Complete mitochondrial genome for the whitemouth croaker *Micropogonias furnieri* (Perciformes: Sciaenidae)

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**ABSTRACT**

This study is the first to research to report the complete 16,496 bp mitochondrial genome of *Micropogonias furnieri*, which consists of 13 protein-coding genes, two ribosomal RNA genes, 22 transfer RNA genes, and a control region (D-loop). The overall base composition of the complete genome is 27.26% A, 25.65% T, 16.46% G, and 30.63% C, with a high A + T content of 52.91%. Phylogenetic analysis showed that *M. furnieri* was most closely related to *Sciaenops ocellatus*. In this study, the mitogenome of *M. furnieri* will provide useful information for phylogenetic and evolutionary understanding in the family Sciaenidae.

Whitemouth croaker *Micropogonias furnieri* (Desmarest 1823) is a fish belonging to the Sciaenidae family, distributed in the Atlantic Ocean from the Gulf of Mexico to the coast of Argentina. *M. furnieri* is a commercially important fishery resource, mainly caught in Brazil and Argentina, and exported to all over the world, including Korea (Vazzoler 1991; Elsdon and Gillanders 2002). *M. furnieri* has a taste and shape similar to that of *Miichthys miiy*, belonging to the family Sciaenidae. For this reason, there is an urgent need to develop markers that can identify species due to illegal sales. Therefore, we wanted to report the mitogenome of *M. furnieri* and the taxonomic position of *M. furnieri* in the family Sciaenidae before developing a species discriminant marker.

*M. furnieri* was imported to Korea in a frozen state after being caught off the coast of Argentina (35°50’S, 57°11’W), and samples were purchased from a Korean importer. Specimens were stored in 99% ethanol after cutting the fin of the fish, and given a voucher number in the Fish Specimen Room of Soonchunhyang University, Asan City, Chungcheongnam-do, Republic Korea (Voucher Storage: Soonchunhyang University; Voucher number: SUC-26732; The person in charge of the collection: KR Kim; email: kimkangrae9586@gmail.com). Genomic DNA was extracted from the fin tissue using the Genomic DNA Prep Kit (Biofact, Korea) and stored in a freezer at –80°C in the sample room of Soonchunhyang University.

For the extracted genomic DNA, a DNA library consisting of 150 bp paired-end read was constructed using the MGI Easy DNA Library Prep Kit (MGI, China). Sequencing was performed using the MGISEQ-2000 platform (MGI). The raw data were assembled using Geneious ver. 11.0.3 program. The complete mitogenome sequence of the assembled *M. furnieri* was annotated using the MITOS web server (Bernt et al. 2013). The complete mitogenome sequence of *M. furnieri* has been deposited with the NCBI GenBank (Accession No. MW646294).

The complete mitochondrial genome of is 16,496 bp, containing 13 protein-coding genes (PCGs), two ribosomal RNAs (rRNA), 22 transfer RNA genes, and a control region (D-loop). The start codons of 13 PCGs all contained ATG. The stop codon of 7 PCGs (ND2, ND3, ND4, CO1, CO2, CO3, and Cytb) were contained incomplete T or TA. The six of the PCGs (ND1, ND4L, ND5, ND6, ATP6, and ATP8) were contained a complete TAA or TAG.

The overall base composition of the *M. furnieri* genome is 27.26% A, 25.65% T, 16.46% G, and 30.63% C, with a high A + T content of 52.91%. The rRNA of *M. furnieri* consists of 16S rRNA (1,697 bp) and 12S rRNA (954 bp).

The phylogenetic tree was constructed and analyzed via the maximum likelihood methods using the PhyML ver. 3.1 (Guindon et al. 2010). We applied a GTR + I + R model to the data based on 13 PCG sequences of a total of 15 species (Guindon and Gascuel 2003; Darriba et al. 2012). Phylogenetic analysis showed that *M. furnieri* was most closely related to *Sciaenops ocellatus*. In this study, the mitogenome of *M. furnieri* will provide useful information for phylogenetic and evolutionary understanding in the family Sciaenidae.

**Disclosure statement**

The authors report no conflicts of interests. The authors alone are responsible for the content and writing of this article.
Figure 1. Phylogenetic trees were constructed based on Bayesian 13 gene coding-based protein inference for 14 genera species including Micropogonias furnieri belonging to the family Sciaenidae. The scale bars represent relative evolutionary distances. The GenBank accession number follows the species name.

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