NOAA Omics FY26Q3 Report

provided to the NOAA Science Council
by the NOAA Omics Working Group
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Administrative and Agency Priorities

- **Seawater to Sequences: NOAA Releases First of Its Kind Deep Sea Environmental DNA Dataset**. NOAA Ocean Exploration, in partnership with NOAA's National Systematics Laboratory at the Smithsonian National Museum of Natural History, the Northern Gulf Institute, and NOAA's Atlantic Oceanographic and Meteorological Laboratory, released its first deep-sea environmental DNA (eDNA) datasets. These biological data were collected during expeditions on NOAA Ship *Okeanos Explorer* in the Pacific and Atlantic oceans between 2021 and 2023 and provide a wealth of information about deep-sea organisms. Data and metadata are now freely available to the public through two repositories: Raw sequences are available from the National Center for Biotechnology Information (NCBI) (BioProject: 1284389) and Organism identifications are available from the Ocean Biodiversity Information System (OBIS). By sharing these economically and scientifically critical data through globally accessible repositories, the partners hope to enable further deep-ocean discoveries and understanding to address current and emerging science and management needs.

- **Environmental DNA (eDNA) in NOAA: Pathways to Implementation to NOAA NOAA Science Advisory Board.** The NOAA Science Advisory Board Ecosystem Science and Management Working Group is actively writing a report on "where is eDNA ready to go to work for NOAA now, under which statutes, at what investment level, and with what standards and infrastructure in place? Its purpose is to rekindle NOAA's whole 'Omics and genomics strategy — now five years after the original 2021 plan, with key milestones unmet and no successor framework in place — and to provide the concrete implementation roadmap that the 2024 national strategy documents called for but did not produce." This report will include an updated Technology Readiness Level assessment for invasive species detection, biodiversity assessment, and transcriptomics/eRNA HAB toxicity; cross-application infrastructure framework; accountability record for unmet commitments to identify gaps since the expiration of plans and strategies; and identify research to operations (R2O) data.

People

- **NOAA Research Determines Lead for Atlantic Omics Program.** NOAA Research Atlantic Oceanographic & Meteorological (AOML) hired Katherine Silliman as the federal lead of the AOML Omics program (**Figure 1**). In her role Katherine will direct the development of omics technologies and data pipelines to enhance marine biodiversity monitoring, support fisheries, and promote coral restoration and resilience.

Figure 1. *Katherine Silliman has joined AOML as the new laboratory Omics Lead.*

- **NOAA Fisheries Welcomes Laboratory Technicians.** Arabella Lewis and Emi Boyd-Tucker recently joined the

Figure 2. *Emi Boyd-Tucker and Arabella Lewis, pictures respectively, have joined the NOAA Fisheries AFSC to support genetic sample processing.*

NOAA Fisheries Alaska Fisheries Science Center (AFSC) Omics team (**Figure 2**). Arabella and Emi will contribute to preparing and processing genetic samples of salmon bycatch in addition to generating data for population genomics projects, that allow for precision management of ecologically sensitive and commercially relevant fisheries.

- **NOAA Research Interns Contribute to Coral Omics and Beyond.** NOAA Research AOML is hosting seven interns to contribute to omics-related projects. University of Miami volunteer Marissa Dallaire, Cooperative Institute for Marine & Atmospheric Studies (CIMAS) Miami-Dade College intern Faith Nunez, NOAA Hollings Scholar Jia Hwang (University of Hawaii Manoa), University of Miami MPS intern Savannah Porcelli, Coral Program intern Diego Ferreira, CIMAS MDC intern Alexis Idun-Ogde, and Nanushka Bonano-Collazo from the University of Maryland Eastern Shore. Faith Nunez will work to develop assays to detect a lobster virus using eDNA. Marissa Dallaire plans to culture coral pathogens to test against coral probiotics. Jia Hwang's analysis on algal symbiont communities of urban corals in southeast Florida will support ongoing laboratory initiatives. Savannah Porcelli will be assessing algal symbiont communities, transcriptomics, and survivorship of cross-bred urban reef genotypes. Diego Ferreira will focus on analyzing gene expression profiles of corals along an ocean acidification gradient at Maug, Central Northern Mariana Islands. Alexis Idun-Ogde's contributions will identify coral spawning activity in timelapse photos of urban coral communities. Nanushka Bonano-Collazo will process data from a 3.5-year moored sediment trap in the northern Gulf of America, analyzing *Sargassum* export and associated microbiome signatures using environmental DNA (eDNA) sequence data. The efforts of this impressive cohort will contribute to AOML's omics mission to integrate omics for mission priorities (**Figure 3**).

