Complete mitochondrial genome of the hybrid grouper *Hyporthodus septemfasciatus* (♀) × *Epinephelus moara* (♂) (Perciformes, Serranidae) and results of a phylogenetic analysis

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**ABSTRACT**

The complete mitochondrial genome of the hybrid grouper *Hyporthodus septemfasciatus* (♀) × *Epinephelus moara* (♂) was obtained by next-generation sequencing. The mitochondrial genome was 16,499 bp long, consisting of 13 protein-coding genes, 22 transfer RNA genes, two ribosomal RNA genes, and a control region (D-loop). The overall base composition is 28.62% A, 28.27% C, 16.27% G, and 26.84% T with 55.46% A+T. In the maximum-likelihood (ML) phylogenetic analysis, the hybrid grouper belonged to the same clade as *H. septemfasciatus* (maternal inheritance).

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the genera \textit{Hyporthodus} and \textit{Epinephelus}. GTR + I + G was confirmed to be the best-fitting evolutionary model based on the corrected Akaike information criterion (AICc), obtained using jModelTest 2.1.10 (Guindon and Gascuel 2003; Darriba et al. 2012). The GTR + I + G model was used for maximum-likelihood (ML) estimation, based on an analysis conducted in RAxML 8.0.11 (Stamatakis 2014) with 1000 bootstrap replicates. In addition, Bayesian inference (BI) tree was run for 1,000,000 generations using MrBayes 3.2.7 (Ronquist et al. 2012). Three species of \textit{Cephalopholis} and \textit{Variola} in the subfamily \textit{Epinephelinae} were used as outgroups (Figure 1).

In the phylogenetic tree of the subfamily \textit{Epinephelinae}, the genera \textit{Epinephelus}, \textit{Hyporthodus}, \textit{Cephalopholis}, and \textit{Variola} each formed a clade, supporting the current taxonomy. The mitochondrial genome of the hybrid grouper \textit{H. septemfasciatus} (♀)×\textit{E. moara} (♂) obtained here was in the same clade as that of \textit{H. septemfasciatus} (maternal inheritance), in accordance with maternal inheritance of mitochondrial DNA in eukaryotes, similar to other hybrid groupers (Sato and Sato 2012). This mitochondrial genome will improve the database for the subfamily \textit{Epinephelinae}, and sheds light on the molecular phylogeny and taxonomy.

**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 of NCBI at https://www.ncbi.nlm.nih.gov, reference number MW151226. The associated BioProject, SRA and Bio-Sample numbers are PRJNA686885, SRR13279997, and SAMN17126625, respectively.

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**Figure 1.** The phylogenetic tree of the genus \textit{Hyporthodus}, obtained from maximum likelihood (ML) and Bayesian inference (BI) analyses of 13 protein-coding genes (PCGs). Bootstrap values above 70% in the ML analysis and posterior probabilities above 0.90 in the BI analysis are shown at the base of each node. The best-fitting evolutionary model was the GTR + I + G model. The GenBank accession numbers follow the scientific names.
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