

MITOGENOME ANNOUNCEMENT

Next-generation sequencing yields the complete mitochondrial genome of the longfang moray, *Enchelynassa canina* (Anguilliformes: Muraenidae)

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Abstract

In this study, the complete mitogenome sequence of the longfang moray, *Enchelynassa canina* (Anguilliformes: Muraenidae) has been sequenced by the next-generation sequencing method. The length of the assembled mitogenome is 16,592 bp, which includes 13 protein coding genes, 22 transfer RNAs, and 2 ribosomal RNAs genes. The overall base composition of longfang moray is 28.4% for A, 28.0% for C, 18.4% for G, 25.1% for T, and show 82% identities to Kidako moray, *Gymnothorax kidako*. The complete mitogenome of the longfang moray provides an essential and important DNA molecular data for further phylogeography and evolutionary analysis for moray eel phylogeny.

Keywords

Longfang moray, mitogenome, next-generation sequencing

History

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Longfang moray, *Enchelynassa canina* (Quoy & Gaimard, 1824) is a special species with anterior nostril bears a bilobate fleshy large projecting tube, posterior nostril in front of and above the eye, surrounded by a fleshy rim. Body color is uniform brownish, and grey color in the belly side. It is a type species (synonyms *E. bleekeri*) and the only member of the genus *Enchelynassa*. This species is widely distributed in Indo-Pacific: Chagos Island and Reunion, to Panama, north to Japan and the Hawaiian Islands, Taiwan, north to China, south to Tonga and Mangareva. Adults live in reef flats and inhabits areas with strong surge in a depth of 2–20 m. This species is very secretive during the day, feeds on fishes and octopus at night. Jaw elongate and arched, elongate canine teeth exposed when mouth closed, it may traumatogenesis to humans when provoked. The establishment of longfang moray mitogenome is useful for further phylogenetic research studies.

Samples (voucher no. 350) of *E. canina* were collected from Changbin, 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 28 × coverage (1390 out of 5,539,274, 0.03%). The complete mitochondrial genome of *E. canina* was 16,592 bp in size (GenBank: KP893074), includes 13 protein coding genes,

22 transfer RNAs, and two ribosomal RNAs genes. The overall base composition of *E. canina* is 28.4% for A, 28.0% for C, 18.4% for G, 25.1% for T, and show 82% identities to Kidako moray, *Gymnothorax kidako*.

The protein coding, rRNA, and tRNA genes of *E. canina* mitogenome were predicted by using DOGMA (Health Effects Research Laboratory, Research Triangle Park, NC) (Wyman et al., 2004), ARWEN (Health Effects Research Laboratory, Research Triangle Park, NC) (Laslett & Canback, 2008), and MitoAnnotator (Health Effects Research Laboratory, Research Triangle Park, NC) (Iwasaki et al., 2013) tools. All protein-coding genes were encoded on the H-strand with exception of protein-coding genes of ND6. All tRNA genes were encoded on the H-strand with the 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 four of the 13 protein-coding genes is inferred to terminate with TAA termination codon (*ND1*, *ATP8*, *ND4L*, and *CYTB*), 2 terminated with TAG codon (*ND5* and *ND6*), 6 of them are terminated with incomplete codons of T- (*ND2*, *CO1*, *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 (949 bp) and 16S rRNA gene (1664 bp), are located between *tRNA-Phe* and *tRNA-Leu* (UAA) and separated by *tRNA-Val*. The length of D-loop control region is 938 bp.

To validate the phylogenetic position of *E. canina*, we have constructed a maximum likelihood phylogenetic tree (with 500 bootstrap replicates) by using the complete mitogenome of

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