**ABSTRACT**
In this study, we first sequenced the mitochondrial genome (mitogenome) of *Schizothorax argentatus*. The circular mitogenome of *S. argentatus* is 16,587 bp long, containing 13 protein-coding genes, 22 tRNA genes, two ribosomal RNA genes, and a control region (D-loop region). The base composition is AT biased (63.11%). A phylogenetic tree confirms monophyly at the genus level within Cyprinidae and supports *S. argentatus* as sister to *Schizothorax pseudoalksaiensis*.

**ARTICLE HISTORY**
Received 24 October 2021
Accepted 4 October 2022

**KEYWORDS**
Mitochondrial genome; *Schizothorax argentatus*; phylogeny; phylogenetic tree

**CONTACT**
Shengao Chen (shengao@taru.edu.cn) College of Animal Science, Tarim University, Alar, Xinjiang 843300, China

**MITOCOHNDRIAL DNA PART B**
2022, VOL. 7, NO. 10, 1834–1836
https://doi.org/10.1080/23802359.2022.2133555

**MITOGENOME ANNOUNCEMENT**

The mitochondrial genome of *Schizothorax argentatus* from Northern Xinjiang and its phylogenetic analysis

Chengxin Wanga, Yong Songa, Fangze Zia, Jianmin Gea and Shengao Chena,b

aCollege of Life Science and Technology/Tarim Research Center of Rare Fishes, Tarim University, Alar, Xinjiang, China; bCollege of Fisheries, Huazhong Agricultural University, Wuhan, Hubei, China

*Schizothorax argentatus* (*Schizothorax argentatus* Kessler 1874) is a species endemic to China that belongs to Schizothorax, Cyprinidae, Cypriniformes, and Osteichthyes. It is distributed in Xinjiang Ili River system rivers and lakes. The species migrates to China’s Ili River basin during the breeding period (Guo et al. 2012). Before the 1960s, it was the main fishing target in the Ili River, accounting for more than 60% of the total catch. Since the 1970s, it has been difficult to catch the fish in China due to the construction of the Karvchagai Reservoir in Kazakhstan. Moreover, the genome of *S. argenta- tus* has not been reported. In this study, we sequenced the complete mitochondrial genome of *S. argentatus* and reconstructed a phylogenetic tree of this species and other taxa in the Cyprinidae to provide more molecular evidence for further research.

Specimens of *S. argentatus* were collected from the Ili River (42°51′N, 80°04′E) (Aquatic Wildlife Special Hunting License of the People’s Republic of China: (new) Shuiye Catching Word [2019] no. 4). Following collection, the specimens were preserved in absolute ethanol and deposited at the Rare Fish Research Center at Tarim University (URL: https://yjsb.taru.edu.cn, contact person: Shengao Chen and email: shengao@taru.edu.cn) under voucher number LFY2020066065. Total genomic DNA was extracted from the back muscle of the specimens using an animal mitochondrial DNA column extraction kit (Sequencing Grade, BioRab, Beijing, China), and the extracted genomic DNA was amplified and sequenced through the Illumina NovaSeq 6000 platform using paired-end (2 × 150 bp) sequencing mode. To improve the accuracy of the assembly, the original data were filtered and evaluated. Subsequently, SPAdes v3.14.1 (http://bioinf.spbau.ru/spades) (Bankevich et al. 2012) was used for sequence assembly, and MITOS (Bernt et al. 2013) was used for sequence annotation. In addition, MEGA 7 (Kumar et al. 2016) was used for sequence analysis. The animal experiments were approved by the Ethical Committee for Animal Experiments of Tarim University and conducted following the Guidelines for Experimental Animals of the Ministry of Science and Technology (Beijing, China).

The mitochondrial genome of *S. argentatus* (accession number MZ958820) was 16,587 bp in length, with a base composition of 31.58% A, 31.53% T, 18.4% C, and 18.28% G, showing the order A > T > C > G. The statistical analysis verified that the A + T ratio was significantly higher than the G + C ratio, which is consistent with findings from previous studies on other fish species (Khan et al. 2016; Li et al. 2016). The genome shows the typical structure, including two ribosomal RNA subunits (12S rRNA and 16S rRNA), 13 protein-coding genes, 22 transfer RNA genes (tRNAs), and a noncoding control region (D-loop region). A phylogenetic tree was constructed based on the complete mitochondrial genome sequences of *S. argentatus* and other Cyprinidae species using the neighbor-joining method and bootstrapping with 1000 replicates (Kumar et al. 2016).

