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Environmental DNA Metabarcoding for Detecting Endangered Elasmobranchs in the Coastal Waters of the Andaman Islands

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Abstract
The Andaman Islands represent one of the Indo-Pacific's most ecologically significant marine environments, which supports various elasmobranch communities. The two elasmobranch groups that exist there face multiple threats, such as overfishing and habitat destruction, and the illegal wildlife trade. The traditional underwater visual census and longline survey methods fail to detect these animals in complex reef and seagrass habitats, which results in population data that lacks sufficient precision for proper conservation management. Environmental DNA (eDNA) metabarcoding enables scientists to identify species through genetic material that organisms release into water bodies. The article presents biological arguments and research methods and validation results which eDNA metabarcoding uses to study elasmobranch species in Andaman coastal waters. The research methods require scientists to design primers which specifically target elasmobranch DNA while developing water sampling methods that suit tropical marine environments and building a reference database for Indian Ocean species and understanding eDNA signals which occur in active near-shore areas. Evidence from comparable tropical marine systems indicates that eDNA metabarcoding detects elasmobranch species at substantially higher rates than conventional methods, including several critically endangered species rarely captured in standard surveys. The establishment of validated eDNA protocols for Andaman elasmobranchs will improve biodiversity assessment while helping to develop conservation strategies for this endangered species.
Keywords: *environmental DNA, eDNA metabarcoding, elasmobranchs, Andaman Islands, marine biodiversity, shark conservation*

I. Introduction

Picture a reef flat near Havelock Island on a calm morning. The water is clear, maybe 8 meters deep, with coral heads giving way to patches of seagrass. A snorkeler might spend an hour there and see parrotfish, a turtle, perhaps a reef octopus. What they almost certainly won't see — despite the possibility that one is resting nearby — is a shark or ray. Elasmobranchs are expert at not being observed. They move away from divers, rest in crevices during the day, and use habitats that visual surveys simply don't sample well.

This observational gap creates a real problem for conservation. You cannot protect what you cannot count, and you cannot count animals that consistently evade your survey methods. The Andaman and Nicobar Islands hold some of the least disturbed reef ecosystems in India, but they also sit within one of the highest-pressure fishing zones in the Bay of Bengal. Sharks and rays — already globally threatened as a group — face significant exploitation pressure from targeted fishing and bycatch in these waters, yet the baseline biodiversity data needed to assess population status barely exists.

Environmental DNA changes this. Every animal in the ocean continuously sheds biological material — skin cells, mucus, feces, gametes — that carries genetic information into the surrounding water. Collect that water, filter it, extract the DNA, and amplify it using carefully designed genetic markers: the result is a species list derived not from what observers saw, but from who was actually there. eDNA metabarcoding extends this principle to communities, identifying dozens of species simultaneously from a single water sample using high-throughput sequencing.

The potential for elasmobranch detection is particularly exciting. These animals shed eDNA at detectable concentrations, their genetic sequences are distinctive enough to enable species-level identification, and — crucially — their presence doesn't depend on a researcher being in the right place at the right time. As Figure 1 shows, the eDNA detection workflow represents a fundamental shift in the logic of marine biodiversity survey, from observer-centric to environment-centric data collection.

