Mitochondrial DNA

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MITOGENOME ANNOUNCEMENT

Next generation sequencing yields the complete mitochondrial genome of the Zebra moray, *Gymnomuraena zebra* (Anguilliformes: Muraenidae)

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Abstract

In this study, the complete mitogenome sequence of the Zebra moray, *Gymnomuraena zebra* (Anguilliformes: Muraenidae) has been sequenced by the next-generation sequencing method. The assembled mitogenome consisting of 16,576 bp includes 13 protein coding genes, 22 transfer RNAs, and two ribosomal RNAs genes. The overall base composition of Zebra moray is 30.2% for A, 26.8% for C, 17.2% for G, and 25.8% for T and show 80% identities to Kidako moray, *Gymnothorax kidako*. The complete mitogenome of the Zebra moray provides an essential and important DNA molecular data for further phylogeography and evolutionary analysis for moray eel phylogeny.

Keywords

Mitogenome, next generation sequencing, zebra moray

History

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The Zebra moray, *Gymnomuraena zebra* (Shaw, 1797) is a special species with densely banded dark and whitish, with round and short snout. This species is widely distributed in Indo-Pacific, eastern coast of Africa, the Red Sea and Oman, east of Galapagos, Hawaii, Maxico, Colombia, north to Japan, Taiwan, and south to Australia. *Gymnomuraena zebra* is the only member of the genus *Gymnomuraena*. It has close-set pebble-like teeth, prey like crustaceans (crabs), mollusks, sea urchins, and fish. It lives in shallow rocky or coral reef on coastal shallow water at the depth from 1 to 39 m, usually at <4 m (Mundy & Press, 2005). The establishment of Zebra moray mitogenome is usefulness for further phylogenetic research of moray eels.

Samples (voucher no. 348) of Zebra moray were collected from Taitung, Taiwan. The methods for genomic DNA extraction, library construction, and next generation sequencing were followed by our previous publication (Shen et al., 2014). The raw next generation sequencing reads generated from MiSeq (Illumina, San Diego, CA) were de novo assembled by commercial software (Geneious V8, Auckland, New Zealand) to produce a single, circular form of complete mitogenome with about an average 99 × coverage (5524 out of 5,063,870, 0.11%). The complete mitochondrial genome of Zebra moray was 16,576 bp in size (GenBank: XXXXX), includes 13 protein coding genes, 22 transfer RNAs, and two ribosomal *RNAs* genes. The overall base composition of Zebra moray is 30.2% for A, 26.8% for C, 17.2% for G, and 25.8% for T and show 80% identities to Kidako moray, *Gymnothorax kidako* (GenBank: NC_004417).

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The protein-coding, rRNA, and tRNA genes of Zebra moray mitogenome were predicted by using DOGMA (Wyman et al., 2004), ARWEN (Laslett & Canback, 2008), and MitoAnnotator (Iwasaki et al., 2013) tools. All protein-coding genes were encoded on H-strand with exception of protein-coding genes of ND6. All *tRNA* genes were encoded on H-strand with exception of *tRNA-Gln*, *tRNA-Ala*, *tRNA-Asn*, *tRNA-Cys*, *tRNA-Tyr*, *tRNA-Ser* (UGA), *tRNA-Glu*, and *tRNA-Pro* genes. All the 13 mitochondrial protein-coding genes share the start codon ATG, except for COX1 (GTG start codon). It also important to note that six of 13 protein-coding genes is inferred to terminate with TAA termination codon (ND1, ATP8, ND4L, ND5, ND6, and CYTB), one terminated with AGA codon (CO1), six of them are terminated with incomplete codons of T-- (ND2, CO2, ND3, and ND4) or TA- (ATP6 and CO3). Many fishes also used such incomplete codon structure as a signal to halt the process of protein translation. The longest one is *ND5* gene (1842 bp) in all protein coding genes, whereas the shortest is *ATP8* gene (168 bp). The two ribosomal *RNA* genes, 12S rRNA gene (948 bp), and 16S rRNA gene (1661 bp) are located between tRNA-Phe and tRNA-Leu (UAA) and separated by tRNA-Val. The length of D-loop control region is 920 bp.

To validate the phylogenetic position of Zebra moray, we have constructed a maximum likelihood phylogenetic tree (with 500 bootstrap replicates) using the complete mitogenome of 22 species derived from 19 different families in order Anguilliformes. By following the analysis method described in previous publication (Inoue et al., 2010), *Notacanthus chemnitzi* and *Elops hawaiensis*, which produce leptocephalus larvae, were used as outgroup to contrast the tree topology. Result shows that Zebra moray can be unambiguously grouped in Muraenidae with high bootstrap value supported (Figure 1). In conclusion, the complete mitogenome of the Zebra moray deduced in this study