

Title: DNA Tracking of Small-Scale Fisheries resources for conservation and management in Latin America

Acronym: FISH e-TRACE

1. Summary/Abstract

FISH e-TRACE is an international SCOR Working Group proposal aiming to coordinate, standardize, and synthesize the use of environmental DNA metabarcoding as a cost-efficient, passive tool for monitoring fish diversity and bycatch in small-scale fisheries. The WG addresses a critical methodological gap in fisheries science, the lack of harmonized, field-tested molecular approaches suitable for data-limited artisanal fisheries, where conventional monitoring is often logistically and economically unfeasible.

FISH e-TRACE will focus on the integration of low-cost, open-source 3D-printed Metaprobes directly into artisanal fishing gears, enabling the collection of eDNA during routine fishing operations. Through international coordination, the WG will develop standardized protocols for Metaprobe design, deployment, biosecurity, and sample preservation, and will harmonize molecular markers, bioinformatic pipelines, and reference library curation for fish and associated bycatch taxa. Also, the Working Group will synthesize regionally coordinated pilot applications in the Latin American Eastern Pacific to generate comparable eDNA-based baselines of fish diversity and bycatch indicators and will intercalibrate these results against conventional fisheries data to assess performance, uncertainty, and management relevance. All outputs will follow FAIR data principles and be released as open-access products.

Led by INVEMAR and comprising experts from molecular ecology, fisheries science, bioinformatics, and participatory monitoring, FISH e-TRACE aligns fully with SCOR's mandate by emphasizing methodological harmonization, synthesis, capacity building, and international coordination rather than primary research funding. Although regionally grounded, its standardized framework is globally transferable, contributing to the advancement of eDNA-based fisheries monitoring within international ocean science and conservation agendas.

2. Scientific Background and Rationale

2.1 Data Gaps in Small-Scale Fisheries and the need for innovative monitoring tools

Small-scale fisheries (SSF) sustain millions of livelihoods across the Pacific coasts of Latin America and provide a critical contribution to regional food security, cultural identity, and coastal economies. Despite their importance, SSF remain among the least monitored marine resource systems worldwide. Challenges such as dispersed fleets, heterogeneous fishing gears, informal markets, limited observer coverage, and financial constraints have resulted in persistent data gaps regarding species composition, spatial dynamics, bycatch, and ecosystem impacts. These knowledge gaps hinder adaptive management, undermine compliance with conservation targets, and limit the capacity of fisheries authorities to align practices with ecosystem-based management frameworks.

In the Eastern Pacific (EP), where artisanal fisheries operate across biodiversity hotspots and multi-use seascapes, these limitations are especially acute. Traditional monitoring approaches such as landing

surveys, self-reported catch logs, and onboard observers, are often costly, logistically challenging, and prone to underreporting or taxonomic uncertainty, particularly for non-target species and incidental catches. There is therefore an urgent need for scalable, cost-efficient, and standardized methods that can complement conventional fisheries monitoring while generating robust biodiversity information directly linked to fishing activities.

2.2 Environmental DNA Metabarcoding as a Transformative Approach

Environmental DNA (eDNA) metabarcoding has emerged over the past decade as a powerful molecular approach for detecting and characterizing biodiversity from genetic traces released into the environment through mucus, scales, feces, gametes, and tissue fragments. Applied in marine systems, eDNA metabarcoding enables the simultaneous detection of multiple taxa from a single sample, improves species inventories, detects rare or elusive organisms, and provides community-level signals that are often overlooked by traditional sampling methods.

Numerous studies have demonstrated the ability of eDNA metabarcoding to recover a high proportion of locally occurring fish species, often exceeding the detection rates of visual censuses, trawl surveys, or landing-based assessments. When coupled with fish-specific (e.g., 12S rRNA) and broad metazoan (e.g., COI) markers, eDNA metabarcoding can capture assemblage structure, trophic diversity, and indicators of ecosystem change. Importantly, eDNA-based approaches are non-invasive, replicable, and increasingly affordable, making them particularly well-suited for data-limited fisheries contexts.

However, the application of eDNA metabarcoding in fisheries monitoring remains uneven, particularly in small-scale fisheries in the Global South. Critical challenges persist, including PCR and primer biases, variable detectability among taxa, incomplete reference libraries, and uncertainties in linking sequence read abundance to biomass or catch volume. These limitations underscore the need for coordinated efforts to standardize protocols, intercalibrate methods, and synthesize best practices, precisely the type of challenge that a Scientific Committee on Oceanic Research (SCOR) Working Group is designed to address.

2.3 Passive eDNA sampling and the emergence of Fishing-Based Metaprobes

Most marine eDNA studies rely on water samples collected from bottles, pumps, or autonomous samplers, which may be spatially or temporally decoupled from fishing operations. In response, recent methodological advances have explored passive eDNA sampling, in which genetic material is accumulated over time onto substrates exposed to moving water. Among these, 3D-printed Metaprobes (perforated spheres containing sterile gauze or membrane filters) have demonstrated a good potential.

