

Intisari

Penelitian ini bertujuan untuk mengidentifikasi dan membandingkan keragaman spesies kembung secara morfologi dan molekuler yang ditemukan di Perairan Selatan Jawa Timur. Sampel ikan diambil dari hasil tangkapan di Perairan Prigi dan Muncar pada bulan Maret 2018 sampai April 2018. Sejumlah 36 karakter truss morfometrik yang terbentuk dan 5 karakter meristik diukur pada masing-masing sampel. Analisis molekuler dilakukan dengan isolasi DNA kemudian dilakukan amplifikasi dan *sequencing* gen dengan target COX1. Analisis data karakter morfometrik menggunakan *Principal Component Analysis* (PCA), *Discriminant Function Analysis* (DFA), dan Analisis Kluster, sedangkan karakter meristik dibandingkan dengan pustaka. Secara genetik, spesies ikan kembung ditentukan menggunakan analisis BLAST pada website NCBI. Berdasarkan identifikasi secara morfologi sampel ikan kembung ada tiga yaitu *R. brachysoma*, *R. kanagurta*, dan *R. faughni*. Berdasarkan analisis PCA dan diskriminan, perbedaan utama antar spesies terletak pada karakter morfometrik sekitar kepala dan tengah tubuh ikan, yaitu jarak awal sirip punggung ke awal sirip perut dan jarak dari ujung mulut ke ujung rahang bawah. Berdasarkan analisis kluster, *R. brachysoma* dan *R. kanagurta* masing-masing perairan berkerabat dekat sedangkan *R. faughni* berkerabat jauh dengan dua spesies lainnya. Analisis filogenetik menunjukkan *R. kanagurta* Prigi dan Muncar berkerabat dekat dengan *R. kanagurta* dengan kemiripan 100%, *R. brachysoma* Prigi dan Muncar berkerabat dekat dengan *R. brachysoma* namun belum dapat dipastikan, sedangkan *R. faughni* berkerabat jauh dengan genus *Rastrelliger*.

Kata kunci: COX1, meristik, molekuler, morfometrik, *Rastrelliger spp.*

Abstract

This study aimed to identify *Rastrelliger* spp. based on morphological and molecular identification from Southern Sea of East Java. The samples were collected from Prigi and Muncar ocean from March 2018 to April 2018. There are 36 truss morphometric characters and 5 meristic characters were measured from each sample. Molecularly, DNA was isolated then used for amplification and sequencing of COX1 gene. Morphometric analysis using Principal Component Analysis (PCA), Discriminant Function Analysis (DFA), and Cluster Analysis, while meristic data were compared to previously reported. For molecular analysis using BLAST through the NCBI website. Based on the morphological analysis, the result showed that Indian mackerel consisted of three species *R. brachysoma*, *R. kanagurta*, and *R. faughni*. Based on the PCA and DFA, these species can be distinguished by head and body area, which are the distance between origin first dorsal fin to origin of pelvic fin, and the distance between snout to the intersection of preopercle and operculum on the ventral side of the body. Cluster analysis showed that *R. brachysoma* and *R. kanagurta* from each water is close enough, while *R. faughni* is separate from two other species. The phylogenetical analysis showed that *R. kanagurta* from Prigi and Muncar are close to *R. kanagurta* with 100% similarity, *R. brachysoma* from Prigi and Muncar are close to *R. brachysoma* but cannot be confirmed to this species, while *R. faughni* is separate to other clade so this species is far from two other species.

Key words: COX1, meristic, molecular, morphometric, *Rastrelliger* spp.