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

Ruoyu Liu\textsuperscript{a, b}, Li Chen\textsuperscript{a}, Site Luo\textsuperscript{c}, Xinglong Zhu\textsuperscript{a}, Zhengwei Jiang\textsuperscript{a}, Hasitha Nethupul\textsuperscript{d} and Xinhua Chen\textsuperscript{a, b}

\textsuperscript{a}Key Laboratory of Marine Biotechnology of Fujian Province, Institute of Oceanology, Fujian Agriculture and Forestry University, Fuzhou, China; \textsuperscript{b}Institute of Deep-Sea Science and Engineering, Chinese Academy of Sciences, Sanya, China; \textsuperscript{c}Southern Marine Science and Engineering Guangdong Laboratory (Zhuhai), Zhuhai, China; \textsuperscript{d}School of Life Sciences, Xiamen University, Xiamen, China

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: Cottoioidei: 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 Cottoioidei confirmed L. tanakae as monophyletic with other snailfishes. This study would provide important genetic resources and could be useful for evolutionary analysis.

The genus Liparis Scopoli, 1777 (Perciformes: Cottoioidei: 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 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 has been assembled by Wang et al. (2019) and Jeong (2020), but no study has 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 Illuma 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

CONTACT Xinhua Chen (chenxinhua@tio.org.cn) Key Laboratory of Marine Biotechnology of Fujian Province, Institute of Oceanology, Fujian Agriculture and Forestry University, Fuzhou, Fujian, China

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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, snailfishes *L. ochotensis* (LC493925) and *L. agassizii* (KX156765, unverified) also contained 23 tRNAs in their mtDNA. *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 nucleotide sequences with of 13 PCGs were aligned with MAFFT v7.407 (Katoh 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 *Liparis* tessellatus specimens clustered into a monophyletic group and diverged with *L. tanakae* (Figure 1). The results were consistent with previous 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.

**Disclosure statement**

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

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**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 PRJNA782839, SRR16996925, and SAMN23377227, respectively. Meanwhile, the assembly and annotation files of this study are also openly available in FigShare (https://doi.org/10.6084/m9.figshare.16783552).

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