Metaprobes are low-cost, reusable, and easily customizable passive samplers that can be integrated directly into fishing gear, allowing them to capture the “water of the net” during active fishing operations. Field trials in trawl fisheries, opportunistic diving surveys, and mobile sampling platforms have shown that Metaprobes deployed in this way can recover over 90% of taxa present in catches, accurately reconstruct demersal assemblage composition, and provide an additional “biodiversity bonus” by detecting species present in the surrounding environment but not retained by the gear.

This approach is highly relevant for small-scale fisheries, where vessels and gear move through ecologically meaningful gradients and interact directly with fish assemblages. By embedding Metaprobes into artisanal nets (e.g., gillnets, trammel nets) or incorporating inline collectors into longlines, it becomes possible to

generate eDNA samples that are inherently linked to fishing effort, gear type, habitat, and location, without requiring additional sampling equipment or specialized personnel and without over complicating the effort for the integration of local communities.

2.4 eDNA-Based assessment of bycatch and community-level impacts

Bycatch remains one of the most critical yet poorly quantified impacts of small-scale fisheries, particularly for vulnerable, protected, or low-value species that are rarely reported. Traditional bycatch assessments rely on observer programs or self-reporting, both of which are often infeasible in artisanal fleets. eDNA metabarcoding offers a complementary pathway to characterize bycatch composition, including cryptic, discarded, or damaged organisms, and to identify interactions with species of conservation concern.

Recent studies suggest that, under controlled conditions, relative eDNA signal strength can correlate with relative biomass or catch fractions, particularly when marker choice, sampling design, and allometric relationships (organism size DNA shedding rates) are considered. While eDNA is not yet a direct substitute for quantitative stock assessment, it provides a powerful tool for comparative analyses across gears, habitats, and management regimes, offering objective indicators of bycatch risk and ecosystem interaction.

In the context of the EP, where artisanal fisheries operate across coral reefs, mangroves, soft-bottom habitats, and offshore seascapes, eDNA-based bycatch monitoring could significantly improve the resolution of impact assessments and support adaptive management strategies aimed at reducing incidental capture of vulnerable species.

2.5 Rationale for a SCOR Working Group: From innovation to standardization

Despite rapid methodological innovation, the use of eDNA Metaprobes in fisheries remains fragmented, with limited protocol harmonization, inconsistent marker selection, and regionally uneven reference databases. Without standardization and intercalibration, results remain difficult to compare across studies, countries, or fisheries, limiting their uptake by management authorities.

The proposed SCOR Working Group “FISH e-TRACE: DNA Tracking of Small-Scale Fisheries Resources for Conservation and Management in Latin America” addresses this gap by focusing explicitly on coordination, synthesis, and standardization, not on funding new research per se. The WG will bring together international experts in molecular ecology, fisheries science, bioinformatics, and participatory monitoring to develop a coherent methodological package for eDNA-based tracing of fish diversity and bycatch in small-scale fisheries.

Consistent with SCOR requirements, FISH e-TRACE targets a well-defined scientific bottleneck: the lack of standardized, field-tested protocols for applying passive eDNA approaches in artisanal fisheries. Over a 4-year timeframe, the WG will deliver best-practice manuals, validated marker and bioinformatics pipelines, intercalibration analyses with traditional fisheries data, and openly available reference libraries tailored to the EP.

2.6 Regional Leadership with Global Relevance

Led by the Instituto de Investigaciones Marinas y Costeras (INVEMAR), the WG will leverage strong regional networks and a proven track record in biodiversity assessment, molecular monitoring, and science–

policy interfacing. Pilot activities in the EP will serve as a testbed for methods that are broadly transferable to other tropical and subtropical regions where small-scale fisheries dominate.

By embedding cutting-edge molecular tools into real-world fishing practices and co-developing protocols with fishing communities and managers, FISH e-TRACE advances both scientific innovation and ethical, inclusive research practices. Importantly, the regional focus does not limit its global relevance: the standardized workflows, open-source Metaprobes designs, and reference curation frameworks developed through the WG will contribute directly to international efforts to harmonize eDNA-based monitoring.

2.7 Expected scientific and management impact

The FISH e-TRACE Working Group will deliver a robust methodological foundation for using eDNA Metaprobes as a cost-efficient, passive monitoring tool in small-scale fisheries. Scientifically, it will reduce uncertainty related to detection biases, marker performance, and bycatch quantification, while improving comparability across studies and regions. From a management perspective, it will provide actionable genetic evidence to inform ecosystem-based fisheries management, bycatch mitigation strategies, and biodiversity conservation planning.

3. Terms of Reference (max. 250 words)

This Working Group will coordinate, standardize, and synthesize methodological approaches for the application of environmental DNA (eDNA) metabarcoding as a cost-efficient, passive tool to track fish diversity and bycatch in small-scale fisheries, with an initial regional focus on the Eastern Pacific (EP) including the participation of Mexico, Costa Rica, Panamá, Colombia, Ecuador, Peru, Chile and Argentina's institutions.

