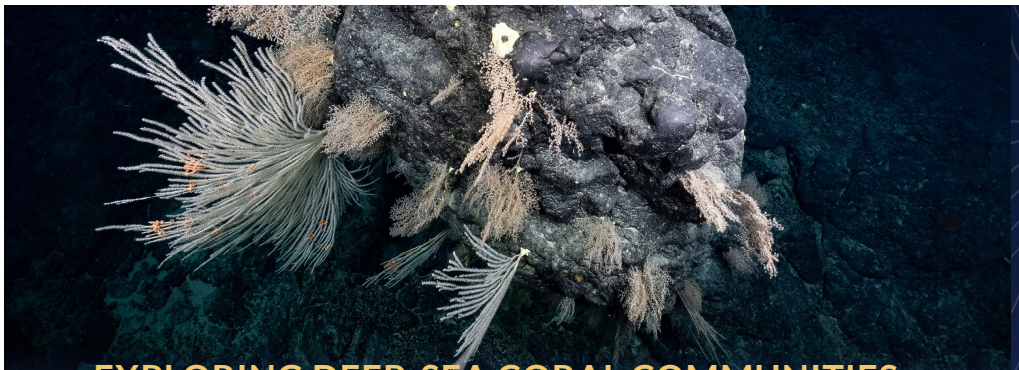

EXPLORING DEEP-SEA CORAL COMMUNITIES IN THE CENTRAL PACIFIC WITH GENOME SKIMMING AND ENVIRONMENTAL DNA

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Deep-sea corals and their wide diversity of associated species are an important contributor to global biodiversity. Currently there is limited understanding of the biodiversity, taxonomy and connectivity of deep-sea coral communities, particularly in remote areas like the Central Pacific. A more clear understanding of this information is important for the conservation of deep-sea coral communities, and is also relevant to the management of marine conservation areas throughout the region, including the Papahānaumokuākea Marine National Monument and the Pacific Remote Islands Marine National Monument.

Environmental DNA (eDNA) based methods can help address these knowledge gaps, as they provide rapid ways to characterize biodiversity, while only requiring minimally invasive water sampling. In addition to biodiversity characterizations, there are many practical applications to the use of eDNA, including the detection and monitoring of species that are of interest to resource management, such as endangered, invasive, or fisheries species. Such eDNA-based approaches can be particularly powerful for the study of difficult to access places like the deep sea, as they have the potential to provide large amounts of information without requiring much time collecting samples. However, success in this space hinges on the ability to collect physical samples that can be paired with detailed imagery whenever possible, so that the detected eDNA can be compared against well-curated reference libraries. Expeditions onboard E/V *Nautilus* provide rare and important opportunities to advance this work.

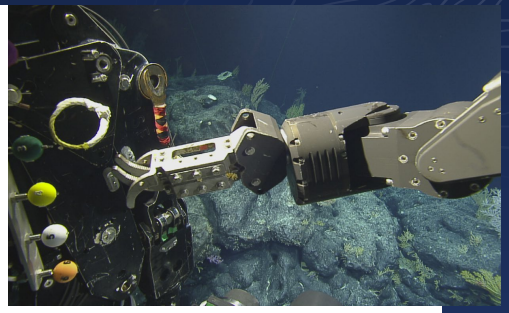
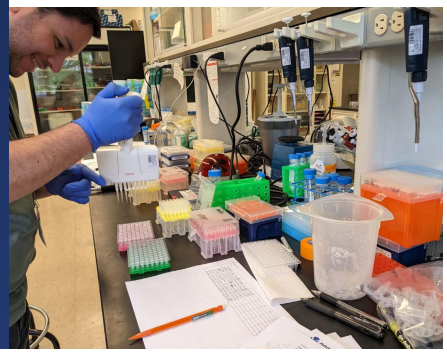


Figure 1. ROV *Hercules* triggering a Niskin bottle mounted on the ROV, thereby collecting a water sample near a deep-sea coral community for the study of eDNA.

Figure 2. University of Rhode Island graduate student Jane Carrick retrieving an eDNA water sample from the Niskin bottle mounted on ROV *Hercules* (photo credit: Steve Auscavitch).

Since 2018 our team has collaborated with the Ocean Exploration Trust to collect eDNA samples and vouchered deep-sea coral specimens on E/V *Nautilus* expeditions across the Central Pacific (Figures 1–2). With support from NOAA Ocean Exploration, we are using these samples to build the first voucher library explicitly targeting octocorals of the Central Pacific. In support of this effort, we are utilizing 170 deep-sea coral samples collected during E/V *Nautilus* expeditions, in addition to octocoral samples collected by other programs that are archived at National Museum of Natural History, Smithsonian Institution. These samples have been subjected to genome skimming using Illumina NovaSeq and HiSeq platforms, a novel sequencing approach that provides insights on biodiversity and evolutionary history at lower costs than traditional methods (Figure 3).

Analyzing these data we have been able to produce 251 novel, draft mitochondrial genomes, and extracted 247 complete sequences of MutS, a DNA repair protein that is useful for studies of evolutionary history and biodiversity of different organisms. These have been combined with previously generated and publicly available MutS sequences to generate an eDNA reference library for octocorals in the Central Pacific. These data represent more than 52 genera within 21 families of deep-sea corals, and include a number of new species that are currently in the process of being described.



Future efforts will include additional analyses to determine the genetic relationships of these species to other octocorals, as well as metabarcoding eDNA samples collected across the Central Pacific. Between 2018–2022, we have obtained 226 eDNA samples from nine separate E/V *Nautilus* expeditions, with 85 additional samples added from three expeditions in 2023. While metabarcoding of these eDNA samples is ongoing, initial tests applying an early version of our updated DNA voucher library have shown promising results, with the ability to detect more species and an increase in the ability to distinguish species. Once data collection is complete, we will apply these data to better characterize patterns of octocoral community biodiversity by geography and habitat variables. Finally, we will compare community structure by geography to better understand patterns of connectivity or dispersal barriers to species distribution.

Figure 3. Steve Auscavitch preparing coral samples collected by E/V *Nautilus* for genome skimming at the Genetics Laboratory of the NOAA Northwest Fisheries Science Center.