The phylogenetic relationships among *S. argentatus* and 18 other Cyprinidae species with complete mitogenome sequences in GenBank were inferred using the neighbor-joining method. As shown clearly in the graph (Figure 1), this
analysis revealed that the Cyprinidae species examined here formed a well-supported monophyletic group and grouped into two major clades. The genera Schizothorax and Oreinus formed one clade that matched the subfamily Schizothoracinae. The other clade consisted of Percocypris, corresponding to the subfamily Barbinae. The constructed phylogenetic tree showed a similar topology, demonstrating that *S. argentatus* was clustered in subfamily Schizothorax and sister to the subfamily Percocypris. *S. argentatus* was sister to *S. pseudoaoksaensis*, both of which are mainly distributed in the Yili River system, clustering with all other congeneric species. Interestingly, *Aspiorhynchus laticeps*, which is closely related to *Schizothorax bidulphi*, did not form a separate branch. The genetic distance between the two genera did not appear to reach the threshold for distinguishing genera; therefore *A. laticeps*, also belonging to the genus Schizothorax, may be a naturalized species (Haisa et al. 2014). Although the support values in the phylogenetic tree are high, some relationships within Nemacheilidae are still vague. In this regard, more genomic datasets are required to better understand the phylogenetic relationships within Schizothorax. We expect the genome sequences obtained in the present study to serve as a valuable genomic resource, to provide useful data for further analysis of evolutionary history and to assist in species identification.

**Figure 1.** Phylogenetic tree of the Cyprinidae family based on the 19 mitochondrial genome sequences in GenBank. GenBank accession numbers are placed next to the species names. Posterior probability values are shown at the nodes.

**Disclosure statement**

The authors report no conflicts of interest, and only the authors are responsible for the content and writing of the article.

**Funding**

This work was supported by the Agricultural Finance Special “Investigation of Fishery Resources and Environment in Key Waters of Northwest China” and the National Natural Science Foundation of China [No. 31360635].

**ORCID**

Shengao Chen http://orcid.org/0000-0003-0716-8511

**Data availability statement**

The genome sequence data that support the findings of this study are openly available in GenBank of the NCBI at https://www.ncbi.nlm.nih.gov/ under accession no. MZ958820. The associated BioProject, SRA, and BioSample numbers are PRJNA820128, SRR18491449, and SAMPN26980527, respectively.

**References**

Bankevich A, Nurk S, Antipov D, Gurevich AA, Dvorkin M, Kulikov AS, Lesin VM, Nikolenko SI, Pham S, Prijibelski AD, et al. 2012. SPAdes: a new genome assembly algorithm and its applications to single-cell sequencing. J Comput Biol. 19(5):455–477.
Bernt M, Donath A, Jühling F, Externbrink F, Florentz C, Fritzsch G, Pütz J, Middendorf M, Stadler PF. 2013. MITOS: improved de novo metazoan mitochondrial genome annotation. Mol Phylogenet Evol. 69(2):313–319.

Guo Y, Zhang R, Cai L. 2012. The fishes of Xinjiang. Urumqi: Xinjiang Science and Technology Press. p. 160–161.

Haisa A, Guo Y, Meng W, Yang T, Ma Y. 2014. Phylogenetic relationship and time of species differentiation of Schizothorax from Xinjiang. Genetic. 36(10):1013–1020.

Khan M, Nasir Khan Khattak M, He D, Liang Y, Li C, Ullah Dawar F, Chen Y. 2016. The mitochondrial genome of *Schizothorax esocinus* (Cypriniformes: Cyprinidae) from Northern Pakistan. Mitochondrial DNA Part A. 27(5):3772–3773.

Kumar S, Stecher G, Tamura K. 2016. MEGA7: molecular evolutionary genetics analysis version 7.0 for bigger datasets. Mol Biol Evol. 33(7):1870–1874.

Li L, Wu J, Zhang S, Wei Q. 2016. Complete mitochondrial genome of *Schizothorax lantsangensis Tsao* (Cypriniformes, Cyprinidae, Schizothoracinae). Mitochondrial DNA Part A. 27(5):3549–3550.