ToR 1 – Standardization of passive eDNA sampling using metaprobes: Develop standardized, field-tested protocols for the design, 3D printing, installation, and operation of low-cost Metaprobes integrated into artisanal fishing gears including guidance on materials, fixation methods, biosecurity, and sample preservation.

ToR 2 – Harmonization of molecular markers and bioinformatics workflows: Define minimum, interoperable molecular and bioinformatic pipelines for fish and associated bycatch detection, prioritizing 12S rRNA (teleosts) and COI (metazoans), including quality control, replication, mock communities, and criteria for curating regional reference libraries for the EP.

ToR 3 – Regional pilot synthesis and baseline generation: Coordinate pilot implementations with small-scale fishing communities to generate harmonized eDNA-based baselines of fish diversity and bycatch indicators, following FAIR data principles and standardized metadata frameworks.

ToR 4 – Intercalibration with conventional fisheries data: Synthesize and intercalibrate eDNA outputs against traditional monitoring approaches (catch records and participatory observations) to evaluate sensitivity, robustness, and uncertainty across gears and habitats.

ToR 5 – Capacity building and knowledge transfer: Deliver training activities, open-access manuals, and

technical guidance to support uptake by researchers, managers, and fishing communities, consolidating a regional FISH e-TRACE network.

4. Deliverables

In direct alignment with its ToR, FISH e-TRACE Working Group will generate a coherent and policy-relevant set of scientific, technical, and capacity-building deliverables that advance the standardized use of eDNA metabarcoding as a passive monitoring tool for Small-Scale Fisheries in Latin America.

First, addressing ToR 1, the WG will produce a Best Practices Manual, an open-access, bilingual technical document detailing standardized protocols for the design, 3D printing, installation, and operation of low-cost Metaprobes integrated into artisanal fishing gears. The manual will include annexes on biosecurity, QA/QC, ethical considerations, and sample preservation logistics.

Second, in support of ToR 2, the WG will deliver a Methodological Guide for eDNA Metabarcoding in Small-Scale Fisheries, defining minimum harmonized molecular markers, bioinformatic pipelines, detection thresholds, and procedures for curating and validating regional reference libraries for the Eastern Pacific.

Third, responding to ToR 3, the WG will coordinate the synthesis of regional eDNA-based baselines of fish diversity and bycatch indicators, released as FAIR datasets with standardized metadata (e.g. OBIS Darwin Core) and accompanied by a regional technical report.

Fourth, aligned with ToR 4, the WG will publish a peer-reviewed synthesis article in an open-access journal presenting intercalibration results between eDNA outputs and conventional fisheries data, including an assessment of uncertainty and gear-specific performance.

Finally, fulfilling ToR 5, the WG will produce a capacity-building package (training modules, outreach materials, and workshop reports) through OTGA platforms and formalize the FISH e-TRACE Latin American network, ensuring long-term uptake and transfer of standardized practices beyond the WG's duration.

5. Working plan

The FISH e-TRACE: DNA Tracking of Small-Scale Fisheries Resources for Conservation and Management in Latin America Working Group (WG) will be implemented over a four-year period, following a phased and coordinated work plan designed to deliver standardized methodologies, synthesis products, and capacity-building outcomes aligned with its Terms of Reference (ToRs). The work plan emphasizes coordination, intercalibration, and methodological harmonization.

Phase 1 (Year 1 – 2026-2027): WG Establishment and methodological harmonization

The first year will focus on establishing the WG, refining scope, and producing standardized methodological foundations addressing ToR 1 and ToR 2.

The WG will be formally constituted with 10 full members and up to 10 associate members, ensuring balanced representation across geography (Latin America and international partners), disciplines (molecular ecology, fisheries science, bioinformatics, participatory monitoring), career stages, and gender. INVEMAR will lead coordination and serve as the institutional anchor, facilitating communication, document management, and engagement with regional partners.

An initial comprehensive state-of-the-art review will be conducted, synthesizing existing applications of passive eDNA sampling, Metaprobe designs, fishing-based eDNA collection, and eDNA metabarcoding in fisheries contexts. Particular attention will be paid to artisanal and data-limited fisheries in the EP.

Drawing on this synthesis, the WG will agree on standard Metaprobe designs, materials, and operational specifications suitable for integration into artisanal fishing gears (e.g., gillnets, trammel nets, longlines). Open-source 3D-printable designs will be selected and documented, with guidance on attachment, deployment duration, biosecurity, contamination prevention, and sample preservation.

In parallel, the WG will harmonize minimum molecular and bioinformatics requirements, defining recommended markers (12S rRNA for fishes; COI for associated metazoans), sequencing strategies, laboratory quality controls, and bioinformatics pipelines. Criteria for reference library curation, including voucher requirements, geographic relevance, and quality thresholds, will be defined with an initial focus on the Tropical Eastern Pacific.

Outputs from Phase 1 will include draft versions of the Best Practices Manual for Metaprobes and the Methodological Guide for eDNA Metabarcoding, as well as a finalized data and metadata framework aligned with FAIR principles. The first WG meeting (hybrid) will be held during this phase to consolidate agreements and plan subsequent activities.

