

INTISARI

ANALISIS KERAGAMAN GENETIK DAN KEKERBATAN IKAN TENGGERI (*Scomberomorus* sp.) ASAL KENDARI, KUPANG, DAN REMBANG BERDASARKAN SEKUEN GEN CYTOCHROME B (*Cytb*)

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Ikan tenggiri merupakan salah satu komoditas unggulan dari sektor perikanan Indonesia yang memiliki nilai ekonomis dan kandungan gizi yang tinggi. Berdasarkan data statistik dari KK, produksi tangkapan ikan tenggiri di Indonesia cenderung mengalami penurunan. Oleh karena itu, diperlukan upaya konservatif untuk mencegah kelangkaan ikan tenggiri. Salah satu upaya yang dapat dilakukan ialah melalui konservasi genetik yang memerlukan kajian genetik. Penelitian ini bertujuan untuk mengetahui keragaman genetik dan hubungan kekerabatan ikan tenggiri (*Scomberomorus* sp.) asal Kendari, Kupang, dan Rembang berdasarkan gen penyandi *cytochrome b* (*cyt b*).

Sembilan sampel diperoleh melalui isolasi jaringan ikan tenggiri yang berasal dari Kendari (AH, BH, CH), Kupang (AU, BU, CU), dan Rembang (1, 2, 3). Seluruh sampel diamplifikasi dengan primer *cytBbaruF* dan *cytBbaruR* dengan metode PCR. Produk PCR yang dihasilkan sebanyak 1311 bp disekuensing dan dianalisis menggunakan aplikasi MEGA 11.0.

Hasil analisis didapatkan gen *cyt b* berukuran 1311 bp memiliki 1141 situs nukleotida yang menyandi 380 asam amino. Analisis menunjukkan adanya variasi antar sampel sebanyak 22 situs nukleotida dan 0 situs asam amino. Hasil analisis kekerabatan berdasarkan sekuen nukleotida dan asam amino gen *cyt b* menunjukkan bahwa seluruh sampel ikan tenggiri asal Kendari, Kupang, dan Rembang berkerabat dengan *Scomberomorus commerson* (EF141176.1) dengan jarak genetik 0% - 1,8%.

Kata kunci: gen *cytochrome b*, ikan tenggiri, *Scomberomorus* sp., sekuensing, PCR

ABSTRACT

ANALYSIS OF GENETIC DIVERSITY AND KINSHIP OF MACKEREL (*Scomberomorus* sp.) THE ORIGIN OF KENDARI, KUPANG, AND REMBANG BASED ON CYTOCHROME B (Cytb) GENE SEQUENCES

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Mackerel is one of the major commodities of the Indonesian fisheries sector which has high economic value and nutritional content. Based on statistical data from KKP, mackerel catch production in Indonesia tends to decrease. Therefore, conservative efforts are needed to prevent the scarcity of mackerel. One of the efforts that can be done is through genetic conservation which requires genetic studies. This study aims to determine the genetic diversity and kinship of mackerel (*Scomberomorus* sp.) from Kendari, Kupang, and Rembang based on the cytochrome *b* (*cyt b*) encoding gene.

Nine samples were obtained through tissue isolation of mackerel fish from Kendari (AH, BH, CH), Kupang (AU, BU, CU), and Rembang (1, 2, 3). All samples were amplified with *cytBbaruF* and *cytBbaruR* primer by PCR method. PCR products produced as much as 1311 bp were sequenced and analyzed using the MEGA 11.0 application.

The results of the analysis found that the *cyt b* gene measuring 1311 bp has 1141 nucleotide sites encoding 380 amino acids. Analysis showed variation between samples of 22 nucleotide sites and 0 amino acid sites. The results of kinship analysis based on nucleotide sequences and amino acids of the *cyt b* gene showed that all mackerel samples from Kendari, Kupang, and Rembang were related to *Scomberomorus commerson* (EF141176.1) with a genetic distance of 0% - 1.8%.

Keywords: cytochrome b gene, spanish mackerel, *Scomberomorus* sp., sequencing, PCR