#### MITOGENOME ANNOUNCEMENT

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# The complete mitochondrial genome of *Paraqianlabeo lineatus* (Cyprinidae: Labeoninae)

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#### ABSTRACT

*Paraqianlabeo lineatus* is a small-sized fish which is endemic to Guizhou province, China. The complete mitochondrial genome of *P. lineatus* is 16,598 bp in total length, with 37 genes, including 13 PCGs, 22 tRNA genes, two rRNA genes (16S and 12S) and a non-coding region (D-loop). The positions and sequences of genes were consistent with congeners of Labeoninae. The nucleotide composition of the mitogenome was A (31.5%), T (26.7%), G (15.9%), C (25.8%) and was slightly A + T biased. Phylogenetic analysis conducted using Bayesian Inference method showed that *P. lineatus* clustered with *Pseudogyrincheilus procheilus* within the subfamily Labeoninae. The results may provide helpful data for further studies of the evolutionary history of Labeoninae.

Paragianlabeo lineatus is a small-sized fish which is endemic to drainages of Yangtze river, Chishui river and Wu-Jiang river, Guizhou province, China (Zhao et al. 2014). This monotypic species is usually found in upper hill streams with rocks. There are few ecological and molecular data about P. lineatus (Li et al. 2016; Zhao 2016). Here, we provide the first description of the complete mitochondrial genome of P. lineatus. The sequence was obtained from a specimen caught in Mengxi river, Shizhi village, Zhengan county (E 107°17'37", N 28°17'17"), Guizhou province, a tributary flowing into Wu-Jiang river. Total genomic DNA was extracted from the pelvic fin preserved in 95% alcohol using the Qiagen QIAamp tissue kit following the manufacturer's protocol. The complete mitochondrial genome was sequenced by next-generation sequencing methods and the annotated sequence was archived at Genebank (accession number MW039085). The specimen (GZ-20170217, 7.7 cm in standard length, 5.0 g in weight) was deposited in the collection of fisheries research institution, Guizhou Academy of Agricultural Sciences.

Structure of the mitogenome of *P. lineatus* was consistent with those of other fishes (Zheng and Yang 2016; Tan et al. 2019; Pan et al. 2020), consisting 13 protein-coding genes, 2 ribosomal RNA (rRNA) genes, 22 transfer RNA (tRNA) genes, and a non-coding regions. Most of the coding regions are encoded on the H-strand except for *ND6*, and there are eight tRNA genes (tRNA<sup>Gln</sup>, tRNA<sup>Ala</sup>, tRNA<sup>Asn</sup>, tRNA<sup>Cys</sup>, tRNA<sup>Tyr</sup>, tRNA<sup>Ser</sup>, tRNA<sup>Glu</sup> and tRNA<sup>Pro</sup>) encoded on H-strand. The base composition of protein-coding genes showed a weak anti-G bias (15.3%) whereas the anti-G bias was strongly observed in the third codon position (6.7%), overall base composition of A + T content (58.2%) is nearly the same with coding region genes (58.8%). Almost all of the 13 protein-coding

genes started with the typical start codon ATG but *COI*, which started with GTG. For the stop codon, six of them share the complete stop codon, while seven shared the incomplete stop codon with a terminal T or TA. The D-Loop was located between tRNA<sup>Pho</sup> and tRNA<sup>Phe</sup> with 936 bp, the base composition reflected a strong A + T-rich (65.7%), richer than the overall average content (58.2%).

We chose Bayesian Inference method to infer evolutionary relationships based on complete mitogenome between *P. lineatus* and 15 other sequences downloaded from Genebank, *Acrossocheilus yunnanensis* (Cyprinidae: Barbinae) was chosen as outgroup here. The phylogenetic tree showed that *P. lineatus* clustered with *Pseudogyrincheilus procheilus* with high Posterior Probability (Figure 1), consistent with previous studies based on short mitochondrial DNA sequences (Zhao 2016; Zheng et al. 2016). this may tell us that genus *Paraqianlabeo* and *Pseudogyrincheilus* have more closely evolutionary relationship, and the results would provide references for further study of subfamily Labeoninae.

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## Disclosure statement

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

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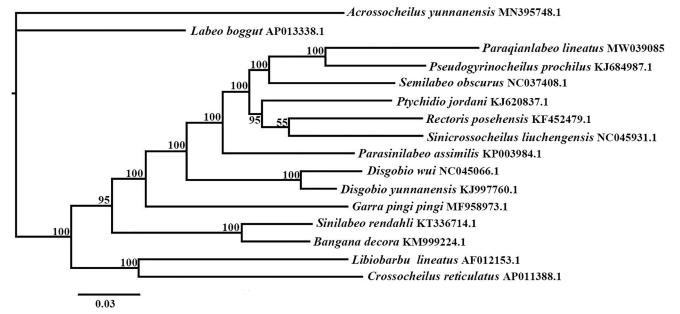


Figure 1. Phylogenetic relationships between *P. lineatus* and 15 other members of Labeoninae based on complete mitochondrial genome sequences. *Acrossocheilus yunnanensis* was used as an outgroup. Numbers on the nodes are Bayesian posterior probability values.

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#### Data availability statement

The genome sequence data that support the findings of this study are openly available in GenBank of NCBI at (https://www.ncbi.nlm.nih.gov/) under the accession no. MW039085. The associated BioProject, BioSample and SRA numbers are PRJNA694796, SAMN17574689 and SRR13664247 respectively.

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