

Original Article

Integrating underwater photo transects and environmental DNA to assess coral genus composition in nearshore reefs of Madura, Indonesia

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Abstract: Understanding coral community composition is essential for reef conservation, particularly in data-limited tropical regions such as Indonesia. This study compares genus-level coral detections from Underwater Photo Transect surveys and environmental DNA metabarcoding on nearshore reefs of Gili Genting and Gili Labak, Madura, Indonesia. Because the molecular component was a preliminary site-level survey using limited water volume and a descriptive presence-absence interpretation, we treat its results as exploratory signals rather than definitive evidence of local occurrence. The photographic survey recorded visually dominant reef-building genera, including *Acropora*, *Montipora*, *Pocillopora*, and *Porites*, whereas environmental DNA detected fewer genera and only partly overlapped with the visual records. Several genera were detected only by environmental DNA, including *Siderastrea*, *Madrepora*, and *Leptoria*, but these records should be interpreted cautiously because they may reflect low DNA concentration, primer bias, hydrodynamic transport, contamination, or taxonomic misassignment. The results indicate that photographic transects provided stronger information on visible coral cover and dominant community structure, while environmental DNA offered a supplementary, though currently limited, signal of potential additional coral taxa. Integrating visual surveys and molecular screening may improve coral monitoring when supported by replicated water sampling, full read-count reporting, curated reference databases, and rigorous contamination controls.

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Introduction

Coral reefs are among the most biodiverse marine ecosystems on Earth and provide essential ecological services, including shoreline protection, fisheries support, and tourism. Indonesia, located within the Coral Triangle, hosts globally significant reef biodiversity; however, effective monitoring remains challenging due to spatial complexity and limited long-term datasets (Alamsyah et al., 2024). Reliable biodiversity assessment methods are therefore critical for supporting adaptive reef management in rapidly changing coastal environments.

Conventional benthic survey techniques, including the Underwater Photo Transect (UPT) method, remain widely used to estimate live coral cover and describe community composition at fine spatial scales. UPT provides a permanent photographic record that can be

rechecked after fieldwork and supports standardized benthic cover assessment, but it still depends on image quality, taxonomic expertise, and colony visibility in photographed quadrats. These limitations have encouraged complementary monitoring approaches (Obura et al., 2019; Cahyani et al., 2024).

Environmental DNA (eDNA) metabarcoding has recently emerged as a useful tool for detecting marine organisms through genetic material released into the surrounding seawater. This approach enables biodiversity detection beyond direct visual observation and has demonstrated strong potential for monitoring reef ecosystems across tropical regions (Shen et al., 2024; Muenzel et al., 2024). Studies in Indonesian waters increasingly show that integrating molecular and visual surveys improves biodiversity detection and conservation-relevant ecological

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interpretation (Facon et al., 2016; Al Malik et al., 2025).

Despite the growing adoption of eDNA methods, comparative evaluations that integrate conventional transect surveys and molecular detection remain limited for nearshore reef systems in the Java Sea. In particular, it remains unclear whether molecular approaches modify ecological interpretations of coral community structure derived from traditional monitoring methods.

This study, therefore, compares coral genus composition at Gili Genting and Gili Labak using UPT and eDNA approaches. Specifically, we aim to (i) quantify overlap and divergence between visual and molecular genus detections and (ii) assess whether site-level biodiversity patterns identified through visual transect surveys are supported by exploratory molecular evidence. Integrating these approaches provides a cautious baseline for reef monitoring and conservation planning in Madura's coastal ecosystems.

Materials and Methods

Study area: Field surveys were conducted at two coral reef systems located southeast of Madura Island, East Java, Indonesia: Gili Genting (7°11'45" S; 113°50'30" E) and Gili Labak (7°13'50" S; 114°03'10" E) (Fig. 1). Both islands are characterized by fringing reef formations influenced by seasonal monsoonal circulation and moderate anthropogenic pressures, including artisanal fisheries and tourism activities. Sea surface temperature ranged between 27-30°C, salinity between 33-35 ppt, and reefs exhibited previously reported live coral cover exceeding 60%.

Survey design: Sampling was conducted during the dry season (July-August 2024) to minimize variability associated with turbidity and sea-state conditions. Coral genus composition was assessed using two complementary approaches: Underwater Photo Transect (UPT) surveys and environmental DNA (eDNA) metabarcoding. The visual survey documented benthic communities through photographs, while eDNA served as an exploratory molecular screening tool.

Underwater photo transect: Coral cover and genus-level visual records were obtained using the Underwater Photo Transect method (Giyanto et al., 2023). A 50 m transect was placed at each observation area, and underwater photographs were taken vertically along the transect using a 58 × 44 cm frame, following the survey approach described by Alamsyah et al. (2024). Coral colonies visible in the photographs were identified to genus level using standard coral identification guides. To compare with molecular data, the visual records were converted into genus-level presence-absence matrices.

