Complete mitochondrial genome of *Stenopsyche tienmushanensis* (Trichoptera: Stenopsycheidae)

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**ABSTRACT**

The complete mitochondrial genome (mitogenome) of *Stenopsyche tienmushanensis* Hwang, 1957 was assembled from Illumina high-throughput sequencing data. The circularized mitogenome has a length of 16,049 bp with a high A + T content of 77.9%, including 13 protein-coding genes (PCGs), 22 tRNA genes, and 2 rRNA genes. Its gene composition and order were the same as *Stenopsyche angustata*. The overall base composition is 42.0% for A, 35.9% for T, 7.6% for C, and 14.5% for G. A phylogenetic analysis based on 13 PCGs of *S. tienmushanensis* and 20 other caddisflies supports the placement of Stenopsycheidae as sister to the Hydropsychidae within Trichoptera.

Trichoptera, also called caddisflies, is the sixth largest order of Insecta. Caddisflies are widely distributed in the world, and play an important role in water monitoring and evaluation of the health of aquatic ecosystems as bio-indicators (Resh and Unzicker 1975). Stenopsycheidae is one of the smallest families in Trichoptera, which only has three genera in the world (Morse et al. 2014). *Stenopsyche* is the largest genus of Stenopsycheidae, most of which live in clean rivers (Morse et al. 2014). The body of *Stenopsyche tienmushanensis* Hwang, 1957 is yellowish brown, with distinct dark punctate pattern of highly sclerotized head and pronotum (Xu et al. 2015). This species widely distributed in China, such as Hubei, Shanxi, Shaanxi, Hunan, Anhui, Zhejiang, Jiangxi, Guizhou and Guangxi Provinces, as well as Hainan Island (Xu et al. 2015). Previously studies focused on ecological surveys and the identification of larvae in *Stenopsyche* genus from China (Tian 1985, 1988; Tian and Zheng 1989). Little is known about the mitogenomes of this genus. To date, whole mitogenome data is available for only one species, *Stenopsyche angustata* (MT677866.1), in Stenopsycheidae (Trichoptera) (Huang et al. 2020). Here, we sequence and annotate the complete mitogenome of *S. tienmushanensis* to facilitate better understanding of the mitochondrial characteristics and the evolutionary history of Stenopsycheidae.

In this study, the specimen of *S. tienmushanensis* was collected from Nanjing, Jiangsu Province, China (32.042°N, 118.848°E). A specimen was preserved at –20 °C and deposited at Nanjing Agricultural University, China (http://www.njau.edu.cn/, Yi Wu, wuyi@nies.org) under the voucher number 33 m-8. Genomic DNA was extracted from one leg of a single individual using the QIAamp DNA Micro Kit (Qiagen, GmbH, Germany). The sample was sequenced on the Illumina HiSeq X 10 platform at Novogene (Tianjin, China) following a PE150 strategy. The sequenced mitogenome was assembled by NOVOPlasty v3.8.2 (Dierckxsens et al. 2017) and annotated by MitoZ v2.4-alpha (Meng et al. 2019).

The circularized mitogenome of *S. tienmushanensis* has a length of 16,049 bp with a high A + T content of 77.9% (42.0% for A, 35.9% for T, 7.6% for C, and 14.5% for G), under GenBank accession number MW201980. It contained an entire set of 37 genes (13 PCGs, 22 tRNA genes, and 2 rRNA genes) plus a control region. Its gene composition and order were same as *S. angustata* (Huang et al. 2020). All 13 PCGs were AT-biased (75.7% on average), with the highest A + T content (81.4%) in ND6 and the lowest (67.9%) in COX3. The l-rRNA and s-rRNA was 1,380 bp and 876 bp in length, with an A + T content of 83.3% and 85.3%, respectively. All tRNAs were ranging from 65 bp (trNA^{Aly}_UUR) to 76 bp (trNA^{Thr}_Leu-UUR) in length with typical cloverleaf secondary structure, except for trNA^{Ser-AGN}_Thr, which has lost the dihydroxyuridine arm. 23 genes (9 PCGs and 14 tRNAs) encoded by the positive strand, and 14 genes (four PCGs, eight tRNAs, and two rRNAs) encoded by the reverse strand. All PCGs were initiated by ATN codons, except for ND4L (GTG). The stop codons of most PCGs were complete (TAA or TAG), except for COX2 and ND5 whose stop codons were incomplete (T).

Nucleotide sequences of 13 PCGs from 21 caddisflies were aligned using MAFFT v7.407 (Katoh and Standley 2013), and trimmed using trimAl v1.4.1 (Capella-Gutiérrez et al. 2009) with heuristic method ‘automated1’. The phylogenetic tree was reconstructed using IQ-TREE v2.0 (Minh et al. 2020). The phylogenetic analyses placed *S. tienmushanensis* as sister to...
S. angustata with high support (Figure 1). It supported the results that the monophyly of Stenopsychidae. This monophylum, as well as its placement as sister to Hydropsychidae, which were consistent with the results from previous studies (Huang et al. 2020).

**Disclosure statement**

No potential conflict of interest was reported by the author(s).

**Data availability statement**

The genome sequence data that support the findings of this study are openly available in GenBank of NCBI at (https://www.ncbi.nlm.nih.gov/) under the accession no. MW201980. The associated Bio-Sample numbers is SAMN16619568.

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