Mitochondrial DNA

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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* is a special species with anterior nostril bears a bilobate fleshy large projectting 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 traumatogenis 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%).

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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 (Wyman et al., 2004), ARWEN (Laslett & Canback, 2008), and MitoAnnotator (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*), 7 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

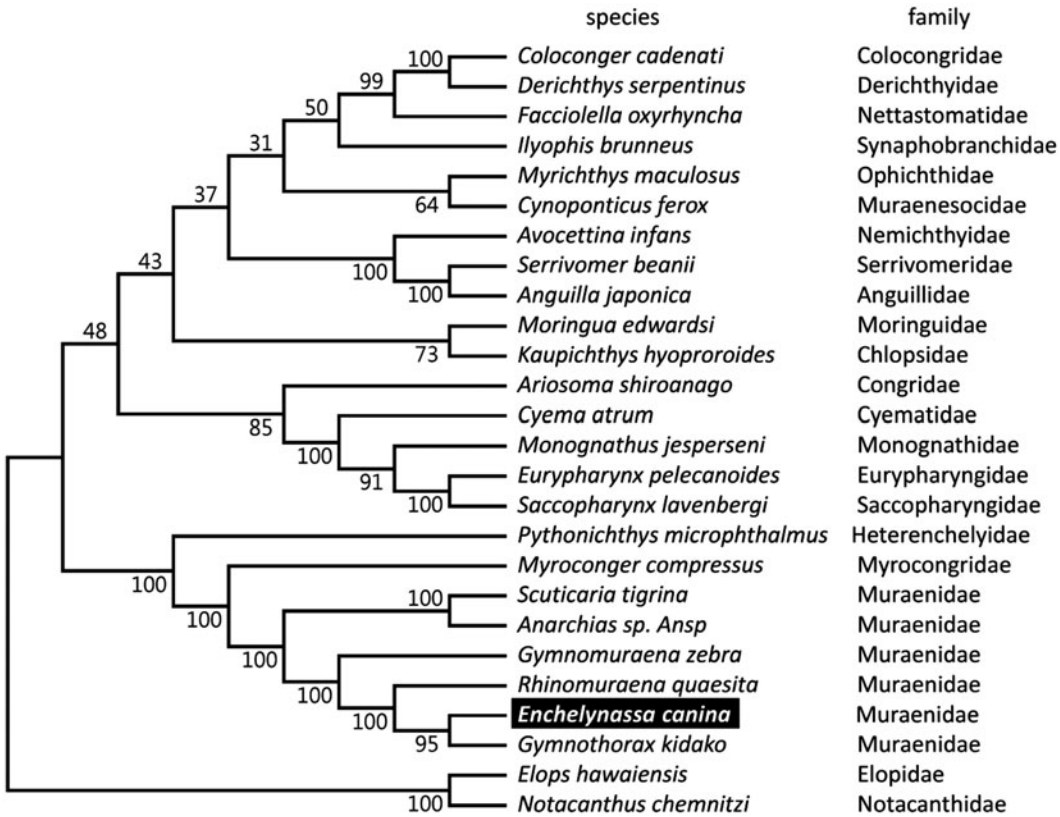

Figure 1. Molecular phylogeny of *Enchelynassa canina* and other related species in Anguilliformes based on complete mitogenome. The complete mitogenomes is downloaded from GenBank and the phylogenic tree is constructed by the maximum likelihood method with 500 bootstrap replicates. The gene's accession number for tree construction is listed as follows: *Coloconger cadenati* (NC_013606), *Derichthys serpentinus* (NC_013611), *Facciolella oxyrhyncha* (NC_013621), *Ilyophis brunneus* (NC_013634), *Myrichthys maculosus* (NC_013635), *Cynoponticus ferox* (NC_013617), *Avocettina infans* (NC_013624), *Serrivomer beanii* (NC_013627), *Anguilla japonica* (NC_002707), *Moringua edwardsi* (NC_013622), *Kaupichthys hyoproroides* (NC_013607), *Ariosoma shiroanago* (NC_013632), *Cyema atrum* (NC_013609), *Monognathus jesperseni* (NC_013612), *Eurypharynx pelecanoides* (NC_005299), *Saccopharynx lavenbergi* (NC_005298), *Pythonichthys microphthalmus* (NC_013601), *Myroconger compressus* (NC_013631), *Scuticaria tigrina* (KP874183), *Anarchias sp. Ansp* (NC_013613), *Gymnomuraena zebra* (KP793920), *Rhinomuraena quaesita* (NC_013610), *Enchelynassa canina* (KP893074), *Gymnothorax kidako* (NC_004417), *Notacanthus chemnitzi* (NC_005144) and *Elops hawaiensis* (NC_005798).

24 species derived from 19 different families in order Anguilliformes. By following the analysis method described in the previous publication (Inoue et al., 2010), *Notacanthus chemnitzi* and *Elops hawaiensis,* which produce leptocephalus larvae, were used as an outgroup for tree rooting. Result shows that *E. canina* can be unambiguously grouped in Muraenidae which is closely related to *Gymnothorax kidako* with high-bootstrap value supported (Figure 1). In conclusion, the complete mitogenome of the *E. canina* deduced in this study provides an essential and important DNA molecular data for further phylogeography and evolutionary analysis for moray eel phylogeny.

Declaration of interest

The authors report that they have no conflicts of interest. The authors alone are responsible for the content and writing of the paper.

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