MITOGENOME ANNOUNCEMENT

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

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Abstract

In this study, the complete mitogenome sequence of two moray eels of Gymnophorax 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.

Anguilliformes is an Order of elongate fishes with pelvic fins and girdle absent or reduced. All the fishes in Anguilliformes have a transparent leptcephalus larval stage during their early life history. The metamorphosis from leptcephalus 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, Gymnophorax 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 (2060 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, tRNA, and tRNA genes of mitogenome were predicted by using DOGMA (Wyman et al., 2004), ARWEN (Laslett & Canback, 2008), MITOS (Bens 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 (1842bp) 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) tRNA genes are located between tRNA-Phe and tRNA-Leu (UUA) 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. Asz 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

Keywords
Gymnophorax formosus, mitogenome, Moray eel, next generation sequencing, Scuticaria tigrina

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