Complete mitochondrial genome of redbreast Wrasse *Cheilinus fasciatus* (Bloch, 1791) and its phylogenetic status within the family Labridae

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**ABSTRACT**

In order to improve our understanding of the characterization of *Cheilinus fasciatus* mitogenome and the classification status in Labridae, the full-length mtDNA of *C. fasciatus* was sequenced, which is 16,872 bp in length with the higher A + T content (53%). It is composed of 37 typical vertebrate mitochondrial genes and a noncoding control region (D-loop). Except for the ND6 gene and eight tRNAs, the rest of the genes are encoded on the heavy strand (H-strand). Subsequent phylogenetic analyses support that *C. fasciatus* belongs to the genus *Cheilinus*, which is closely related to two genera (*Chlorurus* and *Scarus*). The present study will provide important information for future understanding evolutionary theory, population molecular genetics and biological taxonomy of labrid fish.

The redbreast wrasse, *Cheilinus fasciatus*, belongs to the family Labridae that inhabits the reefs across the Indian and Pacific Ocean (Albutra et al. 2014). The family Labridae is the second-largest marine fish family, including more than 600 fish species belonging to 82 genera (Westneat and Alfaro 2005). Due to the structural and ecological diversity of this family, Labrid phylogenetic evolution has been a hot topic of research. Studies on the phylogenetic status in labrid species have been reported (Westneat and Alfaro 2005; Phillips et al. 2016). However, the phylogenetic analysis based on the Labridae mitogenome is unsystematic, hence only 19 Labridae mitogenomes have been published in GenBank. To better understand the phylogenetic status and genetic evolutions of Labridae mitogenome, the mitogenome of *C. fasciatus* was sequenced and its phylogenetic position among labrid species was analyzed.

The specimen used to sequence the whole mtDNA of the redbreast wrasse *C. fasciatus* originated from a wild individual, collected by ‘Nanfeng’ expedition ship of South China Sea Fisheries Research Institute, CAFS in the South China Sea of China (20°29.7'N, 117°56.3'E). Whole genomic DNA was extracted from the muscle tissue. The DNA library of *C. fasciatus* mtDNA is constructed and sequenced following Zhang et al. (2015). The methods of genome annotation and genome sequence analysis were referred to Zhu et al. (2017). All the specimens (accession number: Ssfri-F0092) and the genomic DNA were deposited in Tropical and Subtropical Marine Life Museum of South China Sea Fisheries Research Institute, CAFS, Guangzhou city, Guangdong Province, China.

The mitochondrial genome of *C. fasciatus* (GenBank accession no. KY115687.1) consists of 16,872 bp, and contains an essential set of typical vertebrate mitochondrial genes including 13 protein-coding genes, 22 tRNA genes, two rRNA genes and a noncoding control region (D-loop). Except for the ND6 gene and eight tRNAs, the rest of the genes are encoded on the heavy strand (H-strand). The arrangement of the 13 protein-coding genes in *C. fasciatus* is identical to that of the other sequenced labrid mitogenomes (Guo et al. 2019). The nucleotide composition of the *C. fasciatus* mitogenome is biased toward A + T (53.0%). Except for COXI (GTG), 12 PCGs initiate with a typical ATG start codon. Five genes (ND1, COXI, ATP8, ND4L, and ND5) are terminated in TAA codon and ND6 gene ended with TAG. The other genes are ended with incomplete stop codons (T or TA), expect ND4 with AGG mitochondrial specific stop codons also being found in some other fish (Prosdocimi et al. 2012).

The phylogenetic trees using maximum parsimony (MP), maximum likelihood (ML), and neighbor-joining (NJ) based on the nucleotide of 13 PCGs from 20 labrid species (Figure 1) showed that *C. fasciatus* has a close relationship with *C. undulatus* and the genus *Cheilinus* is closely related to two genera (*Chlorurus* and *Scarus*), which is consistent with the previous studies (Zhu et al. 2017). The current work...
improves our understanding of the mitogenomic structure of C. fasciatus and evolutionary status of Labridae species.

**Disclosure statement**

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

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**Data availability**

The data that support the findings of this study are openly available in the National Center for Biotechnology Information (NCBI) at https://www.ncbi.nlm.nih.gov/nuccore/KY115687.1, reference number [KY115687.1].

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Figure 1. The molecular phylogeny of 20 labrid species based on the nucleotide sequences of 13 PCGs generated by maximum likelihood (ML), maximum parsimony (MP), and neighbor-joining (NJ) method.