Phase 2 (Year 2 – 2027-2028): Pilot Coordination and Reference Library Curation

Year 2 will address ToR 3 by coordinating and synthesizing pilot applications of the standardized FISH e-TRACE framework across selected sites across the 8 participant countries in the Eastern Pacific.

Rather than conducting new funded research, the WG will coordinate existing and in-kind pilot activities implemented by member institutions and partner communities. These pilots will apply the harmonized Metaprobe protocols across representative artisanal fishing gears and habitats, generating comparable datasets for synthesis.

The WG will provide ongoing technical guidance to ensure consistent application of protocols, metadata standards, and quality assurance procedures. Emphasis will be placed on co-design and collaboration with fishing communities, ensuring that sampling integrates naturally into fishing operations and that local knowledge informs interpretation.

Concurrently, the WG will coordinate the construction and curation of a regional reference library for fishes and associated bycatch taxa, prioritizing the Eastern Pacific. Existing sequence repositories will be reviewed, gaps identified, and quality-controlled reference sequences curated and documented. The WG will define transparent criteria for inclusion and versioning of reference libraries.

A regional capacity-building workshop will be organized during this phase, targeting early-career

researchers, fisheries practitioners, and community representatives. Training will focus on Metaprobe deployment, eDNA concepts, data interpretation, and ethical considerations.

Outputs from Phase 2 will include a harmonized, multi-site regional eDNA dataset, a curated reference library resource, and a mid-term technical report summarizing pilot implementation and data readiness.

Phase 3 (Year 3 – 2028-2029): Intercalibration, Synthesis, and Evaluation of Uncertainty

The third year will focus on ToR 4, emphasizing synthesis, intercalibration, and assessment of robustness across methods, gears, and contexts.

The WG will conduct coordinated analyses comparing eDNA-based outputs with conventional fisheries data sources, including catch records, landing surveys, and participatory observations, where available. The objective is not to validate eDNA as a replacement tool, but to evaluate sensitivity, complementarity, and limitations, including uncertainties linked to detection, taxonomic resolution, and relative abundance.

Comparative analyses will assess performance across fishing gears, habitats, and sampling conditions, identifying strengths, caveats, and appropriate use cases for management applications. Particular attention will be given to bycatch detection and the potential for eDNA signals to serve as indicators of incidental capture of vulnerable species.

These analyses will feed into a peer-reviewed synthesis manuscript, integrating results across countries and contexts, and articulating evidence-based recommendations for applying passive eDNA approaches in small-scale fisheries.

A second WG meeting will be convened to review synthesis outcomes, finalize manuals and guidance documents, and engage fisheries authorities and management agencies to ensure relevance and uptake.

Phase 4 (Year 4 - 2029-2030): Knowledge Transfer, Legacy, and Regional Scaling

The final phase will focus on ToR 5, ensuring long-term legacy, transferability, and regional ownership of the FISH e-TRACE framework.

Final versions of all WG products will be published in open access, including manuals, datasets, reference libraries, and scientific articles. Training materials will be adapted for reuse in national and regional capacity-building programs, and guidance will be tailored for fisheries managers and decision-makers.

The WG will formally consolidate the FISH e-TRACE Latin American network, embedded within existing institutional and scientific collaborations (e.g., INVEMAR-led regional initiatives), ensuring continuity beyond the WG's lifetime.

A final WG meeting will synthesize lessons learned, define a roadmap for scaling the approach to other regions, and outline future coordination needs under SCOR or allied programs.

Overall Coordination and Deliverables

Across all phases, coordination will be supported by regular virtual meetings, transparent documentation,

annual progress reports to SCOR, and continuous evaluation against the WG's ToRs. The work plan ensures that all activities remain within SCOR's mandate, prioritizing synthesis, standardization, and capacity development over primary research, while delivering tangible products with lasting scientific and management impact.

6. Capacity Building

The FISH e-TRACE: DNA Tracking of Small-Scale Fisheries Resources for Conservation and Management in Latin America Working Group (WG) is explicitly designed to generate long-lasting global capacity in the application, interpretation, and governance uptake of environmental DNA (eDNA) metabarcoding as a tool for fisheries science and marine conservation. Capacity building is not treated as an ancillary outcome, but as a central and cross-cutting objective embedded in the WG's structure, activities, and deliverables. Through methodological standardization, open knowledge products, training, network consolidation, and sustained engagement with practitioners and decision-makers, FISH e-TRACE will strengthen both the practical and conceptual foundations of this emerging area of marine science well beyond the lifetime of the Working Group.

6.1 Building Capacity through standardization and methodological clarity

A fundamental barrier to the widespread and durable use of eDNA metabarcoding in fisheries contexts is the absence of harmonized, field-tested standards adapted to real-world operational settings, particularly in small-scale fisheries. FISH e-TRACE addresses this challenge by prioritizing the development of clear, accessible, and transferable methodological standards that reduce technical ambiguity and lower barriers to adoption.

