

## INTISARI

### IDENTIFIKASI MOLEKULER DAN ANALISIS KEKERABATAN IKAN BAUNG (*Bagridae*) ASAL SUMATRA DAN JAWA BERDASARKAN SEKUEN GEN NADH DEHIDROGENASE SUBUNIT 6 (ND6)

Muhammad Hesham Maulana  
17/412435/KH/09331

Ikan baung merupakan salah satu dari sekian banyak spesies ikan yang hidup di perairan darat Indonesia. Ikan baung tersebar di Pulau Sumatera, Kalimantan, dan Jawa. Ikan ini memiliki nilai ekonomis yang tinggi. Ikan baung memiliki morfologi yang hampir sama dengan ikan lele ataupun ikan air tawar bersungut lainnya yang ada di perairan darat Indonesia. Kajian molekuler perlu dilakukan untuk mengetahui keragaman genetik dari ikan baung ini. Penelitian ini bertujuan untuk mengidentifikasi gen ND6 secara molekuler pada tiap sampel dan juga hubungan kekerabatan ikan baung asal Pulau Sumatera dan Jawa dengan spesies pembanding dari *Genbank*.

Terdapat 15 sampel ikan baung yang dianalisis sekuen gen ND6-nya menggunakan *software* MEGA X. Sampel-sampel tersebut berasal dari Sungai Kampar di Riau (B1, B2, B3), Sungai Musi di Palembang (D, E, F), Sungai Bengawan Solo di Bojonegoro (BO1, BO2, BO3), Sungai Elo (X1, X2) dan Sungai Progo di Magelang (1.4, 2.4, 3.4). Sampel DNA diperoleh dari isolasi musculus epaxial dan hipoxial. Isolat kemudian di amplifikasi sekuen ND6-nya menggunakan primer ND6F dan ND6R dengan metode PCR. Produk amplifikasi kemudian disekuensing yang selanjutnya dilakukan analisis dengan melihat variasi genetik, asam amino dan jarak genetiknya dengan *software* MEGA X.

Hasil penelitian menunjukkan gen NADH Dehidrogenase Subunit 6 (ND6) memiliki 519 nukleotida dan menyandi 173 asam amino. Setiap sampel dibandingkan dan menunjukkan adanya 139 situs nukleotida dan 23 asam amino yang berbeda. Analisis kekerabatan antara sampel dengan spesies pembanding dari *Genbank* dilakukan dengan menentukan jarak genetiknya yang divisualisasikan dengan pohon filogenetik/filogram. Sampel ikan baung asal Sungai Musi (D, E, F), Sungai Kampar (B1, B2, B3) dan Sungai Progo (1.4, 2.4, 3.4) teridentifikasi ke dalam genus *Hemibagrus* dengan jarak genetik 2.4%-4.2%. Sampel ikan baung asal Sungai Elo (X1, X2) teridentifikasi ke dalam genus *Mystus* dengan jarak genetik 16%. Sampel ikan baung asal Sungai Bengawan Solo (BO1, BO2, BO3) teridentifikasi ke dalam genus *Pangasius* dengan jarak genetik 12 %.

Kata kunci: ikan baung, gen ND6, PCR, sekuensing, *Hemibagrus*, *Mystus*, *Pangasius*

## ABSTRACT

### MOLECULAR IDENTIFICATION AND GENETIC RELATIONSHIP ANALYSIS OF BAUNG FISH (*Bagridae*) FROM SUMATRA AND JAVA BASED ON NADH DEHYDROGENASE SUBUNIT 6 (ND6) GENE SEQUENCES

Muhammad Hesham Maulana  
17/412435/KH/09331

Baung fish is one of the many fish species that live in Indonesia's inland waters. Baung fish scattered on the islands of Sumatra, Kalimantan, and Java. This fish has a high economic value. Baung fish have a morphology similar to catfish or other grumbled freshwater fish in Indonesia's inland waters. Molecular studies need to be carried out to determine the genetic diversity of this baung fish. This study aims to identify the ND6 gene molecularly in each sample and the kinship relationship of the baung fish from Sumatra and Java Islands with the comparison species from Genbank..

There were 15 samples of baung fish whose ND6 gene sequences were analyzed using MEGA X software. The samples came from the Kampar River in Riau (B1, B2, B3), the Musi River in Palembang (D, E, F), the Bengawan Solo River in Bojonegoro (BO1, BO2, BO3), Elo River (X1, X2) and Progo River in Magelang (1.4, 2.4, 3.4). The DNA samples were obtained from the isolation of the epaxial and hypaxial muscles. The isolates were then amplified with the ND6 sequence using the ND6F and ND6R primers by the PCR method. The amplification product is then sequenced, analyzed by looking at genetic variations, amino acids, and genetic distances with MEGA X software.

The results showed that the NADH Dehydrogenase Subunit 6 (ND6) gene has 516 nucleotides and encodes 173 amino acids. Each sample was compared and showed the presence of 139 different nucleotide sites and 23 different amino acids. Genetic relationship analysis between the sample and the comparison species from Genbank was carried out by determining the genetic distance visualized by a phylogenetic tree/phylogram. The fish samples from the Musi River (D, E, F), Kampar River (B1, B2, B3), and Progo River (1.4, 2.4, 3.4) were identified as genus *Hemibagrus* with a genetic distance of 2.4%-4.2%. The fish samples from Sungai Elo (X1, X2) were identified as genus *Mystus* with a genetic distance of 16%. The fish samples from the Bengawan Solo River (BO1, BO2, BO3) were identified as genus *Pangasius* with a genetic distance of 12%.

Keywords: Baung fish, ND6 gene, PCR, sequencing, *Hemibagrus*, *Mystus*, *Pangasius*