

Identification and phylogenetic analysis of the mitochondrial genome of *Hemibarbus labeo* BML (Cypriniformes: Cyprinidae)

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ABSTRACT

The complete mitochondrial genome of *Hemibarbus labeo* BML (Cypriniformes: Cyprinidae) is 16,612 bases in length. It consists of 22 tRNA genes, 13 protein-coding genes, 2 rRNA genes, and 1 non-coding region. Its overall nucleotide composition is A: 29.85%, G: 17.07%, T: 25.86%, and C: 27.23%, respectively, with an A + T rich feature (55.71%). The gene arrangement and organization of the mitochondrial genome from *H. labeo* BML were very similar to other Cyprinidae fishes. The phylogenetic analysis showed that *H. labeo* BML clustered in genus *Hemibarbus*. These results will contribute to the taxonomy and conservation biology studies of *H. labeo*.

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The *Hemibarbus labeo* (Cypriniformes: Cyprinidae) is a small benthic fish distributed widely in China (Xu et al. 2007; Lian et al. 2012; Wu 2015; Lan et al. 2016; Gao et al. 2017). It is artificial cultured (Xu et al. 2009; Li et al. 2015; Zhang et al. 2015; Luo et al. 2016), and used as a commercially important fish because of its tender meat and high nutrition (Gu et al. 2006; Lu et al. 2007; Li et al. 2011; Lian et al. 2011; Lv et al. 2015; Chen et al. 2019; Wei et al. 2020).

The Baima Hu Lake, a small famous lake in Shangyu district, Shaoxing city, East China. The wild population of *H. labeo* in this Lake declines rapidly because of increasing capture pressure and dredging works.

Sequencing and identify the complete mitogenome and analyze its phylogenetic relationships with the related species are necessary for the taxonomy and sustainable utilization of *H. labeo*. In the present study, the complete mitochondrial genome was sequenced and identified from an individual of *H. labeo* sampled from the Baima Hu Lake of eastern China (33°13'47.7"N, 119°08'49.4"E), and was kept in 99% ethanol in the Aquatic Service Platform of Shaoxing (accession no. SXAF20200512). The genomic DNA was extracted and used as template.

Comparison of mitogenome data could be a powerful tool for taxonomy and conservation biology studies (Min and Park 2009; Chen et al. 2013; He et al. 2014).

The complete mitogenome sequence of *H. labeo* BML (GenBank accession no. MT478137) was determined to be 16612 bp in length. It consists of 22 tRNA genes, 13 protein-coding genes (PCDs), 2 rRNA genes, and 1 control region. The gene arrangement and organization of all encoded

genes of the mitogenome from *H. labeo* BML were very identical to other Cyprinidae fishes (He et al. 2014; Wang et al. 2015).

The overall nucleotide composition of the *H. labeo* mitochondrial genome is A: 29.85%, G: 17.07%, T: 25.86%, and C: 27.23%, respectively, which shows an A + T rich feature (55.71%) as that of other vertebrate mitochondrial genomes (Tzeng et al. 1992; Jondeung et al. 2007; He et al. 2014). All of the genes were encoded on the heavy strand (H-strand), except one PCG (*ND6*) and eight tRNA genes (tRNA^{Ala}, tRNA^{Asn}, tRNA^{Cys}, tRNA^{Gln}, tRNA^{Glu}, tRNA^{Pro}, tRNA^{Ser(UCN)}, and tRNA^{Tyr}).

The complete mitogenome sites have 106 variable sites between *H. labeo* BML and *H. labeo* (GenBank accession no. KP064328), accounted for 0.64% of the complete mitogenome sites, these base variation were detected not only in various PCD genes but also in the non-coding region (D-loop).

Based on the complete mitochondrial genome sequences of *H. labeo* BML and other Cyprinidae fishes, a phylogenetic tree was constructed by the NJ method (Figure 1). The mitogenome of *H. labeo* BML shows more closer relationship with other *Hemibarbus* fishes including *H. labeo* (Kim et al. 2009), *H. barbus*, *H. maculatus*, *H. medius*, *H. umbrifer*, *H. mylodon*, and *H. longirostris*. These results showed that, the mitogenome sequence can provide useful information in the taxonomy and conservation biology studies of *H. labeo* and other fish species.

