NOAA Partners Join CalCOFI to Examine the Potential of 'Omic Research

'Omics is the term for a set of genome-based technologies used for biological analysis at the molecular level (i.e., DNA, RNA, or proteins) to identify organisms and their function.

AOML researcher Dr. Kelly Goodwin has teamed with colleagues at the J.C. Venter Institute and Scripps Institution of Oceanography to integrate modern, genome-based technologies ('omics) into the 65-year-old California Cooperative Oceanic Fisheries Investigations (CalCOFI) program.

Microbes underpin the function of the earth's biosphere by regulating marine food web dynamics and associated cycles of carbon, oxygen, metals, toxins, and nutrients. Despite the potential to indicate ocean change, microbial diversity and function represent one of the great data gaps in marine observations. While traditional measurements, such as chlorophyll or total biomass, have long been used by oceanographers to describe this essential component of the earth system, these measurements are unrefined, providing little detailed information.

'Omics, however, can quickly identify the multitude of organisms and enzymes present in a sample. Therefore, "environmental intelligence" (who is there, what they do, and how they are impacted by changing conditions) can be gathered at a scope and detail never before available.

The CalCOFI study area is a productive and economically important ocean region. Like many areas of the ocean, it is under pressure from multiple stressors, including hypoxia, acidification, and warming. Understanding and predicting the impacts of these combined stressors is critical to the long-term economic stability and resiliency of the region.

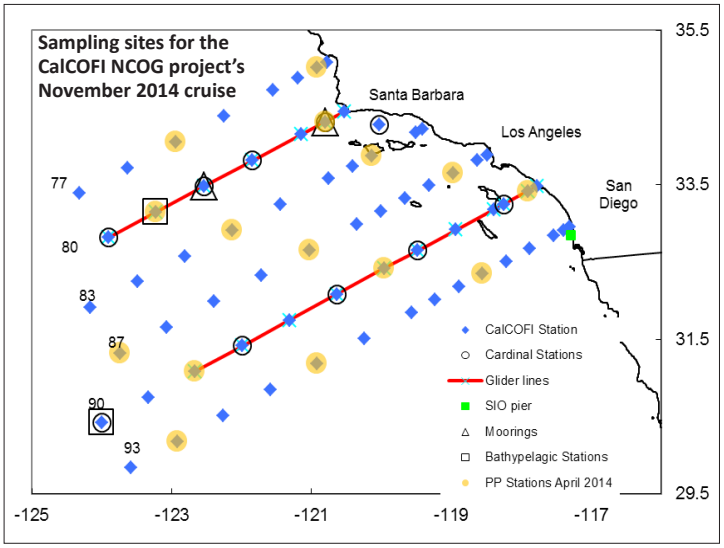
Incorporation of 'omics into CalCOFI will link the diversity and functional activity of microbes (viruses, prokaryotes and eukaryotes) to other measurements of ecosystem productivity in the context of physical and chemical perturbations. The work aims to improve understanding of factors that control ecosystem resiliency and tipping points. This project is a pilot for potential broader applications to other regions and across the NOAA fleet.

CalCOFI is one of the world's longest running ocean observing programs. It is a unique partnership between NOAA's National Marine Fisheries Service, the Scripps Institution of Oceanography, and the California Department of Fish and Game. Originally formed in 1949 to study the ecological aspects of the sardine population collapse off California, the current focus includes understanding this marine environment, managing its living resources, and monitoring the indicators of El Niño and climate change. Quarterly cruises are conducted off southern and central California to collect hydrographic and biological data on station and while underway between stations.

The November 2014 CalCOFI cruise aboard the RV *New Horizon* was the first to gather 'omics observations.

The NOAA-CalCOFI Ocean Genomics (NCOG) project represents a joint activity for NOAA's Office of Oceanic and Atmospheric Research (OAR) and the National Marine Fisheries Service (NMFS). Support was received from the NMFS Office of Science and Technology, OAR's Office of Ocean Exploration and Research (OER) and AOML, and the U.S. Integrated Ocean Observing System (IOOS).

The inaugural CalCOFI expedition for this new project was completed aboard the Scripps Institution of Oceanography RV *New Horizon* in November 2014, with samples presently undergoing metagenomic (DNA identity) and metatranscriptomic (RNA to identity function) processing.



Cisco Werner, Director of NOAA's Southwest Fisheries Science Center, Tilana Konotchic, Ph.D. student on the project, Kelly Goodwin of AOML, and Margot Bohan of NOAA's Office of Ocean Exploration and Research with their poster at the CalCOFI Conference in La Jolla, California.

AOML microbiologist Dr. Kelly Goodwin attended the California Cooperative Oceanic Fisheries Investigations (CalCOFI) conference in December. Kelly and her colleagues presented a poster highlighting a new project that introduces cutting-edge metagenomic and meta-transcriptomic analysis into the 65-year-old CalCOFI program.