ABSTRAK

ANALISIS KERAGAMAN GENETIK IKAN TENGGIRI (*Scomberomorus* sp.) ASAL KENDARI, KUPANG, DAN BANJARMASIN BERDASARKAN GEN *CYTOCHROME B*

Adara Rizkimediani
20/459001/KH/10625

Ikan tenggiri (*Scomberomorus* sp.) merupakan ikan pelagis besar yang tersebar luas di perairan Indonesia. Sebagai komoditas, ikan tenggiri memiliki nilai ekonomis yang tinggi karena dagingnya yang kaya akan protein serta mudah untuk diolah menjadi berbagai macam produk. Nilai ekonomis tinggi dari ikan tenggiri menyebabkan permintaan pasar yang kian meningkat seiring berjalannya waktu. Hal tersebut dapat memicu penurunan populasi secara pesat apabila tidak disertai dengan manajemen pelestarian yang tepat. Kajian mengenai genetik ikan tenggiri dapat membantu dalam upaya menjaga kelestarian ikan tenggiri di perairan Indonesia. Penelitian ini bertujuan untuk menganalisis keragaman genetik dan kekerabatan ikan tenggiri asal Kendari, Kupang, dan Banjarmasin berdasarkan gen penyandi *cytochrome b* (Cyt b). Seluruh sampel diamplifikasi dengan primer cytBbaruF dan cytBbaruR menggunakan metode PCR. Amplikon yang dihasilkan berukuran 1311 bp, kemudian dilakukan sekuensing dan dianalisis menggunakan aplikasi MEGA11. Hasil sekuensing menunjukkan gen *cytochrome b* berukuran 1141 nukleotida yang diterjemahkan menjadi 380 asam amino. Terdapat 167 situs nukleotida dan 15 situs asam amino yang berbeda antar sampel. Hasil analisis sampel didapatkan bahwa sampel ikan tenggiri asal Kendari (kode sampel AH, BH, CH), Kupang (kode sampel AU, BU, CU), dan satu sampel asal Banjarmasin (kode sampel A) merupakan spesies *Scomberomorus commerson* (EF141176.1) dengan jarak genetik sampel asal Kendari dan Kupang 0,1 – 0,2% dan jarak genetik sampel Banjarmasin (kode sampel A) 1,8%. Sementara kedua sampel Banjarmasin lainnya (kode sampel B dan C) merupakan spesies *Scomberomorus commerson* voucher Zhang Q. SCDX1 (AY986968.1) dengan jarak genetik 0%.

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

ABSTRACT

GENETIC DIVERSITY ANALYSIS OF SPANISH MACKEREL (*Scomberomorus* sp.) FROM KENDARI, KUPANG, AND BANJARMASIN BASED ON *CYTOCHROME B* GENE

Adara Rizkimediani
20/459001/KH/10625

Spanish mackerel (*Scomberomorus* sp.) is a large pelagic fish that is widely distributed throughout Indonesian waters. As a commodity, Spanish mackerel holds high economic value due to its protein-rich flesh, which can be easily processed into various products. The high economic value of Spanish mackerel leads to an increasing market demand over time. This demand can trigger a rapid decline in population if not accompanied by proper conservation management. Genetic studies of Spanish mackerel can aid in the efforts to preserve the population of this species in Indonesian waters. This research aims to analyze the genetic diversity and kinship of Spanish mackerel from Kendari, Kupang, and Banjarmasin based on the cytochrome b (Cyt b) gene. All samples were amplified with cytBbaruF and cytBbaruR primers using the PCR method. The resulting amplicons, which were 1311 bp in size, were then sequenced and analyzed using the MEGA11 software. Sequencing results showed that the cytochrome b gene is 1141 nucleotides long and translates into 380 amino acids. There were 167 nucleotide sites and 15 amino acid sites that differed among the samples. Analysis results indicated that the Spanish mackerel samples from Kendari (sample codes AH, BH, CH), Kupang (sample codes AU, BU, CU), and one sample from Banjarmasin (sample code A) belong to the species *Scomberomorus commerson* (EF141176.1) with a genetic distance of 0.1 – 0.2% between samples from Kendari and Kupang, and 1.8% for the Banjarmasin (sample code A) sample. Meanwhile, the other two Banjarmasin samples (sample codes B and C) belong to the species *Scomberomorus commerson* voucher Zhang Q. SCDX1 (AY986968.1) with a genetic distance of 0%.

Keywords: *Scomberomorus* sp., Spanish mackerel, cytochrome b (Cyt b) gene, PCR, sequencing