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The complete mitochondrial genome of the *Aluterus monoceros*

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### Abstract

The complete mitochondrial genome of *Aluterus monoceros* (*A. monoceros*) has been sequenced. The mitochondrial genome of *A. monoceros* is 16,429 bp in length, consisting of 22 tRNA genes, 2 rRNA genes, 13 protein-coding genes and a D-loop region (Gen Bank accession number KP637022). The base A + T of the mitochondrial genome is 63.25%, including 33.16% of A, 30.09% of T and 20.74% of C. Twelve protein-coding genes start with a standard ATG as the initiation codon, except for the COXI, which begins with GTG. Some of the termination codons are incomplete T or TA, except for the ND1, COXI, ATP8, ND4L1, NDS and ND6, which stop with TAA. Construction of phylogenetic trees based on the entire mitochondrial genome sequence of 14 Tetrodontiformes species constructed has suggested that *A. monoceros* has closer relationship with *Acreichthys tomentosus* and *Monacanthus chinensis*, and they constitute a sister group.

### Keywords

*Aluterus monoceros*, mitochondrial genome, sequence analysis

### History

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*Aluterus monoceros*, one of the species belonging to the group Tetrodontiformes, Tetraodontoidae, Monacanthidae and Aluterus, is a warm-water cultured fish in the world, which is mainly distributed in the Atlantic Ocean, the Indian Ocean and the Pacific Ocean, particularly in tropical and subtropical waters. It is an economic species commonly known to produce frozen fillets and fish gelatin. Although the fillet of *A. monoceros* is small, it contains high collagen fiber and is evenly distributed, which makes it wildly used and efficiently characterized (Ahmad & Benjakul, 2011; Ahmad et al., 2011). Meanwhile, it is also used as superior raw material in making leather products (Ahmad et al., 2010; Sadowska et al., 2003). Nevertheless, there is no sufficient information on *A. monoceros*. In this study, we observed and analyzed the complete mitochondrial genome of *Aluterus*. Our purpose was to demonstrate the molecular data and basic gene evidence in terms of systematic classification of *Aluterus*, the analysis of population genomic diversity and the resources protection of population quality. The samples were collected from the South China Sea. Fin samples were immediately preserved in 95% alcohol.

The complete mitochondrial genome of *A. monoceros* is 16,429 bp in length. The gene order and compositions of *A. monoceros* are quite similar to that of most fishes. It contains 37 coding genes (22 tRNA genes, 2 rRNA genes (12s rRNA and 16s rRNA), 13 protein-coding genes) and a D-loop control region, which is 781 bp in length. Most genes were either abutted or overlapped; of which 9 genes (tRNA-Gln, tRNA-Ala, tRNA-Asn, tRNA-Cys, tRNA-Tyr, tRNA-Ser, ND6, tRNA-Glu, tRNA-Pro) were encoded on the L-strand, and the rest 28 genes were encoded on the H-strand. The compositions of the L-strand of the *A. monoceros* revealed are 26.01% of A, 27.35% of T, 29.20% of G and 17.43% of C. The compositions of base A + T of the mitochondrial DNA of *A. monoceros* are 33.16% of A, 30.09% of T, 20.74% of C, 16.01% of G, (A + T)63.25%, (G + C)36.75%, showing moderate preference to AT, which is with the same preference of vertebrates to base A and T. As for the complete mitochondrial genome of *A. monoceros*, it is either abutted or overlapped.

The mitochondrial genome of *A. monoceros* contains 22 tRNA genes. Genes tRNA-Leu and tRNA-Ser have two different sequences, but other 18 genes share only one sequence varying from 67 to 75 bp in length. The 12s rRNA located between tRNA-Phe and tRNA-Val is 947 bp in length, and the 16s rRNA located between tRNAVal and tRNALeu is 1681 bp in length. The mtDNA of *A. monoceros* consists of 13 protein-coding genes (ND1, ND2, COXI, COXII, ATP8, ATP6, COXIII, ND3, ND4L, ND4, NDS, ND6, Cytb), of which 12t protein-coding genes begin with a standard ATG start codon, except for COXI that begins with GTG. Most of the termination codons are incomplete T or TA, except for ND1, COXI, ATP8, ND4L, NDS and ND6, which stop with TAA. The D-loop control region is 781 bp in length, located between tRNA-Pro and tRNA-Phe.

The Neighbor-Joining (NJ) tree based on mitochondrial genome nucleotide sequences of the *A. monoceros* and other 13 kinds of fish were constructed under the Bootstrap method (Figure 1). Compared to the sequences of nucleotide homology of mitochondrial genome in the *A. monoceros* and 13 fishes, it shows that the Tetrodontiformes and 13 fishes have high nucleotide homology. The *A. monoceros* has closer relationship with the...
Acreichthys tomentosus and Monacanthus chinensis, and they constitute a sister group.

Declaration of interest

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References


