

The ocean in a cup: Environmental DNA successfully captures marine biodiversity

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Dolphins in the Port of L.A. eDNA can help researchers identify the breadth of animal life in the oceans through the shed DNA found in as little as a cup of seawater. Credit: Zachary Gold

Measuring marine biodiversity with "environmental DNA"—an

application of gene sequencing to environmental biology—should permit rapid assessment of changes in marine life. That makes environmental DNA (eDNA) a critical tool for managing our response to climate change. But eDNA only works well if key implementation steps are followed, according to a new study of the Los Angeles and Long Beach area published in the journal *PeerJ*.

"What do we need to know to use eDNA in the coastal ocean, and can we make it work well in an important urban setting? Those are the questions that motivated us to launch this study," said Regina Wetzer, Curator and Director of the Marine Biodiversity Center at the Natural History Museum of Los Angeles County (NHM).

Answering those questions involved contributions from a natural history museum, multiple academic institutions, environmental consultants, and government agencies—highlighting the challenges involved in using eDNA, but also the widespread interest in its use.

eDNA uses genetic sequencing of samples from the environment (in this case, ocean water) to inventory biodiversity. "There are genes that differ enough between species that they can be used as identification markers. Every organism sheds DNA by dropping skin cells or other materials, so we can take a cup of seawater, sequence the DNA in it, and use that to inventory organisms in the area," said Zack Gold, lead author of the study.

The neighboring Port of Los Angeles and Port of Long Beach form one of the largest port complexes in the world and are a site of intense environmental interest. That made it an interesting site to test eDNA's ability to act as an effective tool for biodiversity assessment.



NHM's Dean Pentcheff recovering a seawater sample for eDNA. Credit: Janie Chen

This study paired eDNA sampling and conventional ship-based trawl net sampling at seven sites in the port complex. At each site, researchers collected multiple eDNA samples, each about one liter of seawater, just before the trawl net was towed through the same area. That permitted a comparison between eDNA and traditional biodiversity assessment techniques: eDNA detected nearly all of the 17 species of fish found in the trawls, but also detected an additional 55 native fish species. Detecting those additional species through conventional sampling requires many more sampling trips and a very high expense.

"We were happy to see eDNA validated alongside 'conventional' sampling, but we were really excited to see the extra information that came from the eDNA," said Dean Pentcheff, researcher and program manager of the Diversity Initiative for the Southern California Ocean (DISCO) at NHM. But getting that extra information depended on having a complete genetic reference library for all the fish in the area—a [genetic sequence](#) in an eDNA sample can only be resolved to a species if there is a reference sequence on file for that species. All the fish in the eDNA samples in this study were resolved only after the researchers added the last few fish references to the sequence library.

The eDNA samples from different locations in the ports yielded different species inventories at a statistically significant level. That answered an important question: Can eDNA measure variability across an area as small as the port complex, or does seawater mix so thoroughly that local differences are completely blurred? This study demonstrated that eDNA in this ocean environment can expose differences between places as close as a few hundred meters apart.



Recovering sampling trawl net at night. eDNA proved more accurate and would be less expensive than more traditional sampling. Credit: Wood Environment and Infrastructure, Inc.

Based on this pilot project, the authors assembled a set of recommendations for managers considering eDNA as a tool for biodiversity assessments. The recommendations cover careful selection of the identifying genes and specific advice on how to clean up the [sequence data](#) from eDNA samples before searching for sequence matches. Because of the successful species resolution that resulted from building a full sequence reference library, a key recommendation is to create regional reference databases.

"These samples of the environment are like time capsules that we'll be able to exploit in the future," said Adam Wall, Crustacea Collections Manager at NHM. That sentiment prompted another of the group's recommendations: Archive eDNA samples and sequence data for long-term use. As sequencing technology improves, additional information could come from the samples. As genetic data analysis techniques improve and genetic reference libraries are expanded, the sequence data can be analyzed again to get additional results beyond the fish inventories published in this study.

More information: Zachary Gold et al, A manager's guide to using eDNA metabarcoding in marine ecosystems, *PeerJ* (2022). [DOI: 10.7717/peerj.14071](https://doi.org/10.7717/peerj.14071)

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