

FROM SEEPS TO SEAMOUNTS

E/V *Nautilus* Expedition Samples in 2021

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Continued efforts by the Ocean Exploration Trust staff, contractors, and partners to engage the Scientist Ashore community resulted in an increased quantity and diversity of samples collected by E/V *Nautilus* in 2021. Season-wide, over 450 sample collections were recovered, including biological voucher specimens, sediment cores, rocks and crusts, and eDNA extracts. Scientists Ashore were able to connect and participate via the integrated OET Science Portal that allowed more comprehensive interaction with watch standers on board *Nautilus* using collaborative tools. Building on the success of the 2020 season's collaborative sampling effort, a sample request tracker was employed for collections in the Papahānaumokuākea Marine National Monument (PMNM) and the Exclusive Economic Zone (EEZ) surrounding Hawai'i to maximize the availability of sampling products to the scientific community and to minimize disturbance of monument biological, geological, and cultural resources. From these areas, 132 rock samples and cores totaling over 650 kg of material were collected and sent to the Marine Geological Samples Laboratory at the University of Rhode Island Graduate School of Oceanography for curation. In addition, 166 biological samples were deposited at the Museum of Comparative Zoology at Harvard University to facilitate scientific studies of biodiversity in these regions.

CASCADIA MARGIN SEEP ECOSYSTEMS – Tamara Baumberger and Lila Ardor Bellucci

Over the past decade, the number of known active methane seeps along the Cascadia margin has increased dramatically from fewer than 100 to more than 1,000 (Merle et al., 2021). To better understand their influence on the biogeochemistry and ecology of the region, 34 of these sites have now been characterized by E/V *Nautilus* ROVs, and an additional five have been visited by R/V *Falkor's* ROV *SuBastian*. Working with NOAA Ocean Exploration and OET, cruise NA128 investigated diverse seep sites within six regions along the Cascadia margin off the US Pacific Northwest coast to identify relationships among depth,

geological setting, chemical composition, methane output, and the biological community supported. Over 150 bulk samples of gas, methane hydrate, seawater, sediment, rock, and fauna were collected from actively seeping sites, and they were subsampled for a wide range of analyses that are currently underway. Sampling spanned diverse habitats, including bacterial mats, clam beds, tubeworm bushes, background sediments, and the overlying water column (Figure 1). Analysis of these sample collections will increase understanding of the sources and fates of the gas exiting the seafloor, sediment biogeochemistry, microbial and macrofaunal communities in seep-driven ecosystems, and seep-related hard ground formation. An extensive multi-beam sonar data set collected by *Nautilus* provides more constraints on the number of seeps at the Cascadia margin and improves methane flux estimates. The detailed maps constructed from this data set allow more in-depth analysis of seafloor structures. Importantly, the data collected along the Cascadia margin will provide a baseline for studies that inform fisheries management decisions, coastal carbon cycles, climate models, and knowledge of the natural resources and hazards along active margins, all of which have wide-ranging implications for the Blue Economy.



FIGURE 1. Samples of vesicomyid clams collected from a seep site off the Cascadia margin during NA128.

SPONGES IN THE PAPA HĀNAUMOKUĀKEA MARINE NATIONAL MONUMENT – Christopher Kelley

Direct collections of sponges from Papahānaumokuākea Marine National Monument yielded insights into potential new sponge species dwelling in this fully protected marine conservation area. In all, 13 sponge specimens were collected during expedition NA134: 12 glass sponges (Hexactinellida) and one demosponge (Demospongiae). The spicules of 11 of these sponges were examined microscopically and photographed on shore following bleach digestion of small aliquots from each specimen (Figure 2). Hexactinellid specimens included three members of the family Farreidae, two in the genus *Farrea*, and one that could only be identified as being a farreid. Other hexactinellid specimens included three phoronematids, all probably in the genus *Poliopogon*; two euplectellids, one a new species in the genus *Hertwigia* and another that is likely a new species in the subfamily Corbitellinae; and two euretids, one a new species in the genus *Periphragella* and the other a new species in the genus *Heterorete*. One of the *Poliopogon* sp. that was bright yellow when collected was also believed to be dying. The lone demosponge was one of the 11 specimens examined microscopically and was determined to be in the genus *Poecillastra*. Two other hexactinellid specimens were not examined microscopically but are believed to be another phoronematid in the genus *Poliopogon* and the other in the family Rossellidae. The current plan is to submit new species descriptions for the *Periphragella* sp. and the *Heterorete* sp. after additional examination this year.