Figure 3. *From left to Right, Alexis Ogde, Faith Nunez, Jia Hwang, Nanushka Bonano-Collazo, Savannah Porcelli*

Projects

- **Morphology Matters: Comparing eDNA to Traditional Methods.** Scientists from NOAA Fisheries recently concluded a study comparing the effectiveness of beach seines and eDNA to detect the nearshore fish community. The team found that the biological characteristics of

the fish species influence detection probabilities (**Figure 4**). For example, species with scales that shed easily are detected more frequently with eDNA than with beach seines. These efforts provide context for interpreting data sampled with different methods, particularly for studies comparing eDNA observations to net sampling. Overall, the findings encourage the use of multi-method assessments to account for different detection probabilities by both species and gear-type.

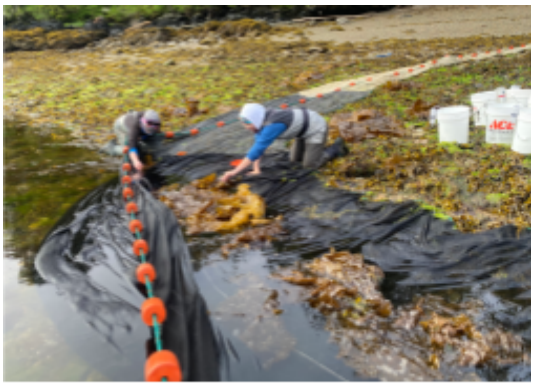

Figure 4. *Science team and partners gather biological samples via beach seines in southeast Alaska.*

- **NOAA Research Coral Program Exceeds One Thousand Coral Tissue Samples.** In a project led by Michael Studivan, the AOML Coral Program has now collected over 1,000 coral tissue samples as part of a population genetics assessment of corals in urbanized habitats in southeast Florida (**Figure 5**). 'Urban coral' communities have appeared on artificial substrates in extremely urbanized habitats in southeast Florida ports in recent decades, and appear to be remarkably resilient to multiple environmental stressors. As part of a NOAA Omics funded project, the team is examining the genetic diversity and gene flow of urban and reef populations across six primary reef-building and disease-susceptible species, to determine whether urban corals are supporting enhanced genetic diversity in the region. To date, the team has collected 1,208 samples from Miami-Dade, Broward, and Palm Beach Counties in Florida!

Figure 5. *AOML Researcher, Michael Studivan collects the team one-thousandth sample next to a curious Goliath Grouper.*

- **Omics Leveraged to Identify a Virulence Source of Coral Disease.** NOAA Research scientist supported a cross-institutional effort that identified lysogenic bacteriophages with virulence factors associated with Stony Coral Tissue Loss Disease (SCTLD). Over the past decade, SCTLD has decimated stony corals across Florida's Coral Reefs, reducing stony coral cover from 30 - 60%. The new study provides an understanding of how bacteriophages (i.e., viruses that infect bacteria) may increase SCTLD virulence through lysogeny (i.e., the integration of a bacteriophage's genome into the bacterial host chromosome). Once the bacteriophage's genome is integrated into the bacteria's genome, the bacteria can utilize virulence and toxin genes carried by the bacteriophage. This work informs potential mechanisms of SCTLD virulence, which in the future can help with disease management and protecting Florida's vulnerable reefs.

- **Researchers Address Epigenetics in Adaptation to Environmental Change.** A NOAA Fisheries Southeast Fisheries Science Center researcher has explored the role of epigenetics in rapid adaptation to environmental change. The efforts solve critical knowledge gaps regarding the timing and fitness impacts of epigenetic shifts, and propose using temporally resolved, multigenerational datasets, such as from fisheries monitoring. Collectively, these efforts help scientists better understand how genetic and epigenetic changes interact during evolutionary rescue, increasing the ability to effectively manage fisheries.

Partnerships

- **NOAA Partners Identify Fish & Dietary Patterns in Cross-Institutional Project.** NOAA Partners at Rockefeller University unveiled fish population dynamics and dietary patterns of human populations within the East River of New York City with a newly released project. The initiative provides evidence and methodologies for efficiently and effectively monitoring wildlife populations within the nearby estuary and surrounding marine areas. To date, fast currents and rocky habitats have reduced scientists' abilities to monitor fisheries within the area using traditional methods. The research team was able to overcome these environmental challenges with the use of eDNA, which allowed effective collection of comparable data. These efforts reinforce eDNA for use by scientists and resource managers to meet research objectives while overcoming the limitations of traditional methods.

