



Short Communication

The Complete Mitogenome of the *Lophius litulon* (Lophioidei: Lophiidae) and Phylogenetic Implications

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ABSTRACT

In this study, the complete mitochondrial genome of *Lophius litulon* was sequenced and assembled by next-generation sequencing techniques. The complete mitochondrial genome of *Lophius litulon* contained 13 protein-coding genes (PCGs), two ribosomal RNA (rRNA) genes, and 22 transfer RNA (tRNA) genes. The total length of the mitochondrial genome of *L. litulon* was 16,430 bp, and the overall base composition of the mitochondrial genome was 26.96% A, 30.13% C, 17.58% G and 25.33% T. Our sequence is consistent with the mitogenome (NCBI accession number AP004413) named *Lophiomus setigerus*, indicating that the latter might be a misidentification. Phylogenetic analysis based on PCGs suggested that genus *Lophius* was more closely related to *Lophiodes* than *Antennatus*.

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Authors' Contribution

TY and XZ were involved in the conception and design. YQ and LL contributed to the analysis and interpretation of the data. TG was involved in the drafting of the paper, revising it critically for intellectual content and we all agree to the final version publication of the article; all authors agree to be accountable for all aspects of the work.

Key words

Mitogenome, Yellow goosfish, *Lophius litulon*, Phylogenetics, *Lophius*

The yellow goosfish, *Lophius litulon* (Jordan, 1902) is a demersal fish species distributed in the coastal waters of the Northwest Pacific, including Japan, Korea, and China (Froese and Pauly, 2021). This species is mainly found in the Yellow Sea in China because of the suitable habitat provided by the Yellow Sea cold water mass (Wei et al., 2016). *L. litulon* has important ecological and economic value. This species exerts top-down control on the Yellow Sea ecosystem (Jin et al. 2010), and has become an important secondary target species in commercial fisheries.

Materials and methods

A specimen of *L. litulon* was collected from the coastal waters of Qingdao, China (35°35'N, 119°30'E) in 2021 and identified morphologically. The fish were stored

at -80°C and the muscle tissues were obtained from the Fishery Ecology and Biodiversity Laboratory (FEBL) of Zhejiang Ocean University (<http://www.zjou.edu.cn/>, Zhoushan, China). The specimen was kept by Tianyan Yang (hellojelly1130@163.com) under voucher number 20200206005. The complete mitochondrial DNA sequence of *L. litulon* was determined by the next-generation sequencing platform. MitoFinder was used for mitogenome assembly (Allio et al., 2020). The assembled mitogenome was annotated using MITOS2 (Donath et al., 2019).

Results and discussion

The complete mitochondrial genome of *L. litulon* (GenBank Number: OL627348) was 16,430 bp in length, including 13 protein-coding genes, 22 transfer RNAs and two ribosomal RNA genes. The overall base composition was 26.96% for A, 30.13% for C, 17.58% for G and 25.33% for T, with a slight A+T bias of 52.29%. Gene arrangement was in accordance with the usual structure of vertebrate mitogenomes. All protein coding genes were encoded on the H-strand with the exception of ND6, and eight tRNA genes were transcribed from the L-strand.

A phylogenetic tree was reconstructed using the mitogenome of *L. litulon* produced in this study and six others available mitogenomes of family Lophiidae with

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Antennatus coccineus of family Antennariidae as the outgroup (Fig. 1). The 13 protein-coding genes of the eight mitogenomes were extracted by PhyloSuite 1.2.2. (Zhang *et al.*, 2020) and aligned by MAFFT (Katoh and Standley, 2013). The aligned sequences were concatenated, and a maximum-likelihood analysis was conducted with IQTREE (Nguyen *et al.*, 2015). The results suggested that sequences of *Lophiomus setigerus* (AP004413) and *L. litulon* (KJ020931) may be identifications. The four species of genus *Lophius* formed a monophyletic group first and clustered with genus *Lophiodes* and next with *Sladenis*, indicating a closer relationship between genus *Lophius* and *Lophiodes*.

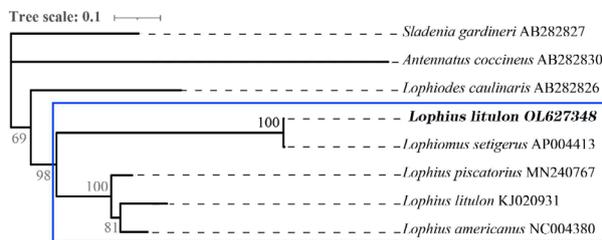


Fig. 1. Phylogenetic tree reconstructed by the maximum likelihood method based on concatenated sequences of protein-coding genes from 7 mitogenomes of Family Lophiidae with *Antennatus coccineus* as the outgroup.

The tree was inferred using IQ-TREE under the best-fit model GTR+F+I+G4 chosen according to BIC for 1,000 ultrafast bootstraps (Minh *et al.*, 2013), as well as the Shimodaira Hasegawa like approximate likelihood-ratio test (Guindon *et al.*, 2010).

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Data availability statement

The genome sequence data of *L. litulon* that support the findings of this study are openly available in GenBank of NCBI at [<https://www.ncbi.nlm.nih.gov>] (<https://www.ncbi.nlm.nih.gov/>) under the accession number OL627348.

The associated BioProject, SRA, and Bio-Sample numbers are PRJNA795006, SRR17477882, and SAMN24669163, respectively.

IRB approval

The fish was collected by trawling by local fishermen for commercial purposes. It was already dead when collected. No of the authors was involved in the collection of the fish. IRB approval was not needed because that no handling of live animals was involved.

Ethics statement

The field studies did not involve any endangered or protected species. *L. litulon* is not protected by Chinese law. No fishing licence was required for the collection of samples from all locations. It is a commercial harvested species in China. The fish were collected by trawling by local fishermen for commercial purposes and were already dead when collected. None of the authors were involved in the collection of the fish. Animal Ethics Committee approval was not needed because no handling of live animals was involved.

Statement of conflict of interest

The authors have declared no conflict of interest.

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