

KEANEKARAGAMAN GENETIK IKAN BIAWAN (*Helostoma temminckii* Cuvier, 1829) DARI PROVINSI RIAU BERDASARKAN GEN MITOKONDRIA COI DAN KARAKTER MORFOLOGIS

INTISARI

Ikan biawan (*Helostoma temminckii*) merupakan ikan air tawar ekonomis yang banyak ditemukan di ekosistem rawa gambut di Provinsi Riau. Penelitian ini bertujuan menganalisis keanekaragaman genetik ikan biawan melalui pendekatan morfologis dan molekuler berdasarkan gen mitokondria *Cytochrome Oxidase Subunit I (COI)*. Sebanyak 30 sampel dikoleksi dari Kampar, Siak, dan Pelalawan. Analisis morfometrik dan meristik menggunakan SPSS V.26 melalui *Principal Component Analysis* menghasilkan 2 fungsi dengan nilai *eigen* 163,127 yang menjelaskan 79,7% variasi morfologis. Karakter dominan pembeda populasi adalah panjang kepala, tinggi badan, dan panjang awal sirip dorsal hingga akhir sirip anal. *Scatter plot* menunjukkan pemisahan individu antar populasi yang mencerminkan adaptasi terhadap kondisi rawa gambut. Analisis molekuler menghasilkan fragmen sepanjang 549 bp dengan similaritas 98,91–99,27% terhadap *H. temminckii* di GenBank. Model evolusi terbaik ditentukan menggunakan *jModelTest*, dan model HKY + G dipilih berdasarkan *Akaike Information Criterion (AIC)* untuk analisis *Bayesian Inference (BI)*. Pohon filogenetik *Neighbor Joining*, *Maximum Likelihood*, dan BI menunjukkan nilai dukungan 100/100/1 dengan satu kluster monofiletik. Jarak genetik 0,00–0,92% menunjukkan variasi rendah dalam kisaran intraspesifik. Komposisi nukleotida didominasi basa A+T (54,5–54,9%), dengan *haplotype diversity* 0,533–0,676 dan *nucleotide diversity* 0,00130–0,00206. Nilai Tajima's mendekati (≈ 0) pada Kampar dan Pelalawan mengindikasikan ekspansi populasi, sedangkan nilai positif di Siak menunjukkan netralitas. Delapan haplotipe dibedakan oleh lima situs polimorfik dengan dominasi mutasi transisi *synonymous*. Analisis AMOVA menunjukkan 20% variasi antar populasi dan 80% dalam populasi dengan nilai F_{st} -0,01852–0,27951. Hasil ini menegaskan bahwa populasi *H. temminckii* di Riau masih satu spesies dengan variasi genetik adaptif terhadap lingkungan rawa gambut.

Kata kunci: DNA *barcoding*, Gen *COI*, Ikan biawan, keanekaragaman genetik, PCA.

GENETIC DIVERSITY OF KISSING GOURAMI (*Helostoma temminckii* Cuvier, 1829) FROM RIAU PROVINCE BASED ON THE MITOCHONDRIAL *COI* GENE AND MORPHOLOGICAL CHARACTERS

ABSTRACT

Kissing gourami (*Helostoma temminckii*) is an economically important freshwater fish commonly found in the peat swamp ecosystems of Riau Province. This study aimed to analyze the genetic diversity of *H. temminckii* using morphological and molecular approaches based on the mitochondrial *Cytochrome Oxidase Subunit I (COI)* gene. A total of 30 samples were collected from Kampar, Siak, and Pelalawan. Morphometric and meristic data were analyzed using SPSS v.26 through Principal Component Analysis (PCA), which produced two functions with eigenvalues of 163.127, explaining 79.7% of total morphological variation. The dominant traits distinguishing populations were head length, body depth, and the distance from the origin of the dorsal fin to the end of the anal fin. The PCA scatter plot showed separation among individuals from different populations, indicating morphological adaptation to peat swamp conditions. Molecular analysis yielded a 549 bp *COI* fragment with 98.91–99.27% similarity to *H. temminckii* sequences in GenBank. The best evolutionary model determined using jModelTest was HKY + G based on the *Akaike Information Criterion (AIC)* for Bayesian Inference (BI). Phylogenetic trees generated by Neighbor Joining, Maximum Likelihood, and BI showed strong support values (100/100/1) with a single monophyletic cluster. Genetic distances ranged from 0.00% to 0.92%, indicating low intraspecific variation. Nucleotide composition was dominated by A+T bases (54.5–54.9%), with haplotype diversity of 0.533–0.676 and nucleotide diversity of 0.00130–0.00206. Tajima's values (≈ 0) in Kampar and Pelalawan indicated population expansion, while a positive value in Siak suggested neutrality. Eight haplotypes were distinguished by five polymorphic sites dominated by synonymous transition mutations. AMOVA revealed 20% variation among populations and 80% within populations, with F_{st} values ranging from -0.01852 to 0.27951 . These results confirm that *H. temminckii* populations in Riau belong to a single species with adaptive genetic variation to peat swamp environments.

Keywords: DNA barcoding, *COI* Gene, kissing gourami, genetic diversity, PCA.