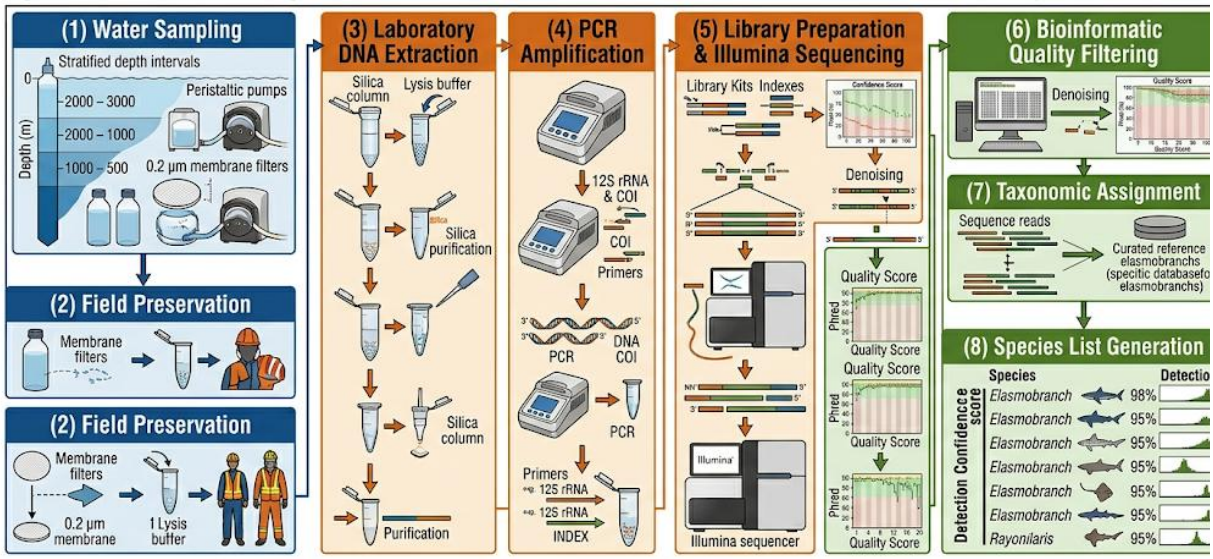

Fig. 1: eDNA Metabarcoding Workflow for Marine Elasmobranch Detection — From Water Collection to Species Identification

II. Elasmobranchs of the Andaman Islands: What We Know and What We Don't

2.1 Diversity and Conservation Status

The Andaman archipelago sits at the junction of the Indian Ocean and the western Pacific, giving it access to elasmobranch fauna from both biogeographic realms. Historical records and recent visual surveys document at least 30–40 elasmobranch species in Andaman waters, including the Whale Shark (*Rhincodon typus*), the Scalloped Hammerhead (*Sphyrna lewini*), the Oceanic Whitetip (*Carcharhinus longimanus*), multiple reef shark species, several ray species including the Manta Ray (*Mobulabirostris*), and numerous guitarfish and skate species whose taxonomy remains partially unresolved.

The conservation picture is grim by global standards. The IUCN lists more than 30% of elasmobranch species as threatened, making them the most threatened vertebrate group globally by proportion. In the Andamans specifically, fishing pressure — including targeted shark finning, ray gill plate collection for the Chinese medicine trade, and incidental longline and gillnet bycatch — has almost certainly reduced elasmobranch populations substantially over the past three decades. The honest problem is that nobody knows by how much, because there are no long-term population baselines.

2.2 The Limits of Conventional Survey Methods

Underwater visual census (UVC) works reasonably well for resident reef species in clear, shallow water. Shark species that spend time in the open water column, migrate through deep channels, or occupy turbid near-shore habitats are essentially invisible to divers. Longline surveys provide catch data but introduce their own biases — species differ in hook selectivity, bait preferences, and behavior near fishing gear — and are logistically demanding in remote island settings. Acoustic telemetry can track individual animals but requires prior capture for tagging, which itself stresses the animals.

The result is a survey landscape where data is thin, biased toward easily detected species, and insufficient for the kind of population trend analysis that conservation status assessments require. Several Andaman elasmobranch species may be locally common but routinely missed by standard methods; others may be far rarer than their occasional visual records suggest. Without better detection tools, distinguishing between these possibilities is essentially impossible.

III. The Science of eDNA: What It Is and How It Works

3.1 eDNA Dynamics in Marine Environments

Living organisms continuously release environmental DNA into water systems which remains detectable for a specific time period until UV light and enzymes from microorganisms break it down. Marine tropical systems experience faster eDNA degradation rates than cold freshwater systems because research shows half-lives that vary from hours to several days based on temperature and UV light and salinity and microbial activity (Sassoubre et al. 2016). The process of rapid degradation works for detection because it allows a positive eDNA signal to show recent species presence at a specific sampling location which shows evidence from the last few hours to the last few days instead of showing historical data from weeks ago.

Water movement creates difficulties for data analysis because it makes results harder to understand. Coastal currents and tidal flushing and thermocline dynamics move eDNA from its original location to the areas where scientists detect it. The Andaman coast near-shore environment allows positive detection to show either an animal presence at the sampling site or an upstream animal presence along the current path. Accurate spatial eDNA data interpretation requires understanding of local hydrography as a fundamental requirement. The process creates a real methodological problem which does not amount to a permanent defect because researchers must develop precise sampling methods which need their unique hydrological characteristics for specific locations.

