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The complete mitochondrial genome of a Pabdah catfish, *Ompok pabda* (Hamilton, 1822)

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ABSTRACT

The complete mitochondrial genome of Pabdah catfish, *Ompok pabda* (Hamilton, 1822) was determined by MiSeq platform. The genome was 16,512 bp in length, in which canonical 13 protein-coding genes, 22 tRNAs, 2 rRNAs, and a control region (D-Loop) were encoded. The overall A + T (55.10%) content was higher than G + C (44.90%). Total nine genes were located at the L strand, and remaining 28 genes were at the H strand. The start codon of 12 protein-coding genes was ATG, except for COX1 (GTG). Incomplete stop codon (TA–/T–) was identified in six genes including COXII, COXIII, ND2, ND3, ND4, and Cytb. The mitogenome of *O. pabda* showed highest sequence identity with *O. bimaculatus* (86%).

ARTICLE HISTORY

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Next-generation sequencing; *Ompok pabda*; mitochondrial genome; phylogeny

The Pabdah catfish, *Ompok pabda* is a silurid fish, widely distributed in freshwaters of Bangladesh, Pakistan, India, Afghanistan, and Myanmar (Talwar and Jhingran 1991; Mukhopadhyay and Ghosh 2007). Although *O. pabda* has been considered as one of the most economically important catfish in Southeastern Asian countries, its population sharply declined due to the overexploitation, pollution, and destruction of habitat due to anthropogenic activities (Chakrabarti et al. 2009; Banik and Bhattacharya 2012; Chaklader et al. 2016). *O. pabda* is currently categorized as the endangered fish species in Bangladesh (Bangladesh 2000) and India (Molur and Walker 1998). *O. pabda* shares habitats with its relatives, such as *Ompok pabo*, and *Ompok bimaculatus* (Talwar and Jhingran 1991; Froese and Pauly 2011), their molecular identification would be an easy alternative way to manage their resources.

O. pabda was collected from the river in Khulna, Bangladesh (22°50'44.3" N, 89°32'27.7" E) in March 2017. The specimen was identified by its morphological characteristics and its identity of COI sequence in the NCBI database (GenBank number: KT762383). The specimen was stored in the Department of Fisheries and Marine Science laboratory, Noakhali Science and Technology University, Noakhali, Bangladesh. The full mitochondrial genome sequence of *O. pabda* was determined by next-generation sequencing (NGS) platform. Mitochondrial DNA was extracted by the mitochondrial DNA isolation kit (Abcam, Cambridge, UK) and the purified mitochondrial DNA was

further fragmented into smaller sizes (~350 bp) by Covaris M220 Focused-Ultrasonicator (Covaris Inc., Woburn, MA). A library was constructed by TruSeq[®] RNA library preparation kit version 2 (Illumina, San Diego, CA), and its quality and the quantity was analysed by 2100 Bioanalyzer (Agilent Technologies, Inc., Santa Clara, CA). The high-throughput sequencing was performed by MiSeq system with 600-cycle kit (Illumina, San Diego, CA). Geneious R11 software (Kearse et al. 2012) was applied for the mitogenome assembly. Phylogenetic tree was constructed by MEGA version 7 software (Kumar et al. 2016) with minimum evolution (ME) algorithm.

The complete mitochondrial genome of *O. pabda* (GenBank Number: MK007074) was 16,512 bp in length, which consisted of 13 protein-coding genes, 22 tRNAs, two ribosomal RNAs (12S and 16S), and a control region (D-Loop). The overall composition of A + T (55.10%) was higher than the G + C (44.90%) content. Total nine genes were located at the L strand, whereas remaining 28 genes were at the H strand. Twelve protein-coding genes showed canonical start codon (ATG), while COX1 starts with GTG. Incomplete stop codon (TA–/T–) was identified in six genes including COXII, COXIII, ND2, ND3, ND4, and Cyt b. Based on the COI region, *O. pabda* was most closely related to *O. pabo* with 99% sequence identity (KX455911) followed by *O. bimaculatus* (88%, NC036233). Genus *Ompok* is recognized to be paraphyletic and *O. pabda* was clustered with the *Siluridae* family group.

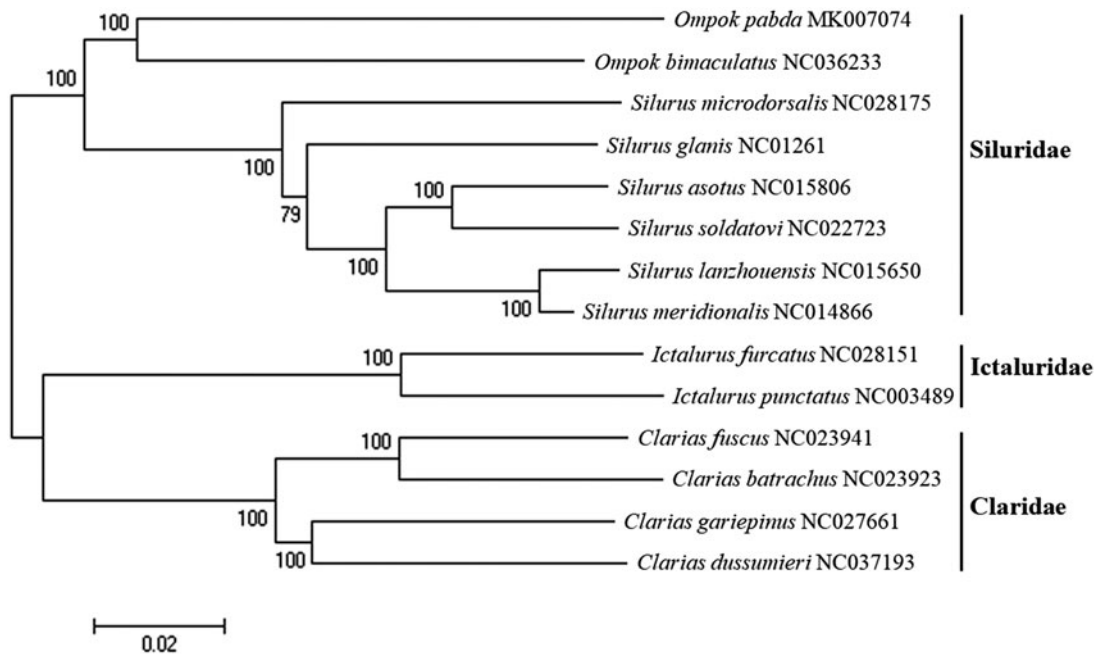


Figure 1. Phylogenetic tree of *Ompok pabda* within Siluridae, Ictaluridae, and Claridae. Phylogenetic tree of *Ompok pabda* complete genome was constructed by MEGA version 7 software with minimum evolution (ME) algorithm with 1000 bootstrap replications. GenBank Accession numbers were shown followed by each species scientific name.

The phylogenetic tree of *O. pabda* was constructed with other seven complete mitogenomes in *Siluridae*, two from *Ictaluridae*, and four from *Claridae* by MEGA version 7.0 program with ME algorithm (Kumar et al. 2016). Based on the full mitogenome sequences to the NCBI database, *O. pabda* showed the highest similarity to *O. bimaculatus* (GenBank number: NC036233) with 86% nucleotide sequence identity (Figure 1).

Disclosure statement

The authors report that they have no conflicts of interest. The authors alone are responsible for the content and writing of the article.

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