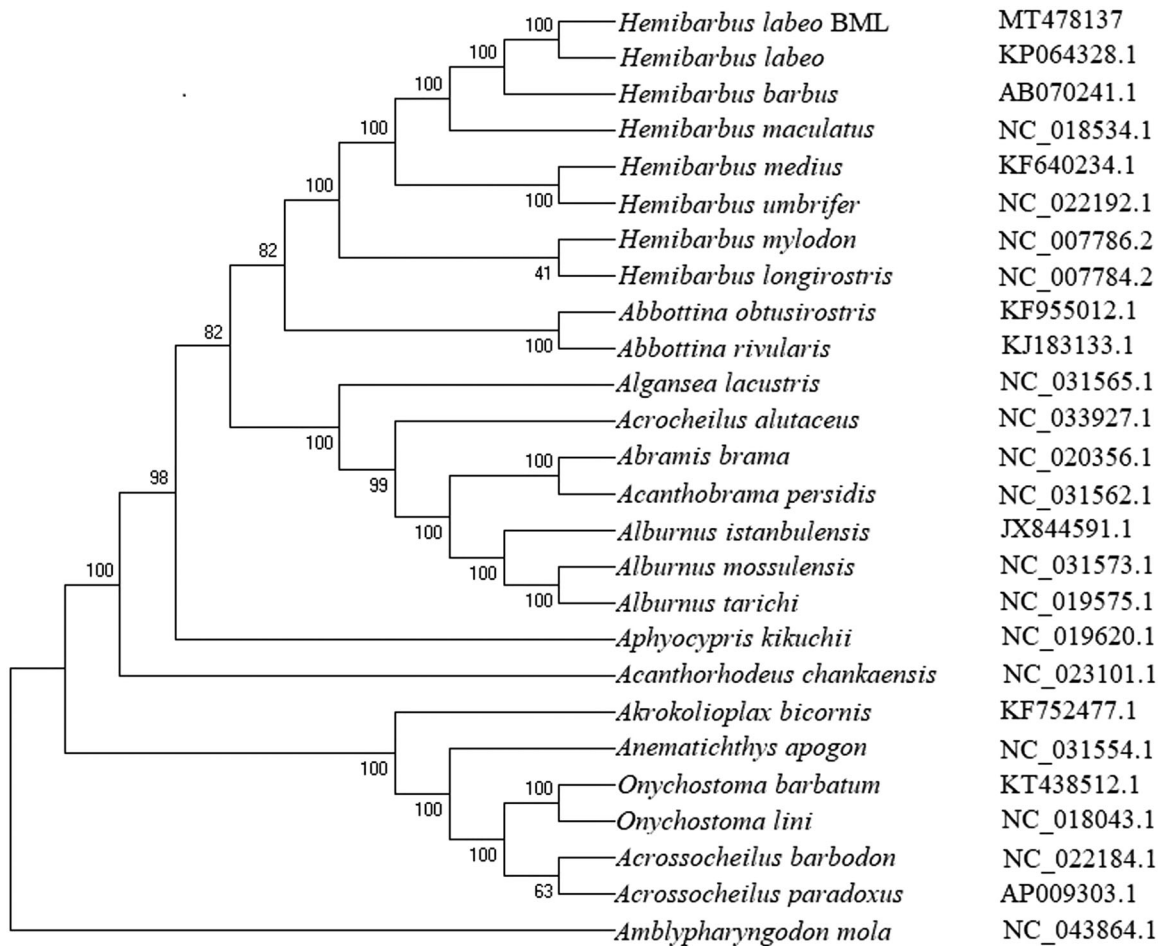


Figure 1. The phylogenetic analysis of *H. labeo* BML and other Cyprinidae fishes based on the mitogenome sequences.

Disclosure statement

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

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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. MT478137. And the data that support the findings of this study are also available from the corresponding author, Dr. Yang, upon reasonable request.