Environmental DNA sampling, filtration, and laboratory workflow: Water sampling was conducted at each reef location to enable an exploratory comparison across contrasting nearshore reef settings. At each location, a 1 L water-column sample was collected and filtered in the field using sterile filtration units with 0.45-micrometer membrane filters (Millipore, USA) to capture extracellular and particle-associated DNA. The filtered membrane was preserved by adding 720 microliters of buffer solution to maintain DNA integrity before extraction (Iturbe-Espinoza et al., 2021). Because the design was intended as a preliminary site-level survey, the dataset does not support estimation of within-site variability. Therefore, inter-site patterns reported in this study are descriptive observations and should guide future replicated sampling designs rather than establish definitive ecological causation.

Environmental DNA was extracted from each filter using the DNeasy PowerWater Kit (Qiagen, Germany) according to the manufacturer's protocol. DNA quantity and purity were checked using a NanoDrop spectrophotometer (Thermo Fisher Scientific, USA), and extracted DNA was stored at -20°C until amplification (Jansson et al., 2024). We assessed DNA integrity by 1% agarose gel electrophoresis and evaluated purity using absorbance ratios at 260 nm and 280 nm (Geller et al., 2013; Ramírez-Amaro et al., 2022).

The mitochondrial cytochrome c oxidase subunit I region was amplified using the jgLCO1490, and jgHCO2198 primer pair, which is commonly used for

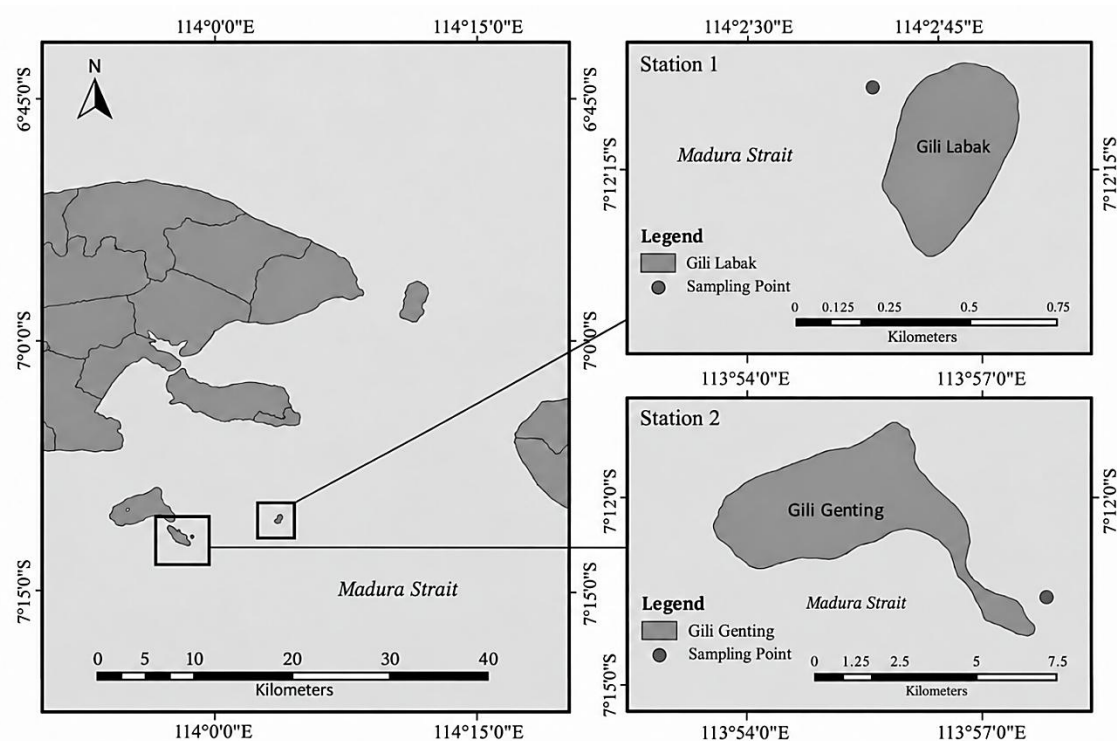


Figure 1. Map of data collection on Gili Labak and Gili Genting, Sumenep, Indonesia.

marine biodiversity metabarcoding (Geller et al., 2013; Xiong et al., 2024). No-template polymerase chain reaction controls were included to monitor reagent contamination, following environmental DNA best-practice recommendations (Hassan et al., 2022; Xiong et al., 2024). Amplicon sequence variants detected in negative controls were treated as potential contaminants and removed before downstream analysis. Polymerase chain reaction products were purified using AMPure XP beads, quantified with a Qubit fluorometer, and sequenced using paired-end Illumina MiSeq technology at Genetika Science Indonesia.

