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The complete mitogenome genome of *Scolopsis vosmeri* and phylogenetic relationship of genus *Scolopsis*

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Abstract

The complete mitogenome genome of *Scolopsis vosmeri* was determined in this study, which is the first recorded for the complete mitogenome in the genus *Scolopsis*. The circular mtDNA molecule was 16 770 bp in size and encoded 13 protein-coding genes, 2 rRNAs, 22 tRNAs and two non-coding regions, with gene arrangement and content basically identical to those of other species of Nemipteridae. The result of phylogenetic analysis strongly supported that *S. vosmeri* was first clustered together with genus Nemipterus and formed a monophyly in the family Nemipteridae, and then they constituted a sister-group relationship with three families Sparidae, Lethrinidae, and Lutjanidae. It concluded that the genus *Scolopsis* should be classified into the family Nemipteridae. The present study also revealed the phylogenetic relationship of this genus at molecular levels.

The complete mitogenome genome of *Scolopsis vosmeri* was determined in this study, which is the first recorded for the complete mitogenome in the genus *Scolopsis*. The circular mtDNA molecule was 16 770 bp in size and encoded 13 protein-coding genes, 2 rRNAs, 22 tRNAs and two non-coding regions, with gene arrangement and content basically identical to those of other species of Nemipteridae. The result of phylogenetic analysis strongly supported that *S. vosmeri* was first clustered together with genus Nemipterus and formed a monophyly in the family Nemipteridae, and then they constituted a sister-group relationship with three families Sparidae, Lethrinidae, and Lutjanidae. It concluded that the genus *Scolopsis* should be classified into the family Nemipteridae. The present study also revealed the phylogenetic relationship of this genus at molecular levels.

The monocode breams of the genus *Scolopsis* (Teleostei, Percoidae) contains approximately 17 species, which are widespread in the tropical and subtropical waters of the Indo-west Pacific region (Russell, 1990; Shao, 2015). The species diversity of genus *Scolopsis* is considered relatively high, but the phylogenetic relationship of this genus has been long controversial by several researchers (Cheng & Zheng, 1987; Russell, 1990). As a representative species of genus *Scolopsis*, *S. vosmeri* (Bloch, 1792) is one of the most economically important marine fishes and widely distributed in Indo-west Pacific, ranging from east African coast, Red Sea and Persian Gulf to northern Australia (Russell, 1990). Here, we determined the complete mitogenome sequence of *S. vosmeri*, which is first recorded for the mitogenomic information in the genus *Scolopsis*. The result of this study is a supplement for the mitogenomes database of the monocode breams, and can be useful for the future analysis of phylogenetic relationship and genetic diversity in this group.

One sample of *S. vosmeri* was collected from Zhanjiang Coast of Guangdong Province, the South China Sea. Muscle tissues were preserved in 95% ethanol for DNA extraction. Total genomic DNA was extracted from the muscle tissue by standard phenol–chloroform procedure (Sambrook & Russell, 1989). Through the high-throughput sequencing in the Illumina HiSeq 2500 System (Illumina Inc, San Diego, CA), we generated totally 8662 sequence reads for the mitogenome of *S. vosmeri* with 64.5 × sequencing depth.

The complete mitogenome sequence of *S. vosmeri* was 16 770 bp and has been deposited in GenBank with accession no. KT692978. It consisted of 13 typical protein-coding genes, 22 transfer RNA genes (tRNAs), two ribosomal RNA genes (12S rRNA and 16S rRNA) and 2 non-coding regions (a light-strand (L-strand) replication origin (O_L) and a control region (D-loop)]. The ND6 and eight *tRNA* (tRNA_Glu, Ala, Asn, Cys, Thr, Ser(UCN), Gln, Pro) genes were encoded on the L-strand and other genes on the H-strand. The overall nucleotide composition of H-strand was 27.8% A, 28.2% T, 17.0% G, and 27.0% C, with an A+T content of 56.0%. In the 13 protein-coding genes, except that COI had a GTG start codon, all other genes started with ATG codon. The ND1, COI, ATPase8, ND4L, and ND5 were terminated with TAA, ND6 with TAG codon, and other protein-coding genes with incomplete stop codon T– or TA–. There were some overlaps between ATPase8–ATPase6 (22 bp), ND4L–ND4 (7 bp), and ND5–ND6 (4 bp). The two rRNA genes were located between tRNA_Glu and tRNA_Lys(UCN), separated by tRNA_Glu. The 22 tRNAs genes ranged in size from 67 bp in both tRNA_Cys and tRNA_Ser(AGY) to 75 bp in tRNA_Ala(UUR). All tRNAs could be folded into typical cloverleaf secondary structure except tRNA_Ser(AGY) losing the dihydrouridine arm. The O_L was found between tRNA_Glu and tRNA_Cys genes in the WANCY region and comprised 37 nucleotides. The D-loop located between tRNA_Pro and tRNA_Phe genes, and was 1031 bp in length. Based on the sequence identity analysis performed in BioEdit version 7.1.9 (Hall, 1999), the mitogenome sequence of *S. vosmeri* shared 72.2–73.7% identities with that of *Nemipterus* (Li et al., 2014; Wu et al., 2015). It indicates that the mitogenome sequence of them is useful for the molecular phylogeny analysis of the family Nemipteridae.

The phylogenetic analysis was performed by MEGA6.06 program (Tamura et al., 2013) based on the complete mitogenome sequence of *S. vosmeri* and those of 13 closely related species belonging to four families Nemipteridae, Sparidae, Lethrinidae, and Lutjanidae, with *Labracinus cyclophthalmus* (AP009125) and *Scatophagus argus* (KC790398) as outgroups. The neighbor-joining tree (Figure 1) showed that *S. vosmeri* first clustered together with three species of genus *Nemipterus* and formed a monophyly in the family Nemipteridae, and then they constituted...
a sister-group relationship with other three families. The present results on the molecular phylogenetic analysis strongly supported that the genus *Scolopsis* should be classified into the family Nemipteridae. This study also revealed the phylogenetic relationship of the genus *Scolopsis* at molecular levels.

**Declaration of interest**

The authors report no conflicts of interest. The authors are responsible for the content and writing of the paper. This study was supported by the National Natural Science Foundation of China (41006084, 31372532, 41276166, and 31172053), Project for Outstanding Young Teachers in Higher Education of Guangdong, China (Yq2013093), and the Open Research Fund Program of Fujian Provincial Key Laboratory of Marine Fishery Resources and Eco-environment (C221502).

**References**


