

ABSTRAK

IDENTIFIKASI MOLEKULER IKAN BAUNG (*Hemibagrus sp.*) DARI BEBERAPA SUNGAI DI KALIMANTAN DAN JAWA BERDASARKAN SEKUEN GEN MITOKONDRIA 12S ribosomal-RNA (12S rRNA)

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Indonesia merupakan wilayah perairan yang menjadikan perikanan Indonesia menjadi sumberdaya alam yang melimpah seperti keanekaragaman jenis ikan air tawar yang tinggi. Salah satunya adalah ikan baung yang tersebar di beberapa wilayah kepulauan Indonesia seperti Sumatera, Jawa, dan Kalimantan. Ikan baung (*Hemibagrus sp.*) sekarang sudah terancam punah akibat perburuan. Oleh sebab itu budidaya ikan baung harus dikembangkan, salah satu upayanya adalah dengan melakukan identifikasi molekuler untuk membedakan spesies ikan baung berdasarkan asalnya. Tujuan dari penelitian ini adalah untuk mengetahui keanekaragaman genetik gen mitokondria 12S rRNA pada ikan baung asal Kalimantan dan Jawa.

Enambelas sampel ikan baung yang diperoleh dari enam sungai di Indonesia, yaitu Sungai Progo Magelang (1.4, 2.4, dan 3.4), Sungai Elo Magelang (X1 dan X2), Sungai Bengawan Solo Bojonegoro (BO1, BO2, dan BO3), Sungai Mahakam Kalimantan Timur (KM1, KM2, dan KM3), Sungai Sintang Kalimantan Barat (A dan B), dan Sungai Martapura Banjarmasin (BJ1, BJ2, dan BJ3). Semua sampel sudah berupa DNA ikan baung yang selanjutnya akan dilakukan amplifikasi dengan teknik PCR. Produk PCR yang dihasilkan adalah 1310 bp kemudian dilakukan sekuensing DNA. Hasil sekuensing gen 12S rRNA dianalisis keragaman genetiknya dengan spesies ikan baung lain dari *GenBank* dengan menggunakan program MEGA X.

Hasil analisis berdasarkan sekuen gen 12S rRNA, ikan baung asal Sungai Progo (1.4, 2.4, dan 3.4), Sungai Martapura (BJ1, BJ2, dan BJ3), Sungai Mahakam (KM1, KM2, dan KM3), dan Sungai Sintang (A dan B) teridentifikasi sebagai *Hemibagrus nemurus* dengan jarak genetik 0,2-0,5% terhadap *H. nemurus* (*GenBank*). Sampel ikan baung asal Sungai Bengawan Solo (BO1, BO2, dan BO3) teridentifikasi sebagai *Pangasianodon sp.* dengan jarak genetik 4,5-4,6% terhadap *P. gigas*. Sampel ikan baung asal Sungai Elo (X1 dan X2) teridentifikasi sebagai *Mystus sp.* dengan jarak genetik 7,6% terhadap *M. cavasius*.

Kata kunci : Ikan baung, *Hemibagrus sp.*, *Pangasianodon sp.*, *Mystus sp.*, gen
12S rRNA

ABSTRACT

MOLECULAR IDENTIFICATION OF BAUNG (*Hemibagrus sp.*) FROM SOME RIVERS IN KALIMANTAN AND JAVA BASED ON MITOCHONDRIA GENE SEQUENCES 12S ribosomal-RNA (12S rRNA)

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Indonesia is a country with vast territorial waters that makes Indonesian fisheries into abundant natural resources such as high diversity of freshwater fish species. One of them is baung fish which is spread in several regions of the Indonesian archipelago such as Java, Sumatera and Kalimantan. Baung fish (*Hemibagrus sp.*) are now threatened with extinction due to hunting activities. Therefore, baung fish cultivation must be developed. One of the efforts is by carrying out molecular identification to differentiate fish species based on their origin. The purpose of this study was to determine the genetic diversity of the mitochondrial gene in baung fish from Kalimantan and Java.

Sixteen samples of baung fish were obtained from six rivers in Indonesia, i.e. Progo river from Magelang (1.4, 2.4, and 3.4), Elo river from Magelang (X1 dan X2), Bengawan Solo river from Bojonegoro (BO1, BO2, dan BO3), Mahakam river from East Kalimantan (KM1, KM2, and KM3), Sintang river from West Kalimantan (A and B), and Martapura river from Banjarmasin (BJ1, BJ2, and BJ3). All samples already in a form of Baung's DNA and then amplified by PCR technique. The PCR product length was 1310 bp which was then sequenced. The result of 12S rRNA gene sequencing were analyzed for genetic diversity with another baung fish from *GenBank* using the MEGA X program.

The result of analysis gene 12S rRNA sequences was that baung fish from Progo river (1.4, 2.4, and 3.4), Martapura river (BJ1, BJ2, and BJ3), Mahakam river (KM1, KM2, and KM3), and Sintang river (A and B) were identified as *Hemibagrus nemurus* with genetic distance 0,2-0,5% against *H. nemurus* (GenBank). Samples of baung fish from Bengawan Solo river (BO1, BO2, dan BO3) were identified as *Pangasianodon sp.* with genetic distance 4,5-4,6% against *P. gigas*. Samples of baung fish from Elo river (X1 and X2) were identified as *Mystus sp.* with genetic distance 7,6% against *M. cavasius*.

Key words: Baung fish, *Hemibagrus sp.*, *Pangasianodon sp.*, *Mystus sp.*, 12S rRNA gene