The complete mitochondrial genome of *Pseudobagrus pratti* and its phylogeny

Yuanchao Zou**, Meng Xie**, Cheng Tang*, Xin Li*, Peng Fu*, Junying Zhang* and Xinbin Duan**

*College of Life Sciences, Conservation and Utilization of Fishes Resources in the Upper Reaches of the Yangtze River Key Laboratory of Sichuan Province, Neijiang Normal University, Neijiang, China; **Fishery Resources and Environmental Science Experimental Station of the Upper-Middle Reaches of Yangtze River Ministry of Agriculture, Yangtze River Fishery Research Institute, Chinese Academy of Fishery Sciences, Wuhan, China

**These authors contributed equally.

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**ABSTRACT**

*Pseudobagrus pratti* (Osteichthyes, Siluriformes, Bagridae, *Pseudobagrus*) is a medium-sized freshwater fish, which mainly distributed in the Yangtze River and Pearl River systems (Cheng and Zheng 1987). This fish is an important economic fish, but study on mitochondrial sequence of the fish has not been reported. In this study, the complete mitochondrial genome was first determined using the next generation sequencing (NGS).

The specimens were obtained from Neijiang, Sichuan Province of China (29°57′61.90″N, 105°06′01.70″E) in July 2018 and were stored in Zoological Specimen Museum of Neijiang Normal University (accession number: 20180724BB05). A 30–40 mg fins clip was collected and preserved in 95% ethanol at 4°C. Total genomic DNA was extracted with a Tissue DNA Kit (OMEGA E.Z.N.A., Norcross, GA) following the manufacturer’s protocol. Subsequently, the genomic DNA was sequenced using the NGS, and then the mitogenome was assembled using *P. ussuriensis* as reference.

The complete mitochondrial genome of *P. pratti* was a circular molecule with 16,533 bp in length (GenBank Accession number MK226735). It is composed of 13 protein-coding genes (PCGs), two tRNA genes, 22 rRNA genes, one D-loop locus, and an origin of replication on the light-strand (OL). The overall nucleotide composition was 31.55% A, 26.76% T, 26.78% C, 14.91% G, with 58.31% AT, respectively. Phylogenetic analysis both highly supported that *P. pratti* showed a close relationship with *P. ussuriensis* and *P. emarginatus*. These data would contribute to elucidate the evolutionary mechanisms and biogeography of *Pseudobagrus* and is useful for the conservation of genetics and stock evaluation for *P. pratti*.

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**CONTACT**

Yuanchao Zou (zou3891@163.com) College of Life Sciences, Conservation and Utilization of Fishes Resources in the Upper Reaches of the Yangtze River Key Laboratory of Sichuan Province, Neijiang Normal University, Neijiang, Sichuan 641100, China; Xinbin Duan (duan@yfi.ac.cn) Fishery Resources and Environmental Science Experimental Station of the Upper-Middle Reaches of Yangtze River Ministry of Agriculture, Yangtze River Fisheries Research Institute, Chinese Academy of Fishery Sciences, Wuhan 430223, China

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The other 11 species were divided into two clades. *P. fulvidraco* and *P. tokiensis* were clustered into clade B, and the rest of species were clustered into clade A. *P. pratti*, *P. sussuriensis*, and *P. emarginatus* were grouped in one clade, suggested the close relationship of these species, and further confirmed that *P. pratti* belongs to the subfamily Bagridae. In addition, two topologies all showed *P. pratti*, *P. sussuriensis* and *P. emarginatus* had a close relationship, which indicated that the rate of evolution of these three species was roughly equivalent.

In summary, the complete mitochondrial genome of *P. pratti* was first determined in present study. It was 16,533 bp long and showed a typical teleost mtgenome order. Phylogenetic analyses indicated that *P. pratti* showed a close relationship with *P. sussuriensis* and *P. emarginatus*. These data would contribute to elucidate the evolutionary mechanisms and biogeography of *Pseudobagrus* and is useful for the conservation of genetics and stock evaluation for *P. pratti*.

**Disclosure statement**

No potential conflict of interest was reported by the authors.

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**Figure 1.** The phylogenetic analyses of *Pseudobagrus* based on 12 protein-coding genes, constructed using the Neighbor-Joining (NJ) and Maximum Likelihood (ML). NJ posterior probabilities (blue number) and ML bootstrap values (black number) are shown at nodes.