

INTISARI

KARAKTERISASI GENETIK IKAN BAUNG ASAL SUNGAI ELO, KAPUAS, MAHAKAM, DAN PROGO MENGGUNAKAN GEN PENYANDI *Cytochrome B*

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Ikan baung merupakan jenis ikan air tawar yang termasuk ke dalam famili Bagridae. Tingkat konsumsi ikan baung semakin meningkat, namun produksi ikan ini dalam memenuhi permintaan pasar dan konsumen sampai saat ini diperoleh dari hasil tangkapan alam. Kondisi ini dikhawatirkan dapat menyebabkan terjadinya kelebihan tangkap dan penurunan populasi ikan baung, sehingga perlu dilakukan kajian penanda genetik untuk mengidentifikasi spesies yang dibudidayakan dalam menjaga kelestarian sumber daya genetiknya. Penelitian ini bertujuan untuk mengidentifikasi ikan baung asal Sungai Elo, Progo, Mahakam, dan Kapuas berdasarkan sekuen gen penyandi *cytochrome b* dan mengetahui kekerabatannya dalam famili Bagridae.

Sampel ikan baung sebanyak sepuluh sampel berasal dari 3 ekor ikan baung asal Sungai Progo, 2 ekor asal Sungai Elo, 3 ekor asal Sungai Mahakam, dan 2 ekor asal Sungai Kapuas. Sampel *deoxyribonucleic acid* (DNA) diisolasi kemudian diamplifikasi dengan teknik *polymerase chain reaction* (PCR). Produk PCR (1420 bp) dilakukan sekuensing. Hasil sekuensing gen *cytochrome b* (1137 nt) dan panjang asam aminonya sebesar 379, kemudian dianalisis keragaman genetik dengan spesies lain dari *Genbank* menggunakan program MEGA versi 7.02.

Hasil analisis menunjukkan sampel ikan baung tergolong menjadi 2 genus, yaitu *Hemibragus* dan *Mystus*. Ikan baung asal Sungai Progo, Sungai Mahakam, dan Sungai Kapuas teridentifikasi sebagai *Hemibragus* sp dengan jarak genetik 3,4-5,2%. Terdapat 23 situs nukleotida sebagai penanda genetik yang membedakan ikan baung asal Sungai Progo, Mahakam, dan Kapuas dengan *Hemibragus*, sedangkan penanda genetik yang membedakan ikan baung Sungai Progo, Mahakam, dan Kapuas terdapat 60 situs nukleotida. Ikan baung asal Sungai Elo teridentifikasi sebagai *Mystus* sp dengan jarak genetik 18,2%.

Kata kunci: ikan baung, gen *cytochrome b*, *Hemibragus* sp, *Mystus* sp

ABSTRACT

GENETIC CHARACTERIZATION OF BAUNG FROM ELO, KAPUAS, MAHAKAM, AND PROGO RIVER USE ENCODING GENE *Cytochrome B*

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Baung is one of the freshwater fish that belongs to Bagridae family. The number of baung consumption is rapidly rising, however the availability of the fish is not sufficient to meet the market needs. The only source of the fish only comes from the nature, by catching them. This condition may cause the population of baung goes down as a result from a rapid fish catching, thus the study of genetic marking to identify the cultivated species to preserve the sustainability of its genetic resource. The objective of this study is to identify baung from Elo, Progo, Mahakam, and Kapuas River according to coded genetic sequent cytochrome b and determine its genetic relationship in Bagridae family.

There are ten samples of baung fish. Three of them are coming from Progo, two samples are coming from Elo, three from Mahakam, and the other two are coming from Kapuas. Deoxyribonucleic acid (DNA) samples are isolated and amplified using polymerase chain reaction (PCR) technique. Polymerase chain reaction product (1420 bp) is sequenced. The sequencing result is cytochrome b gene (1137 nt) and the length of the amino acid is 379, then analyzed its genetic relationship with the other species from Genbank using MEGA Program version 7.02.

The results of the analysis showed samples baung belongs to two genus, namely *Hemibragus* and *Mystus*. Baung from Progo, Mahakam, and Kapuas River identified as *Hemibragus* sp with a genetic distance of 3,4-5,2%. There are 23 nucleotide sites as genetic markers that distinguish fish baung origin of Progo, Mahakam, and Kapuas River with *Hemibragus*, While the genetic markers that differentiate Baung from Progo, Mahakam, and Kapuas River there are 60 sites of nucleotides. Elo River's baung identified as *Mystus* sp with a genetic distance of 18.2%.

Keyword: baung, cytochrome b gene, *Hemibragus* sp, *Mystus* sp