References

- Chen J, Lv YP, Dai QM, Hu ZH, Liu ZM, Li JH. 2019. Host defense peptide LEAP-2 contributes to monocyte/macrophage polarization in barbel steed (*Hemibarbus labeo*). *Fish Shellfish Immunol.* 87:184–192.
- Chen X, Zhou ZM, Chen ZJ, Ai WM. 2013. Complete mitochondrial genome of *Sarcocheilichthys parvus* (Cypriniformes, Cyprinidae). *Mitochondrial DNA.* 24(2):97–98.
- Gao SB, Chi SY, Li SX, Zhen JX, Dong FY. 2017. Fish resource investigation and species diversity analysis of Nanxi river in Zhejiang Province. *J Hydroecol.* 38(6):72–81.
- Gu RB, Wen HB, Xu GC. 2006. Evaluation of nutritive quality and nutritional components in *Hemibarbus maculatus* Bleeker muscle. *J Dalian Fish Univ.* 21(04):378–382.
- He L, Yang S, Zheng D, Li C, Tao G, Wei M, Wang H. 2014. Complete mitochondrial genome of *Pseudorasbora elongata* (Cypriniformes: Cyprinidae): sequencing and analysis. *Mitochondrial DNA.* 25(6):433–434.
- Jondeung A, Sangthong P, Zardoya R. 2007. The complete mitochondrial DNA sequence of the Mekong giant catfish (*Pangasianodon gigas*), and the phylogenetic relationships among Siluriformes. *Gene.* 387(1–2):49–57.
- Kim KY, Lim YH, Bang IC, Nam YK. 2009. Phylogenetic relationships among three new *Hemibarbus* mitogenome sequences belonging to the subfamily Gobioninae (Teleostei, Cypriniformes, and Cyprinidae). *Mitochondrial DNA.* 20(5–6):119–125.
- Lan ZJ, Fan MJ, Huang XL, Zhao J. 2016. Population diversity and phylogeography of *Hemibarbus labeo* and *Hemibarbus medius* in South China. *Acta Ecol Sin.* 36(19):6091–6102.
- Li J, Luo XN, Jin GS, Wei HX. 2015. Growth performance and models of *Hemibarbus labeo* cultured in net cages. *J Guangdong Ocean Univ.* 35(1):99–103.
- Li J, Luo XN, Li JW, Jin GH, Xia DM, Qi Z, Liu ZY, Liu Y, Zhao LW. 2011. Evaluation of nutritive quality and nutrient components in the muscle of *Hemibarbus labeo* pallas. *J Shenyang Agric Univ.* 42(1):59–64.
- Lian QP, Mi GQ, Hu TJ, Wang YC, Shen TS, Yao ZL. 2011. Morphological variations in skin carp *Hemibarbus labeo*, *H. maculatus*

- and their hybrid F1 (*H. labeo*♀ × *H. maculatus*♂). *J Dalian Ocean Univ.* 26(06):493–499.
- Lian QP, Yuan JL, Zhang AJ, Yao ZL, Wang KW, Lu J, Mi GQ. 2012. Preliminary investigation of fishery resources in Lishui section of Oujiang river. *Acta Agric Univ Jiangxi.* 34(2):351–357.
- Lu YP, Cao MF, Yao ZL, Wang MH. 2007. The dressing race and nutritional composition of muscle in spotted steed (*Hemibarbus maculatus*) and skin carp (*Hemibarbus labeo*). *Acta Hydrobiol Sin.* 31(6):843–848.
- Luo XN, Xu ZY, Han RZ, Xu HR, Du Y. 2016. Biological research progress of *Hemibarbus labeo* cultivation: a review. *J East Liaoning Univ (Nat Sci).* 23(2):97–103.
- Lv YP, Yao WJ, Chen J, Bao BL. 2015. Newly identified gene muscle segment homeobox C may play a role in intermuscular bone development of *Hemibarbus labeo*. *Genet Mol Res.* 14(3):11324–11334.
- Min GS, Park JK. 2009. Eurotatorian paraphyly: revisiting phylogenetic relationships based on the complete mitochondrial genome sequence of *Rotaria rotatoria* (Bdelloidea: Rotifera: Syndermata). *BMC Genomics.* 10(533):513–533.
- Tzeng CS, Hui CF, Shen SC, Huang PC. 1992. The complete nucleotide sequence of the *Crossostoma lacustre* mitochondrial genome: conservation and variations among vertebrates. *Nucleic Acids Res.* 20(18):4853–4858.
- Wang H, Li C, Yang X, Yang S, Han J, He L, Wei M, Chen C, Cai L. 2015. The complete mitochondrial genome of *Pseudobagrus ondon* Shaw. *Mitochondr DNA.* 26(4):631–632.
- Wei J, Jie C, Zhi PG, Le Z, Guang PC. 2020. Molecular characterization of a MOSPD2 homolog in the barbel steed (*Hemibarbus labeo*) and its involvement in monocyte/macrophage and neutrophil migration. *J Mol Immunol.* 119:8–17.
- Wu RL. 2015. Study on the correlation between the morphological characters and body weight of two-year-old *Hemibarbus labeo*. *J Anhui Agric Sci.* 43(20):110–138.
- Xu W, Li CT, Cao DC. 2007. Preliminary study on the effects of food and temperature on the growth of *Hemibarbus labeo*. *J Zhejiang Ocean Univ (Nat Sci).* 26(3):339–342.
- Xu W, Li CT, Geng LW, Sun HW, Liu XY. 2009. Growth and reproduction of reared *Hemibarbus labeo* in the Wusuli River. *J Fish Sci China.* 16(4):550–556.
- Zhang JS, Zhang ZP, Chen WQ, Xiong ZS, Mao RX, Hu GH. 2015. Effects of dietary carbohydrate level on growth and feed utilization in skin carp *Hemibarbus labeo*. *Chin J Fish.* 28(1):34–38.