

INTISARI

KERAGAMAN GENETIK IKAN TENGGIRI (*Scomberomorus* sp.) ASAL REMBANG, PALEMBANG, CILACAP, DAN AMBON BERDASARKAN SEKUEN GEN *CYTOCHROME OXIDASE* SUBUNIT II (COX2)

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Ikan tenggiri merupakan kelompok ikan laut pelagis dengan cita rasa khas dan menjadi komoditas perikanan laut utama karena nilai komersil yang tinggi. Persebaran dan komoditas yang tinggi menjadikan ikan tenggiri menjadi salah satu komoditas ekonomi masyarakat sekitar pesisir. Sebagai salah satu komoditas unggulan perikanan di Indonesia, diperlukan informasi mengenai keragaman genetik ikan tenggiri guna menunjang pelestarian, pengelolaan, dan pemanfaatan bagi masyarakat. Penelitian ini bertujuan untuk mengidentifikasi dan mengetahui kekerabatan ikan tenggiri (*Scomberomorus* sp.) asal Rembang (1, 2, 3), Palembang (D, E, F), Cilacap (C1, C2, C3), dan Ambon (M1, M2, M3) berdasarkan gen penyandi *Cytochrome Oxidase* Subunit II (COX2). Seluruh sampel diamplifikasi dengan primer COX2F dan COX2R dengan metode PCR. Produk PCR yang dihasilkan sebanyak 869 bp kemudian disekuensing dan dianalisis menggunakan aplikasi MEGA 11.0. Hasil analisis menunjukkan gen COX2 berukuran 869 bp memiliki 691 situs nukleotida yang menyandi 230 asam amino. Hasil analisis kekerabatan berdasarkan sekuen nukleotida dan asam amino gen COX2 menunjukkan sampel ikan tenggiri asal Cilacap berkerabat dekat dengan *Scomberomorus cavalla* dengan jarak genetik 13,3% namun berdasarkan asam amino berkerabat dekat dengan *Scomberomorus sierra* dan *Scomberomorus concolor*. Sampel asal Rembang, Palembang, dan Ambon memiliki kekerabatan terdekat dengan *Scomberomorus cavalla* dengan jarak genetik 9-9,4%.

Kata kunci: gen COX2, ikan tenggiri, sekuensing, *Scomberomorus* sp., PCR

ABSTRACT

GENETIC DIVERSITY OF SPANISH MACKEREL (*Scomberomorus* sp.) FROM REMBANG, PALEMBANG, CILACAP, AND AMBON BASED ON CYTOCHROME OXIDASE SUBUNIT II (COX2) GENE SEQUENCE

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Mackerel is a group of pelagic marine fish with a distinctive taste for the community and is a major marine fishery commodity because it has high commercial value. Wide and high commodity make mackerel become one of the economic commodities of the people around the coast. As one of the main fisheries commodities in Indonesia, information is needed regarding the genetic diversity of mackerel that can support its conservation, management and utilization for the community. This study aims to identify and determine the kinship of mackerel (*Scomberomorus* sp.) from Rembang (1, 2, 3), Palembang (D, E, F), Cilacap (C1, C2, C3), and Ambon (M1, M2, M3) based on the *Cytochrome Oxidase* Subunit II (COX2) encoding gene. All samples were amplified with COX2F and COX2R primers using the PCR method. The result of the PCR product of 869 bp was then sequenced and analyzed using the MEGA 11.0 application. The results of the analysis showed that the 869 bp COX2 gene has 691 nucleotide sites which encode 230 amino acids. The results of phylogenetic analysis based on the nucleotide and amino acid sequences of the COX2 gene showed that mackerel from Cilacap samples were closely related to *Scomberomorus cavalla* with a genetic distance of 13.3% but based on amino acids that were closely related to *Scomberomorus sierra* and *Scomberomorus concolor*. Samples from Rembang, Palembang and Ambon have the closest kinship with *Scomberomorus cavalla* with a genetic distance of 9-9.4%.

Kata kunci: COX2 gene, Spanish mackerel, sequencing, *Scomberomorus* sp., PCR