By producing open-access manuals and methodological guides for passive eDNA sampling using metaprobes integrated into artisanal fishing gears, the WG will enable practitioners to adopt these tools without relying on ad hoc expertise or proprietary systems. Standardized guidance on Metaprobe design, 3D printing, installation, biosecurity, and preservation ensures that future users whether researchers, fisheries agencies, or community monitoring programs, can replicate and adapt protocols with confidence. This standardization directly contributes to lasting capacity by transforming eDNA approaches from experimental techniques into reliable, operational methods suitable for long-term deployment.

Crucially, methodological clarity also enhances conceptual understanding. Clearly articulated rationales for marker choice, sampling design, quality control, and uncertainty interpretation will help users understand not only how to apply eDNA metabarcoding, but also what the data mean and how they can (and cannot) be used for management purposes. This dual emphasis on practice and interpretation is essential for sustainable capacity development.

6.2 Strengthening Analytical Capacity through Harmonized Pipelines and Reference Libraries

Long-term capacity in eDNA science depends not only on sample collection, but also on the ability to process, analyze, and interpret sequence data in a transparent and reproducible manner. FISH e-TRACE will build this capacity by defining minimum interoperable molecular and bioinformatic pipelines tailored

to fisheries applications, with specific attention to fish diversity and bycatch detection.

By harmonizing the use of complementary genetic markers (e.g., 12S for fishes and COI for associated metazoans), defining quality assurance criteria, and documenting bioinformatic workflows suitable for laboratories with varying levels of infrastructure, the WG will reduce dependence on highly specialized or centralized facilities. This approach empowers regional laboratories and early-career scientists, particularly in the Global South, to generate and interpret eDNA data locally.

In parallel, the WG's emphasis on curating and maintaining regional reference libraries establishes a durable scientific asset that will remain usable long after the WG concludes. Well-documented, quality-controlled reference sequences anchored in regional biodiversity are essential for accurate species identification and for meaningful comparison across studies and time. By aligning reference library curation with FAIR data principles and open repositories, FISH e-TRACE ensures that these resources remain accessible, updateable, and reusable by future generations of scientists worldwide.

6.3 Integrating Capacity Building into Real-World Fisheries Contexts

A defining feature of FISH e-TRACE is its commitment to embedding capacity building within real fisheries operations rather than isolated laboratory exercises. Passive eDNA sampling using Metaprobes integrated into fishing gears allows molecular monitoring to occur within the daily practices of small-scale fisheries, creating a natural interface between science, resource use, and stewardship.

Through coordinated pilot synthesis with fishing communities, the WG will foster experiential learning and mutual understanding between scientists and practitioners. Fishers and local monitors gain exposure to molecular concepts and the value of genetic biodiversity data, while researchers deepen their understanding of operational constraints, gear dynamics, and local ecological knowledge. This reciprocal learning process builds durable social and institutional capacity, reinforcing trust and long-term collaboration.

Importantly, this approach contributes to capacity to ask and answer management-relevant questions. By linking eDNA signals to fishing gears, effort, habitats, and bycatch risks, the WG helps managers and communities understand how molecular data can inform adaptive management, rather than remaining an abstract or externally imposed technology.

6.4 Capacity Development through Training, Mentorship, and Knowledge Transfer

FISH e-TRACE builds long-lasting capacity through targeted training and mentorship at multiple levels. The WG will organize regional workshops, hands-on courses, and virtual training activities focused on eDNA sampling, data interpretation, and ethical considerations in participatory monitoring. These activities are explicitly designed to reach early-career researchers, fisheries practitioners, and community partners, aligning with SCOR's strong emphasis on capacity development.

Training materials will be modular, bilingual where possible, and openly accessible, allowing them to be reused in academic curricula, professional training programs, and community monitoring initiatives. Rather than one-off events, these materials form a capacity package that can be progressively updated and disseminated through institutional and regional networks.

Mentorship within the WG structure further strengthens long-term capacity. By intentionally including

early-career scientists as full or associate members and pairing them with senior experts in molecular ecology, fisheries science, and bioinformatics, the WG promotes skill transfer, leadership development, and sustained engagement in international scientific networks.

6.5 Building Institutional and Network Capacity for Global Reach

Long-lasting capacity in marine science depends on institutions and networks, not only individuals. FISH e-TRACE will consolidate a regional Latin American network of researchers, institutions, managers, and community organizations working on eDNA-based fisheries monitoring. Anchored by INVEMAR and connected to existing regional and international initiatives, this network provides a structural legacy that extends beyond the WG's formal duration.

By fostering collaboration across countries, disciplines, and sectors, the WG enhances the capacity of institutions to coordinate, share data, and align methodologies. This collective capacity is essential for addressing transboundary marine issues and for scaling standardized approaches to new regions.

Importantly, while the WG has a regional focus, its outputs and networks are explicitly designed to be globally transferable. Open-source Metaprobe designs, harmonized pipelines, and reference frameworks can be adapted to small-scale fisheries in other tropical and subtropical systems, contributing to a global community of practice around eDNA-based fisheries monitoring.

