INTISARI

KAJIAN KERAGAMAN GENETIK IKAN TENGGIRI (*Scomberomorus* sp.) ASAL REMBANG, CILACAP, DAN BANJARMASIN BERDASARKAN SEKUEN GEN *CYTOCHROME OXIDASE* SUB-UNIT I (COX1)

Mutiarisa Nur Alifah
19/442216/KH/10140

Ikan tenggiri (*Scomberomorus* sp.) merupakan salah satu spesies ikan yang banyak tersebar di perairan Indonesia. Berbagai olahan makanan dapat dibuat dengan bahan dasar ikan tenggiri sehingga ikan ini merupakan komoditas penting bagi perekonomian dalam negeri maupun kepentingan ekspor. Namun, informasi genetik serta budidaya intensif ikan tenggiri masih sangat terbatas. Oleh karena itu, perlu dilakukan studi genetika untuk meningkatkan efisiensi produksi dan budidaya ikan tenggiri sebagai upaya pelestarian. Penelitian ini bertujuan untuk mengidentifikasi gen *Cytochrome C Oxidase* Sub-Unit I (COX1) secara molekuler dan menganalisis kekerabatan ikan tenggiri asal Cilacap, Rembang, dan Banjarmasin menggunakan sekuen gen penyandi COX1.

Terdapat 9 sampel ikan tenggiri yang diperoleh dari wilayah Cilacap (C1, C2, dan C3), Rembang (R1, R2, dan R3), dan Banjarmasin (BA1, BB2, dan BC1). Hasil isolasi DNA diamplifikasi menggunakan primer COISCOMAF dan COISCOMAR menggunakan metode PCR. Amplifikasi gen COX1 menghasilkan produk PCR sepanjang 1.673 bp yang selanjutnya dilakukan sekuensing DNA. Hasil sekuensing gen COX1 selanjutnya dianalisis keragaman genetik dan filogenetiknya bersama spesies lain dari *genbank* menggunakan program MEGA XI.

Hasil analisis menunjukkan bahwa gen COX1 terdiri dari 1.559 nukleotida yang diterjemahkan menjadi 519 asam amino. Terdapat 185 situs nukleotida dan 22 situs asam amino berbeda antara sesama sampel yang dibandingkan. Analisis filogram menggunakan metode *Neighbor Joining* dengan Bootstrap 1.000x berdasar sekuen nukleotida gen COX1 menunjukkan bahwa sampel ikan tenggiri asal Cilacap, Rembang, dan Banjarmasin berkerabat dekat dengan *Scomberomorus niphonius* dengan jarak genetik 11,1% hingga 11,9%.

Kata kunci: Ikan tenggiri, gen COX1, *Scomberomorus* sp., PCR, sekuensing

ABSTRACT

STUDY OF GENETIC DIVERSITY OF TENGIRI FISH (*Scomberomorus* sp.) FROM REMBANG, CILACAP, AND BANJARMASIN BASED ON CYTOCHROME OXIDASE SUB-UNIT I (COX I) GEN SEQUEENS

Mutiarisa Nur Alifah
19/442216/KH/10140

Tenggiri (*Scomberomorus* sp.) is a fish species that is widely distributed in Indonesian ocean. Various processed foods can be made with the basic ingredients of mackerel so that this fish is an important commodity for the domestic economy as well as for export purposes. However, genetic information and intensive mackerel cultivation are still very limited. Therefore, it is necessary to carry out genetic studies to increase the efficiency of mackerel production and cultivation as a conservation effort. This study aims to identify the *Cytochrome C Oxidase* Sub-Unit I (COX1) gene molecularly and analyze the genetic relationship of mackerel from Cilacap, Rembang, and Banjarmasin using the COX1 encoding gene sequences.

There were 9 samples of mackerel obtained from Cilacap (C1, C2, and C3), Rembang (R1, R2, and R3), and Banjarmasin (BA1, BB2, and BC1) areas. The results of DNA isolation were amplified using COISCOMAF and COISCOMAR primers using the PCR method. COX1 gene amplification resulted in a 1,673 bp long PCR product which was then followed by DNA sequencing. The results of the COX1 gene sequencing were then analyzed for their genetic and phylogenetic diversity together with other species from the genbank using the MEGA XI program.

The results of data analysis showed that the COX1 gene consists of 1,559 nucleotides which are translated into 519 amino acids. There are 185 nucleotide sites and 22 amino acid sites that differ between the samples being compared. Phylogram analysis using the Neighbor Joining method with Bootstrap 1000x based on the nucleotide sequences of the COX1 gene showed that the mackerel samples from Cilacap, Rembang and Banjarmasin are closely related to *Scomberomorus niphonius* with a genetic distance of 11.1% to 11.9%.

Keywords: Mackerel, COX1 gene, *Scomberomorus* sp., PCR, sequencing