

INTISARI

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

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Indonesia merupakan negara kepulauan yang memiliki keanekaragaman ikan yang sangat tinggi. Salah satu jenis ikan Indonesia yang dapat dibudidayakan yaitu ikan baung. Ikan baung (*Hemibagrus sp.*) merupakan jenis ikan air tawar yang keberadaan dan ketersediaannya di alam mulai berkurang akibat penangkapan yang secara terus menerus sehingga terancam punah. Oleh karena itu, diperlukan upaya konservasi untuk mengembangkan budidaya ikan baung. Uji molekuler dilakukan untuk mengidentifikasi spesies dari ikan baung yang akan dibudidayakan. Tujuan dari penelitian ini adalah untuk mengetahui keanekaragaman genetik ikan baung asal Sumatera dan Jawa berdasarkan sekuen gen 12S rRNA.

Sebanyak empat belas sampel ikan baung diperoleh dari lima sungai di Indonesia, yaitu lima sampel berasal dari Sungai Progo dan Elo Magelang (1.4, 2.4, 3.4, X1, dan X2), tiga sampel asal Sungai Bengawan Solo Bojonegoro (BO1, BO2, dan BO3), tiga sampel asal Sungai Kampar Riau (B1, B2, dan B3), dan tiga sampel asal Sungai Musi Palembang (D, E, dan F). Seluruh sampel di amplifikasi dengan PCR dan menghasilkan produk sebesar 1309 bp kemudian disekuensing. Hasil sekuensing gen 12S rRNA (956 nt) selanjutnya dianalisis keragaman genetik antar spesies dengan spesies ikan baung lain dari *GenBank* menggunakan program MEGA X.

Hasil analisis berdasarkan sekuen gen 12S rRNA, ikan baung asal Sungai Progo, Kampar, dan Musi teridentifikasi sebagai *Hemibagrus nemurus* dengan penanda genetik terdiri dari dua situs nukleotida. Sampel ikan baung asal Sungai Elo teridentifikasi satu genus sebagai *Mystus sp.* dengan penanda genetik sebanyak 55 nukleotida, sedangkan sampel ikan baung asal Sungai Bengawan Solo teridentifikasi satu genus sebagai *Pangasianodon sp.* dengan 44 nukleotida sebagai penanda genetik.

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

ABSTRACT

MOLECULAR IDENTIFICATION OF BAUNG (*Hemibagrus sp.*) FROM SUMATERA AND JAWA BASED ON MITOCHONDRIAL 12S rRNA GENE

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Indonesia is a country made up of islands with an extensive variety of fish. One type of fish in Indonesia that could be cultured is baung fish. This fish (*Hemibagrus sp.*) is a type of freshwater species of which its presence and availability is decreasing due to their constant capture that is causing them to become endangered. As a result, a conservation effort is required to boost their cultivation. Molecular testing is developed to identify species from baung fish that would be cultivated. The purpose of the research is to determine the genetic diversity of baung fish originating from Sumatera and Java based on genetic sequence 12S rRNA.

There are fourteen baung fish samples gathered from five rivers in Indonesia, which were five samples from the Progo River and Elo River Magelang (1.4, 2.4, 3.4, X1, and X2), three samples came from Bengawan Solo River, Bojonegoro (BO1, BO2, and BO3), three samples came from the Kampar River, Riau (B1, B2, and B3), and three samples came from Musi River, Palembang (D, E, and F). All samples are amplified with PCR and produced 1309 bp that are then sequenced. The sequence result gen 12S rRNA (956 nt) then undergoes analysis of various genetic inter-species with another species of baung fish from a *GenBank* using the MEGA X program.

The analysis results based on genetic sequence 12S rRNA, the baung fish from Progo, Kampar, and Musi River were identified to be *Hemibagrus nemurus* with a genetic marker consisting of two nucleoid sites. Samples of baung fish from the Elo River is identified as one gene of *Mystus sp.* with a genetic marker consisting of 55 nucleoids, whereas sample from Bengawan Solo River was identified as one gene of *Pangasianodon sp.* with 44 nucleoids as its genetic marker.

Keywords : Baung fish, *Hemibagrus nemurus*, *Mystus sp.*, *Pangasianodon sp.*, 12S rRNA gene, genetic diversity.