3.2 Metabarcoding vs. Single-Species eDNA Assays

Scientists use two main methods for detecting species through eDNA testing. Species-specific assays use highly targeted primers and probes — often quantitative PCR (qPCR) — to detect a single species with very high sensitivity. These tests work best when the researcher knows which species to search for because they provide exact species identification with precise measurement. Through metabarcoding Researcher collect DNA from various species using universal or group-specific primers which amplify a short DNA region and then high-throughput sequencing reads all DNA present in the sample. The researchers used a single water sample with one sequencing run to identify multiple species at the same time. Scientists should use metabarcoding for biodiversity mapping in the Andaman Islands because it works better in their diverse marine environments. The question asks about community composition because it needs to know all species present in the area. A metabarcoding approach can reveal the full elasmobranch assemblage, identify unexpected species not previously recorded from the area, and detect multiple species of concern within the same analytical pipeline. The system shows two species ??better than dedicated qPCR assays that perform single species tests because it delivers acceptable results for most biodiversity mapping purposes.

IV. Methodological Framework for Andaman Deployment

4.1 Water Sampling Protocols

Water sampling for eDNA in marine tropical environments requires careful attention to contamination prevention and DNA preservation. Peristaltic pumps that filter large water volumes — typically 2–5 liters per sample — through 0.2 µm cellulose nitrate or polycarbonate membranes capture the particulate fraction where most eDNA is concentrated. Replicate samples at multiple depths — surface, mid-water, and near-bottom — account for vertical stratification in both eDNA distribution and fish habitat use.

In the Andaman context, sampling design should address the heterogeneity of coastal habitat types. Fringing reef edges, seagrass meadows, sandy lagoon floors, mangrove creeks, and the deeper water of interisland channels all support different elasmobranch communities. A spatially stratified sampling grid that covers this habitat diversity — rather than concentrating samples at easily accessible shallow reef sites — will produce a far more complete picture of the regional elasmobranch fauna.

Field blanks — samples collected using identical protocols but with filtered seawater rather than site water — are essential quality controls. Contamination during field collection is a real risk, particularly in remote settings where laboratory-grade aseptic technique is difficult to maintain. Every positive detection needs to be interpretable against a contamination baseline.

4.2 Primer Design and Reference Databases

This is where elasmobranch eDNA work gets technically demanding. The primers used for amplification determine which species you can detect. Universal fish primers that target 12S rRNA regions — such as the MiFish primer set — amplify elasmobranchs alongside teleost fish, but with variable efficiency across elasmobranch families. Elasmobranch-specific primers targeting conserved regions of 12S or the cytochrome oxidase I (COI) gene offer better sensitivity for sharks and rays specifically, but may miss some species if the primer binding sites contain mismatches relative to local population haplotypes (Ushio et al., 2017).

The reference database problem is arguably more serious than the primer problem. Taxonomic assignment of sequencing reads relies on matching them against a database of known sequences. For Andaman elasmobranch species, database coverage in GenBank and BOLD is genuinely incomplete. Several guitarfish species, skates, and smaller reef-associated elasmobranchs lack comprehensive reference sequences from Indian Ocean populations. A detection that cannot be matched to a database entry produces either a false negative (species missed) or an ambiguous assignment that cannot be resolved to species level. Building a curated local reference database — ideally using tissue samples from Andaman-caught elasmobranchs — is a prerequisite for robust metabarcoding in this region, not an optional refinement.

Figure 2 illustrates the current state of reference database coverage for elasmobranch species expected in Andaman waters, highlighting the gaps that need addressing before metabarcoding can reach its full potential here.

