MITOGENOME ANNOUNCEMENT

The complete mitochondrial genome of Schizothorax yunnanensis paoshanensis (Cyprinidae: Schizothorax)

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Abstract

In this study, the complete mitochondrial DNA (mtDNA) sequence of Schizothorax yunnanensis paoshanensis is determined for the first time. The complete mtDNA genome sequence of S. yunnanensis paoshanensis is 16,585 bp in length. It consists of 13 protein-coding genes, 22 transfer RNA genes, 2 rRNA genes and a putative control region (D-loop region). The gene order of S. yunnanensis paoshanensis mtDNA is identical to most of the vertebrate mtDNAs. The complete mitogenome sequence information of S. yunnanensis paoshanensis can provide useful data for further studies on molecular systematics, taxonomic status and conservation genetics.

Schizothorax yunnanensis paoshanensis is categorized into subfamily Barbinae, family Cyprinidae. It is an endemic species and limitedly distributed in the Baoshan water area of Nujiang River. Schizothorax yunnanensis paoshanensis is deemed as one of the most important commercial fish species. Due to overfishing, environment pollution and illegal fishing, the fish population declined drastically to the extent of commercial exhaustion (reported by local fishermen). The basic biological information of this species is of significance in developing effective strategies for management of this resource. In addition, it may also provide a genetic tool for aquaculture and offer a scientific support for resources conservation. However, the biological information of this species is still unknown. Therefore, the mitochondrial genome data of S. yunnanensis paoshanensis will be useful for resource management, evolutionary biology and conservation genetics studies of the Cyprinid fish.

In this study, Schizothorax yunnanensis paoshanensis were collected from Nujiang River. The muscle was dissected and preserved in 95% alcohol and stored immediately at −20°C. The complete mitogenome sequence of S. yunnanensis paoshanensis was determined. We designed the primers for PCR amplification and sequenced according to the mtDNA sequence of Schizothorax bididulphi (GenBank Accession No. NC_017873) (Gong et al., 2012), a closely related species of S. yunnanensis paoshanensis. After assembling and alignment, we deposited the complete mitogenome sequence of S. yunnanensis paoshanensis into GenBank database with accession number KP892531. The whole length of mitogenome is 16,585 bp, which contains 13 protein-coding genes, 22 tRNA genes, 2 rRNA genes and a control region (detail shown in GenBank KP892531). The structural organization of mitogenome is identical to that of other Schizothorax (Chen et al., 2013; Goel et al., 2014; Zhu et al., 2013). Most of the genes were encoded on the H-strand except ND6 and eight tRNA genes (tRNAGln, tRNAAla, tRNAAsn, tRNAlys, tRNATyr, tRNAser, tRNAglu and tRNApro) those were encoded on the L-strand, showing the typical gene arrangement conforming the Schizothorax (Chen et al., 2013; Zhu et al., 2013). To represent the phylogenetic relationships between Schizothorax yunnanensis paoshanensis and other Schizothorax species, the complete mitochondrial DNA sequences of S. lantsangsensis (Accession number KP143725), S. dolichonema (KJ184546), S. prenanti (KJ126773), S. chongi (KJ718889), S. davidi (KM879227), S. macropogon (KC021013), S. waltoni (JX202592), S. biddulphi (JQ844133), S. progastus (KF739399), S. labiatus (KF739398), S. richardsonii (KC790369), S. esocinus (KF600713), S. plagiostomus (KF928796) and S. pseudoaaskaiensis (KM079630) were obtained. The complete mtDNA genome sequence of 15 Schizothorax species were from 16,575 to 16,592 bp in length. A Neighbor-Joining (NJ) tree was constructed using the Kimura 2-parameter model with MEGA 4.0 (Tamura et al., 2007) (Figure 1). The Schizothorax yunnanensis paoshanensis and Schizothorax lantsangsensis formed a closed group in the tree, with full statistical reliability (bootstrap value, 100%). Schizothorax pseudoaaskaiensis calculated into a separate group faraway from S. yunnanensis paoshanensis indicated that it is the farthest genetic relationship among S. yunnanensis paoshanensis and the other 14 Schizothorax species obtained from Genbank.

Keywords

Conservation genetics, mitochondrial genome, Schizothorax yunnanensis paoshanensis

History

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Declaration of interest

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References


Figure 1. The Neighbor-Joining tree of 15 *Schizothorax* species.