6%), and G (13.0%), with an A + T content of 61.4%, which is consistent with other stoneflies. The total length of 13 PCGs, 22 tRNAs, 2 rRNAs, and control region was 11,229 bp, 1495 bp, 2194 bp, and 832 bp with A + T content of 59.4%, 66.9%, 64.2%, and 73.1%, respectively. Nine PCGs started with the conventional ATN codon, while ND1, ND4, ND5, and COI genes began with TTG, GTG, GTG, and CCG. Only the COII and ND5 genes ended in a single T—, while the remaining 11 genes used the normal complete codon TAA/TAG. All tRNAs could be folded into the typical clover-leaf structures except the *tRNA^{Ser(AGN)}* formed into a loop by the absence of DHU arm.

According to the PCG12R matrix (contains PCGs first and second codons and two rRNAs) from 10 Perlidae and 2 Capniidae species (*Apteroperla tikumana* and *Mesocapnia daxingana* as outgroups) by Maximum likelihood (ML) and Bayesian (BI) methods, we obtained the same topological tree. As shown in Figure 1, the phylogenetic tree inferred that *Claassenia* sp. was the basal taxa of the Perlidae clade, which is consistent with traditional morphologic classification (Sivec et al. 1988; DeWalt et al. 2019). More mitochondrial genome data of genus *Claassenia* probably provide molecular information for further studies in Perlidae.

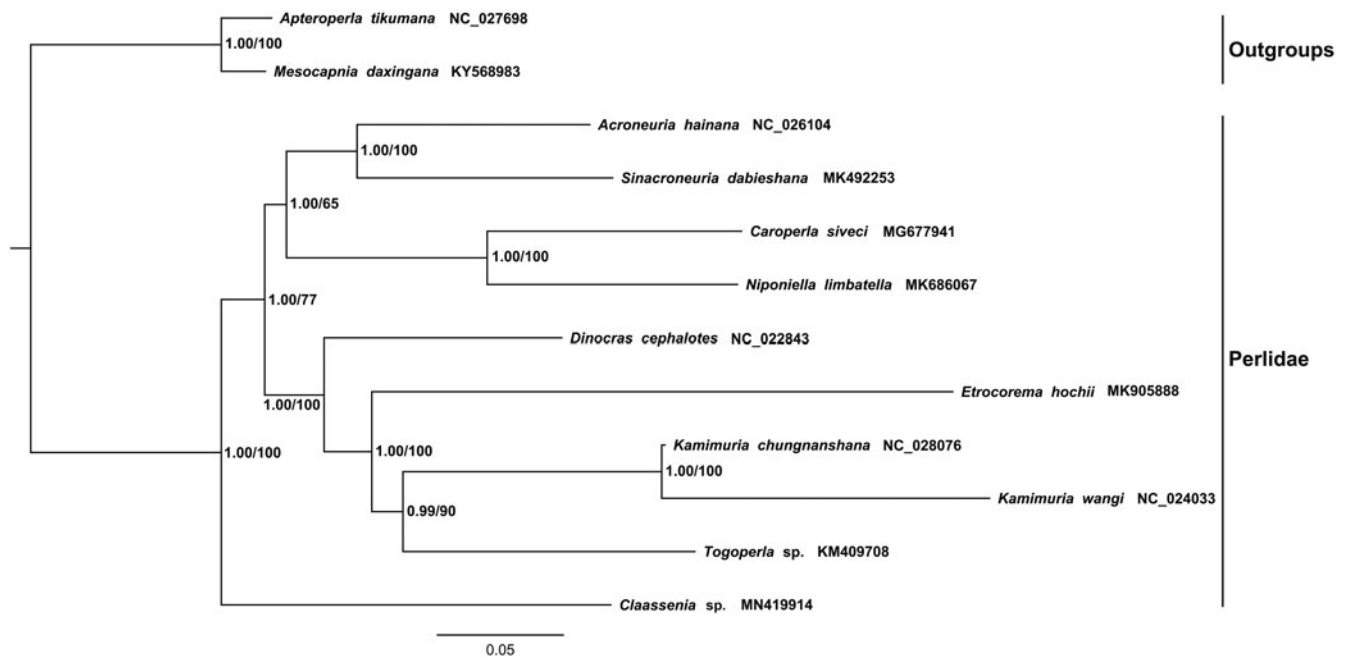


Figure 1. Phylogenetic analyses of *Claassenia* sp. based on the sequences of PCG12R matrix (contains PCGs first and second codons and two rRNAs) by the Maximum likelihood (ML) and Bayesian (BI) methods. The accession number in NCBI of each species is indicated after the scientific name.

Disclosure statement

No potential conflict of interest was reported by the authors.

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References

Bernt M, Donath A, Jühling F, Externbrink F, Florentz C, Fritsch G, Pütz J, Middendorf M, Stadler PF. 2013. MITOS: improved de novo metazoan mitochondrial genome annotation. *Mol Phylogenet Evol.* 69:313–319.

DeWalt RE, Maehr MD, Neu-Becker U, Stueber G. 2019. Plecoptera species file online. [accessed 2019 Sep 16]. <http://Plecoptera.SpeciesFile.org>.

Elbrecht V, Poettker L, John U, Leese F. 2015. The complete mitochondrial genome of the stonefly *Dinocras cephalotes* (Plecoptera, Perlidae). *Mitochondrial DNA Part A.* 26:469–470.

Liu ZZ, Wang Y, Li WH, Cao JJ. 2019. The complete mitochondrial genome of a stonefly species, *Etrocorema hochii* (Plecoptera: Perlidae). *Mitochondrial DNA B Resour.* 4:2690–2691.

Qian YH, Wu HY, Ji XY, Yu WW, Du YZ. 2014. Mitochondrial genome of the stonefly *Kamimuria wangi* (Plecoptera: Perlidae) and phylogenetic position of Plecoptera based on mitogenomes. *PLoS ONE.* 9: e86328.

Sivec I, Stark BP, Uchida S. 1988. Synopsis of the world genera of Perlinae (Plecoptera: Perlidae). *Scopolia.* 16:12.

Wang K, Ding SM, Yang D. 2016. The complete mitochondrial genome of a stonefly species, *Kamimuria chungnanshana* Wu, 1948 (Plecoptera: Perlidae). *Mitochondrial DNA Part A.* 27:3810–3811.

Wang K, Wang YY, Yang D. 2016. The complete mitochondrial genome of a stonefly species, *Togoperla* sp. (Plecoptera: Perlidae). *Mitochondrial DNA Part A.* 27:1703–1704.