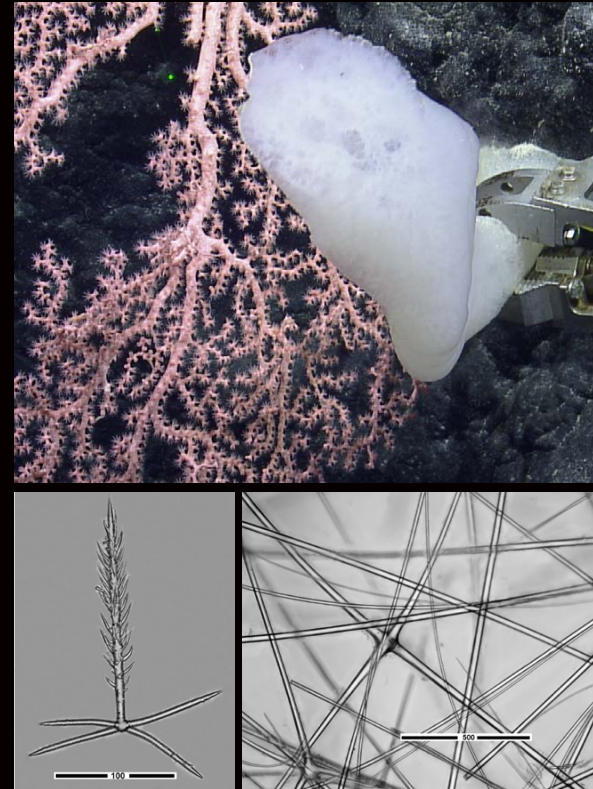


FIGURE 2. Spicule microscopy and in situ imagery for specimen NA134-063, a phoronematid glass sponge in the genus *Poliopogon*. Image credit: C. Kelley

DEEP-SEA FOOD WEBS – Elizabeth Miller

Sea cucumbers are abundant and important members of deep-sea communities that consume low-quality detrital material and make it available for higher trophic levels. They have a variety of strategies for surviving on detritus, but the potential role played by their gut microbiomes remains largely unstudied. Symbioses between animals and microbial communities residing in their guts have been widely documented, especially for animals that consume low-quality food. In 2021, seven deposit-feeding

sea cucumbers were collected between 500 m and 4,000 m depth around the Hawaiian Islands and across the Papahānaumokuākea Marine National Monument during expeditions NA134 and NA135 (Figure 3). To determine the influence of gut microbiota on their diets, the specimens will be dissected to isolate their gut contents from their body tissues. Gut microbial communities will be characterized using 16S rRNA sequencing, and stable isotope analysis will be used to quantify microbial reworking and processing along the length of the animals' gut tracts. The use of stable isotopes will also indicate what types of organic material, detrital versus microbial, are utilized by sea cucumbers at different depths. As food supply and quality decline with depth, we expect to find that gut communities are increasingly utilized to break down detritus. Deeper-living sea cucumbers may also directly consume their gut bacteria as an additional food source. Obtaining specimens across a wide depth range will permit direct examination of how these animal-microbe symbioses vary as a result of environmental conditions.

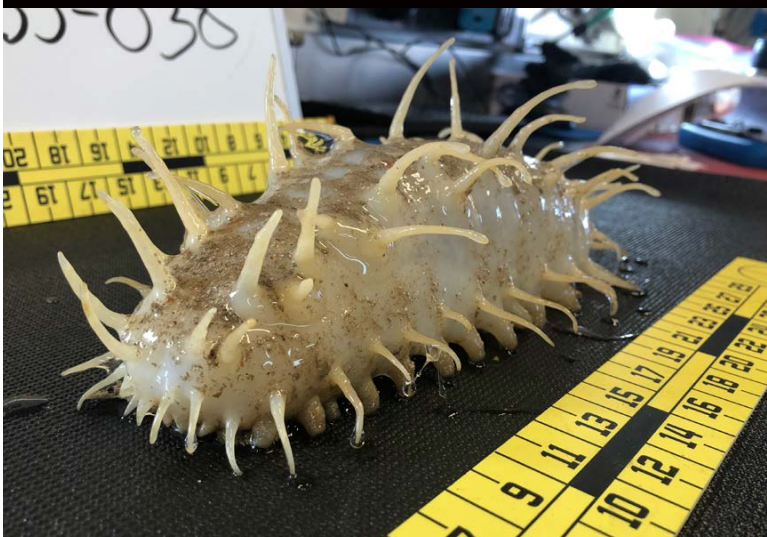


FIGURE 3. A sea cucumber (*Oneirophanta* sp.) collected during NA134 in Papahānaumokuākea Marine National Monument.