


The complete mitochondrial genome of the hybrid grouper *Epinephelus fuscoguttatus* (♀) × *E. polyphekadion* (♂)

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ABSTRACT

This study determined the complete mitochondrial genome of the hybrid grouper *Epinephelus fuscoguttatus* ♀ × *E. polyphekadion* ♂. The complete mitochondrial genome is 16,648 bp and includes 13 protein-coding, 2 ribosomal RNA, 22 transfer RNA genes, and a control region (D-loop). The nucleotide composition of the L-strand was A 29.12%, C 28.33%, G 15.65%, and T 26.90%. All except the NADH dehydrogenase subunit (ND6) and eight tRNA genes are encoded on the H-strand.

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Hybrid groupers have faster growth rates, greater disease resistance, and higher economic value than purebred groupers (James et al. 1999). This study determined data on the Serranidae. We report the complete mitogenome of the novel hybrid grouper *Epinephelus fuscoguttatus* (♀) × *E. polyphekadion* (♂), which was produced in Indonesia (0°58'25.5"N 104°03'20.8"E). Fry of the novel hybrid grouper were preserved in 99% ethyl alcohol immediately after hatching in September 2019. The extracted hybrid grouper DNA specimen is stored at Soonchunhyang University in the Republic of Korea (voucher no. SUC-19259).

The complete mitochondrial genome of the hybrid grouper genome (GenBank accession no. MT709279) is 16,648 bp and consists of 13 protein-coding genes, 22 transfer RNA genes, 2 ribosomal RNA genes, and the control region (D-loop). The encoded genes are similar to those of other Serranidae (Kim et al. 2016; Tang et al. 2016, 2017; Chen et al. 2017). The total length of the 13 protein-coding genes is 11,442 bp or 68.73% of the mitochondrial genome. The nucleotide composition of the L-strand is A 29.12%, C 28.33%, G 15.65%, and T 26.90%. The G + C content (43.98%) is lower than the A + T content (56.02%). All of the genes are encoded on the H-strand, except for the NADH dehydrogenase subunit (ND6) and eight tRNA genes. Most of the coding sequences start with ATG, but COXI and ATP6 start with GTG and ATA, respectively. The 22 transfer RNA genes range from 67 to 76 bp in length. Eight of the protein-coding genes (ND1, COXI, ATP8, ATP6, COXIII, ND3, ND4L, and ND5) stop with TAA, while four of the protein-coding genes end with AGA (ND4, COXII) and TAG (ND6, CYTB). The 12S ribosomal RNA is between transfer RNA-Phe and transfer RNA-Val and is

954 bp in length. The 16S ribosomal RNA is between transfer RNA-Val and transfer RNA-Leu and is 1706 bp in length. The control region (D-loop) is 947 bp long and located between tRNA-Pro (TGG) and tRNA-Phe (GAA). A phylogenetic tree was constructed based on the complete mitochondrial genome and that of other groupers using the neighbor-joining method and two species of *Cephalopholis* were used as the outgroup (Figure 1).

Disclosure statement

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

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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 MT709279.

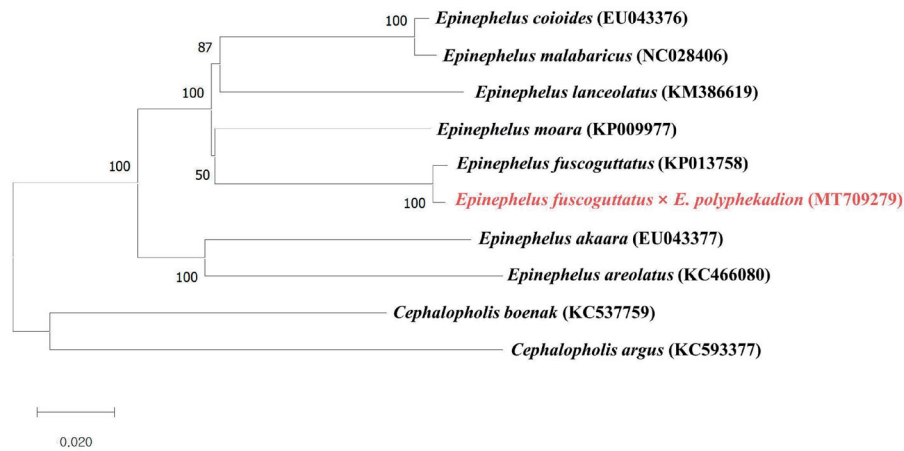


Figure 1. Phylogenetic tree of hybrid grouper *Epinephelus fuscoguttatus* (♀) × *E. polyphkadion* (♂) with 7 *Epinephelus* and 2 out group. The number of each nod is the bootstrap probability. Phylogenetic tree was constructed by neighbor joining.

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