Sequence processing and analytical interpretation:

Sequence processing was conducted in QIIME2 (Bolyen et al., 2019). Primer sequences were removed using Cutadapt before denoising (Martin, 2011). DADA2 was used for quality filtering, trimming, denoising, merging paired-end reads, and removing chimeras (Callahan et al., 2016). Taxonomic assignment was performed using BLAST searches against NCBI reference sequences. However, because public databases can contain contamination, incomplete records, and misannotated entries,

molecular detections were not interpreted as independently validated taxonomic identities (Steinberger and Salzberg, 2020). Because of the exploratory design, limited site-level replication, and the absence of an inferential sampling structure, we did not subject the results to inferential statistical testing.

Data analysis: Genera detected by each method were compiled into presence-absence matrices. Comparative analyses included genus richness, shared versus unique detections visualized using Venn diagrams, and similarity assessment using the Jaccard index. Because the eDNA dataset was collected as a preliminary site-level survey and read-count information was not used for quantitative ecological inference, all comparisons were descriptive, and no inferential statistical tests were performed.

Results

Composition and detection of coral genera: A total of 14 coral genera were recorded across both study sites using the combined UPT and eDNA approaches (Table 1). The UPT survey detected eight genera in Gili Genting and ten in Gili Labak, whereas eDNA

Table 1. Coral genera detected in Gili Genting and Gili Labak using UPT and eDNA methods.

Genus	Gili Genting (UPT)	Gili Labak (UPT)	Gili Genting (eDNA)	Gili Labak (eDNA)
<i>Pavona</i>	-	✓	-	✓
<i>Pachyseris</i>	-	✓	-	-
<i>Pocillopora</i>	✓	✓	-	-
<i>Acropora</i>	✓	✓	-	-
<i>Montipora</i>	✓	✓	-	-
<i>Porites</i>	✓	✓	✓	✓
<i>Stylophora</i>	✓	✓	-	-
<i>Favia</i>	✓	✓	-	-
<i>Oxypora</i>	-	✓	-	-
<i>Fungia</i>	✓	✓	-	-
<i>Seriatopora</i>	✓	-	✓	-
<i>Siderastrea</i>	-	-	✓	✓
<i>Madrepora</i>	-	-	✓	✓
<i>Leptoria</i>	-	-	-	✓

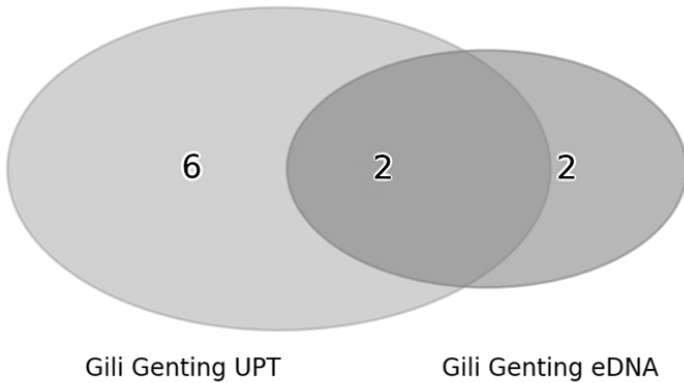


Figure 2. Genera overlap in Gili Genting (UPT versus eDNA).

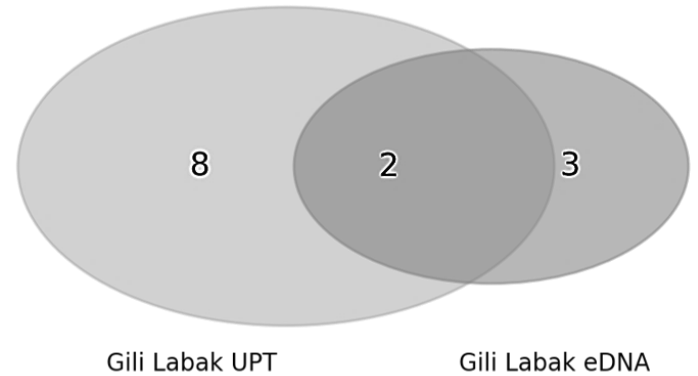


Figure 3. Genera overlap in Gili Labak (UPT versus eDNA).

analysis identified four in Gili Genting and five in Gili Labak. Reef-building genera such as *Acropora*, *Montipora*, *Pocillopora*, and *Porites* were consistently recorded through UPT at both locations. Among all detected taxa, *Porites* was the only genus recorded by both methods at both sites.

