**Characterization and phylogenetic analysis of the complete mitochondrial genome of *Sinocyclocheilus wenshanensis* (Cypriniformes: Cyprinidae)**

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**Abstract**

*Sinocyclocheilus wenshanensis* is a cyprinid fish species endemic to Southwestern China. In this study, we first sequenced and characterized the complete mitochondrial genome (mitogenome) of *S. wenshanensis* by next-generation sequencing method. The entire length of mitogenome is 16,595 base pairs (bp), containing 13 protein-coding genes, two ribosomal RNA genes, 22 transfer RNA genes, and a control region. Its gene arrangement pattern was identical to other previously reported *Sinocyclocheilus* fishes. The overall base composition is 31.12% A, 16.63% G, 25.45% T, and 26.80% C, with AT content of 56.57%. Phylogenetic analysis using mitogenome of 26 Cyprinidae fishes showed that *S. wenshanensis* are closely related to *S. aluensis* and *S. oxycephalus*. This work would provide molecular information fundamental to future phylogenetic analyses among *Sinocyclocheilus* species.

*Sinocyclocheilus wenshanensis* belonging to the genus *Sinocyclocheilus* (Cypriniformes, Cyprinidae) is a freshwater fish species that distributes only in the karst landform areas within Wenshan, belonging to Red River drainage, located in Southeast Yunnan, China (Yang et al. 2017). In the present study, we first sequenced and characterized the complete mitochondrial genome (mitogenome) of *S. wenshanensis* by next-generation sequencing method, which would facilitate future studies on *Sinocyclocheilus* phylogenetics.

The specimen of *S. wenshanensis* under study was collected in Wujiazhai (23.23°N, 104.05°E), Xigu Town, Wenshan, Yunnan Province, China. The specimen was preserved in 95% ethanol and deposited in the Zoological Specimen Museum of Yunnan University (Chunqing Li, lichq@ynu.edu.cn) under the voucher number YNUSW20160703016. Genomic DNA from muscle tissue was extracted by DNeasy Blood & Tissue Kit (Qiagen, Hilden, Germany). The DNA library was prepared following Illumina’s instruction and sequenced on Illumina Miseq (Illumina, San Diego, CA). It generated 3,506,072 clean reads with 699,718,556 base pairs (bp) in total. The complete mitogenome sequence of *S. wenshanensis* was assembled with A5-miseq v20150522 (Coil et al. 2015) and SPAdes (Bankevich et al. 2012). The ND6 gene positions were annotated using the MitoAnnotator on the MitoFish homepage (Iwasaki et al. 2013). All transfer RNA (tRNA) genes were identified by MITOS (Bernt et al. 2013) and tRNA phospho-SE search server (Lowe and Chan 2016). The mitogenome was circularly reconstructed using MrBayes.
v3.2.5 (Ronquist et al. 2012). The mitogenome of *S. wenshanensis*, together with 23 *Sinocyclocheilus* mitogenomes and two outgroup mitogenomes (*Barbodes binotatus* and *Poropuntius huangchuchieni*) available in GenBank database were used to perform phylogenetic analysis. The phylogenetic results (Figure 1) revealed that *S. wenshanensis* was closely related to *Sinocyclocheilus aluensis* (Cui et al. 2021) and *Sinocyclocheilus oxycephalus* (Li et al. 2018), and that 24 *Sinocyclocheilus* species were grouped as a monophyletic clade with strong supports. Phylogenetic analysis reveals *Sinocyclocheilus* form a solid monophyletic group, which was consistent with the traditional morphological classification and previous phylogeny studies based on partial mitochondrial genes or complete mitogenomes (Xiao et al. 2005; Zhao and Zhang 2009; Yang et al. 2021).

**Authors contributions**

Chunqing Li: analysis and interpretation of the data; investigation; drafting of the paper. Fang Hu: analysis and interpretation of the data; investigation. Junxian He: analysis and interpretation of the data; investigation. Xutong Li: formal analysis; methodology. Weixian Li: taxonomic identification. Hongfu Yang: sample collection. Shanyuan Chen: conception and design; funding acquisition; supervision; revising the paper critically for intellectual content. Heng Xiao: conception and design; funding acquisition; supervision; reviewing the final approval of the version to be published. All authors agree to be accountable for all aspects of the work.

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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. OM001088. The associated BioProject, SRA, and Bio-Sample numbers are PRJNA796176, SRR17552844, and SAMN24817860, respectively.

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