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Complete mitochondrial genome of saw-jawed monocle bream *Scolopsis ciliata* and its phylogenetic relationship in genus *Scolopsis*

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ABSTRACT

The complete mitochondrial genome of the saw-jawed monocle bream, *Scolopsis ciliata* was determined by the next generation sequencing (NGS) technique. The circular mitogenome of *S. ciliata* (16,733 bp) encoded the canonical 37 genes including 13 proteins, 22 *tRNA* genes, 2 rRNAs (12S rRNA and 16S rRNA), and two non-coding regions; the origin of light strand replication (OL) and the putative control region (D-Loop). The gene arrangement of the *S. ciliata* mitogenome was identical to its relative, *Scolopsis vosmeri*. Phylogenetic analysis based on the full mitochondrial genome sequences showed that *S. ciliata* is most closely related to *S. vosmeri* with 83% nucleotide sequence identity. The mitogenome information of *S. ciliata* would be the useful information to understand the evolutional relationship of fishes in genus Scolopsis.

Approximately 17 species are currently known in the genus *Scolopsis* and most of which inhabit widly in Indo-West Pacific region (Russell 1990). The *Scolopsis ciliata* is one of economically important marine fishes in Indonesia, which found on the sandy fringe of coastal and lagoon reefs (Kuiter and Tonozuka 2001; Allen and Erdmann 2012). Currently, phylogenetic relationship of fishes in genus *Scolopsis* is still not clearly eastablished (Chen and Zheng 1987; Russell 1990) and only one mitochondrial genome sequence in the genus, *Scolopsis vosmer* is currently reported (Wu et al. 2017). In this study, we report a mitogenome sequence of *S. ciliate*, which would be the useful information to understand the evolutional relationship of fishes in genus *Scloposis*.

The next-generation sequencing (NGS) platform was adopted to read the complete mitochondrial genome sequence of *C. ciliata*. The specimen was collected from the coastal water in Malang, East Java, Indonesia (8°26′05,65"S 112°40′55,31"E) and deposited at the Ichtyology Laboratorium, Universitas Airlangga, Indonesia. Species of the specimen was identified by both its morphological characteristics and DNA sequence identity in COI region to the database (GenBank Accession number: KY362945). Purified mitochondrial DNA by the commercial kit (Abcam, Cambridge, UK) was further fragmented into to the size for library preparation (∼350 bp) by Covaris M220 Focused-Ultrasonicator (Covaris Inc., Woburn, MA). A library was constructed by TruSeq® RNA library preparation kit V2 (Illumina, San Diego, CA) and its quality and the quantity was analysed by 2100 Bioanalyzer (Agilent Technologies, Santa Clara, CA). High-throughput sequencing was performed by Illumina MiSeq system (2 × 300 bp).

The complete mitochondrial genome of *S. ciliata* was circular and 16,733 bp in length (GenBank Number: MH995531). It contained the typical 37 genes coding for two ribosomal RNAs (12S rRNA and 16S rRNA), 22 tRNAs, 13 polypeptides, and two non-coding regions; the origin of light strand replication (OL) and the putative control region (D-Loop). OL was located between tRNA-*Asn* and tRNA-*Cys* at WANCY cluster, while D-Loop (986 bp) was identified between tRNA-*Pro* and tRNA-*Phe*. Besides COX1(GTG) and ATP6 (ATC), 11 protein-coding genes begin with typical ATG. Incomplete stop codons were shown in *ND2*, *COX2*, *COX*3, *ND3*, *ND4*, and *CYTb* genes. The length of tRNAs ranged between 69 and 76 bp, which were located as three conserved tRNA cluster (IQM, WANCY, and HSL)(Satoh et al. 2016). Except for tRNA-*Ser*, 21 tRNAs were predicted to form the typical clover-leaf secondary structures according to ARWEN (Laslett and Canbäck 2008) which has the typical clover-leaf secondary structures except for tRNA-*Ser*. Based on the phylogenetic analysis of the mitogenomes by MEGA7 version 7 software (Kumar et al. 2016), *S. ciliata* was most closely related to *S. vosmeri* (GenBank No. NC029489) with 83% identity forming a genus *Scolopsis* cluster, which is distinct from fishes in genus *Nemipterus* (Figure 1). The mitogenome information of *S. ciliata* would help us understand the evolutional relationship in genus *Scolopsis*.

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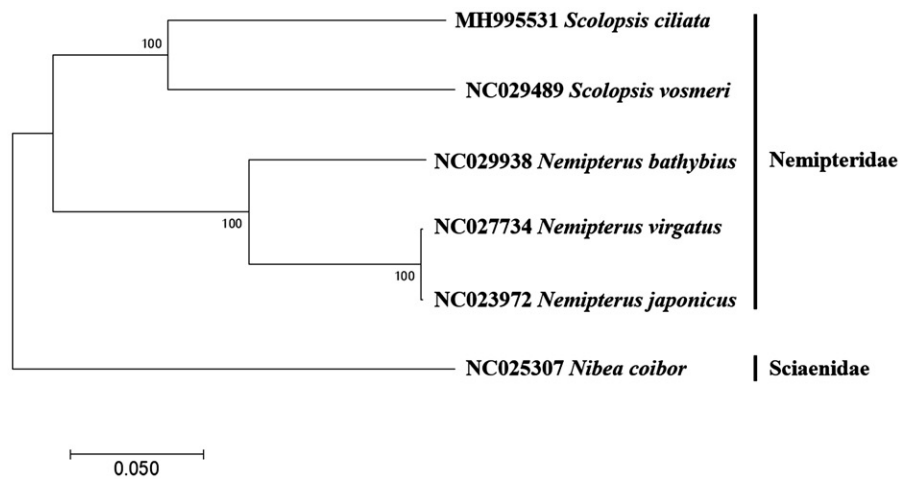
Figure 1. Phylogenetic tree of *Lutjanus vitta* within Lutjanidae. Phylogenetic tree of *Scolopsis ciliata* complete genome was constructed by MEGA7 software with Minimum Evolution (ME) algorithm with 1000 bootstrap replications. GenBank Accession numbers were shown followed by each scientific name.

Disclosure statement

The authors report that they have no conflicts of interest. The authors alone are responsible for the content and writing of the article.

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