

COI-Based Phylogenetic Analysis Uncovers Cryptic Speciation and Misidentification in the Genus *Dermogenys* (Teleostei: Zenarchopteridae)

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INTRODUCTION & AIM

- The family Zenarchopteridae comprises freshwater and brackish water halfbeaks predominantly distributed across Asia and Oceania, with five recognised genera: *Dermogenys*, *Hemirhamphodon*, *Nomorhamphus*, *Tondanichthys*, and *Zenarchopterus* (Fricke et al., 2025).
- Of the 64 valid species described globally, more than half have been recognised post-1950, reflecting the group's taxonomic complexity. The genus *Dermogenys* includes 13 valid species distributed across freshwater habitats in India, Myanmar, Malaysia, Indonesia, the Philippines, and Taiwan (Froese and Pauly, 2025).
- The genus is the smallest in size among zenarchopterids, and inhabits fresh and brackish waters (Meisner & Collette, 1998). *Dermogenys* is well studied, and despite its viviparous nature and limited freshwater–estuarine range, suggesting low dispersal, the genus shows a surprisingly wide distribution (Meisner, 2001).
- Because most *Dermogenys* barcodes in public databases are genus-level entries, leading to misidentification and obscuring possible cryptic speciation, this study tries to find these ambiguities and refine the phylogenetic understanding of the genus.

METHODS

Mitochondrial COI sequences for *Dermogenys* species were obtained from the NCBI GenBank and BOLD repositories, and were aligned using Clustal W algorithm in Bio Edit software (Hall et al. 2011). Based on the aligned COI sequences, the Maximum Likelihood (ML) tree was constructed, and Kimura-2-Parameter (K2P) pairwise genetic distances were calculated using MEGA 11 (Tamura et al., 2021). Average pairwise distances within and between groups were calculated, and standard errors were estimated using 500 bootstrap replicates.

RESULTS & DISCUSSION

- A total of 29 distinct clades were recovered, with *D. siamensis* displaying six different genetic lineages; *D. collettei* having five; *D. pusilla* showing three; *D. bispina*, and *D. sumatrana* having two; and nine additional clades identified solely as *Dermogenys* sp., indicating cryptic speciation and possible misidentifications.

