NOAA ‘Omics Quarterly Report, FY26 Q1

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

Administrative and Agency Priorities

- **NOAA ‘Omics Researchers Consider Machine Learning to Enhance Efficiencies.** Marine metagenomes inform scientists and program managers of microbial function and diversity within coastal and deep-sea environments. Collaboratively, NOAA ‘Omics scientists are investigating machine learning models that identify and address limiting factors of current methods for taxonomic classification and marine metagenome characterization. This adds to the growing understanding of how machine learning can be leveraged toward ‘omics datasets to meet agency and national priorities.
- **NOAA Researchers Outline Roadmap to Integrate eDNA.** NOAA Fisheries geneticists and stock assessors are working to develop a practical approach to integrating eDNA methodologies into fisheries stock assessments. eDNA technologies have the capabilities to inform species' population structure, distribution, and abundance with increased cost-effectiveness and efficiency. In a cross-disciplinary review, scientists outlined critical and limiting factors for incorporating indices of biomass using eDNA directly in fisheries stock assessments. The efforts have resulted in a roadmap for using eDNA in stock assessment models to meet the needs of natural resource managers.

People

- NOAA ‘Omics Coordinator and NOAA Ocean Exploration ‘Omics specialist, Nicole Miller, took part in NOAA Ocean Exploration’s expedition EX2507, from Guam to Palau, during the Beyond the Blue campaign (**Figure 1**). Aboard the *Okeanos Explorer* mapping expedition Nicole led review of current eDNA sampling protocols for efficiencies and enhancements, in addition to studying cutting edge eDNA sample processing techniques of onboard collaborators from the Palau International Coral Reef Center (PICRC) and Stanford University researchers on the Palau eDNA Project. Nicole’s efforts streamlined routine protocols for increased optimization of NOAA Ocean Exploration environmental DNA (eDNA) data.

Figure 1. From left to right, Trish Albano, Rachel Medley, & Nicole Miller process eDNA samples within the Okeanos Explorer wet lab.

Infrastructure

- **NOAA Fisheries Contributes to 'State-of-the Art' Technology Review.** In an international collaborative effort, Ocean Exploration Cooperative Institute and NOAA Fisheries researchers conducted a 'A state-of-the-art review of aquatic eDNA sampling technologies and instrumentation'. The team shared instrument specifications and use cases during the 2023 Marine 'Omics Technology and Instrumentation Workshop and synthesized and reviewed the state of autonomous and programmable eDNA samplers in a recent publication. The manuscript provides scientists with functional comparisons among advanced technologies and will help guide future enhancements and considerations in technology development.

Projects

- **'Omics Influences Ongoing Effort to Enhance National Sequence Repositories.** The NOAA Fisheries National Systematic Laboratory, with support from NOAA Ocean Exploration, has undertaken substantial efforts to fill knowledge and sequence gaps of zooplankton communities sampled from the abyssopelagic zone (0 – 4300 meters) in the Gulf of Alaska. Scientists and sequence repositories still lack significant barcode data from these rarely explored environments. These efforts provide foundational understanding and sequence data that can be used to better characterize community compositions of the Gulf of Alaska and benefit national sequence repositories.
- **eDNA Sampling in the Gulf of America Contributes to Foodweb Dynamics Research.** The National Seafood Inspection Laboratory (NSIL) and the Southeast Fisheries Science Center (SEFSC) Marine Mammal Molecular Genomics Lab (MMMGL) have integrated eDNA sample collection into routine SEFSC plankton surveys during the fall 2025 field season. The eDNA samples are being analyzed to identify marine mammals, plankton, fish, and bacterial communities among survey sampling sites. Concurrent with this project the NSIL is working with the SEFSC trawl survey team to collect fish cloaca and whole gut content for genetic analysis. These efforts will help to identify the essential prey of different fish species and identify pertinent areas of food sources.
- **NOAA Fisheries' Cetacean Genomes Project Advances Genome Libraries.** The Cetacean Genomes Project (CGP), led by the NOAA Fisheries Southwest Fisheries Science Center (SWFSC) Marine Mammal Genetics Program in collaboration with the Vertebrate Genomes Project (VGP), Darwin Tree of Life and others published a report on reference genome sequences from representative species across cetacean families, providing critical infrastructure for research and conservation. The CGP began in early 2020 to facilitate the generation of high quality reference genomes for all cetacean species. Towards that goal, and using the standards of the Vertebrate Genomes Project, the research team generated 13 new reference genomes across eight of the 14 cetacean families, and summarized genome assembly characteristics for 18 species, including

newly-generated and published genome assemblies. In this work, the team found that the reference genomes have enhanced characteristics that will support and promote scientific research in marine mammals.

- **Standardizing and sharing environmental DNA collecting and processing protocols.** NOAA Research ‘omics teams are working toward Gold Standard Science by ensuring laboratory practices are open and accessible. The Better Biomolecular Ocean Practices (BeBOP) initiative pioneered a Minimum Information about an ‘Omics Protocol (MIOP) format to better compare practices and integrate data generated when studying ocean life. BeBOP formatted protocols are accessible, detailed, traceable, machine-readable, and standardized. In the last two months, the NOAA Research ‘omics team has published new protocols online within the OME GitHub and AOML ‘Omics GitHub. The protocols include organismal tissue subsampling and extraction protocols, eDNA gravity filtration collection protocols, and bioinformatics protocols. These efforts ensure metadata readiness for implementing emerging priorities.
- **‘Omics tools detect *Salmonella* in fish meal production and storage facilities.** A recent study evaluated *Salmonella* contamination in feed mill production facilities over a 12-year period, in 12 facilities primarily in the southeastern US. Using high throughput sequencing and evaluation of *Salmonella* genetic diversity, this study revealed possible common sources of contamination including regional fishing waters and shared additives. This study highlights the role of transportation and storage methods as possible sources of cross-contamination. The findings directly support NOAA's mission to ensure a safe and secure seafood supply, by investigating the origins and spread of *Salmonella* in fish meal to identify and reduce risks in the seafood supply chain.

Partnerships

- **Cross-line-office partnership provides insight to near-shore ecosystems.** In a NOAA Research-NOAA Fisheries collaboration, scientists participated in the Mini West Coast Ocean Acidification Cruise aboard the R/V Pacific Storm in July 2025 (**Figure 2**). The cruise focused on sampling along the Newport Hydrographic Line and Heceta Head Line to assess nearshore variability in carbonate chemistry and hypoxia. This effort also included paired environmental DNA and depth-specific sampling to investigate stress markers in key indicator species such as krill, Dungeness crab, and pteropods. The data collected will provide insight into how nearshore ecosystems and sensitive species respond to ocean acidification and hypoxic events.

Figure 2: Front to back: Juan Gutierrez Bravo - graduate student at OSU, Kris Bauer - postdoc at OSU CIMERS, Caroline Fradette - laboratory technician at UW CICOES in the PMEL Carbon Group. (Photo Credit: Zack Gold)