Mitochondrial DNA

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MITOGENOME ANNOUNCEMENT

Complete mitogenome of two moray eels of *Gymnothorax formosus* and *Scuticaria tigrina* (Anguilliformes: Muraenidae)

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Abstract

In this study, the complete mitogenome sequence of two moray eels of *Gymnothorax formosus* and *Scuticaria tigrina* (Anguilliformes: Muraenidae) has been sequenced by the next-generation sequencing method. The assembled mitogenome, with the length of 16,558 bp for *G. formosus* and 16,521 bp for *S. tigrina*, shows 78% identity to each other. Both mitogenomes follow the typical vertebrate arrangement, including 13 protein coding genes, 22 transfer RNAs, two ribosomal RNAs genes, and a non-coding control region of D-loop. The length of D-loop is 927 bp (*G. formosus*) and 850 bp (*S. tigrina*), which is located between tRNA-Pro and tRNA-Phe. The overall GC content is 45.5% for *G. formosus* and 47.9% for *S. tigrina*. Complete mitogenomes of *G. formosus* and *S. tigrina* provide essential and important DNA molecular data for further phylogenetic and evolutionary analysis for moray eel.

Keywords

Gymnothorax formosus, mitogenome, Moray eel, next generation sequencing, *Scuticaria tigrina*

History

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Anguilliformes is an Order of elongate fishes with pelvic fins and girdle absent or reduced. All the fishes in Anguillifomes have a transparent leptocephalus larval stage during their early life history. The metamorphosis from leptocephalus to glass eel is a key process for freshwater eels (Anguillidae) development. Moral eels (Muraenidae) and freshwater eels are in the same suborder Anguilloidei, but living whole their life in coastal marine environment.

Samples of two moray eels, *Gymnothorax formosus* (voucher no. 351) and *Scuticaria tigrina* (voucher no. 347), were collected from Penghu and Changbin in Taiwan, respectively. The methods for genomic DNA extraction, library construction, and next-generation sequencing followed previous publication (Shen et al., 2014). By using commercial software (Geneious V8, Auckland, New Zealand), about 0.09% (3659 out of 4,226,258) and 0.04% raw reads (2660 out of 6,582,060) were *de novo* assembled to produce two circular forms of complete mitogenomes with average 74× and 54× coverage for *G. formosus* and *S. tigrina*, respectively. The assembled mitogenomes of *G. formosus* and *S. tigrina*, consist of 16,558 bp (GenBank: KP874184) and 16,521 bp (GenBank: KP874183), both showing 78% identity each other. Complete mitogenomes of *G. formosus* and *S. tigrina* had the typical vertebrate mitochondrial gene arrangement, including 13 protein coding genes, 22 transfer RNAs, two ribosomal RNAs genes, and a non-coding control region of D-loop. The length of D-loop is 927 bp (*G. formosus*) and 850 bp (*S. tigrina*), which is located between tRNA-Pro and tRNA-Phe.

The protein coding, rRNA, and tRNA genes of mitogenome were predicted by using DOGMA (Wyman et al., 2004), ARWEN (Laslett & Canback, 2008), MITOS (Bernt et al., 2013), and MitoAnnotator (Iwasaki et al., 2013) tools. For *G. formosus*, seven of 13 protein-coding genes are terminated with incomplete stop codons of either T– (*ND2*, *COX1*, *COX2*, *ND3*, and *ND4*) or TA– (*ATP6* and *COX3*). For *S. tigrina*, six of 13 protein-coding genes are terminated with incomplete stop codons of either T– (*ND2*, *COX2*, *ND3*, and *ND4*) or TA– (*ATP6* and *COX3*). For both species, the longest one is ND5 (1842 bp) in all protein coding genes, whereas the shortest is ATP8 (168 bp). The 12S (950 bp for *G. formosus* and 948 bp for *S. tigrina*) and 16S (1654 bp for *G. formosus* and 1673 bp for *S. tigrina*) rRNA genes are located between tRNA-Phe and tRNA-Leu (UAA) and separated by tRNA-Val.

To validate the phylogenetic position, we used MEGA6 (Tamura et al., 2013) software to construct a Maximum likelihood tree (with 500 bootstrap replicates) containing complete mitogenomes of 24 species derived from 19 different genus in Anguilliformes. Tree topology shows that *G. formosus* is closely related to *G. kidako* and supports that *S. tigrina* can be unambiguously grouped in Muraenidae which is closely related to *Anarchias sp. Ansp* with high bootstrap value supported (Figure 1). In conclusion, the complete mitogenome of the *G. formosus* and *S. tigrina* decoded in this study provides an

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