Characterization of the complete mitochondrial genome of *Chrysochir aureus* and phylogenetic studies of Sciaenidae

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**ABSTRACT**

The complete mitochondrial genome of *Chrysochir aureus* was sequenced. The full length of the mitochondrial genome was 16,501 bp, including 13 protein-coding genes (PCGs), two ribosomal RNAs, 22 transfer RNA genes, a non-coding control region (CR) and one origin of replication on the light-strand (OL). The total nucleotide composition of mitochondrial DNA was 26.95% A, 29.99% C, 26.29% T, and 16.77% G. Twelve PCGs used the canonical ATG as their initiation codon, whereas COI gene started with an alternative start codon GTG. The mitochondrial genome of *C. aureus* described in this study could be a useful basis for management of this species and laid a foundation for further research involved with phylogenetic relationship within Sciaenidae.

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*Chrysochir aureus* is widely distributed in southeast India and Sri Lanka to southern China (Yong et al. 2010), it is an important economic fish in many coastal cities and is marketed fresh as well as dried salted (Bianchi 1984). Due to its illegible appearance and high price, fishermen usually use some miscellaneous fish to make up the quantity unintentionally or intentionally; besides, phylogenetic position of *C. aureus* has always been controversial (Yong et al. 2010; Wang et al. 2017). In this study, we described the complete mitochondrial genome of *C. aureus* and explored its phylogenetic position within Sciaenidae, to gain its molecular information which was expected to contribute to purchasing management as well as further phylogenetic studies on its related species.

An individual specimen of *C. aureus* was sampled by commercial bottom trawling in the South China Sea, 20190319YXT78. The total genomic DNA was extracted from a portion of the epaxial musculature using the phenol–chloroform method (Barnett and Larson 2012). The complete mitogenome of *C. aureus* was amplified with the help of universal primers for marine fish species (Cheng et al. 2012; Shao et al. 2014). Fragments generated from PCR amplification were sequenced using Sanger sequencing technology. Sequenced fragments were assembled to create the complete mitogenome using CodonCode Aligner 5.1.5 (CodonCode Corporation, Dedham, MA). The complete mitogenome was annotated using the software of Sequin (version 15.10, [http://www.ncbi.nlm.nih.gov/Sequin/](http://www.ncbi.nlm.nih.gov/Sequin/)). Transfer RNA (tRNA) genes and their potential cloverleaf structures were identified using tRNAscan-SE 1.21 (Lowe and Eddy 1997).

The complete mitogenome of *C. aureus* was 16,501 bp in length (GenBank accession number MW026682), containing 13 protein-coding genes (PCGs), two ribosomal RNA genes (12S and 16S), 22 tRNA genes, one origin of replication on the light-strand (OL) and a putative control region (CR). The overall base composition was 26.95% A, 29.99% C, 26.29% T, and 16.77% G, respectively, with a slight AT bias of 52.24%. The gene arrangement, composition, and size were quite similar to the teleost fish mitogenomes published previously (Jing et al. 2010; Zhu et al. 2018). The total length of 13 PCGs of *C. aureus* mitogenome was 11,409 bp, encoding 3792 amino acids. Similar to the typical vertebrate mitogenome (Miya and Nishida 2000), 12 of them were located on the H-strand, except for ND6 which was detected on the L-strand. All of the PCGs used the canonical ATG initiation codon with the exception of COI gene, which started with an alternative start codon GTG. Seven PCGs (ND1, ND2, ATP8, ATP6, COIII, ND4L, and ND6) terminated with the stop codon TAA, two (COI, ND5) with AGA, one (ND3) with TAG, the genes ended with a single T were COII, ND4, and Cytb, the presence of an incomplete stop codon is a common phenomenon in vertebrate mitochondrial genes (Zhu et al. 2018; Lee et al. 2019). Twenty-two tRNAs that dispersed between rRNAs and PCGs were identified by their specific anticodon sequences. All the tRNAs were capable of folding into the archetypal cloverleaf
structure except for tRNA^Ser (AGC) that lacked a dihydrouridine arm (Garey and Wolstenholme 1989). The lengths of the two rRNA genes were 954 bp (12S rRNA) and 1707 bp (16S rRNA), respectively, which located between the tRNA^Phe and tRNA^Leu(UUA) and interposed by the tRNA^Val. The CR was detected between tRNA^Phe and tRNA^Pro, consisting of 821 nucleotides, G-C content (35.45%) was significantly lower than that of A-T (64.55%).

