

Environmental Studies Program: Ongoing Study

Title	Harnessing the Power of eDNA as a Real-time Assessment tool of Nearshore Arctic Marine Communities (AK-19-02-13)
Administered by	Alaska Regional Office
BOEM Contact(s)	Rick Raymond (richard.raymond@boem.gov)
Procurement Type(s)	Cooperative Agreement
Conducting Organization(s)	University of Alaska Coastal Marine Institute
Total BOEM Cost	\$200,766 plus Joint Funding (\$200,766)
Performance Period	FY 2021–2024
Final Report Due	January 31, 2024
Date Revised	September 14, 2022
PICOC Summary	
<i><u>Problem</u></i>	Climate change is rapidly reshaping Arctic marine ecosystems creating challenges to Arctic research and biological monitoring. New tools and approaches are needed to detect and quantify changes in Arctic food-webs and species diversity.
<i><u>Intervention</u></i>	Environmental DNA (eDNA) metabarcoding is a relatively new cost-effective genomic tool that can be used to quantify fine-scale changes in coastal communities, allowing for rapid standardized collection of data about species distribution and relative abundance of nearshore fish, invertebrate, seabird, and marine mammal communities.
<i><u>Comparison</u></i>	Genomic sequencing tools using eDNA metabarcoding complements more traditional sampling approaches such as using nets and local Indigenous knowledge by providing rapid assessments of species composition.
<i><u>Outcome</u></i>	This study would be the first step towards creating a georeferenced Arctic eDNA Atlas that will show nearshore community composition over space and time, which can then be used to inform decision making.
<i><u>Context</u></i>	Beaufort Sea

BOEM Information Need(s): BOEM needs updated information regarding temporal and spatial changes to species populations and diversity resulting from environmental change. This study will use a cost-effective sampling system to monitor potential ecosystem level changes to update existing baseline descriptions, and offer further insight into changes in fish, seabirds, and marine mammal populations. Study results will support impact analyses and documentation required under NEPA, ESA, MMPA, and other requirements.

Background: As climate change continues to rapidly reshape Arctic marine ecosystems; scientists have identified tools and approaches that will accurately quantify changes in Arctic food-webs and the structure of coastal biological communities. The eDNA metabarcoding genomic sequencing tools complement traditional fisheries approaches and local Indigenous knowledge by providing assessments of biological species composition in coastal communities. As an emerging technology, eDNA addresses the challenges associated with Arctic research and biological monitoring by quantifying species

responses in nearshore biological communities resulting from environmental change. Using eDNA will allow for rapid, cost-effective, and standardized collection of data about species distribution and their relative abundance. For small, rare, cryptic, and other species that are difficult to detect, eDNA provides an alternative for marine inventory and monitoring of nearshore species composition. Past evidence using eDNA demonstrates improved species detection and catch-per-unit effort compared with other current traditional field methods. Detection of species using eDNA would expand biodiversity assessments and provide additional information about status, distribution, and habitat requirements for lesser-known species. Study results would build on existing baseline data to document changes in a region undergoing potential oil and gas development with the goal of developing an Arctic eDNA Atlas identifying nearshore community composition.

Objectives:

- Test the efficacy of newly available automated eDNA sampling by characterizing the biodiversity and phenology of nearshore fish, invertebrate, seabird and mammal communities.
- Compare eDNA results to traditional fish catching methods as part of the Beaufort Sea long-term monitoring program.

Methods: This study will use eDNA autosamplers affixed to fyke nets to collect water samples in conjunction with the BSFMS program. Water samples will be vacuum filtered by an autosampler through 0.45-micron nitrocellulose membranes that will be preserved in Longmire's buffer. The eDNA samples will be extracted from a filter membrane and amplified with primers specific to fish, including Pacific salmon, marine invertebrates, seabirds, and marine mammals. Libraries will be prepared using a modified genotyping in sequencing protocol and sequenced on an Illumina MiSeq platform at the UAF Genomics Core Lab.

Specific Research Question(s):

1. Can eDNA expand capabilities for population assessment of all coastal species, facilitate research on their behavior and habitat requirements, and improve understanding about their population status and habitat use in a warming Arctic?
2. Can eDNA also be an effective tool for early detection of aquatic invasive species?
3. How effective is eDNA to capture species distribution changes in response to various changes in environmental and anthropogenic parameters?

Current Status: Ongoing, fieldwork underway

Publications Completed: N/A

Affiliated WWW Sites:

<http://www.boem.gov/akstudies/>

<https://www.uaf.edu/cfos/research/cmi/>