6.6 Enhancing Capacity at the Science–Policy Interface

A critical dimension of durable capacity is the ability to translate scientific knowledge into policy-relevant information. FISH e-TRACE strengthens this capacity by producing synthesis products explicitly tailored to management audiences, including technical notes and guidance documents for fisheries authorities.

By rigorously evaluating the strengths, limitations, and uncertainties of eDNA approaches through intercalibration with conventional monitoring methods, the WG equips policymakers with realistic expectations and scientifically grounded decision support tools. This enhances institutional confidence in molecular methods and builds long-term capacity for evidence-based governance.

INVEMAR's leadership and experience at the science–policy interface further ensures that WG outputs are embedded within existing advisory and management frameworks, reinforcing continuity and uptake.

6.7 Cultural and Ethical Dimensions of Capacity Building

FISH e-TRACE also contributes to long-lasting capacity by promoting ethical, inclusive, and culturally sensitive approaches to marine science. By co-developing monitoring frameworks with fishing communities and clearly addressing data ownership, bioethics, and benefit sharing in its manuals and training, the WG strengthens social legitimacy and long-term stewardship.

This ethical grounding is essential for the sustainability of eDNA-based monitoring, particularly in contexts where external scientific interventions have historically been extractive or mistrusted. Capacity built on trust, transparency, and shared ownership is far more likely to persist.

6.8 Enduring Impact Beyond the Working Group

Taken together, FISH e-TRACE will leave a durable legacy of skills, standards, resources, networks, and understanding that extends well beyond the four-year timeframe of a SCOR Working Group. By transforming eDNA metabarcoding into an accessible and interpretable tool for small-scale fisheries monitoring, the WG consolidates a new area of marine science practice that is inclusive, scalable, and globally relevant.

Through open knowledge products, empowered practitioners, strengthened institutions, and sustained networks, FISH e-TRACE will build long-lasting global capacity to practice, understand, and responsibly apply eDNA-based approaches in support of marine biodiversity conservation and sustainable fisheries management.

7. Working Group composition

The composition of the FISH e-TRACE Working Group has been carefully designed to achieve a balanced, inclusive, and effective team capable of addressing the scientific, methodological, and capacity-building objectives set out in the Terms of Reference. The proposed membership reflects a deliberate balance across career stages (from early-career to senior researchers), geographical representation, disciplinary expertise, and institutional roles, in full alignment with SCOR principles.

Balance Across Career Stages

The Working Group combines early-career researchers (≈ 5 years since degree) with mid-career and senior scientists (8–10+ years since degree). Early-career members bring high technical proficiency in emerging tools such as eDNA metabarcoding, bioinformatics, digital workflows, and FAIR data practices, as well as strong motivation for international collaboration and capacity development. Their involvement ensures innovation, methodological rigor, and long-term continuity of expertise beyond the lifetime of the WG.

Senior and more experienced members contribute strategic oversight, institutional memory, and experience in leading large-scale monitoring programs, synthesis efforts, and science–policy interfaces. This vertical integration across career stages enables effective mentorship, skill transfer, and leadership development, while ensuring that WG outputs meet the expectations of scientific, management, and policy audiences.

Geographic and Regional Balance

The WG has strong representation from Latin America, particularly countries of the Eastern Pacific, where small-scale fisheries play a dominant socio-ecological role. Members from Colombia, Chile, Peru, Panama, Costa Rica, Mexico, and Argentina ensure deep regional knowledge of artisanal fisheries operations, governance contexts, and data limitations. This regional grounding is essential for adapting eDNA-based methods to real operational conditions and ensuring relevance for local management.

At the same time, the inclusion of associate members from Australia, the United States, and Europe provides global perspective, access to cutting-edge methodological developments, and alignment with international observing systems and data infrastructures. This balance ensures that, while regionally focused, the WG's

outputs are globally transferable and internationally credible, consistent with SCOR’s mandate.

Disciplinary Complementarity

The membership spans a complementary set of disciplines, including molecular ecology, fisheries biology, ichthyoplankton and early life-stage ecology, bioinformatics, marine biodiversity monitoring, data management, and fisheries governance. This interdisciplinary composition is essential for addressing the full methodological chain of FISH e-TRACE, from passive eDNA sampling design and molecular analysis to data synthesis, interpretation, and management uptake. In particular, the combination of molecular experts with fisheries scientists and managers ensures that eDNA-based indicators are not developed in isolation but are explicitly intercalibrated with conventional fisheries data and framed in ways that are meaningful for decision-making.

Institutional and Role Balance

The WG includes representatives from research institutes, fisheries agencies, and data infrastructure organizations, enabling effective linkage between science, operations, and policy. Full members primarily drive methodological synthesis, standardization, and scientific outputs, while associate members strengthen links to global observing systems, biodiversity data platforms, and management authorities. This structure maximizes impact without duplicating efforts or exceeding SCOR’s remit.

