VARIASI MORFOLOGIS DAN MOLEKULAR LIMA POPULASI *Meretrix* spp. (BIVALVIA:VENERIDAE) DI INDONESIA DENGAN PENANDA *INTER SIMPLE SEQUENCE REPEATS*

ABSTRAK

Perubahan lingkungan dan eksploitasi berlebihan menjadi faktor penyebab turunnya populasi *Meretrix* spp. dibeberapa daerah di Indonesia. Salah satu langkah antisipasinya melalui pengelolaan berbasis budidaya. Informasi mengenai karakter morfologis dan molekular dibutuhkan agar budidaya yang dilakukan lebih efektif dan efesien. Penelitian ini bertujuan mengetahui variasi morfologis dan molekular populasi *Meretrix* spp. serta menentukan populasi yang potensial untuk dikembangkan. Pengambilan sampel berdasarkan distribusi penyebarannya di lima populasi berbeda yaitu Tarakan, Ketapang, Takalar, Trenggalek dan Demak. Analisis karakter morfologis dan molekular dilakukan di Laboratorium Sistematika Hewan dan Laboratorium Genetika Fakultas Biologi Universitas Gadjah Mada mulai bulan April hingga Agustus 2015. Tahapan penelitian terdiri dari pengambilan sampel, preservasi dan pengamatan karakter morfologis, isolasi DNA genom, amplifikasi DNA dengan metode PCR-ISSR menggunakan primer ISSR 5 dan ISSR 6, elektroforesis dan pengamatan pita DNA. Data morfometri dianalisis rasio dan regresinya menggunakan SPSS 21 sedangkan data pita DNA dianalisis persentase polimorfisme dan similaritas berdasarkan metode UPGMA dengan menggunakan software MVSP 3.1. Hasil penelitian menunjukan bahwa spesies *M. meretrix* ditemukan di semua populasi sedangkan spesies *Meretrix* sp. hanya ditemukan di populasi Takalar. Populasi Ketapang memiliki keunggulan yaitu persentase polimorfisme sebesar 100%, similaritas intrapopulasi terendah (56%), diameter *pallial line* tertinggi (5,72cm) dan rerata panjang cangkang tertinggi (7,01cm). Populasi Tarakan memiliki keunggulan yaitu tingkat persentase polimorfisme sebesar 100%, variasi warna corak terbanyak (5 jenis) dan persentase berat daging tertinggi (25%). Berdasarkan data morfologis dan molekular maka *M. meretrix*. populasi Ketapang dan Tarakan direkomendasikan untuk dibudidayakan agar mendapatkan hasil yang maksimal.

Kata kunci : *Meretrix meretrix*, Variasi genetik, Penanda molekular ISSR.

MORPHOLOGY AND MOLECULAR VARIATION IN FIVE POPULATIONS OF INDONESIAN *MERETRIX* SPP. (BIVALVIA : VENERIDAE) USING INTER SIMPLE SEQUENCE REPEATS

ABSTRACT

Environmental change and overexploitation were the main factors causing the decline of *Meretrix* spp. population in several regions in Indonesia. The conservation and sustainable management of aquaculture-based can be used to anticipate these. Information on morphological and molecular characters are needed for effectively and efficiently cultivation. This study aimed to determine the morphology and molecular variation of five populations of *Meretrix* spp. in Indonesia and to determine the potential population for further developing. Sampling was based on the distribution of *Meretrix* spp. in five different populations include Tarakan, Ketapang, Takalar, Trenggalek, and Demak. Analysis of morphological characters and molecular systematics were carried out in the Laboratory of Animal Systematic Laboratory and Genetic Laboratory in Faculty Biology, Gadjah Mada University from April to August 2015. Stages of the study consisted of sampling, preservation and observation of morphological characters, DNA genome isolation, DNA amplification using PCR-ISSR by ISSR 5 and 6 primer, electrophoresis and DNA bands observation. Data morphometric ratios and regression were analyzed using SPSS 21 software. DNA polymorphisms and similarity percentage, to reconstruct the dendrogram, were determined by UPGMA method using MVSP 3.1 software. The results showed that Ketapang population has the highest polymorphism percentage (100%), the lowest intra-population similarity (56%), the longest pallial line (5.72 cm), and the longest shell length (7.01cm). While, Tarakan population has the highest polymorphism percentage rate of (100%), the most variance in colors and patterns (5 types), and the highest meat weight (25%). Based on data, Ketapang and Tarakan population were recommended for cultivation.

Keywords: *Meretrix* spp., genetic variation, ISSR molecular markers.