



NOAA
FISHERIES

Alaska Fisheries
Science Center

Auke Bay
Laboratories

Alaska Fisheries Science Center: Genetics Program

What We Do

We use genetic tools to inform fish and shellfish management in the marine environments of Alaska. Genetic tools empower us to gather intricate data that remains hidden from traditional methods. For example, environmental DNA (eDNA) shed by marine species can be used to track their presence and abundance without ever observing them. Tools in our genetics program have many applications that range from identifying digested diet items to tracking the origin of salmon to understanding the genes that have allowed organisms to successfully adapt to their environments. Our three focal areas of research are:

1. Identifying the stock of origin of salmon caught as bycatch or in targeted fisheries to provide required information for regional, national, and international agreements and treaties.
2. Investigating the genetic stock structure and stock-specific distribution patterns of federally managed species to inform stock assessments and fisheries management.
3. Using eDNA and other molecular tools to understand species diversity, distribution, phenology, and ecology.



Genetics program biologist Natasha Howe along with other crew members from the University of Washington catch sockeye salmon for genetic sampling in Bristol Bay, Alaska. Credit: NOAA Fisheries



Collected water samples to test for DNA. Credit: NOAA Fisheries



Genetics program biologist Katie D'Amelio filters eDNA samples. Credit: NOAA Fisheries

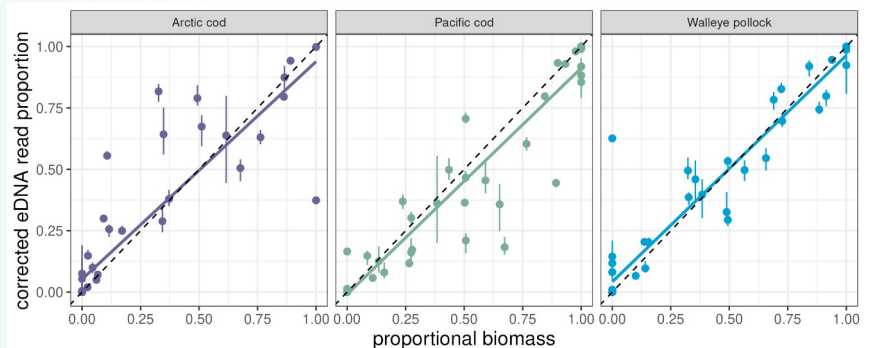


Genetics Program biologist, Juliana Cornett prepares seawater samples for eDNA analysis to detect harmful algal blooms. Credit: NOAA Fisheries/Jessica Whitney.



2024 Accomplishments

- **Salmon bycatch:** Assigned over 10,000 salmon to stock of origin. Data were used to understand the impacts of bycatch, especially on stocks from western Alaska. Partnered with Bristol Bay Science and Research Institute (BBSRI) to analyze in-season data and estimate the origin of chum salmon bycatch in near real time.
- **Environmental DNA:** Continued to develop and apply eDNA for assessing distribution and abundance of marine species.
- Developed new eDNA tools for monitoring gadids, rockfish, and harmful algal blooms.
- Identified prey from northern fur seal fecal DNA.
- **Population genomics:** Generated data to assist with defining management units for sablefish, king crab, and rockfish. Discovered a significant genetic control for migration timing in 4 species of salmon. This finding has major implications for salmon management. We are working with the Alaska Department of Fish and Game and the Department of Fisheries and Oceans Canada to integrate the markers that we discovered into their genetic panels for further analysis and salmon management.



Results from an aquarium eDNA validation study for three species of cod. The proportion of DNA metabarcoding reads was positively correlated to proportion of fish biomass. Published as Ledger et al., 2024 in Environmental DNA.



Howard Lutnick
Secretary of Commerce

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Acting Under Secretary of Commerce
for Oceans and Atmosphere

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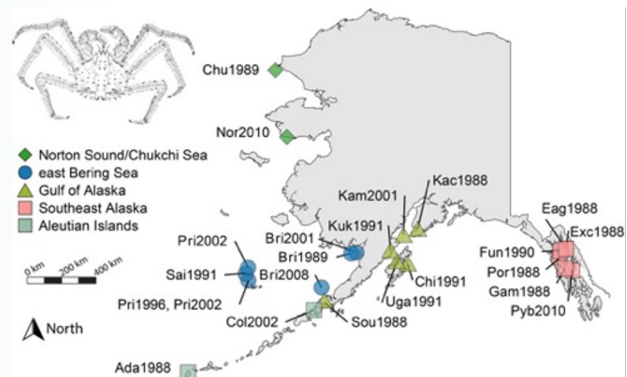
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www.fisheries.noaa.gov

OFFICIAL BUSINESS

National Marine
Fisheries Service

Alaska Fisheries Science Center
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Seattle, WA 98115 6349



Sampling locations for Alaska king crab population genetic study. King crab in this study showed more genetic diversity on smaller spatial scales than expected. Published as St. John et al., 2024 in Evolutionary Applications.

2025 Preview

- **Integrating eDNA into stock assessments:** Building a road map that can be used across NOAA to guide the integration of eDNA into stock assessments.
- **A new genetic baseline for Chinook salmon:** Working with Alaska Department of Fish and Game on an updated baseline that will allow for more precise estimates of stock of origin. This will be particularly useful for understanding bycatch impacts in western Alaska.
- **eDNA time series from the northern Bering Sea:** Analyzing four years of eDNA data to understand how the interannual high latitude environment influences fish communities and abundance. We will compare eDNA species to data collected from surface trawl nets.