INTISARI

ANALISIS KEKERABATAN IKAN BAUNG ASAL PULAU JAWA DAN KALIMANTAN BERDASARKAN SEKUEN GEN NADH DEHYDROGENASE SUBUNIT 2 (ND2)

Kessar Athallah Putra
18/427329/KH/09703

Ikan baung adalah ikan air tawar golongan *catfish* yang terdistribusi di perairan Indonesia. Ikan baung memiliki daging tebal dengan cita rasa khas sehingga digemari oleh masyarakat. Permintaan pasar yang tinggi tanpa pembudidayaan yang signifikan mengakibatkan penurunan populasinya di alam. Perlu dilakukan studi genetika untuk melestarikan ikan baung dan meningkatkan efektivitas budidayanya. Penelitian ini bertujuan untuk mengetahui kekerabatan genetik ikan baung asal Pulau Jawa dan Kalimantan dengan memanfaatkan sekuen gen NADH *Dehydrogenase* Subunit 2 (ND2).

Terdapat 16 sampel ikan baung asal Sungai Bengawan Solo (BO1, BO2, BO3), Sungai Elo (X1, X2), Sungai Progo (1.4, 2.4, 3.4), Sungai Martapura (BJ1, BJ2, BJ3), Sungai Mahakam (KM1, KM2, KM3), dan Sungai Kapuas (A, B). Sampel tersebut diamplifikasi dengan primer ND2F dan ND2R melalui metode PCR dan hasilnya kemudian disekuensing. Hasil sekuensing dianalisis menggunakan aplikasi MEGA versi 11 untuk melihat kekerabatan genetik terhadap spesies dari *Genbank.*

Hasil analisis kekerabatan menunjukkan bahwa sampel ikan baung asal Sungai Bengawan Solo tergolong ke dalam genus *Pangasius* dengan jarak genetik sebesar 12-12,1%, sampel ikan baung asal Sungai Elo tergolong ke dalam genus *Mystus* dengan jarak genetik sebesar 17-17,1%, dan sampel ikan baung asal Sungai Progo, Martapura, Mahakam, dan Kapuas tergolong ke dalam genus *Hemibagrus* dengan jarak genetik sebesar 3,0-3,8%.

Kata kunci: gen ND2, ikan baung, PCR, sekuensing.

ABSTRACT

GENETIC RELATIONSHIP ANALYSIS OF BAUNG FISH FROM JAVA AND KALIMANTAN BASED ON NADH DEHYDROGENASE SUBUNIT 2 (ND2) GENE SEQUENCE

Kessar Athallah Putra
18/427329/KH/09703

Baung fish is a freshwater fish of the catfish group which is distributed in Indonesian waters. Baung fish has thick meat with a distinctive taste so it is favored by the community. High market demand without significant cultivation has resulted in a decrease in its population in the wild. It is necessary to conduct genetic studies to preserve baung fish and increase the effectiveness of its cultivation. This research aims to determine the genetic relationship between baung fish from Java and Kalimantan by utilizing the NADH Dehydrogenase Subunit 2 (ND2) gene sequence.

There were 16 samples of baung fish from Bengawan Solo River (BO1, BO2, BO3), Elo River (X1, X2), Progo River (1.4, 2.4, 3.4), Martapura River (BJ1, BJ2, BJ3), Mahakam River (KM1, KM2, KM3) and Kapuas River (A, B). The samples were amplified with ND2F and ND2R primers through the PCR method and the results were sequenced. The results of the sequencing were analyzed using the MEGA version 11 application to see genetic relationship with species from Genbank.

The results of the genetic relationship analysis showed that the baung fish sample from the Bengawan Solo River belongs to the genus *Pangasius* with a genetic distance of 12-12.1%, the baung fish sample from the Elo River belongs to the genus *Mystus* with a genetic distance of 17-17.1% and baung fish samples from the Progo, Martapura, Mahakam, and Kapuas Rivers belong to the genus *Hemibagrus* with a genetic distance of 3.0-3.8%.

Keywords: baung fish, ND2 gene, PCR, sequencing.