

ABSTRAK

KAJIAN KERAGAMAN GENETIK IKAN TENGGIRI (*Scomberomorus* sp.) ASAL GRESIK, BANJARMASIN, MOROWALI UTARA, AMBON, DAN FAKFAK BERDASARKAN SEKUEN GEN ATP SINTASE 6

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Ikan tenggiri (*Scomberomorus* sp.) merupakan ikan pelagis yang tersebar luas di perairan tropis, termasuk perairan Indonesia dan kawasan Indo-Pasifik. Ikan tenggiri (*Scomberomorus* sp.) memiliki nilai ekonomis tinggi mendorong tingginya penangkapan secara terus-menerus tanpa memperhatikan ketersediaan di perairan. Status konservasi ikan tenggiri berada pada *Near Threatened* (NT) yang berarti populasi cenderung menurun dan dapat terancam punah apabila upaya konservasi tidak berjalan dengan optimal. Hingga kini, hubungan filogenetik dan taksonomi ikan tenggiri di Indonesia belum lengkap, sehingga menghambat upaya konservasi. Penelitian ini bertujuan untuk mengetahui keragaman genetik dan hubungan filogenetik ikan tenggiri (*Scomberomorus* sp.) yang berasal dari beberapa daerah di Indonesia berdasarkan sekuen gen ATP sintase 6. Sampel yang digunakan berjumlah 12 muskulus *epaxial* ikan tenggiri yang berasal dari Gresik, Morowali Utara, Banjarmasin, Ambon, dan Fakfak. Sampel ikan tenggiri diisolasi kemudian diamplifikasi dengan metode PCR menggunakan *forward primer* (ATPScomF) dan *reverse primer* (ATPScomR) sehingga diperoleh 1.072 bp produk PCR dan dilanjutkan dengan sekuensing. Hasil sekuensing dianalisis menggunakan MEGA 11 untuk mengetahui keragaman genetik sampel ikan tenggiri dengan sekuens pembandingan yang diperoleh dari *Genbank*. Hasil analisis diketahui bahwa gen penyandi ATP sintase 6 ikan tenggiri asal Gresik, Banjarmasin, Morowali Utara, Ambon, dan Fakfak terdiri atas 684 basa nukleotida yang diterjemahkan menjadi 228 asam amino dengan 257 nukleotida dan 42 asam amino yang bervariasi. Analisis filogenetik menunjukkan bahwa sampel ikan tenggiri asal Gresik (TB1, TB2), Banjarmasin (KA), Morowali Utara (TM), Ambon (M1, M2, M3) berkerabat dekat dengan spesies *Scomberomorus commerson* (PP437202.1) dengan jarak genetik 0.15–1.78%, sampel ikan tenggiri asal Banjarmasin (KB, KC) berkerabat dekat dengan spesies *Scomberomorus aff. guttatus* (OM36353) dengan jarak genetik 0.15%, sampel ikan tenggiri asal Fakfak (P1, P2, P3) berkerabat dekat dengan spesies *Scomberomorus semifasciatus* (NC021391.1) dengan jarak genetik 0–0.15%.

Kata kunci: gen ATP sintase 6, ikan tenggiri, PCR, *Scomberomorus* sp., sekuensing

ABSTRACT

STUDY OF GENETIC DIVERSITY OF MACKEREL (*Scomberomorus* Sp.) ORIGIN OF GRESIK, BANJARMASIN, NORTH MOROWALI, AMBON, AND FAKFAK BASED ON ATP SYNTHASE 6 GENE SEQUENCE

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Mackerel (*Scomberomorus* sp.) is a pelagic fish widely distributed in tropical waters, including Indonesian waters and the Indo-Pacific region. Mackerel (*Scomberomorus* sp.) has high economic value, which drives continuous intensive harvesting without adequate consideration of stock availability in the wild. The conservation status of mackerel is at *Near Threatened* (NT) which means that the population tends to decline and can be endangered if conservation efforts do not run optimally. To date, the phylogenetic and taxonomic relationships of mackerel in Indonesia remain unresolved, thereby hindering effective conservation and management efforts. This study aims to determine the genetic diversity and phylogenetic relationship of mackerel (*Scomberomorus* sp.) which originated from several regions in Indonesia based on the ATP synthase 6 gene sequence. The samples used amounted to 12 *epaxial* muscle of mackerel from Gresik, North Morowali, Banjarmasin, Ambon, and Fakfak. Mackerel samples were isolated and then amplified by PCR method using *forward primer* (ATPScomF) and *reverse primer* (ATPScomR) so that 1,072 bp of PCR product were obtained and continued with sequencing. The sequencing results were analyzed using MEGA 11 to determine the genetic diversity of mackerel samples with comparative sequences obtained from *Genbank*. The results of the analysis found that the ATP synthase 6 encoding genes of mackerel from Gresik, Banjarmasin, North Morowali, Ambon, and Fakfak consisted of 684 nucleotide bases which were translated into 228 amino acids with 257 nucleotides and 42 amino acids that vary. Phylogenetic analysis showed that mackerel samples from Gresik (TB1, TB2), Banjarmasin (KA), North Morowali (TM), Ambon (M1, M2, M3) were closely related to the species *Scomberomorus commerson* (PP437202.1) with a genetic distance of 0.15–1.78%, mackerel samples from Banjarmasin (KB, KC) were closely related to the species *Scomberomorus aff. guttatus* (OM36353) with a genetic distance of 0.15%, mackerel samples from Fakfak (P1, P2, P3) are closely related to the species *Scomberomorus semifasciatus* (NC021391.1) with a genetic distance of 0–0.15%.

Keywords: ATP synthase 6 gene, mackerel, PCR, *Scomberomorus* sp., sequencing