# INTISARI

## IDENTIFIKASI MOLEKULER DAN ANALISIS KEKERABATAN IKAN BAUNG (Bagridae) ASAL PULAU KALIMANTAN DAN SUMATERA BERDASARKAN SEKUEN GEN PENYANDI NADH DEHYDROGENASE SUBUNIT 6 (ND6)

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Ikan baung merupakan salah satu spesies ikan air tawar asli di Indonesia yang mudah ditemukan di area rawa, sungai, dan danau di perairan kepulauan Indonesia. Ikan baung digemari masyarakat karena dagingnya putih, tebal dan rasanya yang lezat. Budidaya yang belum efektif dan permintaan pasar yang meningkat menyebabkan populasinya semakin menurun. Oleh karena itu, perlu dilakukan studi genetika untuk meningkatkan efisiensi budidaya ikan baung serta untuk menjaga agar tidak punah. Kajian molekuler terhadap keragaman genetik ikan baung sangat diperlukan untuk keberhasilan budidayanya. Penelitian ini bertujuan untuk mengidentifikasi gen ND6 secara molekuler dan menganalisis kekerabatan ikan baung asal Kalimantan dan Sumatera menggunakan sekuen gen penyandi ND6.

Terdapat 12 sampel ikan baung yang berasal dari Banjarmasin (BJ1, BJ2, BJ3), Samarinda (KM1, KM2, KM3), Palembang (D, E, dan F), dan Pekanbaru (B1, B2, B3). Sampel DNA total diperoleh dari isolasi musculus epaxial dan hepaxial ikan baung. Hasil isolasi DNA diamplifikasi menggunakan primer ND6F dan ND6R1 dengan metode PCR. Hasil produk PCR sebesar 921 bp kemudian dilakukan sekuensing DNA. Hasil sekuensing gen ND6 selanjutnya dianalisis keragaman genetik dan filogenetiknya bersama spesies lain dari *Genbank* menggunakan program MEGA X.

Hasil analisis data menunjukkan bahwa gen ND6 terdiri dari 561 nukleotida yang diterjemahkan menjadi 171 asam amino. Analisis filogram berdasar sekuen nukleotida dan sekuen asam amino gen ND6 menunjukkan bahwa sampel ikan baung asal Kalimantan dan Sumatera berkerabat dekat dan teridentifikasi sebagai *Hemibagrus sp.* dengan jarak genetik 2,2% - 7%. Terdapat 61 situs nukleotida dan 40 situs asam amino yang dapat digunakan sebagai penanda genetik gen ND6 antara sampel ikan baung dengan spesies yang memiliki kekerabatan dekat dalam genus *Hemibagrus sp*.

Kata kunci: ikan baung, gen ND6, *Hemibagrus sp.*, PCR, sekuensing.

# *ABSTRACT*

## MOLECULAR IDENTIFICATION AND KINSHIP ANALYSIS OF BAUNG FISH (Bagridae) FROM BORNEO AND SUMATRAN ISLAND BASED ON NADH DEHYDROGENASE SUBUNIT 6 (ND6) GENE SEQUENCES

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The baung fish is a native Indonesian freshwater species that can be found in wetlands, rivers, and lakes throughout the Indonesian archipelago. People likes it because of its white, thick flesh and delicious taste. The population of baung has declined due to ineffective cultivation, and rising market demand. As a result, genetic study is needed to improve the effectiveness of baung production in order to prevent the species from becoming extinct. Molecular study on the genetic variety of baung fish is important to their cultivation success. This study aims to identify the ND6 gene molecularly and analyze the kinship of baung fish from Borneo and Sumateran using the gene squence encoding ND6.

There were 12 samples of baung fish obtained from Banjarmasin (BJ1, BJ2, BJ3), Samarinda (KM1, KM2, KM3), Palembang (D, E, F), and Pekanbaru (B1, B2, B3). Total DNA samples was isolated from epaxial and hepaxial muscles of baung fish. The results of DNA isolation were amplified using ND6F and N6R1 primers by PCR method. The PCR product had a length of 921 bp, which was followed by DNA sequencing. The results of the ND6 gene sequencing were analyzed to other *Genbank* species for genetic and phylogenetic variety using the MEGA X program.

The results of data analysis showed that the ND6 gene has 561 nucleotides, that are translated into 171 amino acids. The phylogram analysis based on the nucleotide and amino acid sequences showed that the baung fish samples from Borneo and Sumateran island were closely related and identified as *Hemibagrus sp* with a genetic distance of 2.2%-7%. There are 61 nucleotide and 40 amino acid sites that can be used as genetic markers ND6 gene between samples and closely related species of *Hemibagrus sp*.

Key words: baung fish, ND6 gene, *Hemibagrus sp.*, PCR, sequencing.