



The complete mitochondrial genome of the longneck croaker, *pseudolithus typus* Bleeker, 1863 from Sierra Leone

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ABSTRACT

The complete mitochondrial DNA information of *Pseudolithus typus* Bleeker, 1863, collected from Sierra Leone was determined using next-generation sequencing (NGS) and bioinformatic analysis. Its mitogenome (16,504 bp) encoded the typical 13 protein-coding genes (PCGs), 2 ribosomal RNAs (12S & 16S), and 22 tRNAs. All 13 PCGs showed a standard start codon (ATG) but an unusual stop codon (AGA) was identified in COX1 gene. Except for ND6, all 12 PCGs were encoded on the light strand. Except for tRNA^{Ser-GCT}, 21 tRNAs formed the typical clover-leaf structures. Phylogenetic analysis showed three mitochondrial genomes in the genus *Pseudolithus* formed a clade distinct from the other species in the same family. The mitogenome of *P. typus* identified in this study exhibited 96.27% and 88.86% identity to *T. typus* in the Guinean water and *P. elongatus*, respectively. Additional mitogenome sequences of *Pseudolithus* species will provide useful information for their scientific management in western African countries.

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Fish in the *Pseudolithus* (Family: Sciaenidae) are widely distributed along the coast of West Africa from Senegal to Angola, most of which have been economically important in those countries (Bayagbona 1969). Although six species are currently reported in the genus *Pseudolithus*, it is difficult to identify a species from the others in the genus mainly due to the morphological similarity and the shared geographical distribution. Discrimination of *Pseudolithus senegalensis* from *Pseudolithus typus* is particularly challenging, even though the numbers of spines at dorsal fin and inter-orbital length are considered as the keys to differentiate them (Sossoukpe 2011). Therefore, those six species in the genus *Pseudolithus* have been recorded in the fishery data, which is problematic for the efficient management of the resources along the West African countries. In this study, *P. typus* Bleeker, 1863, was collected from the offshore of Sierra Leone, and its complete mitochondrial DNA information was determined using next-generation sequencing (NGS) and bioinformatic analysis as a part of effort for its scientific management.

The specimen was collected from the offshore of Sierra Leone (8°00'00.0"N 14°03'36.0"W) during the 2019 FAO/EAF-NANSEN transboundary survey. The specimen's identity was confirmed by 99.6% identity in the COI region to database (KP722770) and its morphological characteristics. The specimen and its DNA are stored at the Marine Biodiversity

Institute of Korea (<https://www.mabik.re.kr/html/en/>, Ha Yeun Song, and hysong@mabik.re.kr) under the number GR00004774. For the mitogenome sequencing, mitochondrial DNA was extracted by a commercial DNA isolation kit (Abcam, Cambridge, UK), which was further sheared by Covaris M220 Focused-Ultrasonicator (Covaris Inc., San Diego, CA). The library for sequencing was constructed using TruSeq[®] RNA library preparation kit (Illumina, San Diego, CA) according to manufacturer's manual. Assembly of the obtained raw reads and gene annotation was performed by Geneious[®] 11.0.2 software (<https://www.geneious.com>). The locations and structures of 22 tRNAs were predicted by tRNAScan-SE software (Lowe and Chan 2016). A phylogenetic tree was constructed with 12 mitogenome sequences using MEGA X software with a maximum likelihood (ML) algorithm (Kumar et al. 2018). *Oplegnathus fasciatus* in the family Oplegnathidae was used as an outgroup member.

The complete mitochondrial genome of *P. typus* (MW465657) was 16,504 bp in length, which encoded the typical 13 protein-coding genes (PCGs), 2 ribosomal RNAs (12S & 16S), and 22 tRNAs. Among two non-coding regions, the control region (828 bp) was identified between tRNA^{Pro} and tRNA^{Phe}, while the putative origin of light-strand replication (O_L) was found within a cluster of five tRNA genes (WANCY). The ratio of [A + T] to [G + C] was 1.09, exhibiting slightly higher A + T content. All 13 PCGs begin with a typical

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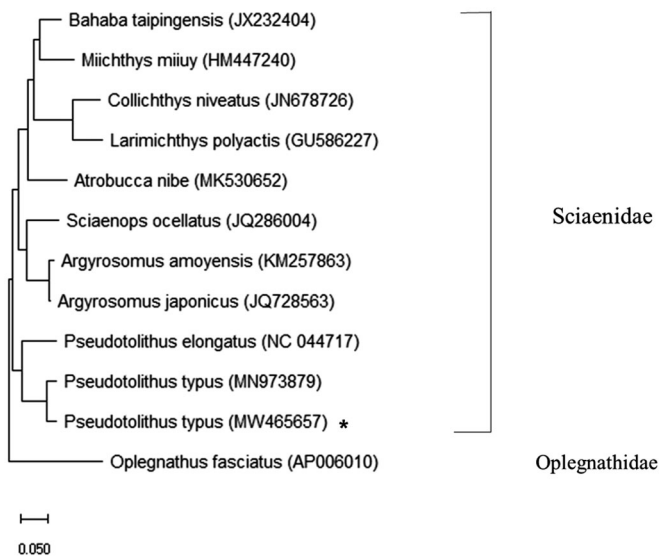


Figure 1. Evolutionary analysis by maximum likelihood method. The evolutionary history was inferred by using the Maximum Likelihood method and Tamura-Nei model with 1000 bootstrap replicates. GenBank accession number was shown next to each scientific name. *Oplegnathus fasciatus* was used for an out-group member. Asterisk (*) indicates the mitogenome identified in this study.

start codon (ATG), while an unusual stop codon (AGA) was identified in *COX1* gene. Incomplete stop codons (T–TA–) were identified in seven genes, including *ND2*, *ND3*, *ND4*, *COX2*, *COX3*, *ATP6*, and *CytB*. Except for *ND6*, all 12 PCGs were encoded on the light (L) strand. The predicted size of 22 tRNAs varied from 66 to 74 bp. Twenty-one of them formed the typical clover-leaf structures, except for tRNA^{Ser-GCT}, which lacked D-arm as shown in the typical metazoans (Watanabe et al. 2014).

Phylogenetic analysis showed that 11 species in the family Sciaenidae were clustered together distinctly from *O. fasciatus* in the family Oplegnathidae (Figure 1). Three mitochondrial genomes in the genus *Pseudotolithus* formed a clade distinct from the other species in the same family, supporting the accuracy of mitogenome information in this study. The mitogenome of *P. typus* identified in this study exhibited 96.27% identity to the previously reported one, which was caught in the Guinean water. Given the wide distribution of *P. typus*, it is postulated that genetic distance within the species would be high. Therefore, additional mitochondrial genome sequences in various locations would be required to understand its population structure in western Africa. The other species in the same genus, *P. elongatus* showed only

88.86% identity to *P. typus* in this study. Unfortunately, the complete mitogenome of *P. senegalensis*, the most closely related species to *P. typus*, has not yet been reported. Additional mitogenome sequences of *Pseudotolithus* species will provide useful information for their scientific management in western African countries.

Disclosure statement

No potential conflict of interest was by reported the authors.

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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. MW465657. The associated BioProject, SRA, and Bio-Sample numbers are PRJNA706871, SRX10243190, and SAMN18147058, respectively.

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