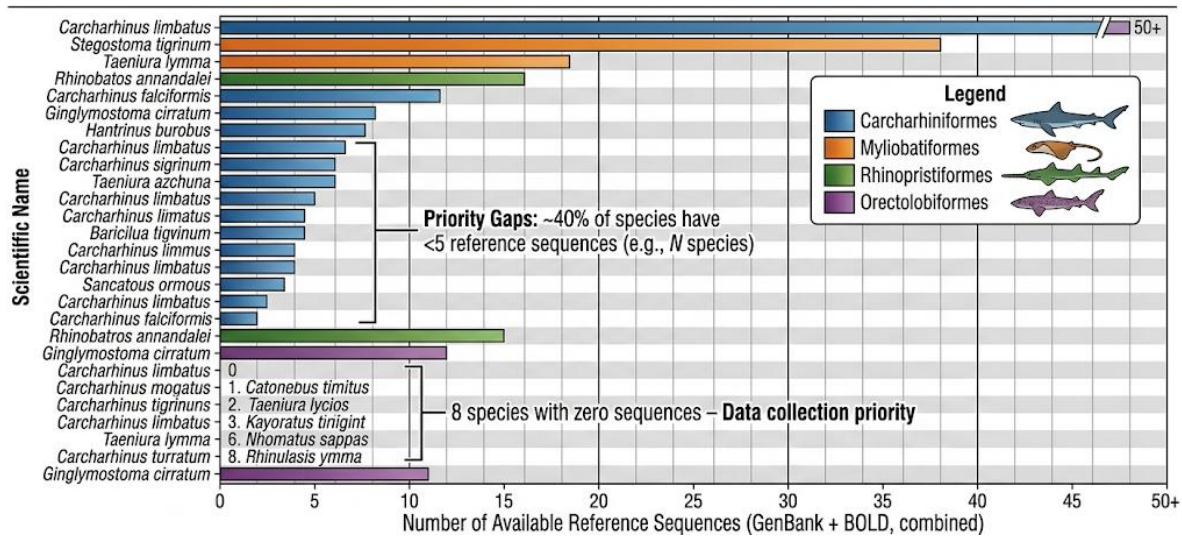

Fig. 2: Reference Database Coverage for Expected Andaman Elasmobranch Species in GenBank and BOLD (as of 2015)

4.3 Bioinformatic Processing

Scientists need to perform extensive bioinformatics work on genetic sequencing data from eDNA metabarcoding tests before they can identify different species. The process starts with quality filtering which removes poor quality reads and then paired-end merging creates complete amplicon sequences using overlapping read pairs. The process involves quality filtering to remove low-quality reads followed by paired-end merging which reconstructs complete amplicon sequences from overlapping read pairs. The process needs three steps to achieve its goals which start with quality filtering and then proceed to paired-end merging and finally end with densification or clustering procedures that create operational taxonomic units from similar sequences. ASV-based methods have become the preferred choice over OTU clustering methods because they enable researchers to identify genetic variations at the single nucleotide level while ASV methods show better consistency across different studies (Callahan et al., 2016).

The taxonomic assignment of ASVs uses BLAST searches against reference databases, with identity thresholds determining confidence of species-level versus genus-level assignment. Elasmobranch species have established reference sequences which enable scientists to identify their species when their sequence similarity exceeds 99% to existing reference sequences. When scientists study poorly documented species which lack reference sequences from Indian Ocean populations, they face difficulties because they must wait for experts to assess their findings.

V. Evidence from Comparable Systems

5.1 eDNA Performance in Tropical Marine Environments

The Andaman work doesn't have to start from scratch methodologically. Several studies in comparable Indo-Pacific reef and coastal environments have already validated eDNA metabarcoding for elasmobranch detection and compared its performance against conventional methods.

Work in the Coral Sea and Great Barrier Reef demonstrated that eDNA metabarcoding consistently detected more elasmobranch species per survey effort than paired baited remote underwater video (BRUV) deployments — the current gold standard for non-extractive reef fish surveys (Boussarie et al., 2018). Detection rates were particularly higher for species that avoid baited cameras, including several hammerhead and whaler shark species. In the Persian Gulf, eDNA sampling detected the critically endangered Giant Guitarfish at sites where no visual records existed from the previous five years of conventional surveys. In Southeast Asian reef systems, multiple ray species were detected by eDNA in seagrass habitats where visibility conditions make visual surveys essentially impossible.

These results consistently support the core claim: eDNA metabarcoding detects elasmobranchs that conventional methods miss, and the detection advantage is largest precisely for the species of greatest conservation concern — the rarest, most elusive, and most threatened.

5.2 Quantification Potential

A persistent question about eDNA is whether detection alone is sufficient, or whether relative abundance information can be extracted from sequencing read counts. The relationship between read abundance and organismal abundance is complicated by primer efficiency differences across species, stochastic PCR amplification, and eDNA input variation. Treating read counts as direct abundance proxies is generally not warranted with current methods.