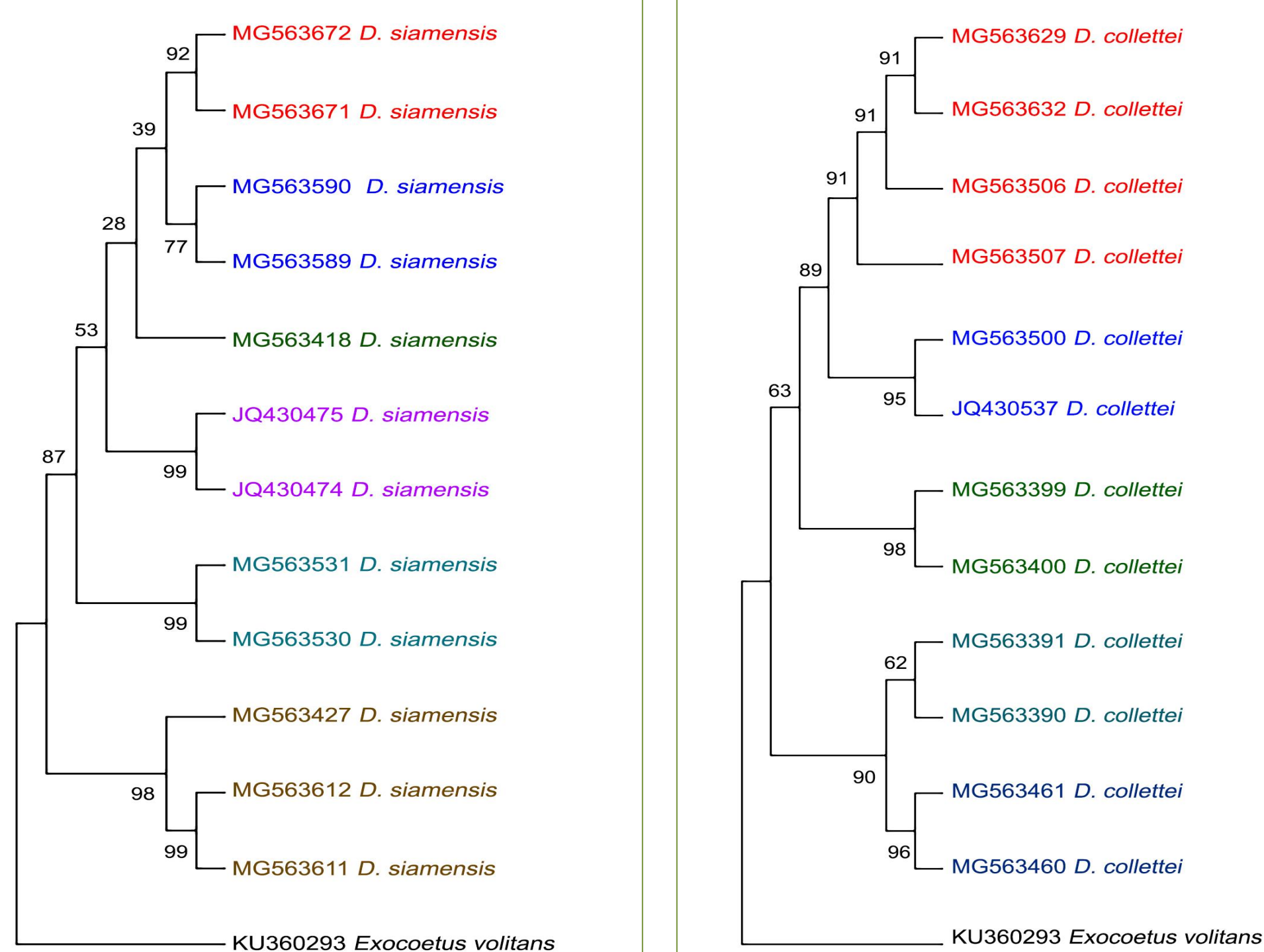


Figure 1. ML phylogenetic tree of genus *Dermogenys* using COI sequences: (a) records labelled *D. siamensis* and (b) records labelled *D. collettei*.

