

INTISARI

IDENTIFIKASI MOLEKULER IKAN BAUNG (Bagridae) ASAL KALIMANTAN DAN SUMATRA BERDASARKAN SEKUEN GEN PENYANDI NADH DEHYDROGENASE SUBUNIT 1

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Ikan baung merupakan salah satu spesies ikan air tawar asli perairan umum di Indonesia. Kandungan protein dalam daging ikan ini sangat baik, sehingga menjadikannya salah satu komoditas ikan air tawar ekonomis penting di Indonesia. Walaupun demikian, budidaya intensif dan informasi genetik terhadap spesies ini masih terbatas. Oleh karena itu, perlu dilakukan studi genetika untuk meningkatkan efisiensi produksi dan budidaya ikan baung agar tidak punah. Kajian molekuler terhadap keragaman genetik ikan baung sangat diperlukan untuk keberhasilan pelestariannya. Penelitian ini bertujuan untuk mengidentifikasi gen ND1 secara molekuler dan menganalisis kekerabatan ikan baung asal Kalimantan dan Sumatra menggunakan sekuen gen penyandi ND1.

Terdapat 12 sampel ikan baung yang diperoleh dari Sungai Martapura (BJ1, BJ2, dan BJ3), Sungai Mahakam (KM1 dan KM3), Sungai Musi (D, E, dan F), Sungai Kampar (B1 dan B2), dan Sungai Kapuas (A dan B). Sampel DNA total diperoleh dari isolasi musculus epaxial dan hepaxial ikan baung. Hasil isolasi DNA diamplifikasi menggunakan primer ND1F dan ND1R dengan metode PCR. Produk PCR sebesar 1327 bp kemudian dilakukan sekuensing DNA. Hasil sekuensing gen ND1 selanjutnya dianalisis keragaman genetik dan filogenetiknya bersama spesies lain dari *Genbank* menggunakan program MEGA X.

Hasil analisis data menunjukkan bahwa gen ND1 terdiri dari 975 nukleotida yang diterjemahkan menjadi 325 asam amino. Terdapat 81 situs nukleotida dan 16 situs asam amino yang dapat digunakan sebagai penanda genetik antara sampel ikan baung dengan *Hemibagrus nemurus*. Analisis filogram menggunakan metode *Neighbor Joining* dengan *Bootstrap* 1000x berdasar sekuen nukleotida gen ND1 menunjukkan bahwa sampel ikan baung asal Kalimantan dan Sumatra berkerabat dekat dan teridentifikasi sebagai *Hemibagrus sp.* dengan jarak genetik 2,9% - 4,9%.

Kata kunci: ikan baung, gen ND1, *Hemibagrus nemurus*, PCR, sekuensing

ABSTRACT

MOLECULAR IDENTIFICATION OF BAUNG FISH (Bagridae) FROM KALIMANTAN DAN SUMATRA BASED ON NADH DEHYDROGENASE SUBUNIT 1 GENE SEQUENCES

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Baung fish is one of the indigenous species in Indonesia. Their protein content is excellent, making it one of the economically essential fish commodities in Indonesia. However, intensive cultivation and genetic information on this species are still limited. Therefore, it is necessary to carry out genetic studies to increase the production efficiency and cultivation of baung fish not to become extinct. Molecular studies of the genetic diversity of baung fish are needed for the success of their conservation. This study aims to identify the ND1 gene molecularly and analyze the kinship between baung fishes from Kalimantan and Sumatra using the ND1 coding gene sequence.

There were 12 samples of baung fish obtained from the Martapura River (BJ1, BJ2, and BJ3), Mahakam River (KM1 and KM3), Musi River (D, E, and F), Kampar River (B1 and B2), and Kapuas River (A and B). Total DNA samples isolated from epaxial and hepaxial muscles of baung fish. The results of DNA isolation were amplified using ND1F and ND1R primers by PCR method. The PCR product was 1327 bp and then DNA sequenced. The results of the ND1 gene sequencing were then analyzed for genetic diversity and phylogenetic with other species from Genbank using the MEGA X program.

Data analysis results showed that the ND1 gene consists of 975 nucleotides, which are translated into 325 amino acids. There were 81 nucleotide sites and 16 amino acid sites that could be used as genetic markers between baung fish samples and *Hemibagrus nemurus*. Filogram analysis using the Neighbor Joining method with Bootstrap 1000x based on ND1 gene nucleotide sequence showed that baung fishes from Kalimantan and Sumatra were closely related and identified as *Hemibagrus sp.* with 2.9% - 4.9% of genetic distance.

Key words: baung fish, ND1 gene, *Hemibagrus nemurus*, PCR, sequencing