The complete mitochondrial genome of *Nematobrycon palmeri* (Characiformes:Nematobrycon) and phylogenetic studies of Characidaes

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**ABSTRACT**

Complete mitochondrial genome of the Characiform fish *Nematobrycon palmeri* was characterized in the present study. The whole mitogenome was 17,340bp in size and the proportion of coding sequences with a total length of 11,448bp was 66.02%, which encodes 3805 amino acids. The base composition of the genome was 30.92% for A, 23.92% for C, 14.88% for G, and 30.28% for T. All protein-coding genes were started with ATG, CO1 and ATP8 ended by AGG, TAG respectively, whereas CO2, ATP6, ND4 ended by a single T, the other PCGs commonly ended by TAA. The length of 12S and 16S ribosomal RNA was 949bp and 1675bp, respectively. The control region (D-loop) ranging from 15,654bp to 17,340bp was 1687bp in size. It showed negative GC skew value (−0.2329) and positive AT skewness (0.0105). Phylogenetic analysis showed that *N. palmeri* was most closely related to *Gephyrocharax atracaudatus*. The complete mitochondrial genome sequence would provide a new insight into taxonomic classification, and help to draw a more complete picture of species diversity within the Characidae.

*Nematobrycon palmeri* belongs to the family Characidae and the order Characiformes, a species of characid fish found in the Atrato and San Juan river basins in western Colombia. Though diverse species based on anatomical diversity have been added to each genus, but there is hardly any sequences on the Nematobrycon. We are at loss here to assess properly the status of species of Nematobrycon relevant to our review because their descriptions are incomplete and/or misleading. In this study, we determined the complete mitochondrial genome of *N. palmeri*, which would supplement the limited data on molecular level and even be reference for systematics.

Specimens of *N. palmeri* were collected from San Juan river basin of Colombia (4°02’42”N, 77°26’29”W) and stored in a refrigerator of –80 °C in Zhejiang Engineering Research Center for Mariculture and Fishery Enhancement Museum (Accession number: PH181922). Total genomic DNA was extracted from muscle of three different individuals using the phenol–chloroform method (Barnett and Larson 2012). The calculation of base composition and phylogenetic construction were conducted by MEGA6.0 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 *N. palmeri* was sequenced by Sanger dideoxy and assembled by CodonCode Aligner 5.1.5 (CodonCode Corporation, Dedham, MA), the annotated genes was deposited in GenBank with the accession number MN861079.

Similar to the typical mitogenome of vertebrates, the mitogenome of *N. palmeri* is a closed double-stranded circular molecule of 17,340bp including 13 protein-coding genes, 2 ribosomal RNA genes, 22 tRNA genes and two main non-coding regions (Boore 1999; Zhu et al. 2018). The contents of A, C, G, and T are 30.92%, 23.92%, 14.88%, and 30.28%, 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 Pro), which are encoded on the L-strand. The proportion of coding sequences with a total length of 11,448bp is 66.02%, 13 protein-coding genes (PCGs) encode 3805 amino acids in total. A-T and G-C contents of mitochondrial genome were 61.21% and 38.79%, respectively, thereby with a high AT bias. Besides, it showed negative GC skew value (−0.2329), indicating that C base was more common than G base, whereas AT skewness was positive (0.0105), suggesting A base occurs more frequently than T base in the *N. palmeri* mitochondrial genome.

All the protein-coding genes use the initiation codon ATG, which is quite common in vertebrate mtDNA (Miya et al. 2001; Liu et al. 2017). ND1, ND2, CO3, ND3, ND4L, ND5, ND6 and CytB end by TAA as a stop codon, CO1 and ATP8 end by AGG, TAG respectively, and three incomplete termination codons (T) were found in the other genes (CO2, ATP6, and ND4). The content of Cys in 13 PCGs was the lowest accounting for 0.79% and there were 5 amino acids (from high to low: Leu 16.35%, Ala 8.36%,...
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Data availability statement
The data that support the findings of this study are openly available at NCBI (https://www.ncbi.nlm.nih.gov), GenBank accession no. MN861079. And the data that support the findings of this study are also available from the corresponding author, Dr. Liu, upon reasonable request.

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