MITOGENOME ANNOUNCEMENT

The complete mitochondrial genome of variegated lizardfish
_Synodus variegatus_ (Aulopiformes, Synodontidae)

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Abstract

In this study, the complete mitogenome sequence of variegated lizardfish _Synodus variegatus_ (Lacepède, 1803) (Perciformes, Synodontidae) has been amplified and sequenced employing the long polymerase chain reaction method. The mitogenome, consisting of 16,448 base pairs (bp), had the typical vertebrate mitochondrial gene arrangement, including 13 protein-coding, 22 transfer RNAs, 2 ribosomal RNA genes and a noncoding control region (CR). The CR of 830 bp length is rather compact and located between tRNA<sup>Pro</sup> and tRNA<sup>Ser(UCN)</sup>. The overall base composition of _Myxocyprinus asiaticus_ is 26.36% for A, 27.69% for C, 26.99% for T and 18.95% for G, with a slight AT bias of 53.36%. The complete mitogenome may provide important DNA molecular data for further phylogenetic analyses for higher taxa of teleost fishes, especially for the fishes of order Aulopiformes.

DNA genes, 2 ribosomal RNA genes and a CR (Table 1). All genes were encoded on H-strand with the exception of one protein-coding gene (ND6) and eight tRNA genes (tRNA<sub>Glu</sub>, tRNA<sub>Arg</sub>, tRNA<sub>Asp</sub>, tRNA<sub>Gln</sub>, tRNA<sub>Tyr</sub>, tRNA<sub>Val</sub>, tRNA<sub>Met</sub>, tRNA<sub>Glu</sub> and tRNA<sub>Pro</sub>). The overall base composition of _M. asiaticus_ is 26.36% for A, 27.69% for C, 26.99% for T and 18.95% for G from which a slight AT bias could be easily found due to AT 53.36% >GC 46.64% in both strands.

All 13 mitochondrial protein-coding genes share the start codon ATG, except for COI (GTG start codon). It also important to note that three of 13 protein-coding genes are inferred to termination with an incomplete stop codon T- (COII, ND4 and Cyt b); eight of them share typical termination codon TAA (ND1, ND2, COI, ND3, ATP8, ATP6, ND4L and ND5); two of them share typical termination codon TAG (COIII and ND6). Many other Perciform fish species also have such incomplete codon structure as a signal to halt the process of protein translation (e.g. Chen et al., 2012; Cheng et al., 2012; Jin et al., 2012; Miya & Nishida, 1999; Shi et al., 2012; Song et al., 2012). The longest one is the ND5 gene (1833 bp) in all protein-coding genes, whereas the shortest is ATP8 gene (168 bp). The CR (D-loop) is 830 bp in length, which is very compact compared to most of the other marine teleost fishes except for the European sand goby, Pomatoschistus minutus, having the most compact D-loop length as 773 bp among the teleost fishes (Stefanni et al., 2002), and is located between the tRNA<sup>Pro</sup> and tRNA<sup>Pro</sup>. The two ribosomal RNA genes, 12S rRNA gene (945 bp) and 16S rRNA gene (1668 bp), are located between tRNA<sup>Pro</sup> and tRNA<sup>Pro</sup>(UUR) and separated by tRNA<sup>Val</sup>. We expect that the present result will contribute for elucidating the further phylogenetic approach among different taxa of marine teleost fishes.

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