

## INTISARI

### **KAJIAN PENANDA GENETIK IKAN BAUNG (*Hemibagrus sp.*) ASAL SUNGAI MUSI, KAMPAR, ELO, DAN PROGO BERDASARKAN SEKUEN GEN PENYANDI *Cytochrome B***

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Indonesia adalah negara kepulauan yang memiliki sumber daya alam yang melimpah. Salah satu jenis sumberdaya perikanan di Indonesia adalah ikan air tawar golongan *catfish*. Ikan baung merupakan jenis ikan air tawar golongan *catfish* yang berasal dari beberapa sungai di Indonesia. Banyak dari jenis ikan baung (*Hemibagrus sp*) yang terancam punah karena perburuan dan ketersediaan yang terbatas. Oleh karena itu, budidaya ikan baung perlu dikembangkan. Upaya yang dapat dilakukan untuk membedakan spesies ikan baung agar diketahui asalnya adalah dengan melakukan uji molekular. Tujuan dari penelitian ini adalah untuk mengetahui keragaman genetik ikan baung asal Magelang dan Sumatera berdasarkan gen penyandi *CYTB*.

Sebelas sampel ikan baung diperoleh dari empat sungai di Indonesia, yaitu lima sampel berasal dari sungai Progo dan Elo Magelang (1.4, 2.4, 3.4, X1, dan X2), tiga sampel berasal dari Sungai Musi Palembang (D, E, dan F), dan tiga sampel berasal dari Sungai Kampar Riau (Beong 1, Beong 2, dan Beong 3). Seluruh sampel di isolasi DNA dan amplifikasi dengan teknik PCR. Produk PCR yang dihasilkan adalah 1.420 bp kemudian disekuensing. Hasil sekuensing gen *CYTB* kemudian dianalisis keragaman genetik antar spesies dengan spesies ikan baung lain dari *Genbank* menggunakan program MEGA 6.

Hasil analisis berdasarkan sekuen gen *CYTB*, ikan baung asal Magelang (1.4, 2.4, 3.4), Palembang (D, E, F), dan Riau (Beong 1, Beong 2, Beong 3) teridentifikasi sebagai *Hemibagrus nemurus* dengan jarak genetik 3-3,2% terhadap *H. nemurus* (*Genbank*). Sampel ikan baung asal Magelang (X1 dan X2) teridentifikasi satu genus sebagai *Mystus sp* dengan jarak genetik 19,1% terhadap *Mystus cavasius* (*Genbank*). Sebanyak 35 nukleotida dan 24 asam amino sebagai penanda genetik sampel ikan baung Magelang (1.4, 2.4, 3.4), Palembang (D, E, F), dan Riau (Beong 1, Beong 2, Beong 3) dengan *Hemibagrus nemurus*.

**Kata kunci :** Ikan baung, *Hemibagrus nemurus*, gen penyandi *Cytochrome B*, keragaman genetik, sekuen DNA.

## ABSTRACT

### STUDY OF GENETIC MARKERS IN BAUNG FISH (*Hemibagrus* sp.) FROM THE MUSI, KAMPAR, ELO, AND PROGO RIVERS BASED ON THE CYTOCHROME B CODING GENE SEQUENCE

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Indonesia is an archipelago that has abundant natural resources. One type of fisheries resource in Indonesia is freshwater fish, the catfish group. Baung fish is a type of freshwater fish group of catfish originating from several rivers in Indonesia. Many species of baung fish (*Hemibagrus* sp) are endangered due to hunting and limited availability. Therefore, baung fish cultivation needs to be developed. Efforts that can be made to differentiate baung fish species so that their origin is known is by conducting molecular tests. The purpose of this study was to determine the genetic diversity of baung fish from Magelang and Sumatra based on *CYTB* encoding genes.

Eleven samples of baung fish were obtained from four rivers in Indonesia. Five samples originating from the Progo River and Elo River, Magelang (1.4, 2.4, 3.4, X1, and X2), three samples came from the Musi River, Palembang (D, E, and F), and three samples came from Kampar River, Riau (Beong 1, Beong 2, and Beong 3). All samples were DNA isolated and amplified by PCR technique. The PCR product produced was 1.420 bp which was then sequenced. The result of *CYTB* gene sequencing were analyzed for genetic diversity between species with other baung fish species from Genbank using the MEGA 6 program.

The result of analysis based on *CYTB* gene sequences was that baung fish from Magelang (1.4, 2.4, 3.4), Palembang (D, E, F), and Riau (Beong 1, Beong 2, Beong 3) were identified as *Hemibagrus nemurus* with genetic distance 3-3,2% against *H. nemurus* (Genbank). Samples of baung fish from Magelang (X1 and X2) were identified as one genus as *Mystus* sp with a genetic distance of 19.1% against *Mystus cavasius* (Genbank). There were 35 nucleotides and 24 amino acids as genetic markers of samples of Magelang baung fish (1.4, 2.4, 3.4), Palembang baung fish (D, E, F), and Riau baung fish (Beong 1, Beong 2, Beong 3) with *Hemibagrus nemurus*.

**Keywords :** Baung fish, *Hemibagrus nemurus*, Cytochrome B, genetic diversity, DNA sequence