Although the complete mitogenome had been reported by Wang et al. (2017) that revealed C. aureus was closely related to the species of genera Nibea instead of Protonibea, phylogenetic relationship of C. aureus remains uncertain and related research still needs further development. In this study, a total of 29 mitogenomes were downloaded from NCBI website for constructing by far the most comprehensive phylogenetic tree of Sciaenidae based on 13 PCGs. The ML tree showed different clustering results and indicated C. aureus was first clustered with Protonibea diacanthus (Figure 1), being consistent with previous studies (Chen 2007; Yong et al. 2010). The present study might give more thought to phylogenetic position of C. aureus and was expected be helpful for further phylogenetic analysis of Sciaenidae.

**Disclosure statement**

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

**Funding**

The study was supported by Open Foundation from Marine Sciences in the First-Class Subjects of Zhejiang; Open Foundation from Key Laboratory of Tropical Marine Bio-resources and Ecology, Chinese Academy of Sciences (LM202010005); 2019 Zhejiang Province Public Welfare Technology Application Research Project (LGN19C190001); Starting Research Fund from the Zhejiang Ocean University.

**Data availability statement**

The genome sequence data that support the findings of this study are openly available in GenBank of NCBI at https://www.ncbi.nlm.nih.gov/ under the accession no. MW026682.
References

Barnett R, Larson G. 2012. A phenol–chloroform protocol for extracting DNA from ancient samples. Methods Mol Biol. 840:13–19.

Bianchi G. 1984. FAO species identification sheets for fishery purposes, Western Indian Ocean (fishing area 51)/edited by W. Fischer and G. Bianchi. Eur J Radiol. 45:208–213.

Chen Q. 2007. Molecular phylogeny of the Sciaenidae in China. Guangzhou: Jinan University.

Cheng YZ, Xu TJ, Jin XX, Tang D, Wei T, Sun YY, Meng FQ, Shi G, Wang RX. 2012. Universal primers for amplification of the complete mitochondrial control region in marine fish species. Mol Biol. 46(5):727–730.

Garey JR, Wolstenholme DR. 1989. Platyhelminth mitochondrial DNA: evidence for early evolutionary origin of a tRNA (serAGN) that contains a dihydrouridine arm replacement loop, and of serine-specifying AGA and AGG codons. J Mol Evol. 28(5):374–387.

Jing H, Zhang D, Hao J, Huang D, Cameron S, Zhu C. 2010. The complete mitochondrial genome of the yellow coaster, Acraea issoria (Lepidoptera: Nymphalidae: Heliconiinae: Acraeini): sequence, gene organization and a unique tRNA translocation event. Mol Biol Rep. 37(7):3431–3438.

Lee S-H, Kang C-B, Shin M-H, Lee S-H, Yoon M, Kim HJ. 2019. The complete mitochondrial genome of a marbled eelpout Lycodes raihens (Perciformes: Zoarcidae). Mitochondrial DNA Part B. 4(2):4043–4044.

Lowe T, Eddy S. 1997. tRNAscan-SE: a program for improved detection of transfer RNA genes in genomic sequence. Nucleic Acids Res. 25(5):955–964.

Miya M, Nishida M. 2000. Use of mitogenomic information in teleostean molecular phylogenetics: a tree-based exploration under the maximum-parsimony optimality criterion. Mol Phylogenet Evol. 17(3):437–455.

Shao W, Wei L, Li L, Wang H, Lin Z, Chen J. 2014. Universal DNA primers for amplification complete mitochondrial genome for sturgeons. Conserv Genet Resour. 6(2):305–307.

Wang Y, Chai X, Hu Z, Xu T. 2017. Complete mitochondrial genome of the golden drum Chrysochir aurenus (Perciformes, Sciaenidae) and its phylogeny. Mitochondrial DNA Part A. 28(1):54–55.

Yong Z, Chun-Yan MA, Ling-Bo MA, Yong NI, Ang-Lv S. 2010. Molecular phylogenetic relationships of 13 Sciaenidae species in China sea areas based on 16SrRNA fragment sequences. Mar Fish. 32:276–282.

Zhu K, Lü Z, Liu L, Gong L, Liu B. 2018. The complete mitochondrial genome of Trachidermus fasciatus (Scorpaeniformes: Cottidae) and phylogenetic studies of Cottidae. Mitochondrial DNA Part B. 3(1):301–302.