

Mitochondrial DNA Part B Resources

ISSN: (Print) (Online) Journal homepage: <https://www.tandfonline.com/loi/tmdn20>

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To cite this article: Ruoyu Liu, Li Chen, Site Luo, Xinglong Zhu, Zhengwei Jiang, Hasitha Nethupul & Xinhua Chen (2022) The complete mitochondrial genome of snailfish *Liparis tanakae* Gilbert & Burke, 1912 (Perciformes: Cottoidei: Liparidae), Mitochondrial DNA Part B, 7:4, 649-651, DOI: [10.1080/23802359.2022.2060767](https://doi.org/10.1080/23802359.2022.2060767)

To link to this article: <https://doi.org/10.1080/23802359.2022.2060767>



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Published online: 11 Apr 2022.



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The complete mitochondrial genome of snailfish *Liparis tanakae* Gilbert & Burke, 1912 (Perciformes: Cottioidei: Liparidae)

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ABSTRACT

Mitochondrial genome is maternal inheritance that provides higher resolution in taxonomic and phylogenetic research. The absence of complete mitogenome becomes an obstacle to further research. Here, we reported the complete mitogenome of *Liparis tanakae* Gilbert & Burke, 1912 (Perciformes: Cottioidei: Liparidae), which has a length of 17,860 bp. It comprised 39 genes, including 13 protein-coding genes (PCGs), 23 transfer RNA genes (tRNAs), 2 ribosomal RNA genes (rRNAs), and 1 control region (D-loop). The 23 tRNAs in this mitogenome included two tRNA-Ala genes on the light strand. Maximum-likelihood (ML) phylogenetic analysis based on 14 available mitogenomes of 10 species in suborder Cottioidei confirmed *L. tanakae* as monophyletic with other snailfishes. This study would provide important genetic resources and could be useful for evolutionary analysis.

ARTICLE HISTORY

Received 4 November 2021
Accepted 25 March 2022

KEYWORDS



Liparis tanakae; snailfish; mitochondrial genome; phylogenetic analysis

The genus *Liparis* Scopoli, 1777 (Perciformes: Cottioidei: Liparidae) is a large group of snailfish including 98 species, which is commonly found in the temperate and cold seas from the northern hemisphere (Froese and Pauly 2021). Due to its similarity and plasticity in morphology, similar ecological niche, and interchangeable common names, taxonomy of *Liparis* confused taxonomists and fishermen (Orr et al. 2019). For example, *L. ochotensis*, *L. tessellatus*, and *L. tanakae* were reported as morphologically similar, and their nomenclature is confused, especially in larval stage (Jeon et al. 2020; Sim et al. 2020). Mitochondrial genes are maternally inheriting and regularly used in taxonomic and phylogenetic analysis (Liu et al. 2016; Orr et al. 2019). The use of complete mitochondrial genomes for evolutionary reconstruction has higher coverage and resolution than using only a single gene, and thus could more accurately resolve evolutionary relationships (Satoh et al. 2016). The complete mitogenome of *L. ochotensis* and *L. tessellatus* has been published by Jeon et al. (2020) and Sim et al. (2020). The nuclear genome of *L. tanakae* had been assembled by Wang et al. (2019) and Jeong (2020), but no study had been published on the complete mitogenome sequence (LC493937, incomplete). It is necessary to report the complete mitogenome of *L. tanakae* for further studies.

In this study, we adopted the paired-end Illumina data from a muscle tissue for mitogenome assembly. The sequenced specimen was a juvenile female of *L. tanakae* that was deposited at Fujian Agriculture and Forestry University

under the voucher number SAMN23377272 (chenli28113 94514@163.com). The genomic DNA was extracted, then the 350 bp DNA Library was constructed for 150 bp paired-end sequencing in HiSeq-4000 platform (Jeong 2020). The studies were performed in strict accordance with the Regulations of the Administration of Affairs Concerning Experimental Animals established by the Fujian Provincial Department of Science and Technology (PZCASFAFU2019019). All efforts were made to minimize suffering. The quality of data were evaluated with FASTQC v0.11.8 (Andrews 2010) and filtered with FASTP v0.21 (Chen et al. 2018). The mitogenome was *de novo* assembled using GetOrganelle v1.7.5.0 (Jin et al. 2020). The mitogenome was annotated by GeSeq v2.0.3 (Tillich et al. 2017) which 'BLAT' with *L. tessellatus* (NC046407), and manually corrected according to its closely related species *L. tessellatus* (NC046407) and *L. ochotensis* (MG718032). The complete circle mitogenome was deposited at the NCBI GenBank (OL321962).

