The complete mitochondrial genome of Slender Giant Moray *Strophidon sathete* (Hamilton, 1822)

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**ABSTRACT**

The whole mitochondrial genome of the Slender Giant Moray *Strophidon sathete* (Hamilton, 1822) from the Hainan island was characterized using next-generation sequencing for the first time. The circular mitogenome of *S. sathete* is 16,568 bp, with 13 protein-coding genes (PCGs), 22 tRNA genes, two rRNA genes, and a D-loop region. The base composition is little biased (A, G, T, and C was 30.95%, 16.73%, 27.09%, and 25.23%, respectively) with A + T contents of 58.04%. Among 13 PCGs, 12 PCGs use a normal ATG as the start codon except COX1 use GTG; four of them end with TAA or TAG, others terminate with an unusual stop codon. The phylogenetic tree showed that *S. sathete* was first clustered with *Rhinomuraena quaesita* and *Gymnothorax minor*, which further clarify the phylogenetic and evolution position of the genus *Strophidon* in the family Muraenidae.

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The 22 tRNA genes in the mitogenome of the slender giant moray vary from 67 bp to 76 bp. Two tRNA are present more than once: tRNA-Leu and tRNA-Ser both have two type copies, respectively. The 12S rRNA is 949 bp, located between tRNA-Val and tRNA-Phe; the 16S rRNA is 1660 bp, located between tRNA-Val and tRNA-Leu. There are six overlapping regions of 1–9 bp in length. The longest overlapping region is located between ATP8 and ATP6. The mitochondrial genome has 16 intergenic sequences varying from 1 to 915 bp in length (Supply Table S1). The largest intergenic sequence is the D-loop region located between tRNA-Pro and tRNA-Phe. Twelve PCGs use a normal ATG as the initiation codon except COX1 start with GTG. Four genes (ND1, ND4L, ND6, CYTB) end with TAA or TAG, other genes terminate with unusual stop codon: ATP8, ATP6, and COX3 use TA; ND2 and COX2 use T; COX1 uses AGA; ND3 uses GAA; ND4 uses TGT; ND5 uses ACC.

The phylogenetic tree (Figure 1) showed that S. sathete was first clustered with Rhinomuraena quaesita and Gymnothorax minor, which further elucidate the phylogenetic and taxonomic position of the genus Strophicdon in the family Muraenidae. The results are largely similar to previous studies based on mitochondrial COI fragments, 12S and 16S rRNA genes (Tang and Fielitz 2013; Huang et al. 2020). Taken together, the newly sequenced mitochondrial genome of S. sathete characterized here should contribute to a better understanding of phylogenetic relationships of species in the family Muraenidae, and molecular identification, population genetic and evolutionary biological studies of the slender giant moray.

The GenBank accession number for each species is indicated after the scientific name. Anguilla marmorata was used as outgroup.

**Disclosure statement**

No potential conflict of interest was reported by the authors.

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**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. MW035594. The associated BioProject, SRA, and Bio-Sample numbers are PRJNA703745, SRR13758977, and SAMN18022891, respectively.

**Figure 1.** Phylogenetic tree of the complete mitogenome of 13 fish species in Anguilliformes.
References

Böhlke EB. 1997. Notes on the identity of elongate unpatterned Indo-Pacific morays, with description of a new species (Muraenidae, Subfamily Muraninae). Proc Acad Nat Sci Philadelphia. 147:89–109.

Chen H-M, Shao K-T, Chen C-T. 1994. A review of the muraenid eels (family Muraenidae) from Taiwan with descriptions of twelve new records. Zool Stud. 33:44–64.

Huang WC, Mohapatra A, Thu PT, Chen HM, Liao TY. 2020. A review of the genus Strophidon (Anguilliformes: Muraenidae), with description of a new species. J Fish Biol. 97:1462–1480.

Jin J-J, Yu W-B, Yang J-B, Song Y, Depamphilis CW, Yi T-S, Li D-Z. 2020. GetOrganelle: a fast and versatile toolkit for accurate de novo assembly of organelle genomes. Genome Biol. 21(1):31.

Loh K-H, Hussein MAS, Chong V-C, Sasekumar A. 2015. Notes on the moray eels (Anguilliformes: Muraenidae) of Malaysia with two new records. Sains Malay. 44:41–47.

Nguyen L-T, Schmidt HA, Von Haeseler A, Minh BQ. 2015. IQ-TREE: a fast and effective stochastic algorithm for estimating maximum-likelihood phylogenies. Mol Biol Evol. 32:268–274.

Tang KL, Fielitz C. 2013. Phylogeny of moray eels (Anguilliformes: Muraenidae), with a revised classification of true eels (Teleostei: Elopomorpha: Anguilliformes). Mitochondrial DNA. 24:55–66.