

## INTISARI

### **ANALISIS KERAGAMAN GENETIK DAN KEKERABATAN IKAN BAUNG ASAL JAWA DAN SUMATERA BERDASARKAN SEKUEN GEN NADH DEHYDROGENASE SUBUNIT 2 (ND2)**

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Ikan baung merupakan salah satu ikan dari golongan *catfish* yang banyak hidup di perairan darat Indonesia. Ikan ini banyak digemari masyarakat dan memiliki nilai ekonomis yang tinggi. Upaya budidaya ikan ini sudah mulai dikembangkan, namun masih mengalami berbagai kendala. Ikan baung memiliki morfologi yang mirip dengan ikan golongan *catfish* lain serta memiliki tingkat migrasi yang tinggi, sehingga perlu dilakukan kajian genetik untuk mengidentifikasi spesies ikan baung yang akan dibudidayakan serta untuk meningkatkan efisiensi produksi pada budidaya ikan baung. Penelitian ini bertujuan untuk mengetahui keragaman genetik serta kekerabatan antar spesies ikan baung asal Jawa dan Sumatera menggunakan sekuen gen NADH *Dehydrogenase* Subunit 2 (ND2).

Sebanyak 14 sampel diperoleh melalui isolasi jaringan pada ikan baung asal Sungai Progo (1.4, 2.4, 3.4), Sungai Elo (X1, X2), Sungai Bengawan Solo (BO1, BO2, BO3), Sungai Kampar (B1, B2, B3), serta Sungai Musi (D, E, F). Seluruh sampel diamplifikasi menggunakan primer ND2F dan ND2R dengan metode PCR. Produk PCR sebanyak 1303 bp kemudian disekuensing dan hasilnya dianalisis menggunakan aplikasi MEGA versi 11 untuk melihat keragaman genetiknya dengan spesies pembanding asal *Genbank*.

Hasil analisis data menunjukkan bahwa gen ND2 memiliki 1.045 nukleotida dan menyandi 348 asam amino. Terdapat 295 situs nukleotida dan 59 situs asam amino yang dapat dijadikan penanda genetik antar sampel. Hasil analisis kekerabatan antara sampel dengan spesies pembanding dari *Genbank* menunjukkan bahwa sampel ikan baung asal Sungai Progo (1.4, 2.4, 3.4), Sungai Kampar (B1, B2, B3) dan Sungai Musi (D, E, F) teridentifikasi ke dalam genus *Hemibagrus* dengan jarak genetik 2,8-3,6%, sampel asal Sungai Elo (X1, X2) teridentifikasi ke dalam genus *Mystus* dengan jarak genetik 17-17,1% serta sampel asal Sungai Bengawan Solo teridentifikasi ke dalam genus *Pangasius* dengan jarak genetik 12-12,1%.

Kata kunci: gen ND2, *Hemibagrus*, ikan baung, *Mystus*, *Pangasius*, PCR, sekuensing.

## ABSTRACT

### **ANALYSIS OF GENETIC DIVERSITY AND KINSHIP OF BAUNG FISH FROM JAVA AND SUMATERA BASED ON THE NADH DEHYDROGENASE SUBUNIT 2 (ND2) GENE SEQUENCE**

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Baung fish is one of the fish from the catfish group that is indigenous to the Indonesian inland waters. This fish is tremendously favored by society and has a high economic value. Efforts to cultivate this fish have begun to be developed but are still experiencing various obstacles. Baung fish has a similar morphology to the other catfish groups and has a high migration rate, therefore it is necessary to conduct a genetic study to identify the baung fish species for cultivation purposes and to increase production efficiency in said cultivation. This study intends to determine the genetic diversity and kinship between baung fish species from Java and Sumatra by utilizing the NADH Dehydrogenase Subunit 2 (ND2) gene sequence.

A total of 14 samples were acquired through tissue isolation in baung fish originated from the Progo River (1.4, 2.4, 3.4), Elo River (X1, X2), Bengawan Solo River (BO1, BO2, BO3), Kampar River (B1, B2, B3), and the Musi River (D, E, F). All the samples were amplified using the ND2F and ND2R primers by PCR method. The PCR product consisting of 1303 bp was sequenced and then analyzed using the Mega version 11 to observe its genetic diversity with the other species from Genbank.

The results of data analysis showed that the ND2 gene has a total of 1.045 nucleotides and codes for 348 amino acids. There are 295 nucleotide sites and 59 amino acid sites that can be used as genetic markers between samples. The results of the kinship analysis between the sample and the other species from Genbank showed that the baung fish samples from the Progo River (1.4, 2.4, 3.4), Kampar River (B1, B2, B3) and Musi River (D, E, F) were identified as part of the genus *Hemibagrus* with a genetic distance of 2.8-3.6%, samples from the Elo River (X1, X2) were identified as part of the genus *Mystus* with a genetic distance of 17-17.1% and samples from the Bengawan Solo River were identified as part of the genus *Pangasius* with a genetic distance of 12 -12.1%.

**Keywords:** baung fish, *Hemibagrus*, *Mystus*, ND2 gene, *Pangasius*, PCR, sequencing.