- **NOAA Research contributes to microbial source tracking in Miami-Dade County**. NOAA Research Laboratory (AOML), in partnership with the UM CIMAS, is investigating sources of land-based pollution in Miami-Dade County and throughout the Florida Keys. This project utilizes Microbial Source Tracking to explain how contamination, in the form of bacterial communities, can change as they progress from nearshore source inputs onto critical coral reef habitats, informing resource managers and communities of the microbial 'highways' that influence ecosystem, reef, and human health.

- **New eDNA tool to help track recovery of sunflower sea star, a Pacific Coast 'apex predator'.** NOAA PMEL has been deploying their recently developed sunflower star eDNA assay with partners across the U.S. West Coast including Northwest Fisheries Science Center as well as Olympic, Greater Farallones, Cordell Bank, Monterey Bay, Chumash Heritage, and Channel Islands National Marine Sanctuaries. These efforts are helping identify and monitor remaining populations of this important apex predator that feed on sea urchins and other kelp grazers to help keep vital kelp forest ecosystems in balance.

Recent Publications

Diet composition of data-limited marlins (Istiophoridae) in the Northwest Atlantic

Genome sequence of Fraser's dolphin morbillivirus isolated from a stranded Fraser's dolphin (*Lagenodelphis hosei*) in Hawai'i

Recent Publications Continued

Brevetoxicosis in Florida manatees (*Trichechus manatus latirostris*): Plasma proteomics for Florida red tide biomarkers

Reference genome assembly of the false killer whale (*Pseudorca crassidens*)

Ensuring the future of Atlantic bluefin tuna

Applications of active-acoustic and complementary technologies in marine ecosystem science

Optimized methods for obtaining sequencing-quality RNA from blubber of free-ranging cetaceans collected under field conditions

Success of restoration strategies in preventing extirpation of 2 critically endangered coral species

Molecular relatedness-based analyses reveal breeding site philopatry in female bluntnose sixgill sharks (*Hexanchus griseus*)

Assessing differences among elasmobranch nurseries to aid conservation based on a genomics framework

Mapping the marine distribution of eulachon (*Thaleichthys pacificus*) in the Northeast Pacific using environmental DNA

Genomic selection for low salinity tolerance in the eastern oyster *Crassostrea virginica* in Louisiana and Chesapeake Bay populations

Tolerance to future elevated CO_2 conditions in sablefish (*Anoplopoma fimbria*), a deep-water benthic dwelling fish species

The bacterial community composition of American Lobster (*Homarus americanus*) embryos and recently hatched larvae held under experimental laboratory conditions

DNA-based identification of anadromous fishes (*Alosa* spp., Family Clupeidae) in stomach contents of marine groundfish

Accounting for Intra- and Intergenomic Sequence Variation in Reference Barcodes Improves eDNA Metabarcoding Biodiversity Assessment

Biomonitoring in the Anthropocene: Urban estuary environmental DNA tracks marine fish, terrestrial wildlife, and human diet

Beyond Biodiversity: Incorporating UncertaintyInto Metabarcoding Data for Improved Inference ofEcological Relationships

Characterization of Marine Fauna Assemblages in the Presence of Upside-Down Jellyfish (Genus *Cassiopea*) at Jobos Bay National Estuarine Research Reserve (JBNERR), Puerto Rico

Ancient DNA from shells reveals delayed genomic erosion and rapid immune adaptation in the critically endangered black abalone

Evaluation of siRNA-mediated knockdown of heat shock protein 16.2 in adult *Acropora cervicornis*

Recent Publications Continued

Organic matter respiration stoichiometry in the Arctic Ocean is linked to shifts in plankton community composition

Adaptive genomic divergence parallels migratory behavior in Atlantic bluefin tuna

Prospects of multipurpose biomonitoring for fisheries assessment based on environmental nucleic acids

Estimating genetic diversity of abundant oceanic dolphins through repeated environmental DNA sampling

One Assay to Rule Them All: Development of a Global Environmental DNA Tool to Support Range-Wide Surveys of an Imperiled Sawfish and Its Application in the Eastern Tropical Pacific

Diverse Cyanopeptides follow distinct temporal succession patterns in freshwater harmful algal blooms