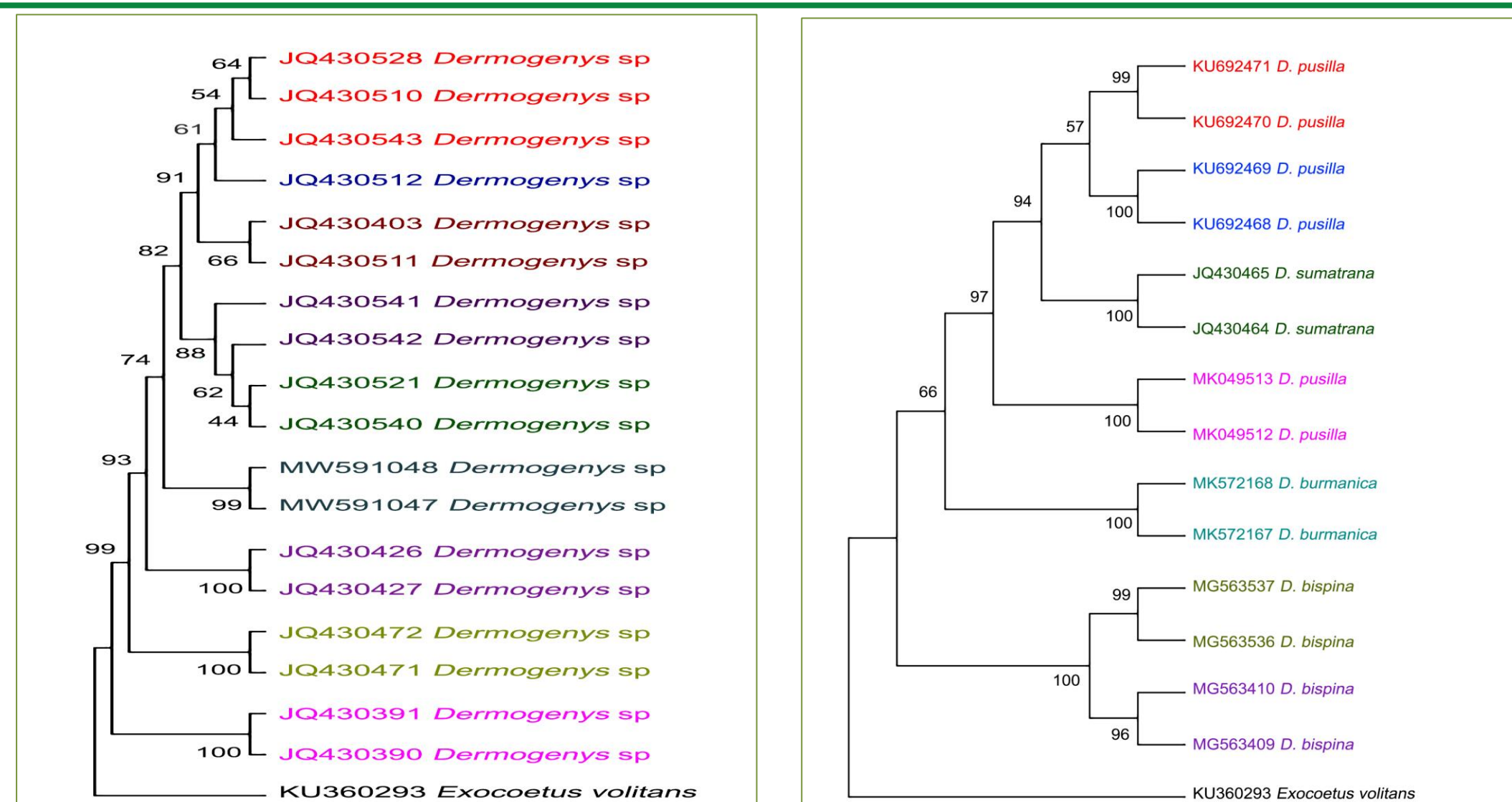


Figure 2. ML phylogenetic tree of genus *Dermogenys* based on mitochondrial COI sequences: (a) records labelled *Dermogenys* sp., and (b) sequences representing the remaining available species.

- Low intraspecific COI divergence (0.2%–1.2%) and high interspecific divergence (3.5%–12%) confirmed clear genetic separation among species, supporting the effectiveness of DNA barcoding for species delimitation in fishes (Herbert et al., 2003).
- The high genetic divergence within *D. siamensis*, *D. collettei*, *D. bispina*, *D. pusilla*, and *D. sumatrana* suggests the presence of a cryptic species complex (Figure 1 & 2), a pattern commonly reported in Indo-Pacific fishes (Nurul et al., 2018).
- The identification of multiple clades labelled only as *Dermogenys* sp. highlights unrecognised lineages and the need for integrative taxonomic approaches combining molecular and morphological data (Meisner & Collette, 1998; Nurul et al., 2018).
- These findings reveal hidden diversity and misidentification within the genus, providing new insights into its taxonomy and evolutionary relationships across the Indo-Pacific region (Meisner, 2001).

CONCLUSION

- All Beloniformes families except Zenarchopteridae remain understudied. Compared to the well-studied Belonidae and Hemiramphidae,
- This study reveals that morphological taxonomy alone is insufficient for species delimitation in *Dermogenys*, highlighting the need for integrative approaches.
- The findings have important implications for species validation, conservation, and resource management in Southeast Asia.

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