THE BENTHIC ZONE NEWSLETTER

PUBLISHED
September 2025

Unlocking the Future of Environmental Monitoring: Environmental DNA as a Tool for Biological Characterization and Site Management (Part One of a Two-Part Series)

By Jennifer Wollenberg, Ph.D., *Principal*
Daniel Doolittle, *Principal*
Sadie McGarvey, *Consultant*

Biological monitoring is a common requirement in many environmental site management contexts, such as contaminated site assessment, ecological risk assessment, regulatory permitting, and ecological restoration. Traditional biological monitoring methods involve time- and labor-intensive field surveys and species identification by trained biologists.

Over the past decade, an innovative new analytical tool for biological monitoring has emerged: **environmental DNA (eDNA)**. This noninvasive sampling method can provide robust community data to supplement traditional survey methods and to provide an additional line of evidence to assess biodiversity, monitor ecological health and recovery, and efficiently manage environmental and greenfield sites.

This article is Part 1 of Integral's two-part series on the cutting-edge applications of eDNA. This installment provides an introduction to eDNA and explores the advantages and challenges of eDNA analysis for site management applications. Our future installment will highlight how eDNA can be a useful component of the sediment practitioner's toolbox across a range of project types.

Traditional Biological Assessments: Strengths and Limitations

Biological assessments can establish baseline conditions at a site, demonstrate impacts of cleanup or management actions, and/or show changes in the ecological community over time. Example applications of such surveys include:

- Characterization of benthic invertebrate or fish communities during the remedial investigation and risk assessment phases under Superfund and state cleanup programs
- Assessment of marine mammal populations near offshore development projects
- Monitoring of vegetation for wetland restoration projects
- Analysis of benthic invertebrate communities for National Pollutant Discharge Elimination System discharge permit monitoring
- Early detection of the presence of invasive species before their establishment—saving significant time and resources at eradication once established.

In all instances, traditional methods involve direct observation and capture of organisms, followed by field or laboratory-based taxonomic identification.

The information collected through these survey methods provides quantitative data regarding populations and supports calculation of ecological metrics that have long been relied upon to characterize communities. While effective and part of the lexicon, these methods:

- Are labor-intensive, time consuming, and costly
- Require detailed subject matter expertise, expertise that is waning in supply as classical taxonomists retire and are not replaced
- Are potentially limited in their ability to detect rare or cryptic species
- Are limited by the ability to catch certain species and members of their subpopulations (age class, sex)
- Are dependent on seasonal and environmental conditions
- May be injurious or lethal to targeted individuals
- May be injurious or lethal to nontarget individuals (e.g., trawling bycatch)
- Can be biased by survey methods, locations, and researchers' ability to identify species.

These limitations have prompted the search for more efficient, comprehensive, more objective, and less intrusive alternatives—leading to the rise of eDNA.

What is eDNA?

Environmental DNA refers to genetic material shed by organisms into their surroundings through skin cells, mucus, feces, or other biological processes. This DNA can be collected from environmental media, such as water or sediment, as well as from tree canopies and from vegetation—basically from anything that may have been a receptor to genetic material. The media are then processed to collect genetic material and analyzed to determine which species are or were recently present in an environment.

The process typically involves:

1. Sample collection (e.g., filtering water or collecting sediment from a water body)
2. DNA extraction and amplification using polymerase chain reaction (PCR) techniques
3. High-throughput DNA sequencing systems (aka Next Generation Sequencing or NGS) and bioinformatics to match DNA fragments to known species libraries.

There are two general approaches that may be employed for species identification: targeted analysis for specific species or metabarcoding to assess groups of species. For target species identification, a DNA sequence (or "primer") specific to the species of interest is amplified using quantitative PCR (qPCR) to confirm presence/absence of the species. In some instances, validated qPCR assays may be able to provide some insight on abundance, as well. Metabarcoding uses a universal primer (i.e., a sequence of DNA that is consistent across a group of organisms) to amplify DNA for many species using one reaction.

With either method, the best results are achieved with newly emerging high-throughput sequencing systems and sample processing technologies that allow for millions to billions of "reads" of that DNA sequence of interest. These systems provide deeper sequencing coverage, meaning more reads are obtained for a given region of a genome, leading to more accurate variant detection and the ability to detect species of interest when limited genetic material is present in the sample. An abundance of information increases the statistical power of the bioinformatic analyses and enables questions to be answered with greater sensitivity and precision.

After sequencing, the results enter the bioinformatics phase of the process and are compared to a database to determine which species are present. Genetic libraries are growing in both depth and breadth—allowing genomic approaches to be more widely implemented—for example, the GEANS project (Genetic Tools for Ecosystem Health Assessment in the North Sea Region) has recently released a curated DNA barcode library for common macroinvertebrates of soft bottom habitats, which represents 29 percent of the known North Sea macrobenthos species (Christodoulou et al. 2025). Bioinformatic computing systems, the application of AI, and other continuous improvements in genomic technology are increasing the depth and breadth of barcode libraries at an incredibly rapid pace, thus the abilities of eDNA are continually improving.

