

RINGKASAN

MEGA ANANDA PUTRI. Keanekaragaman Eukaryota Di Ekosistem Padang Lamun Desa Pengudang, Bintan Dengan eDNA Metabarkoding Marka Gen 18S rRNA. Dibimbing oleh ARIEF PRATOMO dan TRY FEBRIANTO.

Ekosistem padang lamun merupakan salah satu ekosistem pesisir dengan produktivitas tinggi yang berperan penting sebagai habitat, daerah asuhan, pemijahan, dan sumber pakan bagi berbagai organisme laut. Namun, identifikasi keanekaragaman biota menggunakan metode konvensional masih memiliki keterbatasan dalam mendeteksi organisme berukuran kecil, kriptik, maupun spesies dengan kelimpahan rendah. Penelitian ini bertujuan mengungkap dan mengidentifikasi keanekaragaman Eukaryota pada ekosistem padang lamun Desa Pengudang, Kabupaten Bintan, Kepulauan Riau menggunakan pendekatan *environmental DNA* (eDNA) metabarkoding dengan marka gen 18S rRNA. Penelitian dilaksanakan pada Juli 2025 di Desa Pengudang, sedangkan analisis laboratorium dilakukan di Laboratorium Oceanogen Bogor dan pengolahan data berlangsung pada Desember 2025 hingga Mei 2026. Sampel eDNA berupa air laut, sedimen, dan epifit pada daun lamun *Enhalus acoroides* dikumpulkan menggunakan metode *purposive sampling*, kemudian difiltrasi, diekstraksi, dan diamplifikasi menggunakan mesin *Polymerase Chain Reaction* (PCR), dan disekuensing dengan *platform* Illumina. Analisis bioinformatika dilakukan menggunakan QIIME2 dan DADA2 untuk menghasilkan *Amplicon Sequence Variants* (ASV) serta klasifikasi taksonomi menggunakan database PR2, kemudian dianalisis menggunakan indeks Shannon, Bray Curtis, dan *Principal Coordinates Analysis* (PCoA). Hasil penelitian menghasilkan 1.298 ASV yang teridentifikasi ke dalam lima kingdom Eukaryota dengan total 115 genera. Komposisi komunitas berbeda pada setiap habitat, yaitu air laut didominasi oleh Copepoda dan Dinophyceae, epifit daun lamun Ea didominasi diatom dan mikroalga, sedangkan sedimen didominasi Gastropoda, Annelida, dan Foraminifera. Nilai keanekaragaman Indeks Shannon tertinggi terdapat pada sedimen, sedangkan nilai disimilaritas Bray Curtis sebesar 0,98–0,99 dan visualisasi PCoA menunjukkan perbedaan komunitas yang jelas tipe sampel. Penelitian ini menunjukkan bahwa eDNA metabarkoding merupakan metode non-invasif yang efektif untuk mengungkap keanekaragaman Eukaryota serta karakteristik mikrohabitat pada ekosistem padang lamun secara komprehensif.

Kata kunci: eDNA metabarkoding, Ekosistem Padang Lamun, Eukaryota, Desa Pengudang, Keanekaragaman Hayati.

SUMMARY

MEGA ANANDA PUTRI. Keanekaragaman Eukaryota Di Ekosistem Padang Lamun Desa Pengudang, Bintan Dengan eDNA Metabarkoding Marka Gen 18s rRNA. Dibimbing oleh ARIEF PRATOMO dan TRY FEBRIANTO.

Seagrass ecosystems are among the most productive coastal ecosystems and play a crucial role in supporting marine biodiversity by providing habitat, nursery grounds, spawning areas, and feeding grounds for a wide range of marine organisms. However, conventional biodiversity assessment methods remain limited in detecting small, cryptic, and low-abundance organisms. This study aimed to identify and characterize Eukaryotic communities in the seagrass ecosystem of Pengudang Village, Bintan Regency, Riau Islands, Indonesia, using an environmental DNA (eDNA) metabarcoding approach targeting the 18S rRNA gene. Field sampling was conducted in July 2025 at the Pengudang seagrass ecosystem, while laboratory analyses were performed at Oceanogen Laboratory, Bogor, and bioinformatic analyses were carried out between December 2025 and May 2026. Environmental DNA samples were collected from three habitat types, namely seawater, sediment, and epiphytes associated with the leaves of *Enhalus acoroides*, using a purposive sampling approach. Samples were subsequently filtered, subjected to DNA extraction, amplified using Polymerase Chain Reaction (PCR), and sequenced on the Illumina platform. Bioinformatic processing was performed using QIIME2 and DADA2 to generate Amplicon Sequence Variants (ASVs), followed by taxonomic assignment based on the PR2 database. Community diversity was evaluated using the Shannon diversity index, Bray–Curtis dissimilarity, and Principal Coordinates Analysis (PCoA). A total of 1,298 ASVs representing five Eukaryotic kingdoms and 115 genera were identified. Community composition differed markedly among habitat types, with seawater dominated by Copepoda and Dinophyceae, epiphytes by diatoms and microalgae, and sediment by Gastropoda, Annelida, and Foraminifera. Sediment exhibited the highest Shannon diversity, whereas Bray–Curtis dissimilarity values (0.98–0.99) and PCoA revealed clear community separation among habitats. These findings demonstrate that eDNA metabarcoding is an effective non-invasive approach for assessing Eukaryotic biodiversity and provides a comprehensive understanding of microhabitat characteristics within seagrass ecosystems.

Keywords: Environmental DNA Metabarcoding, Seagrass Ecosystem, Eukaryota, Pengudang Village, Biodiversity.