

The complete mitochondrial genome of *Thalassoma lunare* (Labriformes, Labridae)

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ABSTRACT

Thalassoma lunare is one of most important genera of Labridae. However, the systemically classification and taxonomic studies have so far been limited. In this study, we report the complete mitochondrial genome sequence of *T. lunare*. The mitogenome has 17,073 base pairs (57.7% A + T content) and made up of total of 37 genes (13 protein-coding, 22 transfer RNAs and 2 ribosomal RNAs), and a putative control region. This study will provide useful genetic information for future phylogenetic and taxonomic classification of Labridae.

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Thalassoma lunare belongs to the Family Labridae and the Order Labriformes, it also named the Moon Wrasse because of its yellow caudal fin shapes like crescent moon with long upper and lower lobes (Fulton et al. 2016).

There is no report of the complete genome of this fish *T. lunare*, which was developed in Shenzhen, Guangdong Province, Republic of China (N22°37'34", E114°41'06") in October 2018. Therefore, it is very important to characterize the complete mitogenome of this species, which can be utilized in research on taxonomic resolution, population genetic structure and phylogeography, and phylogenetic relationship. Total DNA was extracted from muscle following TIANamp Marine Animals DNA Kit (Tiangen, China), and NOVOPlasty software was used to assemble the mitogenomes, the mistake parameter was set by default (Dierckxsens et al. 2017). The samples were stored in -80 °C in Key Lab of South China Sea Fishery Resources Exploitation & Utilization, Ministry of Agriculture and Rural Affairs, South China Sea Fisheries Research Institute, Chinese Academy of Fishery Sciences, Guangzhou, China. Number is TL-1.

In this study, we obtained the complete mitochondrial genome of the fish *T. lunare*. Its mitochondrial genome has been deposited in the GenBank under accession number MN170516. For a better understanding of genetic status and the evolutionary study, we focused on the genetic information contained in the complete mitochondrial genomes of the fish.

The complete mitogenome of the fish *T. lunare* was 17,073 bp in length. The genomic organization was identical to those of typical vertebrate mitochondrial genomes, including two rRNA genes, 13 protein-coding genes, 22 tRNA

genes, a light-strand replication origin (OL), and a putative control region (CR). The overall base composition was 28.5% of A, 26.0% of T, 29.2% of C, and 16.4% of G with a slight A + T bias (57.7%) like other vertebrate mitochondrial genomes. The features mentioned above were accordant with typical *Labridae* fish mitogenome.

For the 13 protein-coding genes, 12 genes started with ATG while only *COI* started with GTG. Four genes shared the termination codon TAA (*ATPase8*, *ND1*, *ND5*, and *ND4L*), one with TAG (*ND6*), the remaining with incomplete stop codon (*COI*, *COII*, *COIII*, *ND2*, *ND3*, *ND4*, *ATPase6*, and *Cytb*). This feature was common among vertebrate mitochondrial protein-coding genes. *T. lunare* had two non-coding regions, the L-strand replication origin region (36 bp) locating between tRNA-Asn and tRNA-Cys, and the control region (1,229 bp) locating within the tRNA-Pro and tRNA-Phe. Except for eight tRNA (tRNA-Ser, tRNA-Pro, tRNA-Glu, tRNA-Tyr, tRNA-Cys, tRNA-Asn, tRNA-Ala, and tRNA-Gln) and the *ND6* gene were encoded on the L-strand, the others were encoded on the H-strand. This feature is similar to other fish mitochondrial genes. The complete mitogenome sequence had 16 s RNA (1,693 bp) and 12 s RNA (944 bp), which were located between tRNA-Phe and tRNA-Leu and separated by tRNA-Val gene. The location is same with most vertebrates that have high conservation.

To determine taxonomic status of *T. lunare*, we reconstructed the phylogeny of this species with other natural populations based on the *COI* gene, *Salvelinus malma* as a foreign group (Yang et al. 2017).

The phylogenetic tree showed that the *T. lunare* has the closer relationship with *Halichoeres nigrescens* (Figure 1).

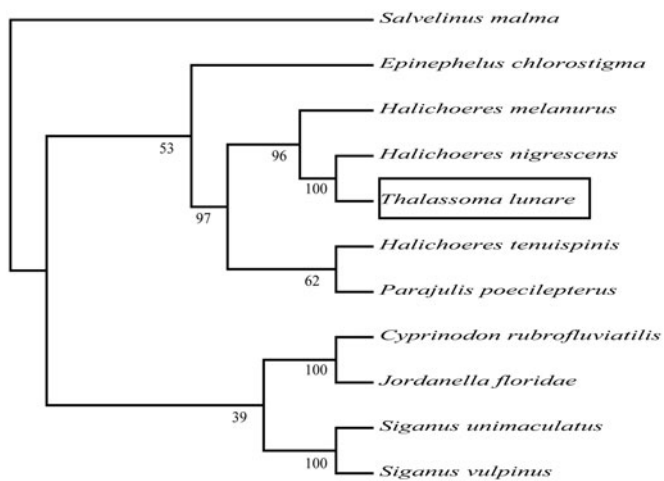


Figure 1. The phylogenetic relationship was estimated using the Maximum Likelihood method for the COI genes. Genbank accession Numbers: *Halichoeres nigrescens* (NC_041194), *Halichoeres melanurus* (AP006018), *Halichoeres tenuispinis* (EU082205), *Parajulis poecilepterus* (EF192032), *Siganus vulpinus* (KM233212), *Siganus unimaculatus* (AP006031), *Cyprinodon rubrofluvialtilis* (EF442803), *Epinephelus chlorostigma* (KR872887), *Jordanella floridae* (AP006778), *Salvelinus malma* (MF680544) and *Thalassoma lunare* (MN170516). The numbers at the nodes are bootstrap percent probability values based on 1000 replications.

The phylogeny was reconstructed based on the General Time Reversible + Invariant + gamma sites (GTR + I + G) model of nucleotide substitution using Mega7 (Kumar et al. 2016). The complete mitochondrial genome sequence of the *T. lunare* provided an important dataset for a better understanding of the mitogenomic diversities and evolution in fish as well as novel genetic markers for studying population genetics and species identification.

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Disclosure statement

No potential conflict of interest was reported by the authors.

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