Advantages of eDNA

Incorporation of eDNA analysis as a part of the modern site assessment toolkit can provide several advantages for any project where biological monitoring is being implemented, such as:

- **Cost-Effective:** Requires fewer personnel and less field time
- **Autonomous:** New remote sampling systems are being deployed
- **Scalable:** Enables more frequent and widespread sampling
- **Straightforward:** Samples can be collected with minimal training
- **Non-invasive:** Reduces harm to organisms and habitats
- **Greater Sensitivity:** Detects species that are rare, elusive, or present in low abundance
- **Complementary:** Enhances traditional methods rather than replacing them.

Studies comparing eDNA with traditional trawl and benthic surveys (e.g., Stoeckel et al. 2021; Ji et al. 2023) show that eDNA often identifies more species and provides a broader picture of community composition. A study in Swiss streams (Brantschen et al. 2021) demonstrated strong alignment between eDNA and traditional biotic indices, supporting its regulatory use.

Challenges and Considerations

Despite its promise, broader acceptance of eDNA is not without hurdles, which include:

- **Regulatory Acceptance:** Although many regulatory frameworks are still built around traditional methods, some agencies at state and federal levels in the U.S. and abroad are encouraging adoption of eDNA as a tool for environmental management. For example, the National Science & Technology Council published its Aquatic Environmental DNA Strategy, which recommends a "nationwide eDNA network to inform decisions that promote resilient ecosystems" (NSTC 2024). This acceptance is expected to grow over time. But broader adoption of eDNA will require:
  - Education of regulators and stakeholders
  - Demonstration of equivalency to or superiority over existing methods
  - Integration into existing biotic indices and assessment protocols.
- **Standardization:** Efforts to develop best practices and standards across the industry are well underway (e.g., by the International Standards Organization and industry groups such as IOGP[1] and others[2]). To ensure consistency and reliability, the field needs:
  - Standardized sampling and analysis protocols
  - Quality assurance and control measures
  - Increased laboratory capacity to provide results in a timely fashion as use increases.
- **Interpretation of Results:** eDNA data can be influenced by a range of environmental factors, species-specific considerations, and methodological differences. Understanding these nuances is essential for developing suitable sampling approaches and data quality objectives, accurate data interpretation, and application to decision-making.

The Path Forward

The integration of eDNA into environmental monitoring represents a paradigm shift. As methods become more refined and regulatory frameworks evolve, eDNA is poised to become a mainstream tool in site assessment and ecological management.

To fully realize the potential of eDNA, the environmental science community must:

- Continue validating eDNA against traditional methods
- Develop robust standards and best practices
- Foster collaboration between researchers, regulators, and industry
- Continue to build genetic libraries validated against traditional assessments of species type
- Promote genomic methods as a complementary and efficient way to gain comprehensive ecological and biological data.

Stay tuned for Part 2 in this series, which will present case studies of eDNA applications within Superfund sites and greenfield applications.

---

[1] International Association of Oil and Gas Producers https://www.iogp-edna.org/publications/

[2] For example, International eDNA Standardization Task Force https://iestf.global/, iTrackeDNA https://itrackdna.ca/, and the Centre for Environmental Genomics Applications https://www.cegacanada.com/

Jennifer L. Wollenberg, Ph.D.
Principal
jwollenberg@integral-corp.com
View Bio

Daniel Doolittle
Principal, Offshore Wind
ddoolittle@integral-corp.com
View Bio

Sadie McGarvey
Consultant
smcgarvey@integral-corp.com
View Bio

References

Brantschen, J., R.C. Blackman, J.-C. Walser, and F. Altermatt. 2021. Environmental DNA gives comparable results to morphology-based indices of macroinvertebrates in a large-scale ecological assessment. PLoS ONE 16(9):e0257510. . https://doi.org/10.1371/journal.pone.0257510

Christodoulou et al. 2025. A taxonomically reliable DNA barcode reference library for North Sea macrobenthos. Jul 11;12:1198. doi: 10.1038/s41597-025-05500-z.

Ji et al. 2023. Comparison of environmental DNA metabarcoding and bottom trawling for detecting seasonal fish communities and habitat preference in a highly disturbed estuary. Ecological Indicators. Volume 146, February 2023, 109754.

NSTC. 2024. National aquatic environmental DNA strategy. National Science & Technology Council. June.

Stoeckel, M.Y., J. Adolf, Z. Charlop-Powers, K.J. Dunton, G. Hinks, and S.M. VanMorter. 2021. Trawl and eDNA assessment of marine fish diversity, seasonality, and relative abundance in coastal New Jersey, USA. ICES Journal of Marine Science 78(1):293–304. doi:10.1093/icesjms/fsaa225.