


Complete mitochondrial genome of the hybrid grouper *Hyporthodus septemfasciatus* (♀) × *Epinephelus lanceolatus* (♂)

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ABSTRACT

The complete mitochondrial genome of the novel hybrid grouper (*Hyporthodus septemfasciatus* ♀ × *Epinephelus lanceolatus* ♂) includes 13 protein-coding genes, 2 ribosomal RNAs, 22 transfer RNA genes, and 1 control region (D-loop) for a total length of 16,559 bp. The overall nucleotide composition encoded on the heavy strand comprises 28.64% A, 28.26% C, 16.26% G, and 26.84% T.

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In this study, we report the complete mitogenome of the novel hybrid grouper *Hyporthodus septemfasciatus* (♀) × *Epinephelus lanceolatus* (♂) in Tongyeong, Republic of Korea (34°49'36.8"N, 128°20'01.6"E). Fry of the hybrid were sampled immediately after hatching and preserved in 99% ethyl alcohol in September 2019. The extracted hybrid grouper DNA specimen is stored at Soonchunhyang University in Republic of Korea (voucher no. SUC-19260). The complete mitochondrial genome (GenBank accession no. MT709278) includes 13 protein-coding genes, 2 ribosomal RNAs (rRNA), 22 transfer RNA (tRNA) genes, and 1 control region (D-Loop), for a total length of 16,559 bp. The encoded genes are similar to those of other Serranidae species (Kim et al. 2016; Tang et al. 2016; Wang et al. 2016). Most genes are encoded on the heavy strand, except for NADH dehydrogenase subunit 6 (ND6). Eight tRNA genes (tRNA-Gln, Ala, Asn, Cys, Tyr, Ser, Glu, and Pro) are encoded on the light strand. The total length of the 13 protein-coding genes (PCGs) is 11,469 bp. Among these, 12 PCGs start with ATG; the one remaining PCG is COX1 (starting with GTG). We identified three types of stop codons: TAA, with nine PCGs (ATP6, ATP8, COX1, COX3, ND1, ND2, ND4L, ND5, and ND6); AGA, with three PCGs (COX2, CYTB and ND4); and TAG, with one PCG (ND3). The overall nucleotide composition encoded on the heavy strand was 28.64% A, 28.26% C, 16.26% G, and 26.84% T. G + C content (44.53%) is less than that of A + T (55.48). The length of the mitochondrion DNA is 16,559 bp, which is 184 bp shorter than that of *E. lanceolatus* (Wang et al. 2014). Composition analysis

revealed differentiation from *E. lanceolatus* in nucleotide frequencies, as 2.09% A, 0.50% C, 2.83% G, and 1.28% T. The 22 tRNA genes vary in length from 67 to 76 bp. The 12S rRNA, with a length of 956 bp, is located between tRNA-Phe and tRNA-Val, and the 16S rRNA, with a length of 1,709 bp, is located between tRNA-Val and tRNA-Leu. The control region (D-loop), with a length of 851 bp, is located between tRNA-Pro and tRNA-Phe. A molecular phylogenetic tree was constructed using the neighbor joining method based on complete mitochondrion genes among five species of *Epinephelus*, two species of *Cephalophis*, and two species of *Hyporthodus* (Figure 1).

Disclosure statement

No potential conflict of interest was reported by the author(s).

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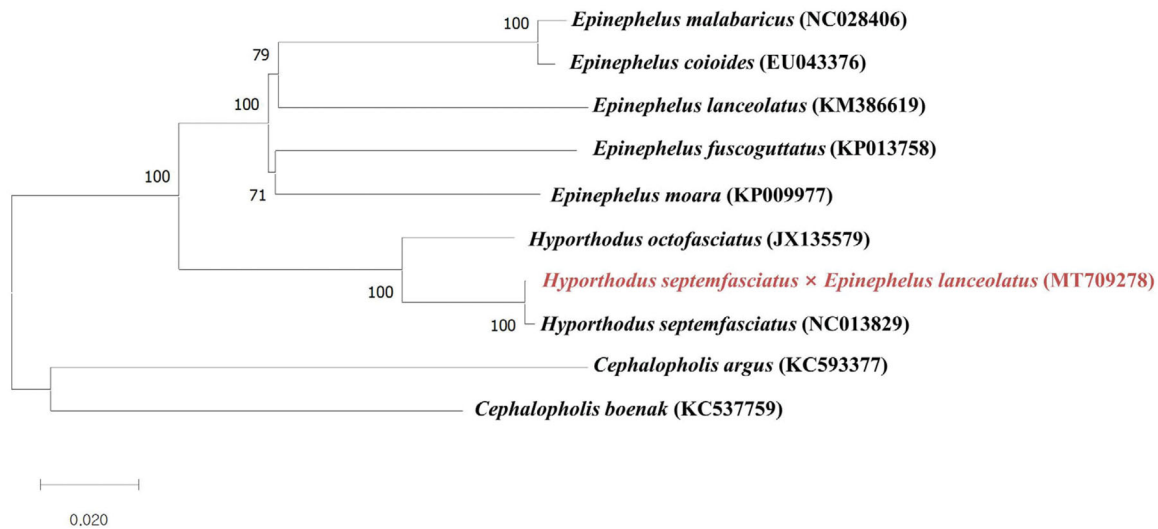


Figure 1. Molecular phylogenetic tree of complete mitochondrial genes among 5 species of *Epinephelus*, 2 species of *Cephalopholis*, and 2 species of *Hyporthodus*. The phylogenetic tree was constructed using neighbor joining.

Data availability statement

The data that support the findings of this study are openly available in GenBank at <https://www.ncbi.nlm.nih.gov/>, reference number MT709278.

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