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MITOGENOME ANNOUNCEMENT



The complete mitochondrial genome of *Xenocypris yunnanensis* (Nichols, 1925), threatened fishes of the world

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ABSTRACT

Xenocypris yunnanensis is an endemic species subsisted in Dianchi Lake in China and has been listed as one of the most dangerous species due to the invasion of alien species. In the present study, we determined the first complete mitochondrial genome of *X. Yunnanensis*. This genome was 16,630 bp in size and contained 37 genes (13 protein-coding genes, two ribosomal RNA, 22 transfer RNA genes and one control region). The overall base composition of the heavy strand is that the 31.25% for A, the 27.20% for C, the 16.15% for G and the 25.40% for T. In this study, the complete mitochondrial genome sequencing for *X. yunnanensis* was determined for the first time. The result of phylogenetic analysis indicated is that *X. yunnanensis* is clustered in genus *Xenocypris* as expected. Also, The mitochondrial genome sequencing of *X. yunnanensis* provided important molecular data for conservation genetic studies.

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Xenocypris yunnanensis;
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Introduction

Xenocypris yunnanensis belongs to the order Cypriniformes, Cyprinidae family, and genus *Xenocyprinae*. *Xenocypris yunnanensis* is an endemic species in Dianchi Lake, Kunming, Yunnan, China which is (24°40'–25°02' N, 102°36'–102°47' E, 1,885 m above sea level and covered 306.3 km² (Liu et al. 2009). It has not been seen by frequent aquatic biodiversity surveys (GEF/The World Bank) in the lake and it is considered endangered now. Their greatest threats came through introduction of commercial fishes, such as *Hemibarbus prognathus* into Dianchi Lake. *X. yunnanensis* has already been listed as the most endangered species by the red list of IUCN (2008), as endangered in China Red Data Book of Endangered Animals (Wang and Xie 2004) and China Species Red List, Vol. 1 Red List (Sung et al. 1998).

In this work, a matured *X. yunnanensis* collected from Dianchi Lake during catching season in 2016 by accident was used for the complete mitochondrial DNA sequencing. The total genomic DNA was extracted from alcohol-preserved fin using the traditional phenol-chloroform method (Taggart et al. 1992). Total genomic DNA was extracted from tail tip using the Ezup pillar genomic DNA extraction kit (Sangon Biotech, Shanghai, China). A total of 13 pairs of primers, designed based on the mitochondrial genome of *Xenocypris davidi* (KF039718.1) (Liu 2014), were used to amplify the complete mitochondrial genome. The PCR products were

sequenced using the Sanger method and further assembled into a sequence with CAP3 (Huang and Madan 1999).

The complete mitogenome sequence of *X. yunnanensis* is 16,630 bp in length (GenBank accession number KY993905) and consists of 13 protein-coding genes, two ribosomal RNA, 22 transfer RNA genes and one control region. Among these genes, ND6, tRNA-GAA, tRNA-CCA, tRNA-CAA, tRNA-GCA, tRNA-CGA, tRNA-UAC, and tRNA-UCA are located on the light strand (L-strand), while all the remaining genes on the heavy strand (H-strand). The overall base composition of the heavy strand is 31.25% for A, 27.20% for C, 16.15% for G and the 25.40% for T. The percentage of GC content is 43.35% and AT content is 56.65%.

We constructed a phylogenetic tree including *X. yunnanensis* and the other 20 fish. Phylogenetic relationships obtained with the maximum likelihood approach were identical to those of the Bayesian analysis (Posada and Buckley 2004; Wang et al. 2015). As shown in the phylogenetic tree (Figure 1), *X. yunnanensis* sequence was clustered in genus *Xenocyprinae*, including *Xenocypris argentea*, *Xenocypris davidi*, *Distoechodon tumirostris* and *Plagiognathops microlepis*. Phylogenetic analysis revealed that *X. yunnanensis* is closely related to *X. argentea* and *X. davidi*.

Disclosure statement

No potential conflict of interest was reported by the authors.

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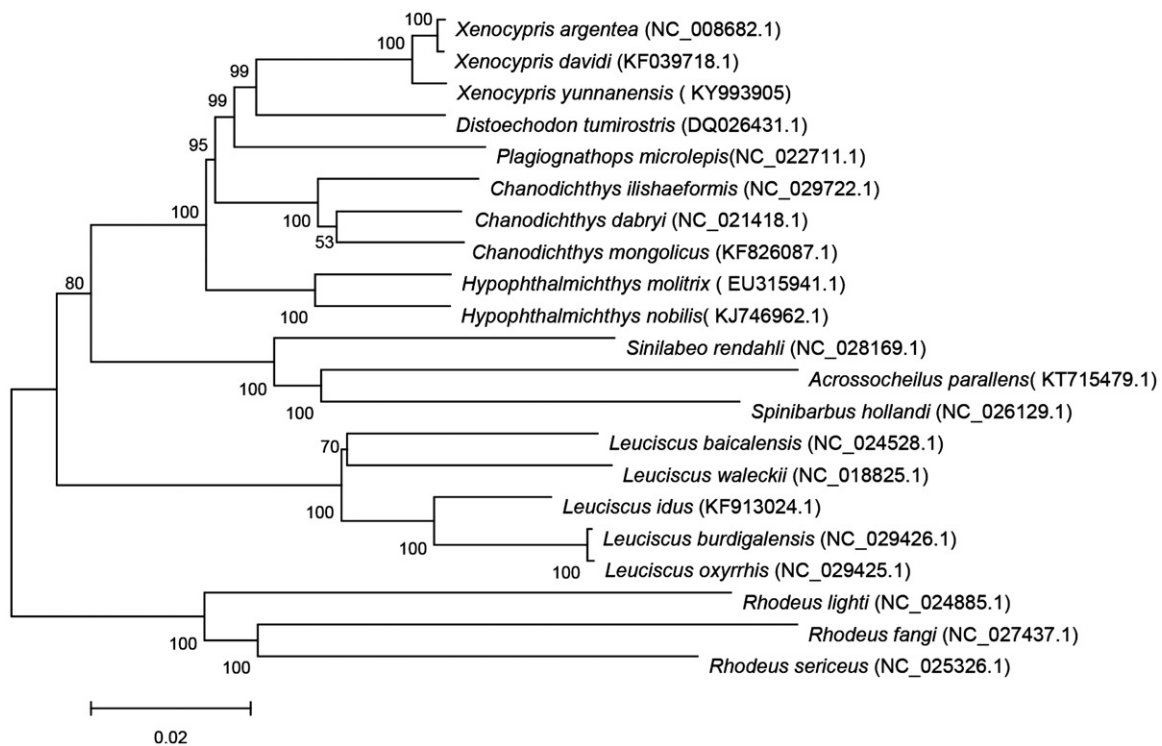


Figure 1. The phylogenetic tree of the 21 species from Cyprinidae was constructed based on complete mitochondrial genome data.

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