Several genera, including *Siderastrea*, *Madrepora*, and *Leptoria*, were detected exclusively through eDNA analysis, while others such as *Favia*, *Stylophora*, and *Oxypora* were identified only through UPT observations. Gili Labak exhibited higher overall genus richness than Gili Genting across both sampling approaches.

Methodological overlap between UPT and eDNA:

A comparison of detection methods revealed low overlap in coral genus identification. In Gili Genting, two genera (*Porites* and *Seriatopora*) were detected

by both approaches, with six genera detected only by UPT and two detected only by eDNA (Fig. 2). In Gili Labak, two genera were shared, eight were detected only by UPT, and three were detected only by eDNA (Fig. 3). Based on these presence-absence matrices, the Jaccard similarity was 0.20 for Gili Genting and 0.15 for Gili Labak, indicating substantial divergence rather than moderate agreement between visual and molecular datasets.

Site-level biodiversity patterns: The genus richness was consistently higher at Gili Labak than at Gili Genting. UPT surveys recorded 10 genera in Gili Labak and 8 in Gili Genting, whereas eDNA detected 5 and 4 genera, respectively. This site-level pattern suggests that both methods identified relatively greater genus richness at Gili Labak. However, because eDNA missed several major UPT-recorded

genera and produced several eDNA-only detections, use the eDNA results only as supporting qualitative evidence for this pattern.

Discussions

Complementarity between visual and molecular detection: The present study shows that UPT and eDNA generated markedly different genus-level inventories. UPT detected more genera than eDNA at both sites and recovered the visually dominant reef-building taxa that structure the local reef community (McGeady et al., 2023). This is expected because UPT directly documents benthic organisms visible within photographed transect frames and is therefore better suited for describing coral cover and dominant community structure.

In contrast, eDNA detected only a subset of visually recorded genera and produced several eDNA-only detections. This pattern should not be interpreted simply as evidence that eDNA detected hidden diversity (Cahyani et al., 2024). The failure to detect several major UPT-recorded genera suggests possible false negatives caused by limited 1 L sampling volume, low coral DNA concentration, primer mismatch, stochastic amplification, hydrodynamic dilution, or incomplete capture of spatial heterogeneity (Collins et al., 2019).

The eDNA-only records of *Siderastrea*, *Madrepora* and *Leptoria* should therefore be treated as provisional molecular signals. They may reflect true local occurrence of rare, juvenile, or cryptic colonies, but they may also arise from transported DNA, low-level contamination, index hopping, or taxonomic misassignment against incomplete or incorrectly annotated public reference sequences.

Ecological differences between Gili Genting and Gili Labak: Higher coral genus richness recorded in Gili Labak suggests more favorable environmental conditions supporting reef development. Field observations indicating clearer water and reduced sediment influence may promote larval settlement, coral growth, and long-term colony persistence (Hughes et al., 2017). Similar environmental filtering processes have been reported in reef systems

characterized by stronger water circulation and lower anthropogenic disturbance.

The consistent occurrence of framework-building genera across both islands indicates relatively stable reef structure; however, the additional genera detected in Gili Labak imply greater habitat heterogeneity. This site-level pattern is supported by UPT and eDNA richness values, although the low overlap between methods means that eDNA should be interpreted as supportive rather than confirmatory evidence.

Implications for coral reef monitoring: Integration of UPT and eDNA can provide a useful monitoring framework only when the strengths and limitations of each method are clearly separated. UPT remains essential for estimating benthic cover, documenting visible colony structure and providing spatially explicit photographic evidence (Caldwell et al., 2016; Cahyani et al., 2024). eDNA may complement UPT by screening for molecular traces of rare, cryptic, or early-stage taxa, but its detections require careful validation when based on limited water volume and public reference databases (Alexander et al., 2020; Skelton et al., 2023; Steinegger and Salzberg, 2020).

For future monitoring in Madura reefs, eDNA protocols should include larger or replicated water volumes, field and extraction blanks, positive controls, full primer and polymerase chain reaction reporting, sample-specific sequencing-depth summaries, per-genus read counts, and locally curated coral reference libraries. These improvements are necessary before eDNA results can be compared quantitatively with UPT observations or used to infer ecological abundance.

Conclusion

This study provides a cautious comparison of Underwater Photo Transect surveys and eDNA metabarcoding for coral genus detection in nearshore reefs of Madura. UPT recorded more genera and provided a stronger basis for interpreting visible reef community structure, whereas eDNA produced a smaller and partly divergent set of molecular detections. Some eDNA-only records may indicate additional coral taxa, but they should be interpreted as

provisional because they may also reflect low DNA concentration, contamination, transported DNA, or taxonomic misassignment. The combined approach remains promising for coral reef monitoring, but future applications should use replicated sampling, complete sequence-read reporting, and curated reference databases to strengthen reliability and reproducibility.

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