Full Members

Name	Gender	Years since degree*	Country and institution of affiliation(s)	Expertise relevant to proposal
1 Vanessa Yepes Narváez (Co-Chair)	F	5	Colombia, INVEMAR	Molecular approaches for marine biodiversity assessment
2 Jessica Bonicelli Proaño (Co-Chair)	F	5	Chile, IFOP	Field and analytical experience on early life stages of small pelagic fishes, with focus on the population dynamics and reproductive strategies. implement FAIR data practices.
3 Giovanna Sotil (Co-Chair)	F	8	Peru, IMARPE	Fisheries monitoring, ecosystem-based management, and assessment of small-scale and industrial fisheries
4 Verónica Jurquiza	F		INIDEP, Argentina	Fisheries biology, monitoring programs, and applied research for sustainable fisheries management
5 María Hozbor	F		INIDEP, Argentina	Fisheries science, resource assessment, and methodological development

				for monitoring exploited marine species
6 Patricia Zárate	F	5	IFOB, Chile	Fishery-dependent data collection, biological sampling, and applied research in support of fisheries management
7 Laura Molina	F	5	ARAP, Panama	Fisheries governance, monitoring, and institutional coordination
8 Lilia Soler	F		IMIPAS, Mexico	Fisheries research, marine resource management, and participation in national monitoring programs
9 Deivis Cueva	M	5	Peru, IMARPE	Knowledge of artisanal fisheries operations
10 Pilar Arguedas	F	5	INCOPECA, Costa Rica	Fisheries management, regulatory frameworks, and technical advisory processes.

* Field only required for members identified as early career: 10 years or less post-degree, not counting time off for family leave.

Associate Members

Name	Gender	Years since degree*	Country and institution of affiliation(s)	Expertise relevant to proposal
1 Mario Rueda Hernández	M	10	Colombia, INVEMAR	Marine fish biodiversity assessment and applied research for management and conservation
2 Rodrigo Bustamante	M	10	Australia, CSIRO	Development of indicators for marine biodiversity and fisheries impacts
3 Jatinder Sidhu	M	10	Australia, CSIRO	Marine data systems, analytical workflows, and the application of emerging technologies for environmental monitoring
4 Annette Govindarajan	F	10	USA, Woods Hole Oceanographic Institution	Molecular ecology, marine biodiversity, and the application of genetic tools to ocean science

5 Carlos Alvarado	M	10	Costa Rica, INCOPECSA	Fisheries management, governance, and technical advisory processes
6 Pascal Hablutzel	M	8	Belgium, VLIZ	Marine data management, biodiversity information systems, and international data infrastructures

* Field only required for members identified as early career: 10 years or less post-degree, not counting time off for family leave.

Working Group contributions

Full members

1. Vanessa Yepes Narváez (Co-Chair): Experience in molecular approaches for marine biodiversity assessment. She will provide scientific leadership, ensure alignment with SCOR objectives, coordinate synthesis activities, and guide the development of best-practice manuals, reference frameworks, and capacity-building outputs.

2. Jessica Bonicelli Proaño (Co-Chair): She will contribute to field sampling design, integration of molecular tools with fisheries surveys, sample handling protocols, and the interpretation of genetic signals in relation to population dynamics and fisheries management.

3. Giovanna Sotil (Co-Chair): Experience in fisheries monitoring, ecosystem-based management, and assessment of small-scale and industrial fisheries. Her expertise includes fisheries data analysis, biological sampling programs, and integration of scientific evidence into management advice.

4. Verónica Jurquiza: Expertise in fisheries biology, monitoring programs, and applied research for sustainable fisheries management. She brings experience in national fisheries assessment frameworks, biological sampling, and institutional data reporting.

5. María Hozbor: Expertise in fisheries science, resource assessment, and methodological development for monitoring exploited marine species. She will contribute to intercalibration between eDNA outputs and conventional fisheries data, and to the translation of scientific results into management-oriented guidance.

6. Patricia Zárate: Experience in fishery-dependent data collection, biological sampling, and applied research in support of fisheries management. She will contribute to the design and evaluation of sampling strategies that integrate passive eDNA collection into routine fisheries operations.

7. Laura Molina: Expertise in fisheries governance, monitoring, and institutional coordination. Her experience at the science-management interface will support stakeholder engagement, co-design of pilots with fishers, and the articulation of WG outputs with national fisheries authorities.

8. Lilia Soler: Expertise in fisheries research, marine resource management, and participation in national monitoring programs. She will contribute regional experience, support comparative synthesis across

countries, and strengthen links to fisheries institutions in the Eastern Pacific and Gulf of Mexico.

9. Deivis Cueva: He will contribute deep regional knowledge of artisanal fisheries operations, support pilot coordination, and ensure that eDNA-based indicators are relevant and interpretable for fisheries management agencies.

10. Pilar Arguedas: Expertise in fisheries management, regulatory frameworks, and technical advisory processes. She will contribute a management and policy perspective to ensure that WG outputs are directly relevant to decision-makers and aligned with national and regional fisheries governance needs.

