NOAA ‘Omics Strategy Report, FY25 Q2

provided to the NOAA Science Council *by* the NOAA ‘Omics Working Group

Project Highlights

- **Effective Resource Management: Genetic Data Points to King Crab Resiliency.** The fishery for Alaska red king crab (Figure 1) is embedded in Alaska’s working waterfronts, but it collapsed in the 1980s. Recent ‘omics research provides hope that genetic resilience can provide a buffer against disease and other stressors**.** Researchers from the Alaska Fisheries Science Center (AFSC) along with colleagues from Cornell, University of Alaska Fairbanks, and the Alaska Department of Fish and Game found more genetic diversity than expected and high levels of population structure suggesting that populations are locally adapted, which confirmed the current management approach by region in Alaska. These findings harnessed the power of whole genome sequencing, providing improved resolution of population structure compared to older techniques, and they can inform hatchery enhancement efforts.

Figure 1. Red king crab on the deck of a research vessel. Credit: NOAA Fisheries / Erin Fedewa

- **Benefits for Fisheries: ‘Omics Integrated into Stock Assessments.** Pacific hake adds millions of dollars to the U.S. fishing industry, and stock assessments are key to sustaining this benefit. Applying non-invasive eDNA analysis to stock assessments is a challenging ambition for NOAA ‘Omics because there is a need to estimate biomass as well as spatial/temporal mapping. In an international first, researchers from the Northwest Fisheries Science Center (NWFSC) successfully included an eDNA index of abundance into a 2025 stock assessment for Hake. Using data collected during surveys in 2019, 2021, and 2023, this first integration of eDNA data for Hake in the eastern Pacific lays the groundwork for similar assessments in the future. In addition, this approach provided information on a number of other important fisheries stocks, such as sardine and anchovy, marking a major advancement (Figure 2).

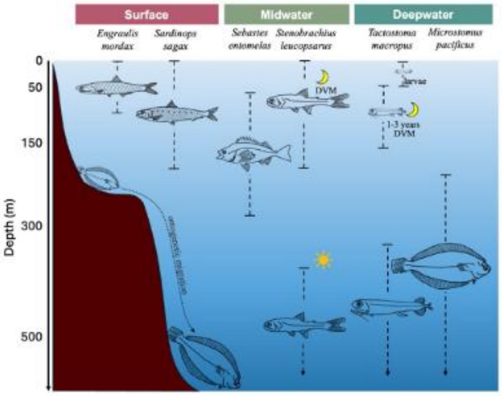

Figure 2. Known depth distribution of species for which eDNA abundance is evaluated using eDNA metabarcoding. Credit: NWFSC

- **Top Five Manuscript.** A team of NOAA Fisheries scientists working on killer whale genetics revealed that one of the world's most recognizable creatures in the North Pacific Ocean is actually two separate species. The manuscript was ranked in the top 5% of all research outputs scored by Altmetric, downloaded over 29,000 times in the first 6 months, and was broadly accessible as indicated by 97% of those downloading the article identifying themselves as members of the public rather than as scientists. The Royal Society Open Science journal ranked this paper in their top five for the year.

- **Training to Make Workflows Machine Readable and AI-ready.** NOAA 'Omics hosted a hands-on workshop that helped users convert protocols and data into machine-readable and standardized Better Biomolecular Ocean Practices (BeBOP) formats. Sharing the resulting protocols on the NOAA 'Omics Technical Portal will aid consistency and efficiency across the agency and enhance the ability to compare data sets at large geographic scales.

- **'Omics Applied to Ocean Acidification.** The NOAA Ocean Acidification Program will support development of gene expression assays to signal ocean acidification stress in an indicator species commonly known as sea butterflies, or pteropods (*Limacina helicina*) (Figure 3). These microscopic snails are an important part of the food web because they serve as prey for a wide variety of species, including juvenile salmon. Pteropods are sensitive to ocean acidification and thus serve as sentinels for biological impacts. A team led by Dr. Zack Gold at the Pacific Marine Environmental Research Laboratory (PMEL) will leverage the NOAA West Coast Ocean Acidification 2025 cruise for animal collection and bring together chemical and biological measurements to understand how changes in ocean chemistry impact productive West Coast ocean ecosystems.

