The complete mitochondrial genomes of *Gobiobotia meridionalis* (Cypriniformes: Cyprinidae)

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**ABSTRACT**

In this study, we sequenced the complete mitogenome of *Gobiobotia meridionalis* (Chen et Tsao, 1982). The genome is 16,609 base pair (bp) in length, encoding 13 protein-coding genes (PCGs), 22 tRNA genes, 2 rRNA genes, and 1 non-coding control region (D-loop). The nucleotide composition is A: 30.34%, T: 26.88%, G: 16.49%, and C: 26.29% (AT content: 55.22%). The complete mitogenome of *G. meridionalis* provides essential and important DNA molecular data for the genetic diversity conservation of this species.

**ARTICLE HISTORY**

Received 7 March 2021
Accepted 12 April 2021

**KEYWORDS**

Gobiobotia meridionalis; mitochondrial genome; phylogeny

*Gobiobotia meridionalis* (Chen et Tsao, 1982), is a small-sized bottom-dwelling fish endemic to China, mainly distributed in Zhuijiang basin, the tributaries of the middle Yangtze River, the Yuanjiang River, and the lower reach of the Lancang River (Chen 1998). It is easy to distinguish *G. meridionalis* from other species of genus *Gobiobotia*, for absence of the basal process of the pelvic fin bone (He 1997). Here, we first determined the complete mitochondrial genome of *G. meridionalis* and reconstructed the phylogenetic relationship with other Gobiobotinae species. It may shed light on some genetic background of *G. meridionalis*, and could provide essential and important DNA molecular data for the genetic diversity conservation of this species.

The specimen of *G. meridionalis* used in this study were obtained from the Fuhe River (116°14′10″E, 26°33′03″N), Jiangxi, China. Muscles were immediately fixed in 95% ethanol until it was picked out for DNA extraction. Some specimens of *G. meridionalis* were deposited in Nanchang Normal University (maqindoris@163.com) under the Voucher number NCNU20200828032.

Total genomic DNA was extracted from muscle samples of *G. meridionalis* using E.Z.N.A.® Tissue DNA Kit (OMEGA,Guangzhou, China) following the manufacturer’s instructions and then sequenced on the Illumina HiSeq platform. The reads were assembled in NOVOPlasty version 4.0 (Dierckxsens et al. 2017, https://github.com/ndierckx/NOVOPlasty) and annotated using MITOS webserver (Bernt et al. 2013). Protein-coding genes (PCGs) and rRNAs were rechecked by aligning them with the published mitogenomes of the *Gobiobotia filifer* (Garman, 1912) (Li et al. 2016).

The complete mitogenome of *G. meridionalis* was a circular DNA of 16,609 bp in length (GenBank with the accession number of MW442088) and contained 13 PCGs (cyt b, ATP6, ATP8, COX1-3, ND1-6, and ND4L), 22 tRNA genes, 2 rRNA genes (12S and 16S rRNA), and 1 control region (CR or D-Loop). It played similar patterns in gene arrangements, codon use, and gene overlaps, which have been reported in other Gobioninae mitogenomes (Hwang et al. 2013; Li et al. 2018).

Eight tRNA genes (Ala, Asn, Cys, Gin, Glu, Tyr, Ser, and Pro) and NADH dehydrogenase subunit 6 (ND6) are encoded on the light strand (L-strand), the other 29 genes are encoded on the heavy strand (H-strand). The nucleotide composition is A: 30.34%, T: 26.88%, G: 16.49%, and C: 26.29% (AT content: 55.22%). Almost all 13 PCGs for *G. meridionalis* share the regular initiation codon ATG except COI gene with GTG. There are three different patterns of termination codons: nine PCGs (terminated with the stop codons TAA or TAG, while three PCGs (cyt b, COX2, COX3, and ND4) use incomplete stop codon (TA– or T–).

The phylogenetic trees of Gobiobotinae were reconstructed based on whole mitogenome dataset. Phylogenetic relationships of Gobiobotinae were reconstructed based on the multiple alignments of 17 mitochondrial genomes within this subfamily (Hwang et al. 2013; Hwang et al. 2014a, 2014b; Li et al. 2015, 2016, 2018; He et al. 2016; Tao and Zhao 2016). Outgroup taxa were selected based on a previous study (Tang et al. 2011). Neighbor-joining (NJ) analysis was conducted using MEGA version 7 (Kumar et al. 2016, https://www.megasoftware.net) with 1000 bootstrap replicates. As in the previous study, our phylogeny also revealed that the
genera *Gobiobotia* was monophyletic (Tang et al. 2011; Li et al. 2018). The phylogenetic tree strongly supported the close relationship of *Gobiobotia naktongensis* (Mori, 1935), *Gobiobotia pappenheimi* (Kreyenberg, 1911), *Gobiobotia intermedia* (Banarescu et Nalbant, 1968), *G. filifer*, and *G. meridionalis* (Figure 1). In the tree, *G. naktongensis*, *G. pappenheimi*, *G. intermedia*, and *G. filifer* formed a clade sister to *G. meridionalis*, which was also congruent with the previous studies (Tang et al. 2011).

**Disclosure statement**

No potential conflict of interest was reported by the author(s).

**Funding**

This work was supported by Scientific Research Project of Jiangxi Provincial Education Department [GJJ191133], Startup Foundation of Doctor Scientific Research Projects of Nanchang Normal University [NSBSJJ2018029] and Natural Science Foundation of Jiangxi Province [20161BAB214154].

**Data availability statement**

The data that support the findings of this study are openly available in Genbank with the accession codes MW442088 (https://www.ncbi.nlm.nih.gov/nuccore/MW442088).

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