The complete mitogenome of *L. tanakae* (OL321962) was 17,860 bp in length, comprised of 13 typical vertebrate protein-coding genes (PCGs), 23 transfer RNA genes (tRNAs), two ribosomal RNA genes (12S rRNA and 16S rRNA), and one control region (D-loop). The ND6 gene and nine tRNA genes were encoded at the light strand, other genes were located at the heavy strand. Only COX1 gene initiated with GTG, other 11 PCGs started with ATG. The stop codons of PCGs were TAA, incomplete codon TA– or T–. A control region with 1,098 bp was located at the heavy strand between

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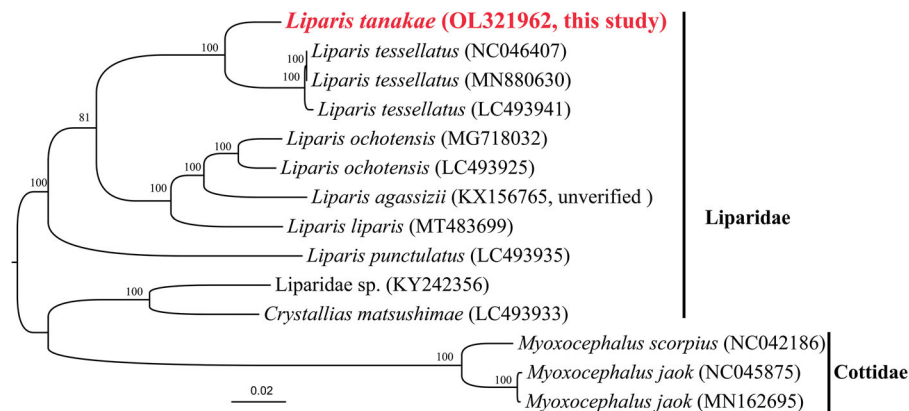


Figure 1. Maximum-likelihood (ML) phylogenetic analysis of 10 species based on the concatenated protein-coding genes (PCGs). Accession numbers of mitogenome sequences are listed in brackets after species.

thetRNA-Phe and -Pro. The overall base composition of the mitogenome was 29.34% A, 28.38% T, 25.39% C, and 16.06% G. The structure and composition of *L. tanakae* mitogenome were similar with those of typical mitogenomes of previously reported *Liparis* species (Jeon et al. 2020; Jeong 2020; Sim et al. 2020). As for tRNA genes, the mitogenome of *L. tanakae* from this study contains 23 tRNAs, which is different from most *Liparis* species and teleosts that only contain 22 tRNAs (Satoh et al. 2016). However, snailfish *L. ochotensis* (LC493925) and *L. agassizii* (KX156765, unverified) also contained 23 tRNAs in their mitogenome. *L. tanakae* (OL321962, this study) had two tRNA-Ala in its light strand. Similarly, *L. ochotensis* (LC493925) and *L. agassizii* (KX156765, unverified) also had duplicated tRNA-Cys in their light strand. The duplicated tRNAs in these three *Liparis* species were located at the same location which was between tRNA-Trp and COX1.

A phylogenetic analysis was performed using nine mitogenomes of six species in the genus *Liparis*, and five mitogenomes from four species in suborder Cottioidei were serving as outgroup taxa (Figure 1). A concatenated nucleotides sequences with of 13 PCGs were aligned with MAFFT v7.407 (Kato and Standley 2013). Maximum-likelihood (ML) tree was constructed by FastTree v2.1.10 with JC + CAT model (Price et al. 2009). Phylogenetic tree indicated *L. tanakae* and *L. ochotensis* are grouped into different branches. Three *L. tessellatus* specimens clustered into a monophyletic group and diverged with *L. tanakae* (Figure 1). The results were consistent with previously reports based on the conserved molecular sequences and RADseq (Orr et al. 2019; Sim et al. 2020). Our results made a good distinction across the three species which were confused previously. The complete mitochondrial genome of *Liparis tanakae* obtained here will provide a valuable resource for phylogenetic and taxonomic analyses in future studies.

Authors contributions

R Liu and X Chen designed and wrote the paper; R Liu and S Luo analysed the data; L Chen, S Luo, X Zhu, and Z Jiang collected materials, and H Nethupul proofed language. All authors agreed to be accountable for all aspects of the work.

Disclosure statement

No potential conflict of interest was reported by the author(s).

Funding

This work was supported by the China Agriculture Research System of MOF and MARA under Grant [CARS-47] and funding from Institute of Oceanography of Fuzhou under Grant [2021F02].

Data availability statement

The genome sequence data that support the findings of this study are openly available in NCBI GenBank under the accession number OL321962. The associated BioProject, SRA, and Bio-Sample numbers are PRJNA782389, SRR16996925, and SAMN23377272, respectively. Meanwhile, the assembly and annotation files of this study are also openly available in FigShare (<https://doi.org/10.6084/m9.fig-share.16783552>).

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