

## The complete mitochondrial genome of longhorn cowfish, *Lactoria cornuta*

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### ABSTRACT

We determined the complete mitochondrial genome of *Lactoria cornuta*, which is 16,495 bp in length with an A + T content of 57.37%, and contains 13 protein-coding genes, 2 rRNAs, 22 tRNAs and a complete control region. The total base composition of the mitogenome is 28.2% T, 26.7% C, 29.2% A and 15.9% G. Of the 13 protein-coding genes, 12 genes start with an ATG codon, except for COX1 with GTG. Ten genes use TAA or AGA as the termination codon, whereas three (COX2, ND4, and Cyt *b*) have incomplete stop codon T. This study would provide useful genetic information for phylogenetic and species identification of the family Ostraciidae.

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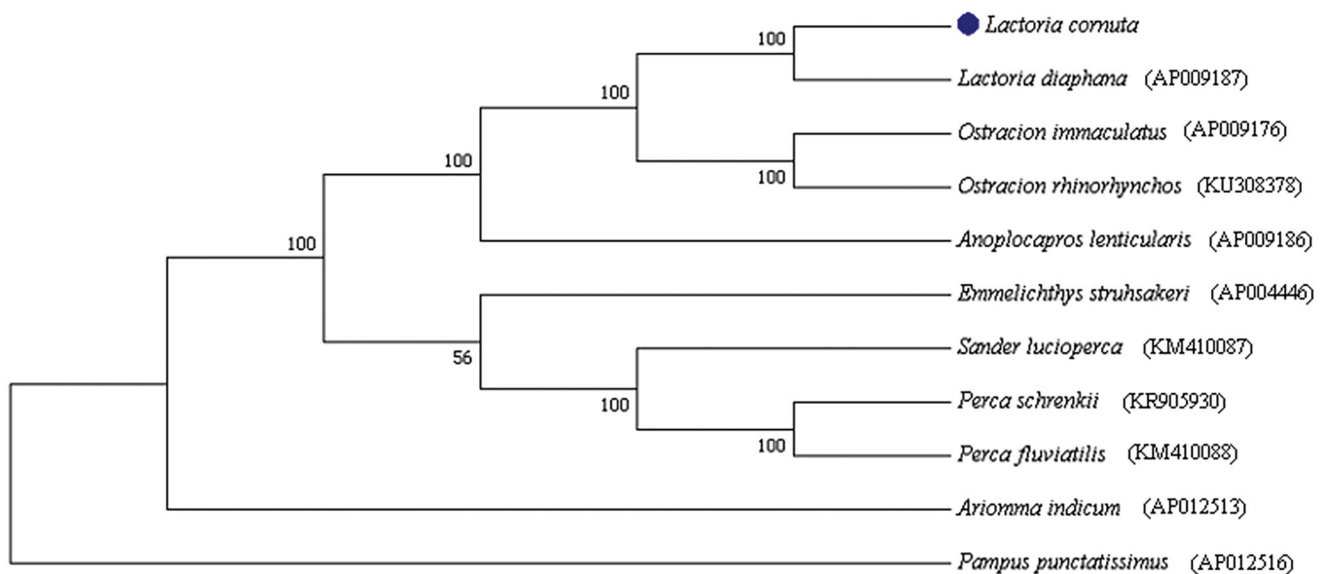
### KEYWORDS

Mitochondrial genome;  
Ostraciidae; *Lactoria cornuta*



*Lactoria cornuta* is a small box-like fish belongs to the family Ostraciidae, which are widely distributed in coral reefs from the Indian Ocean to the Pacific Ocean. When threatened or harassed, they can exude ostracitoxin. In spite of their peculiar morphology, the family Ostraciidae have received relatively scant attention from fish systematists, and the relationships within genera appeared to be uncertain (Santini et al. 2013). Until now, only rare studies have reported the

complete mitochondrial genome of the family Ostraciidae, such as *Lactoria diaphana* (NC\_011330; Yamanoue et al. 2008), *O. immaculatus* (NC\_009865; Yamanoue et al. 2007) and *Ostracion rhinorhynchos* (KU308378; Huang et al. 2016). Hence, we sequenced its mitochondrial genome of *L. cornuta* and analyzed its phylogenetic position.

The specimen of *L. cornuta* was collected from Guangdong Lanhai Marine Technology Co., Ltd, Guangzhou



**Figure 1.** The phylogenetic relationships of the family Ostraciidae based on the nucleotide sequence of 13 protein-coding genes in the mitochondrial genome. The bootstrap support values with 1000 replicates are shown on the nodes. The *Pampus punctatissimus* (AP012516) was used as outgroup.

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City, Guangdong Province, China (23° 12'51"N, 113° 28'06"E). Genomic DNA was extracted from muscle using Tissue DNA Kit (OMEGA E.Z.N.A). The samples were stored in -80 °C in National Freshwater Aquatic Germplasm Resource Center in Guangzhou city, Guangdong Province in China. Number is OS-LC-1. The mitogenome was sequenced by the next-generation sequencing using an Illumina HiSeq 2000 system and assembled using SPAdes v.3.5.0 software (<http://cab.spbu.ru/software/spades/>) (Lapidus et al. 2014).

The complete mitogenome of *L. cornuta* was 16,495 bp in length, containing 22 transfer RNA genes (tRNAs), 13 protein-coding genes (PCGs), 2 ribosome RNA genes (rRNAs), and a control region (CR), which was similar to those of the family Ostraciidae (Yamanoue et al. 2007; Huang et al. 2016). The total nucleotide composition is a 28.2% T, 26.7% C, 29.2% A and 15.9% G, respectively. Of the 13 protein-coding genes, 12 genes start with an ATG codon, except for COX1 with GTG. Ten use TAA or TAG as the termination codon, whereas three (COX2, ND4, and Cyt *b*) have incomplete stop codon T.

Among the 13 PCGs ranging in size from 168 bp (*ATPase8*) to 1839 bp (*ND5*), 12 PCGs are coded on the H-strand, while *ND6* is coded on the L-strand. The 12S and 16S rDNA are 949 bp and 1687 bp in length, respectively. The length variations of 22 tRNAs range from 67 bp (tRNA<sup>Cys</sup>) to 75 bp (tRNA<sup>Lys</sup>). There are two non-coding regions, the L-strand replication origin region (38 bp) locating between tRNA<sup>Asn</sup> and tRNA<sup>Cys</sup>, and the control region (833 bp) locating within the tRNA<sup>Pro</sup> and tRNA<sup>Phe</sup>.

To determine taxonomic status of *L. cornuta*, we reconstructed the phylogeny of the family Ostraciidae based on the nucleotide sequence of 13 protein-coding genes in the mitochondrial genome. Phylogenetic analyses highly supported the close relationship of *L. cornuta* and *L. diaphana*. The genus *Lactoria* and the genus *Ostracion* were clustered (Figure 1), consistent with previous study (Yamanoue et al. 2008). The complete mitochondrial genome sequence of *L. cornuta* would provide useful genetic markers for population genetics and species identification of fish.

## Disclosure statement

The authors report no conflicts of interests. The authors alone are responsible for doing the research and writing the paper.

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## Data availability statement

The data that support the findings of this study are openly available in GenBank at <https://www.ncbi.nlm.nih.gov/genbank/>, accession number MT712150.

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