

INTSARI

Ikan gabus (*Channa striata*) dengan isolasi geografi dari populasi perairan yang berbeda yaitu perbedaan kawasan daerah aliran sungai (DAS) dapat berdampak pada variasi karakter morfologi dan genetik. Penelitian ini bertujuan untuk mengidentifikasi subspecies ikan gabus potensial untuk pengembangan akuakultur berdasarkan keragaman morfologi dan genetik dari sembilan populasi yang berbeda di Sumatera, yaitu Sungai Kampar (SK), Sungai Merang (SM), Sungai Batang Hari Sembilan (SB), Danau Cala (DC), Danau Ranau (DR), Danau Singkarak (DS), Rawa Banjiran Siak (RS), Rawa Banjiran Kumpeh (RK), dan Rawa Banjiran Lubuk Lampam (RL). Analisis morfologi penelitian ini meliputi variasi karakter morfometrik-*Truss Network Measurement* (m-TNM), hubungan berat-panjang standar (B-SL), faktor kondisi (CF) sebagai indikator daya dukung lingkungan ikan gabus, dan reproduksi. Kemudian keragaman molekuler dari populasi berbeda menggunakan gen *Growth hormone* (GH) dan *cyt. b*, dan uji performa pertumbuhan post-larva ikan gabus menggunakan analisis protein pertumbuhan dengan metode *Enzyme-Linked Immunosorbent Assay* (ELISA). Tiga ratus sembilan puluh empat spesimen ikan gabus dikoleksi untuk pengukuran 38 karakter m-TNM, B-SL dan 196 ekor ikan betina untuk diamati reproduksinya. Dua puluh tujuh isolat DNA gen GH *region* exon 4 ikan gabus dikumpulkan dari sembilan lokasi dengan analisis keragaman polimorfisme *Single Nucleotide Polymorphism* (SNP) dan *insert-deletion*. Dua belas ikan gabus dari populasi Sumatera budidaya dianalisis molekuler dengan ELISA protein GH dan dilengkapi dengan uji performa pertumbuhan. Uji statistik untuk karakter morfologi dan genetik menggunakan analisis koefisien keragaman, analisis diskriminan fungsi (DFA), analisis kluster (CA), korelasi bivariate, dan *Analysis of Variance* (ANOVA), dan *Analysis of Molecular Variance* (AMOVA). Dua puluh karakter pembeda m-TNM mengelompokkan ikan gabus Sumatera menjadi empat kluster dan pohon filogeni juga membagi ikan gabus menjadi empat kluster. Ikan gabus SM memiliki rerata diameter telur ($1,26 \pm 0,5 \text{ mm}$) tertinggi yang signifikan berbeda. Ikan gabus populasi SM memiliki badan ramping (allometrik negatif) dan semua populasi memiliki daya dukung lingkungan yang baik dengan nilai faktor kondisi (CF) >1 . Polimorfisme indel exon 4 gen GH ikan gabus tertinggi (1-3) pada populasi SM yang berpengaruh sedang (0,40-0,421) terhadap morfologi (bobot, panjang standar, dan tinggi badan). Populasi SM memiliki keragaman gen GH exon 4 tertinggi untuk *Nucleotide Diversity* dan persen identifikasi NCBI terendah (96,94%) dibandingkan populasi lain. Ikan gabus budidaya populasi SM memiliki konsentrasi protein GH tertinggi yang berbeda nyata ($1,77 \pm 0,11 \text{ pg } \mu\text{l}^{-1}$), sehingga ikan gabus populasi SM lebih bervariasi secara morfologi dan genetik yang direkomendasikan sebagai kandidat *strain* ikan gabus baru untuk pengembangan akuakultur dimasa yang akan datang.

Kata Kunci: Ikan Gabus, Morfometrik, Genetik, Reproduksi, Budidaya

ABSTRACT

The morphological analysis of this study includes variations in morphometric Characters-Truss Network Measurement (m-TNM), standard weight-length relationship (B-SL), condition factor (CF) as an indicator of the environmental carrying capacity of snakehead fish, and reproduction. Then the molecular diversity of different populations using *Growth hormone* (GH) and *cyt b* genes, and test the growth performance of snakehead fish post-larvae using growth protein analysis using the Enzyme-Linked Immunosorbent Assay (ELISA) method. Three hundred and ninety-four specimens of snakehead fish were collected for measurement of 38 characters of m-TNM, B-SL and 196 female fish were taken to observe their reproduction. Twenty-seven DNA isolates of GH gene exon 4 snakehead fish region were collected from nine locations by analysis of the diversity of Single Nucleotide Polymorphism (SNP) and insert-deletion polymorphisms. Twelve snakehead fish from cultured Sumatran populations were analyzed molecularly by ELISA GH protein and supplemented with growth performance tests. Statistical tests for morphological and genetic characters used the coefficient of diversity analysis, discriminant function analysis (DFA), cluster analysis (CA), bivariate correlation, and Analysis of Variance (ANOVA), and Analysis of Molecular Variance (AMOVA). Twenty distinguishing characters of m-TNM classifies the Sumatran snakehead fish into four clusters and the phylogenetic tree of *cyt. b* classified into four clusters. The SM population had the highest mean egg dimension ($1.26 \pm 0.5\text{mm}$) which was significantly different. The snakehead fish population of SM has a slender body (negative allometric) and all populations have good environmental carrying capacity with the value of the condition factor ($CF > 1$). The highest indel exon 4 polymorphism of snakehead fish GH gene (1-3) in SM population had a moderate effect (0.40-0.421) on morphology (weight, standard length, and body height). The SM population had the highest GH exon 4 gene diversity for Nucleotide Diversity and the lowest percentage of NCBI identification (96.94%) compared to other populations. Cork cultured SM population had the highest GH protein concentration which was significantly different ($1.77 \pm 0.11 \text{ pg } \mu\text{l}^{-1}$), with the result that the SM snakehead fish population was more varied morphologically and genetically which was recommended as a candidate for new snakehead fish strains future.

Key words: *Channa striata*, Morphometric, Genetic, Reproduction, Aquaculture

