

EKSPLORASI DIVERSITAS FAUNA DI GUA LAULAWI, PULAU MUNA, SULAWESI TENGGARA MELALUI PENDEKATAN *ENVIRONMENTAL* DNA

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INTISARI

Gua Laulawi di Kabupaten Buton Tengah, Pulau Muna, Sulawesi Tenggara memiliki area akuifer yang menjadi habitat unik dan menyimpan diversitas yang belum pernah dieksplorasi selama ini. Penelitian ini bertujuan sebagai kajian awal monitoring diversitas fauna di akuifer menggunakan pendekatan *environmental* DNA. Sampel air diambil dari 5 titik dengan volume kurang lebih 1,5 liter. Sampel air kemudian difiltrasi menggunakan membran penyaringan dan dilanjutkan dengan ekstraksi, amplifikasi dan sekuensing. Analisa *metabarcoding* menggunakan *pipeline* DADA2 pada Galaxy dan Geneious Prime serta penentuan taksonomi dengan dibandingkan database MIDORI Reference 2. Dari lima sampel eDNA, satu sampel berhasil disekuensing dan dianalisis, dengan hasil taksonomi divisualisasikan dalam bentuk diagram Krona. Berdasarkan algoritma *Amplicon Sequence Variant* (ASV), filum dengan kelimpahan terbesar adalah Arthropoda (76%), diikuti oleh Chordata (24%). Proporsi serupa dihasilkan dari pendekatan algoritma *Operational Taxonomic Unit* (OTU), dengan Arthropoda sebesar 76% dan Chordata sebesar 16%. Salah satu sekuens eDNA berhasil diverifikasi melalui DNA *barcoding* dari spesimen hasil koleksi lapangan dan berpotensi sebagai spesies baru dari kelompok amphipoda. Hasil ini menunjukkan bahwa metode eDNA efektif sebagai alat awal pemantauan biodiversitas di ekosistem akuatik bawah tanah, namun tetap memerlukan verifikasi lanjutan melalui metode konvensional untuk identifikasi spesies secara akurat.

Kata kunci: Gua Laulawi, *environmental* DNA, akuifer, *metabarcoding*

**FAUNA DIVERSITY EXPLORATION OF LAULAWI CAVE, MUNA ISLAND,
SOUTHEAST SULAWESI USING ENVIRONMENTAL DNA APPROACH**

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ABSTRACT

Laulawi Cave, located in Central Buton Regency, Muna Island, Southeast Sulawesi, contains a submerged aquifer that serves as a unique and understudied subterranean habitat. This study aimed to conduct a preliminary diversity assessment of the aquifer using environmental DNA (eDNA) approach. Water samples were collected from five sites with volume approximately 1.5 liters per sample. The samples were filtered using membrane filters, followed by DNA extraction, amplification, and sequencing. Metabarcoding analysis was performed using the DADA2 pipeline on the Galaxy platform and Geneious Prime, with taxonomic assignments against the MIDORI Reference Database 2. Of the five samples, one successfully yielded sequencing data. Taxonomic composition was visualized using a Krona chart. Based on the Amplicon Sequence Variant (ASV) algorithm, the most abundant phylum was Arthropoda (76%), followed by Chordata (24%). Similar proportions were obtained using the Operational Taxonomic Unit (OTU) approach, Arthropoda for 76% reads and Chordata for 16% reads. One eDNA sequence was verified through DNA barcoding of a collected specimen and potential identified as a new amphipod species. The results demonstrate the utility of eDNA as a non-invasive, preliminary tool for biodiversity monitoring in subterranean aquatic ecosystems, while emphasizing the need for complementary conventional methods for species verification.

Key word: Laulawi Cave, environmental DNA, aquifer, metabarcoding