General role of the Associate members

1. Mario Rueda Hernández (Connections)

Senior researcher with experience in marine biodiversity assessment and applied research for management and conservation. His expertise will support the integration of eDNA-based indicators into broader biodiversity assessment programs. As an associate member, he will contribute to the synthesis of regional datasets, the interpretation of biodiversity signals in coastal and artisanal fishing contexts, and the linkage of WG outputs with national monitoring initiatives.

2. Rodrigo Bustamante (Mentorship)

Senior scientist with experience in the development of indicators for marine biodiversity and fisheries impacts. He will contribute to the conceptual framing of eDNA-based monitoring within global fisheries and ecosystem assessment contexts. He will support methodological synthesis, scalability assessment, and the articulation of WG products with international observing and management frameworks.

3. Jatinder Sidhu (Mentorship)

Researcher with expertise in marine data systems, analytical workflows, and the application of emerging technologies for environmental monitoring. His experience in data processing, standardization, and interoperability will be particularly relevant to ToRs related to harmonized bioinformatic pipelines and FAIR data practices. As an associate member, he will contribute to the development of reproducible analytical frameworks and guidance for managing and sharing eDNA-derived fisheries data.

4. Annette Govindarajan (Mentorship)

Researcher with recognized expertise in molecular ecology, marine biodiversity, and the application of genetic tools to ocean science. Her experience spans marker selection, molecular data interpretation, and methodological rigor in DNA-based biodiversity studies. She will provide strategic input on molecular standards, quality control, and the positioning of WG outputs within the broader evolution of biomolecular ocean observing.

5. Carlos Alvarado (Connections)

Decision-maker in Costa Rica with experience in fisheries management, governance, and technical advisory processes. His perspective from a national fisheries authority will ensure that WG products are relevant,

interpretable, and actionable for managers and decision-makers. He will support the translation of eDNA-based indicators into policy-relevant contexts and facilitate connections with regulatory institutions.

6. Pascal Hablützel (Mentorship)

Researcher with expertise in marine data management, biodiversity information systems, and international data infrastructures. His experience in supporting platforms such as OBIS and in advancing FAIR and interoperable marine biodiversity data will be instrumental for ToRs related to data standardization and open access. As an associate member, he will contribute guidance on metadata frameworks, data publication pathways, and the long-term usability of eDNA-based datasets generated by the WG.

8. Relationship to other international programs and SCOR Working Groups

The Working Group FISH e-TRACE: DNA Tracking of Small-Scale Fisheries Resources for Conservation and Management in Latin America is strategically aligned with existing international initiatives and with SCOR's portfolio of Working Groups, while addressing a clearly defined methodological gap not currently covered by other programs. Its contribution is complementary rather than duplicative, focusing on coordination, standardization, and synthesis of environmental DNA (eDNA) applications in small-scale fisheries.

At the international level, FISH e-TRACE is closely aligned with the Ocean Biomolecular Observing Network (OBON), a UN Ocean Decade endorsed program aiming to develop global biomolecular observation systems to monitor marine life. While OBON operates at a broad systemic scale, integrating multiple platforms and omics technologies across coastal and open-ocean environments, FISH e-TRACE contributes a specific operational component, standardized protocols for passive eDNA sampling integrated directly into artisanal fishing gears. In this way, the Working Group strengthens the fisheries dimension of OBON and provides ready-to-implement methodologies that can be incorporated into broader biomolecular observing frameworks.

The Working Group is also strongly aligned with the objectives of GBIF and OBIS, particularly in the context of the rapid growth of DNA-derived marine biodiversity data. FISH e-TRACE will contribute practical guidance for the generation, curation, and publication of FAIR eDNA datasets derived from fishing activities, tailored to tropical and small-scale fisheries contexts. By doing so, it enhances data interoperability and increases the value of eDNA-based observations for both scientific synthesis and policy-relevant decision-making.

From a policy and governance perspective, the WG is conceptually consistent with the FAO Voluntary Guidelines for Securing Sustainable Small-Scale Fisheries (SSF Guidelines). While FAO focuses on normative guidance, governance frameworks, and socio-economic dimensions of small-scale fisheries, FISH e-TRACE contributes complementary scientific tools that can strengthen the evidence base for ecosystem-based management, bycatch mitigation, and transparency in artisanal fisheries value chains, without overlapping FAO's mandate.

In relation to existing and past SCOR Working Groups, FISH e-TRACE complements efforts that have

addressed marine biodiversity observation, biological standards, and methodological harmonization, but distinguishes itself through its explicit focus on small-scale fisheries, the direct integration of molecular tools into extractive activities, and the combination of eDNA metabarcoding, genetic traceability, and participatory science. As such, it fills a methodological niche within SCOR's portfolio by targeting data-limited fisheries systems where conventional monitoring is least effective and innovation is most urgently needed.

Finally, FISH e-TRACE will strengthen coherence across SCOR activities by delivering products such as best-practice manuals, methodological guides, intercalibrated syntheses, and open datasets, that can be reused and scaled by other SCOR Working Groups and international programs. Although regionally grounded in the Eastern Pacific, its methods and standards are globally transferable, fully consistent with SCOR's mission to advance ocean science through international coordination and methodological innovation.

9. Key References

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Appendix

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