Figure 3. Photograph of a microscopic pteropod in a state of dissolution due to ocean acidification conditions. Credit: NOAA

- **Statistical Methodology and Software Infrastructure for a Common Fishery Management Application with Genomic Sequencing Data**. In collaboration with computational biologists at Colorado State University, Southwest Fisheries Science Center (SWFSC) researchers developed and released a program for conducting population assignments from low-coverage whole genome sequencing data. This approach allows the population of origin of harvested individuals to be inferred in species with little population structure, enabling more precise management of mixed-stock fisheries. The program is currently being used in studies of Atlantic bluefin tuna and anadromous American shad and has been proposed as a solution to poor resolution of stocks of Chinook and chum salmon in Western Alaska.

- ***Acropora cervicornis* Data Coordination (AcDC) Hub Now Accepts Data from Other Coral Species.** Through support from NOAA 'Omics and the Coral Reef Conservation Program, the NOAA Research Atlantic Oceanographic and Meteorological Laboratory (AOML) Coral Program, developed an open-access database as a central repository for all genotype performance data related to the endangered coral species *Acropora* *cervicornis*. The AcDC database has now expanded to include multiple coral species. The hub allows the direct comparison of coral genotypes used in restoration across many different trait measurements, providing a user-friendly tool for restoration practitioners and researchers to identify priority genotypes for their efforts.

Partnerships

- In partnership with the Smithsonian National Museum of Natural History and Jonah Ventures, the NOAA National Systematics Lab released a new tool called MitoPilot for assembling, annotating and publishing mitochondrial genomes from voucher specimens of fishes. MitoPilot is publicly available on GitHub, along with Documentation and Instructions for Implementing on NOAA Fisheries HPCC SEDNA. This work supports the creation of reliable, voucher-based genetic reference data in support of eDNA analyses for biodiversity surveys, fisheries monitoring, and invasive species detection conducted by NOAA and other organizations. Future work will expand MitoPilot to handle taxa beyond fishes and additional reference markers to improve eDNA capabilities for understudied marine species.

- **Pushing the Boundaries of Innovation.** Dr. Charles Gumbi joined the Alaska Fisheries Science Center (AFSC) and the University of Washington Cooperative Institute for Climate, Ocean, and Ecosystems Studies (UW-CICOES) as a postdoctoral scholar to develop tools for epigenetic aging of groundfish. Age is a vital input for many fisheries stock assessments that are the primary tool used to set harvest quotas. Traditional aging methods such as counting rings on otoliths are time intensive and potentially inaccurate. Epigenetic aging can produce accurate estimates of a fish age with genetic methods, which could substantially increase accuracy and decrease costs of aging. Charles will focus on developing epigenetic aging methods for two species of commercially important rockfish.

Figure 4. Dr. Charles Gumbi to work on epigenetic aging methods.

- **Introduction to Developing DNA Reference Barcode Sequences.** NOAA scientists at NOAA Pacific Marine Environmental Laboratory, Smithsonian National Museum of Natural History, NOAA ‘Omics, and NOAA Northwest Fisheries Science Center created a guide for generating and disseminating voucher-based DNA reference barcode sequences. It provides a general step-by-step approach to collecting and processing specimens/vouchers, as well as generating and reporting the resulting nucleotide sequence data.

- **Increased ‘Omics Data Processing Capabilities.** Five bioinformaticians are helping NOAA Fisheries develop shared ‘omics support and resources across all Fishery Management Councils and the Office of Science and Technology. Their mission is to use ‘omics data to enhance stock assessments, model protected and essential species, and study population biology and health of managed species. In addition, their efforts increase the bioinformatic capacity at NOAA via the expansion of computing infrastructure, establishment of training and resources, and increased FAIR (Findable, Accessible, Interoperable, Reusable) ‘omics data generated by NOAA.

- **Support Grows for Shrimp Metagenomics.** Liyah Smith joined the Key Species and Bioinformatics Branch of National Centers for Coastal and Ocean Science (NCCOS) as an Oak Ridge Institute for Science and Education (ORISE) Fellow. Liyah will work on a collaborative project with NCCOS and the Southeast Fisheries Science Center (SEFSC) and leverage metagenomics to analyze the gut content of the keystone species brown shrimp. This project will enhance our understanding for both the range of species inferred to be regulated by brown shrimp and the efficiency of using metabarcoding for dietary analysis, especially in cases of matter that has been distorted by the organisms’ digestive processes.

Infrastructure

- **Aiding Seafood Inspection.** The NOAA Fisheries National Seafood Inspection Laboratory (NSIL) has acquired a QuantStudio 5 Real-Time PCR system to help with future qPCR analysis. NSIL has also expanded its lab space for PCR amplification and qPCR analysis. These enhancements will improve the detection and quantification of DNA targets in eDNA samples.