

**KEANEKARAGAMAN GENETIK KERANG POKEA,
Batissa violacea (Lamarck, 1818), DARI SULAWESI TENGGARA
BERDASARKAN GEN MITOKONDRIA COI
DAN KARAKTER MORFOLOGIS**

INTISARI

Pokea merupakan kerang air tawar konsumsi yang banyak ditemukan di sungai wilayah Provinsi Sulawesi Tenggara dan saat ini mengalami overeksploitasi akibat aktivitas antropogenik. Strategi konservasi diperlukan untuk menjaga stabilitas populasi pokea di habitat aslinya. Berdasarkan hal tersebut, maka keakuratan identifikasi spesies menggunakan integrasi data morfologis dan *DNA barcoding* serta evaluasi keanekaragaman genetik dan struktur populasi pokea penting dilakukan sebagai dasar informasi upaya konservasi hewan tersebut. Pada penelitian ini dilakukan identifikasi spesies menggunakan integrasi data morfologis dan *DNA barcoding* serta melakukan analisis variasi genetik dan struktur populasi pokea yang disampling dari tiga sungai di Sulawesi Tenggara (Sungai Lasolo, Sungai Pohara dan Sungai Konawehe). Karakter morfologis yang digunakan adalah karakteristik cangkang dan hasil pengukuran morfometrik cangkang dianalisis menggunakan program PAST. Selanjutnya untuk karakter molekuler, gen mitokondria *COI* kerang pokea diisolasi dan diamplifikasi menggunakan metode PCR dengan primer universal LCO1490 dan HCO2198. DNA gen mitokondria *COI* yang sudah didapatkan disekuensing untuk memperoleh data sekuens DNA. Data sekuens DNA yang diperoleh selanjutnya dianalisis menggunakan GeneStudio, DNASTAR, BLAST, Mesquite, MEGA11, jModelTest, BEAST, DnaSP, POPART, dan GenAlex. Analisis data sekuens gen *COI* dilakukan untuk mendapatkan data persentase similaritas, jarak genetik, variasi genetik, rekonstruksi pohon filogenetik, dan struktur populasi kerang pokea. Hasil penelitian menunjukkan bahwa seluruh sampel terkonfirmasi sebagai spesies *Batissa violacea* berdasarkan analisis morfologi dan molekuler. Analisis variasi genetik menunjukkan terdapat 5 haplotipe dan 4 *variable site*. Rerata keragaman haplotipe dan keragaman nukleotida adalah $0,3665 \pm 0,235$ dan $0,000845 \pm 0,0007$. Berdasarkan hasil AMOVA, sumber utama variasi genetik terjadi dalam populasi. Secara keseluruhan, penelitian ini memberikan dasar yang penting untuk pengelolaan sumber daya genetik *B. violacea* di habitat alaminya.

Kata Kunci: Pokea, *DNA Barcoding*, Keanekaragaman Genetik, Struktur Populasi

**GENETIC DIVERSITY OF POKEA,
Batissa violacea (Lamarck, 1818), FROM SOUTHEAST SULAWESI BASED
ON THE *MITOCHONDRIAL COI* GENE AND MORPHOLOGICAL
CHARACTERS**

ABSTRACT

Pokea is an edible freshwater clam found in many rivers in the Province of Southeast Sulawesi and is currently overexploited due to anthropogenic activities. Therefore, conservation strategies are needed to maintain the establishment of pokea populations in their natural habitat. The accuracy of species identification using the integration of morphological and molecular data (DNA barcoding) as well as evaluation of genetic diversity and population structure of pokea is important for database information on this species conservation efforts. In this study, species identification was carried out using the integration of molecular data with DNA barcoding and morphological character data, and then genetic variation and population structure of Pokea sampled from three rivers in Southeast Sulawesi (Lasolo River, Pohara River, and Konawe River) were analyzed. The morphological characters used are shell characteristics and shell morphometric measurements was analysed using PAST program. Next, the mitochondrial *COI* gene isolated and amplified using the PCR method with universal primers LCO1490 and HCO2198. The DNA sequence data obtained were then analysed using GeneStudio, DNASTAR, BLAST, Mesquite, MEGA11, jModelTest, BEAST, DnaSP, POPART, and GenAlex. Analysis of *COI* gene sequence data was carried out to obtain data on similarity, genetic distance, genetic variation, phylogenetic tree reconstruction and population structure of pokea. The results revealed that all samples belonged to *Batissa violacea* species according to both morphological and molecular analyses. Genetic variation analysis showed 5 haplotypes and 4 variable sites. The average haplotype diversity and nucleotide diversity were 0.3665 ± 0.235 and 0.000845 ± 0.0007 , respectively. According to AMOVA, the primary source of genetic variation occurs within populations. Overall, this study provides a valuable basis for the management of genetic resources of the *B. violacea* in their natural habitat.

Keywords: Pokea, DNA Barcoding, Genetic Diversity, Population Structure