Complete mitogenome genome of the hybrid loach of Paramisgurnus dabryanus ssp. (female) and Misgurnus bipartitus (male)

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ABSTRACT

The hybrid loach of Paramisgurnus dabryanus ssp. (female) and Macrobrachycephalus rubripinnis (male) have the desirable trait of growth performance. In this study, the complete mitogenome of this hybrid loach was obtained, and the genome is 16,569 bp in length, including 2 ribosomal RNA genes, 13 proteins-coding genes, 22 transfer RNA genes, and a non-coding control region. Sequence analysis showed that the overall base composition is 29.4% for A, 27.5% for T, 26.4% for C, and 16.7% for G. The phylogenetic tree showed the hybrid loach to be one of the Paramisgurnus. Also, the mitochondrial genome sequence of loach was aligned by BLAST, when compared with Cobitinae the sequence similarity could reach >90%, and the similarity to Paramisgurnus was >99%. Mitogenome information from this study could be a useful basis for conservation and phylogenetics of this hybrid loach.

Taiwanese loach (Paramisgurnus dabryanus ssp.) was bred in Formosa and then widely cultivated in China. The Taiwanese loach and Misgurnus bipartitus is a commercially important Cypriniformes fish species in Asia. The hybrid loach of P. dabryanus ssp. (female) and M. bipartitus (male) have the desirable trait of growth performance. Recently, farming scale of the hybrids has been gradually increased in Asia, promising a new variety for loach. There is no report of the complete genome of this hybrid. Therefore, it is very important to characterize the complete mitogenome of this species, which can be utilized in research on taxonomic resolution, population genetic structure and phylogeography, and phylogenetic relationship (Zhang, Wang et al. 2016).

In this study, we sequenced the complete mitogenome of this hybrid with a GenBank accession number MK714038. The voucher specimen was collected from Zhili Fanyi aquaculture base, north latitude 30°22' and east longitude 120°25', Huizhou city, China, which were stored in biology herbarium of Heze University. Its tailfins were preserved in 95% alcohol. All DNA were extracted using phenol–chloroform extraction methods and stored at –80°C (Zhang, Tao et al. 2016). The complete mitochondrial genome sequences were amplified by primers which were initially published for P. dabryanus (Dai et al. 2016).

The complete mitochondrial genome was 16,569 bp in length, including 2 ribosomal RNA genes, 13 proteins-coding genes, 22 transfer RNA genes, and a non-coding control region, which was similar to other fishes. The overall base composition was 29.4% for A, 27.5% for T, 26.4% for C, and 16.7% for G. Most of the protein genes used ATG as the initiation codons (ND1, ND2, COX2, ATP8, ATP6, COX3, ND3, ND4L, ND4, ND5, Cytb), except for COX1 and ND6 genes, which used GTG and ATA instead of ATG. Eight protein-coding genes ended with incomplete stop codon, except for COX1 and ND6 genes, which used TAG as termination codons. Gene ND4 used TAG as termination codons, and ND6 use CAT instead of TAA. COX2, COX3, and Cytb share the incomplete stop codon T–. Except for eight tRNA, (tRNASer, tRNAPro, tRNAHis, tRNAAsp, tRNAAla, tRNAThr, tRNAArg, tRNAVal) and the ND6 gene encoded on the L-strand, the other genes were encoded on the H-strand. The 21 kinds of tRNA, tRNALeu, and tRNAVal repeated in the complete mitochondrial genome, respectively. This feature is similar to other fish mitochondrial genes. The complete mitogenome sequence had 16s RNA (1678 bp) and 12s RNA (953 bp), which were located between tRNAPro and tRNALeu, and were separated by tRNAVal genes. The location is same with most vertebrates that has high conservative. As in most vertebrates, two non-coding regions were found in the hybrid loach mtgenome, the only CR (913 bp) gene located between tRNAPro and tRNAVal, and an OL

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(30 bp) was located between tRNA^{Asn} and tRNA^{Cys}. The 21 tRNA genes, ranging from 66 to 76 bp in size, except for tRNA^{Ser(AGY)} which lacks a dihydrouridine arm, could be folded into cloverleaf secondary structure. The origin of L-strand was in the WANCY region including five tRNA genes (tRNA^{Trp}, tRNA^{Ala}, tRNA^{Asn}, tRNA^{Cys} and tRNA^{Tyr}) and it can fold into a stem-loop secondary structure with the conserved motif 50-GCCGG-30.

To determine the taxonomic status of the hybrid loach, we performed the phylogenetic relationship of this loach stock with other natural populations in loach as inferred by entire mitogenome (Fan et al. 2018). The phylogenetic tree showed the hybrid loach to be one of the Paramisgurnus species (Figure 1). Also, the mitochondrial genome sequence of loach were aligned by BLAST, when compared with Cobitinae the sequence similarity could reach >90%, and the similarity to Paramisgurnus was >99%.

**Disclosure statement**

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**References**

Dai L, Guo B, Chu Z, Wang Y, Wang X, Huang T. 2016. Complete mitochondrial genome of Paramisgurnus dabryanus. Mitochondrial DNA A. 27:1257–1258.

Fan L, Tan H, Fazhan H, Xie Z. 2018. The complete mitochondrial genome and phylogenetic analysis of Matuta planipes (Decapoda: Brachyura: Matutidae), Mitochondrial DNA B. 3:157–158.

Zhang G, Tao P, Chen J, Wang R, Zang X, Yin S. 2016. The complete mitochondrial genome of the hybrid of Pelteobagrus fulvidraco (♀) × Pelteobagrus vachelli (♂), Mitochondrial DNA A. 27:2–5.

Zhang G, Wang R, Mao J, Yin S, Tao P, Chen J, Yu X, Tang Z, Chen S. 2016. The complete mitochondrial genome and phylogenic analysis of Pseudobagrus vachelli. Mitochondrial DNA A. 27:3551–3355.