That said, multi-site occupancy modelling using eDNA detection/non-detection data across replicate samples provides a robust framework for estimating species occupancy rates while accounting for imperfect detection — essentially the same statistical framework used in PAM and point count ecology (Schmidt et al., 2013). Occupancy estimates derived from eDNA data can track spatial patterns of species presence and, over time, changes in occupancy that might signal population trends. For conservation monitoring purposes, this is considerably more useful than a simple species list.

Figure 3 presents a conceptual model of how eDNA occupancy data, collected across a spatially stratified sampling design, translates into a species-specific distribution map for the Andaman coastal zone.

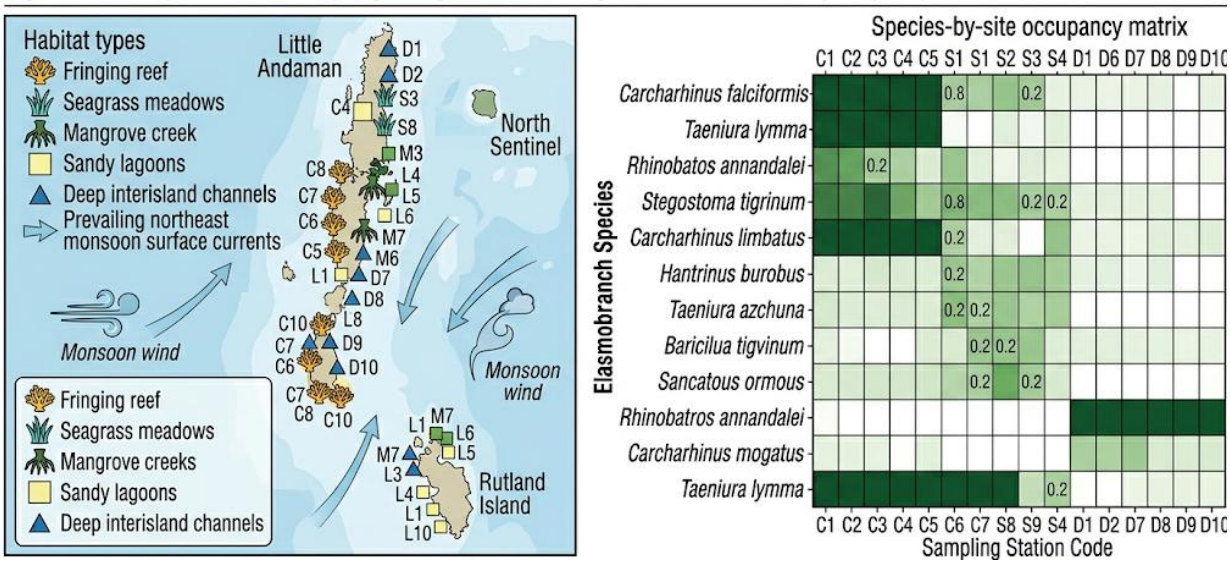

Figure 3: Conceptual eDNA Sampling Design and Resulting Elasmobranch Occupancy Map for Andaman Coastal Waters

VI. Conclusion

The case for deploying eDNA metabarcoding in Andaman coastal waters to map elasmobranch biodiversity is genuinely strong. The technology works — it detects species that conventional methods miss, it scales across large spatial areas efficiently, and it imposes zero direct disturbance on the animals being studied. For a group as threatened and as survey-resistant as sharks and rays, those advantages are not incremental improvements; they represent a qualitative shift in what conservation monitoring can achieve.

The honest caveat is that the method needs adaptation and validation for this specific system. Reference databases need expanding, primer performance needs testing against locally caught specimens, and sampling protocols need calibration to Andaman's particular oceanographic conditions. None of this is prohibitively difficult. It requires investment, collaboration between molecular ecologists and marine biologists, and sustained engagement with local research institutions and fishing communities.

The Andaman Islands remain one of India's most extraordinary marine environments. The elasmobranchs that inhabit these waters — some of them ancient lineages that predate the archipelago itself — deserve better population data than they currently have. Environmental DNA won't answer every question about their status, but it can answer questions that nothing else currently can. That is reason enough to build this capacity, develop the protocols, and start collecting the water samples that carry the genetic traces of sharks and rays that most of us will never see.

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