Complete mitochondrial genome sequence for the cuneate drum *Nibea miichthioides* (Perciformes, Sciaenidae) and its phylogeny

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**ABSTRACT**

The cuneate drum, *Nibea miichthioides*, is a native sciaenid species with relevant commercial importance in China. However, the wild resource represented by this species has been severely damaged owing to overfishing and water pollution. For conserving and recovering the species through appropriate measures, genetic studies on the population are necessary. The complete mitochondrial genome of *N. miichthioides* is a supplement to the mitogenome database for giant croakers and can be used to address taxonomic problems and phylogenetic relationships in Sciaenidae. In this study, we sequenced and characterized the complete mitochondrial genome of *N. miichthioides*. The full length of the complete mitochondrial DNA was 16,490 bp. It contained 13 protein-coding genes, 22 tRNA genes, two rRNA genes and a control region. All 21 tRNA genes can fold into a typical cloverleaf structure except for tRNA^Ser^ (AGY), which lacks a dihydrouridine arm. The phylogenetic analysis using the complete mitochondrial genome revealed that *N. miichthioides*, *A. amoyensis*, *N. japonica* and *A. japonicus* might be grouped in Argyrosomus, but not belonged to *Nibia* of Argyrosominae, which was highly consistent with the proposal of Talwar. This investigation provides an effective molecular tool for genetic research on and protection of this endangered species.

In this study, the specimen of *N. miichthioides* sampled from Ningde city, Fujian, South China Sea was stored in the fish collection of Zhejiang Marine Fisheries Research Institute. The caudal fins of *N. miichthioides* were scissored for genomic DNA isolation. Total genomic DNA was isolated using the high-salt procedure (Aljanabi & Martinez 1997). PCR primers were initially designed according to *N. albiflora* (HQ890947.1), *Sciaenops ocellatus* (JQ286004.1) and *Miichthys miiyu* (HM447240.1). Subsequently, based on the received sequences, some additional primers were designed to supplement residual gaps. Finally, ContigExpress software was used for sequence analysis and assembly. The assembled mitochondrial genome was annotated with MitoFish (Iwasaki et al. 2013). All tRNA genes were reappraised by trRNAscan-SE1.21 (Lowe & Eddy 1997), which was also used to characterize the anti-codons of all tRNAs. Simultaneously, we downloaded 18 complete mitochondrial genomes of the Sciaenidae, which were aligned by means of Clustal W using BioEdit (Hall 2004). The best-fit model to nucleotide substitution of these genomes were Jmodeltest2 (Darriba et al. 2012), via Akaike information criteria (AICc). Finally, the phylogenetic analysis of Maximum Likelihood (ML) was performed using MEGA 5.0 (Tamura et al. 2011), and the number of bootstrap replicates is 1000.
The complete mitochondrial genome of *N. miichthioides* was 16,490 bp in length (KU738606). It contained 22 tRNA genes, 13 protein-coding genes, two rRNA genes and a control region. All genes were encoded on the heavy strand except ND6 and eight tRNAs. The length of all tRNAs ranged from 66 to 74 bp and their anti-codons were consistent with other fish of Sciaenidae. All 21 tRNA genes can fold into a typical cloverleaf structure except for tRNA$^{	ext{Ser}}$(AGY) which lack a dihydrouridine arm. Usually, the function of tRNAs is mainly determined by anticodon stem-loop and amino acid stem. Hence, the lack of dihydrouridine arm does not affect the function (Hanada et al. 2000). All the 13 protein-coding genes were initiated with the orthodox ATG. They had three types of intact stop codons (TAG, AGA and TAA) and two types of incomplete stop codons (TA– and T–). The two rRNA genes (125 rRNA and 16S rRNA) were typically isolated by tRNA$^{	ext{Val}}$, located between tRNA$^{	ext{Phe}}$ and tRNA$^{	ext{Leu}}$. The control region is located between the tRNA$^{	ext{Phe}}$ and tRNA$^{	ext{Thr}}$ genes on the heavy strand with the size of 824 bp. Some intergenic nucleotides (from -10 to 36) were also recognized. The mitogenome base composition was 27.0% for A, 25.3% for T, 31.0% for C and 16.7% for G. The A + T content (52.3%) was higher than the G + C content.

The best-fit model to nucleotide substitution of these genomes was HKY$+G+I$. Phylogenetic analysis revealed that *N. miichthioides*, *A. amoyensis* and other eight fish first clustered into the Argyrosominae clade (Figure 1). Then, the Argyrosominae, Pseudoscaieninae and Sciaeninae formed the sister group, while the Johniniinae became a separate clade, which is accordant with the researches (Chen 2007). In the present study, the phylogenetic analysis showed that *N. miichthioides*, *A. amoyensis*, *N. japonica* and *A. japonicus* were clustered into sister group (Figure 1), being inconsistent with the previous reports (Zhu et al. 1963; Cheng et al. 1987). Due to high bootstrap values’ support, phylogeny validated that *N. miichthioides*, *A. amoyensis*, *N. japonica* and *A. japonicus* might be grouped in *Argyrosomus*, but not belonged to *Nibea* of Argyrosominae, which was highly consistent with the proposal of Talwar (1995).

**Disclosure statement**

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

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