Complete mitochondrial genome of *Onychostoma leptura* and phylogenetic analysis of *Onychostoma*

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**ABSTRACT**

In this study, we first sequenced and characterized the complete mitochondrial genome of *Onychostoma leptura*. The complete mitochondrial genome was 16,601 bp in length and included 13 protein-coding genes (PCGs), 22 transfer RNA genes (tRNA), two ribosomal RNA genes (12S rRNA and 16S rRNA), and one non-coding control region (D-loop). The overall nucleotide composition was A: 31.31%, T: 23.89%, G:16.16%, and C: 28.64%, and the A + T content (55.20%) was much higher than G + C content (44.80%). The phylogenetic tree indicated that nine species belong to *Onychostoma* in the present study were classified into two clades. These results can provide basic genetic information for population genetic research of *O. leptura* and phylogenetic analysis of *Onychostoma*.

*Onychostoma leptura* (genus: *Onychostoma*, subfamily: Barbinae, family: Cyprinidae), an endemic fish in East Asia, is mainly distributed in Laos, Vietnam, and China (Kottelat 2001). It has a slender and laterally compressed body, a thin caudal peduncle, and a dark stripe along the lateral line of the body. The edges of anal, dorsal, and caudal fins of *O. leptura* are light red (Yue 2000). It feeds on scraping algae attached to rocks and inhabits streams with turbulent and clear water (Kottelat 2001). It has a certain population and is the main economic fish in some places, such as Hainan Island of China (Zhou et al. 2016). Here, we first sequenced the complete mitochondrial genome of *O. leptura*, which will provide basic genetic information for population genetic research of *O. leptura* and phylogenetic analysis of *Onychostoma*.

Specimen of *O. leptura* was collected from Shibizhen (N19°09′46″ E110°18′30″) section of the Wanquan River in Hainan Island in 2018. The collected specimen was deposited in 95% alcohol and stored at −20 °C in Specimen Room of School of Life Sciences, Jianghan University (Specimen code: *O. leptura* 20180413001). The total genomic DNA was extracted from dorsal muscle by using the animal tissue DNA kit. The complete mitochondrial genome was sequenced using the Illumina high-throughput sequencing technology and de novo assembled using NOVOPlasty ver 2.6 (Dierckxsens et al. 2017). Protein-coding genes and rRNA genes were predicted using web server DOGMA (Wyman et al. 2004), and tRNA genes were created using the program ARWEN (Laslett and Canback 2008).

The complete mitochondrial genome of *O. leptura* was 16,601 bp in length (NCBI GenBank accession number: MT449680). The overall nucleotide composition was A: 31.31%, T: 23.89%, G:16.16%, and C: 28.64%, and the A + T content (55.20%) was much higher than G + C content (44.80%). The complete mitochondrial genome included 13 protein-coding genes (ND1, ND2, ND3, ND4, ND4L, ND5, ND6, COI, COII, COIII, ATP6, ATP8, Cyt b), 22 transfer RNA genes (tRNA), two ribosomal RNA genes (12S rRNA and 16S rRNA), and one non-coding control region (D-loop). All the genes were encoded on the heavy strand, except for one protein-coding gene (ND6) and eight tRNA genes (tRNA^Glu^, tRNA^Ala^, tRNA^Asn^, tRNA^Cys^, tRNA^Ile^, tRNA^Ser^, tRNA^Glu^ and tRNA^Pro^) were encoded on the light strand.

A phylogenetic tree was constructed using Neighbour-Joining method using MEGA7 (Kumar et al. 2016) based on the whole mitogenome sequences of nine species belong to *Onychostoma* and *Sinilabeo rendahli* that was used as the outgroup (Figure 1). The complete mitochondrial genome of other species used for the construction of phylogenetic tree were downloaded from NCBI GenBank. The phylogenetic tree indicated that nine species belong to *Onychostoma* in the present study were classified into two clades: *O. lini*, *O. macrolepis*, *O. barbatum*, *O. rara*, and *O. barbatulum* in clade1, *O. alticorpus*, *O. leptura*, *O. gerlachi*, and *O. simum* in clade2.
Disclosure statement

There are no conflicts of interest for all the authors including the implementation of research experiments and writing this article.

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Data availability statement

The data that support the findings of this study are openly available in GenBank of NCBI at https://www.ncbi.nlm.nih.gov, reference number MT449680.

Figure 1. A phylogenetic tree was constructed using Neighbour-Joining method based on the mitochondrial genome of nine species belong to Onychostoma and Sinilabeo rendahli that was used as the outgroup. The O. leptura sequenced in this study was shown in bold.

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