

ABSTRAK

IDENTIFIKASI MOLEKULER IKAN BAUNG (*Hemibagrus sp.*) ASAL SUMATERA DAN KALIMANTAN BERDASARKAN SEKUEN GEN PENYANDI 12S rRNA

Catrine Relia Patrecia Gultom
16/398173/KH/08944

Ikan baung merupakan jenis ikan air tawar golongan *catfish* yang berasal dari beberapa sungai di Indonesia. Ikan ini cukup populer di Indonesia sebagai ikan konsumsi dan memiliki nilai ekonomi tinggi. Budidaya ikan baung mulai dikembangkan dan diperkenalkan sebagai upaya untuk menjaga kelestarian ikan baung di alam dan dalam rangka memenuhi permintaan masyarakat yang terus meningkat. Kajian variasi genetik penting dilakukan untuk mendukung usaha konservasi dan budidaya ikan baung. Penelitian ini bertujuan untuk mengetahui keragaman genetik ikan baung asal Sumatera dan Kalimantan berdasarkan sekuen gen penyandi 12S Ribosomal. Empat belas sampel ikan baung diperoleh dari lima sungai di Indonesia, yaitu tiga sampel berasal dari Sungai Kampar Riau (B1, B2, dan B3), tiga sampel berasal dari Sungai Musi Palembang (D, E, dan F), tiga sampel berasal dari Sungai Mahakam Kalimantan Timur (KM1, KM2, dan KM3), dua sampel berasal dari Sungai Kapuas Kalimantan Barat (A dan B), dan tiga sampel berasal dari Sungai Martapura Kalimantan Selatan (BJ1, BJ2, dan BJ3). Seluruh sampel diamplifikasi dengan teknik PCR menggunakan primer *forward* (12SF) dan primer *reverse* (12SR). Produk PCR yang dihasilkan adalah 1309 bp dan kemudian disekuensing. Hasil sekuensing gen 12S rRNA kemudian dianalisis keragaman genetik antar spesies dengan spesies ikan baung lain dari *GenBank* menggunakan program MEGA X. Hasil analisis berdasarkan sekuen gen 12S rRNA menunjukkan bahwa ikan baung asal Sumatera (B1, B2, B3, D, E, dan F) dan Kalimantan (KM1, KM2, KM3, A, B, BJ1, BJ2, dan BJ3) teridentifikasi sebagai *Hemibagrus nemurus* dengan jarak genetik 0,2-0,8% terhadap *H. nemurus* (*GenBank*). Terdapat 2 situs nukleotida sebagai penanda genetik sampel ikan baung asal Sumatera dan Kalimantan dengan *Hemibagrus nemurus*.

Kata kunci: Ikan baung, Sekuensing, Keragaman genetik, gen 12S rRNA

ABSTRACT

MOLECULAR IDENTIFICATION OF BAUNG (*Hemibagrus* sp.) FROM SUMATERA AND KALIMANTAN BASED ON ENCODING GENE SEQUENCES 12S rRNA

Catrine Relia Patrecia Gultom
16/398173/KH/08944

Baung fish is one of the freshwater catfish that come from several river in Indonesia. It is quite popular in Indonesia as a consumption fish and has a high economic value. Baung fish cultivation has been developed and introduced as an effort to maintain baung fish in nature and to fulfil the increasing demands of society. Research on the genetic variation is important to support the conservation and cultivation of baung fish. This research is purposed to determine the genetic variation of baung fish from Sumatera and Kalimantan based on encoding gene sequences 12S rRNA. Fourteen samples of baung fish were obtained from five rivers in Indonesia. Three samples came from the Kampar River, Riau (B1, B2, dan B3), three samples came from the Musi River, Palembang (D, E, and F), three samples came from the Mahakam River, East Kalimantan (KM1, KM2, dan KM3), two samples came from the Kapuas River, West Kalimantan (A and B), and three samples came from the Martapura River, South Kalimantan (BJ1, BJ2, dan BJ3). All samples were amplified by PCR technique using forward primer (12SF) and reverse primer (12SR). The PCR product produced was 1309 bp and then it was sequenced. The result of 12S rRNA gene sequencing were analyzed for genetic variation between species with other baung fish species from *GenBank* using the MEGA X program. The result of analysis based on 12S rRNA gene sequences showed that baung fish from Sumatera (B1, B2, B3, D, E, dan F) and Kalimantan (KM1, KM2, KM3, A, B, BJ1, BJ2, dan BJ3) were identified as *Hemibagrus nemurus* with genetic distance 0,2-0,8% against *H. nemurus* (*GenBank*). There were two nucleotide site as genetic markers of samples from Sumatera and Kalimantan with *Hemibagrus nemurus*.

Keywords: Baung fish, Sequencing, Genetic variation, 12S rRNA gene