

INTISARI

KAJIAN KERAGAMAN GENETIK IKAN TENGGIRI (*Scomberomorus* sp.) ASAL SUMATRA, KALIMANTAN, DAN AMBON BERDASARKAN SEKUEN GEN *CYTOCHROME C OXIDASE* SUBUNIT II (COX II)

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Ikan tenggiri merupakan ikan pelagis yang ditemukan hampir di seluruh perairan Indonesia karena habitatnya yang cocok di daerah iklim tropis. Masyarakat di Indonesia memanfaatkan kondisi ini untuk menjadikannya sebagai komoditas ekonomi karena kebutuhan produk perikanan yang terus meningkat sehingga berpotensi menimbulkan kecurangan perdagangan untuk meningkatkan keuntungan sepihak. Penelitian ini bertujuan untuk menganalisis keragaman genetik ikan tenggiri (*Scomberomorus* sp.) yang berasal dari Banjarmasin, Ambon, dan Palembang menggunakan sekuen gen *Cytochrome c Oxidase* subunit II (COX II) sehingga bermanfaat untuk memberikan informasi mengenai keragaman genetik ikan tenggiri dalam upaya pengelolaan sumber daya ikan tenggiri. Terdapat sembilan sampel DNA total hasil isolasi jaringan ikan tenggiri yang berasal dari Banjarmasin (A, B, C), Ambon (M1, M2, dan M3), dan Palembang (D, E, F). Sampel DNA tersebut diamplifikasi menggunakan primer COX subunit II *forward* dan *reverse* dengan metode PCR. Produk PCR yang diperoleh sebesar 871 bp kemudian dilakukan sekuensing DNA. Selanjutnya, hasil sekuensing dianalisis untuk menentukan keragaman genetik dengan spesies pembanding dari *GenBank* menggunakan perangkat lunak MEGA 11.0. Hasil analisis data menunjukkan bahwa gen COX II terdiri dari 691 nukleotida yang menyandi 230 asam amino. Analisis filogram berdasarkan sekuen nukleotida dan asam amino gen COX II menunjukkan adanya perbedaan kekerabatan antar sampel ikan tenggiri yang berasal dari Banjarmasin, yaitu berdasar sekuen nukleotida berkerabat dekat dengan *Scomberomorus niphonius* dengan jarak genetik 12,6%, sedangkan berdasar sekuen asam amino berkerabat dekat dengan *Scomberomorus concolor* dan *Scomberomorus sierra*. Sampel asal Ambon dan Palembang berkerabat dekat dengan *Scomberomorus cavalla* dengan jarak genetik sebesar 9-9,5%.

Kata kunci: ikan tenggiri, *Scomberomorus* sp., gen COX II, sekuensing, PCR

ABSTRACT

STUDY OF GENETIC DIVERSITY OF SPANISH MACKEREL (*Scomberomorus* sp.) FROM BANJARMASIN, AMBON, AND BASED ON CYTOCHROME C OXIDASE SUBUNIT II (COX II) GENE SEQUENCE

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Spanish mackerel is a pelagic fish that is found in almost all Indonesian waters because of its suitable habitat in tropical climates. Communities in Indonesia take advantage of this condition to make it an economic commodity because the need for fishery products continues to increase, which has the potential to cause trade fraud to increase one-sided profits. This study aims to analyze the genetic diversity of spanish mackerel (*Scomberomorus* sp.) originating from Banjarmasin, Ambon, and Palembang using the Cytochrome c Oxidase subunit II (COX II) gene sequence so that it is useful to provide information about the genetic diversity of spanish mackerel in efforts to manage natural resources spanish mackerel. There were nine total DNA samples isolated from mackerel tissue from Banjarmasin (A, B, C), Ambon (M1, M2, and M3), and Palembang (D, E, F). The DNA samples were amplified using COX subunit II forward and reverse primers using the PCR method. The PCR product obtained was 871 bp and then DNA sequencing was performed. Next, the sequencing results were analyzed to determine genetic diversity with comparison species from GenBank using MEGA 11.0 software. The results of data analysis showed that the COX II gene consists of 691 nucleotides which encode 230 amino acids. Phylogram analysis based on the nucleotide and amino acid sequences of the COX II gene showed that there were differences in the kinship between mackerel samples from Banjarmasin, namely based on nucleotide sequences that were closely related to *Scomberomorus niphonius* with a genetic distance of 12.6%, while based on amino acid sequences that were closely related to *Scomberomorus concolor* and *Scomberomorus sierra*. Samples from Ambon and Palembang are closely related to *Scomberomorus cavalla* with a genetic distance of 9-9.5%.

Key words: spanish mackerel, *Scomberomorus* sp., COX II gene, sequencing, PCR