The complete mitochondrial genome of *Pseudomugil furcatus* (Atheriniformes: Pseudomugil) and phylogenetic studies of Atheriniformes

Qi Wang\(^a\), Jian Chen\(^b\), Zengliang Miao\(^b\), Youkun Huang\(^a\),b, Fang Meng\(^a\),b, Kehua Zhu\(^a\),b, Bingjian Liu\(^a\),b and Yifan Liu\(^a\),b

\(^a\)National Engineering Research Center for Marine Aquaculture, Zhejiang Ocean University, Zhoushan, PR China; \(^b\)National Engineering Laboratory of Marine Germplasm Resources Exploration and Utilization, Marine Science and Technology College, Zhejiang Ocean University, Zhoushan, PR China

**ABSTRACT**

Complete mitochondrial genome of the atheriniform fish *Pseudomugil furcatus* was characterized in this study. The whole mitogenome was 16,753 bp in size and consisted of 13 protein-coding genes (PCGs), 22 tRNAs, 2 rRNA genes, a control region, and origin of light-strand replication. The proportion of coding sequences with a total length of 11,499 bp was 68.64%, which encoded 3869 amino acids. The base composition of the genome was 27.00% for A, 27.31% for C, 15.56% for G, and 30.13% for T. Most mitochondrial genes are encoded on the H-strand except for ND6 and eight tRNA genes (*Gln*, *Ala*, *Asn*, *Cys*, *Tyr*, *Ser*, *Glu*, and *Gly*), which are encoded on the L-strand. The proportion of coding sequences with a total length of 11,499 bp is 68.64%, 13 PCGs encode 3869 amino acids in total. A-T and G-C contents of mitochondrial genome are 57.13% and 42.87%, respectively.

All the PCGs use the initiation codon ATG, which is quite common in vertebrate mtDNA (Miya et al. 2001; Liu et al. 2017). ND1, ND2, CO1, CO3, ND4L, and CytB end by TAA as a stop codon, ATP8, ND3, ND5, and ND6 end by TAG, whereas CO2, ATP6, ND4 ended with single T, the other PCGs commonly ended with TAA. The length of 12S ribosomal RNA was 948 bp, while that of 16S ribosomal RNA was 1744 bp. The control region (D-loop) ranging from 15,774 to 16,753 bp was 980 bp in size. The complete mitochondrial genome sequence provided here could be a useful information for the management of *P. furcatus*.

**CONTACT** Yifan Liu et999927@163.com National Engineering Laboratory of Marine Germplasm Resources Exploration and Utilization, Marine Science and Technology College, Zhejiang Ocean University, Zhoushan, PR China

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*Pseudomugil furcatus* belongs to the family Melanotaeniidae and the order Atheriniformes, distributed in rainforest streams. However, few reports about its basic biology data including genetic information have been indexed up to the present. In this study, we determined the complete mitochondrial genome of *P. furcatus*, which would supplement the limited data on molecular level and be reference for systematics.

Specimens of *P. furcatus* were collected from Papua New Guinea south-east of Popondetta (8°45′56″S, 148°14′05″E) and stored in a refrigerator for −80°C in Zhejiang Engineering Research Center for Mariculture and Fishery Enhancement Museum (Accession number: PH180341). Total genomic DNA was extracted from the muscle of three different individuals using the phenol–chloroform method. The calculation of base composition and phylogenetic construction was conducted using MEGA version 6.0 software (Tamura et al. 2013). The transfer RNA (tRNA) genes were generated with the program tRNAscan-SE (Lowe and Eddy 1997). The mitochondrial genome sequence of *P. furcatus* with the annotated genes was deposited in GenBank with the accession number MT112897.

Similar to the typical mitogenome of vertebrates, the mitogenome of *P. furcatus* is a closed double-stranded circular molecule of 16,753 bp including 13 protein-coding genes (PCGs), 2 ribosomal RNA genes, 22 tRNA genes, and 2 main noncoding regions (Boore 1999; Zhu et al. 2018). The contents of A, C, G, and T are 27.00%, 27.31%, 15.56%, and 30.13%, respectively. Most mitochondrial genes are encoded on the H-strand except for ND6 and eight tRNA genes (*Gln*, *Ala*, *Asn*, *Cys*, *Tyr*, *Ser*, *Glu*, and *Gly*), which are encoded on the L-strand.

All the PCGs use the initiation codon ATG, which is quite common in vertebrate mtDNA (Miya et al. 2001; Liu et al. 2017). ND1, ND2, CO1, CO3, ND4L, and CytB end by TAA as a stop codon, ATP8, ND3, ND5, and ND6 end by TAG, besides three incomplete termination codons (T) were found in the other genes (CO2, ATP6, and ND4). The lengths of 12S ribosomal RNA and 16S ribosomal RNA are 948 and 1744 bp, which are both located in the typical positions between tRNA-Phe and tRNA-Leu (UUA), separated by tRNA-Val (Petillo et al. 2006; Huang et al. 2019). The length of control region (D-loop) is 980 bp, ranging from 15,774 to 16,753 bp.

The neighbor-joining (NJ) tree results suggested that *P. furcatus* was most closely related to *Craterocephalus stramineus* among all the Atheriniformes species included in the analysis. This result is consistent with the conventional morphological taxonomy (Figure 1).
Disclosure statement
No potential conflict of interest was reported by the author(s).

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