

The Complete Mitogenome and Phylogenetic Analysis of *Acrossocheilus wuyiensis* (*Osteichthyes Cyprinidae*)

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Abstract

Acrossocheilus wuyiensis is an endemic south China stream-dwelling cyprinid species. In this study, we decoded the complete mitogenome of *Acrossocheilus wuyiensis* for the first time by using whole genome sequencing approach. The complete mitogenome is 16,594 bp in length, consisting of 13 protein-coding genes, 22 tRNA genes, 2 rRNA genes and one D-loop control region. Only ND6 and other eight tRNA genes are encoded on the L-strand while most of these genes are located in the H-strand. Its overall base composition is A: 31.1%, C: 28.0%, G: 16.2% and T: 24.7%. The complete mitogenome of the Chinese barred species of *Cyprinidae* could provide a basic data for further phylogenetic and conversational analysis.

Keywords: Barred species; Mitogenome; *Acrossocheilus wuyiensis*; Next generation sequencing

Introduction

Acrossocheilus wuyiensis is a fresh water fish that live in benthopelagic area in subtropical climate. This species was found in Wuyishan Nature Reserve, Fujian, China [1]. *Acrossocheilus* is also known to be found in Southern part of China and northern part of Laos. The *Acrossocheilus genera* has a distinctive characteristic from the family of *Barbinae*, a rostral fold between the lip and the snout, fleshy and continuous lips around the corners of the mouth, horny sheath and two pairs of barbels around the jaw, serrated or smooth posterior margin [2]. This genus is divided into two species groups: a striped or barred species, and non-barred species. The barred species group are characterized by possessing several dark vertical bars on each side of the body [3]. *A. wuyiensis* is considered to be in the barred species group. *A. wuyiensis* can be distinguished from other *Acrossocheilus* species in having black blotches along the back, longer maxillary barbel, and no weak serrate on the last dorsal spine [1]. This species has forked caudal fins, 8 soft-rays in anal fins, 12 soft rays in dorsal fins, dark yellow body color and also can grow up to 15.9 cm. The complete mitogenome of *A. wuyiensis* will benefit our knowledge on phylogeny and conservation of Chinese barred species of *Cyprinidae*.

Materials and Methods

Sample of *A. wuyiensis* was collected in April 2015 from the Wuyishan county (Min Jiang, flowing to East Sea), Fujian Province of China and deposited to the Zhejiang Museum of Natural History (ZMNH 2015040001). The complete mitogenome of *A. wuyiensis* has

been obtained from high-throughput sequencing on whole genomic DNA with HiSeq 2000 platform (Illumina, San Diego, CA). We used next generation sequencing to perform low-coverage whole genome sequencing according to previous protocol [4]. About 0.11% raw reads (29,959 out of 26,785,944) were de novo assembly by using commercial software (Geneious V9, Auckland, New Zealand) to produce a single, circular form of complete mitogenome with about an average 268 X coverage. The protein coding, rRNA and tRNA genes of *A. wuyiensis* mitogenome were predicted by using DOGMA [5], ARWEN [6], MITOS [7] tools and manually inspected. To validate the phylogenetic position of *A. wuyiensis*, we used MEGA6 software [8] to construct a Maximum likelihood tree (with 500 bootstrap replicates and Kimura 2-parameter model [9]) containing complete mitogenomes of 12 species derived from *Acrossocheilus* genus. Two species of the genus *Onychostoma* (*O. gerlachi* and *O. barbatulum*) were included as the ingroup in this study as they are thought to be closely related to the barred species of *Acrossocheilus* [10]. *Barbonymus gonionotus* was utilized as out-group for tree rooting [11].

Results and Discussion

The complete mitochondrial genome of *A. wuyiensis* has been submitted to GenBank under accession no. KY131977. The length of complete mitochondrial genome of *A. wuyiensis* is 16,594 bp, includes 13 protein-coding genes, 22 tRNA genes (ranging from 67 bp in tRNACys to 76 bp in tRNALeu and tRNAlys), 2 rRNA genes (957 bp in 12S rRNA and 1682 bp in 16S rRNA), and 1 D-loop control region (939 bp) (Figure 1). The complete mitogenome of *A. wuyiensis* showing 99% identities to *A. stenotaeniatus* (GenBank KJ909660) after BLAST search against NCBI nr/nt database. Only ND6 and other eight tRNA (tRNACys, tRNAAla, tRNAGlu, tRNAPro, tRNAGln, tRNASer, tRNATyr and tRNAAsn) genes are encoded on the L-strand while

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