Complete mitochondrial genome and phylogenetic analysis of black-fin stream jewel goby *Stiphodon percnopterygionus* (Gobiiformes: Gobiidae) from Taiwan

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**ABSTRACT**

The complete mitochondrial genome of the black-fin stream jewel goby *Stiphodon percnopterygionus* has been amplified and sequenced. The whole mitochondrial genome is 16,502 base pairs (bp) in total length and consisting of 13 protein-coding genes, 2 ribosomal RNA genes, 22 transfer RNA genes, and 1 control region (CR). The overall base composition is 28.1% for A, 17.1% for G, 28.7% for C and 26.0% for T with AT comprising 54.1%. A phylogenetic tree was constructed using mitochondrial protein-coding genes (PCGs) sequence data for 34 related taxa of the order Gobiiformes showed that *S. percnopterygionus* is closely related to *S. tuivi*. These findings will contribute for phylogenetic, phylogeography and further genetic studies in genus *Stiphodon* and related gobiiid fishes.

**KEYWORDS**

Mitogenome; Gobiidae; phylogenetic analysis; *Stiphodon percnopterygionus*;

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separated by the tRNA-Val gene. The control region (D-loop) was 841 bp in length, located between the tRNA-pro and tRNA-Phe genes.

Phylogenetic analysis of *Stiphodon percnopterygionus* and its relatives was performed using maximum likelihood (ML) and Bayesian inference (BI) methods based on the sequences of 13 mitochondrial PCGs from 34 taxa of the order Gobiiformes retrieved from GeneBank. ML and BI analysis were conducted using standard RAxML (Stamatakis 2014) and MrBayes (Ronquist et al. 2012), respectively. ML was performed with 1000 bootstrap replicates and BI was performed as follow: Markov chains were run for 5,000,000 generations with trees being sampled every 500 generations, four chains and a burn-in step for the first 500 generations. GTR + G + I was used as the substitution model based on Akaike Information Criterion (AIC) estimated by MrModeltest (Nylander 2004). The phylogenetic tree (Figure 1) confirms that the 28 taxa were found within Gobiidae clade and remains constituted Eleotridae clade, and Rhyacichthyidae clade which is concordant with the result previous classifications of Order Gobiiformes (Pezold 1993; Gill and Mooi 2012; Agorreta et al. 2013; Fricke et al. 2022). The tree also demonstrated that, *S. percnopterygionus* is most closely related to *S. tuivi*. The further phylogenetic approach of the congeners would be in process to facilitate the detailed phylogenetic perspectives of *Stiphodon*.

**Author contributions**

Tonisman Harefa: Conception and design, PCR experiments, analysis and interpretation of the data, drafting of manuscript, revising manuscript, final approval of the version to be published. I-Shiung Chen: Conception and design, analysis and interpretation of the data, revising manuscript, final approval of the version to be published. All authors agree to be accountable for all aspects of the work.

**Disclosure statement**

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

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**Data availability statement**

Mitochondrial genome sequence can be accessed via accession number MW548257 in GenBank of NCBI at [https://www.ncbi.nlm.nih.gov/nuccore/MW548257](https://www.ncbi.nlm.nih.gov/nuccore/MW548257). The associated BioProject, SRA, and Bio-Sample numbers are PRJNA786405, SRR19216410, and SAMN23671125, respectively.

**Ethic approval**

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