# Schmidt Ocean Institute Expedition Report

## Deep Coral Diversity at Emperor Seamount Chain 2019

Chief Scientist Dr. Les Watling

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# 1 Overview

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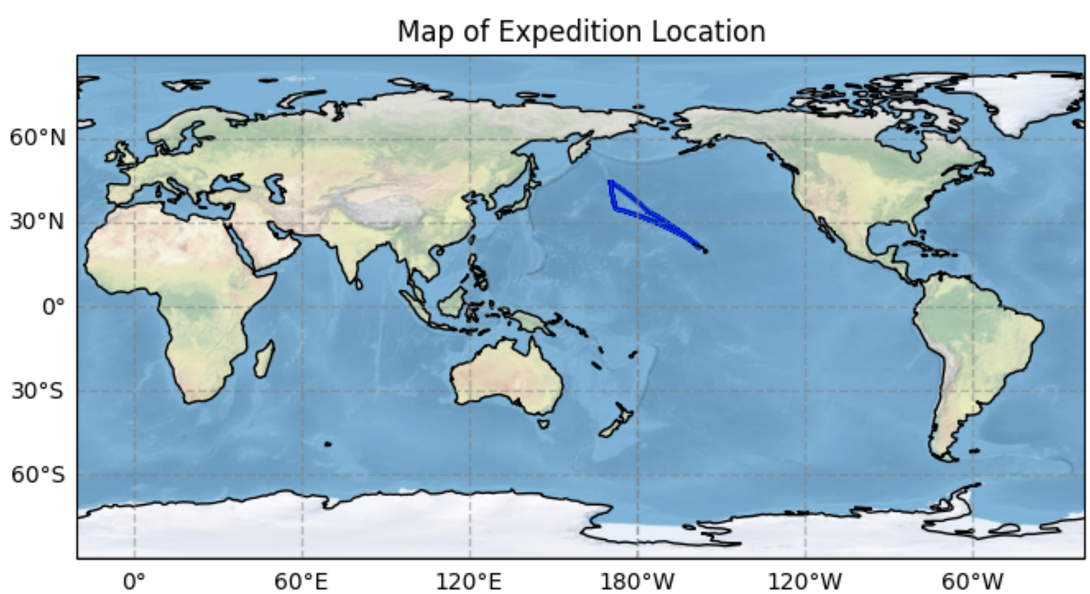
|---|---|
| SOI Expedition ID | FK190726 |
| Vessel | *R/V Falkor* |
| Expedition Name | [Deep Coral Diversity at Emperor Seamount Chain 2019] |
| Expedition Dates | 2019/07/26 - 2019/08/26 |
| Departure Port | Honolulu, Hawaii |
| Termination Port | Honolulu, Hawaii |
| Ocean | Pacific |



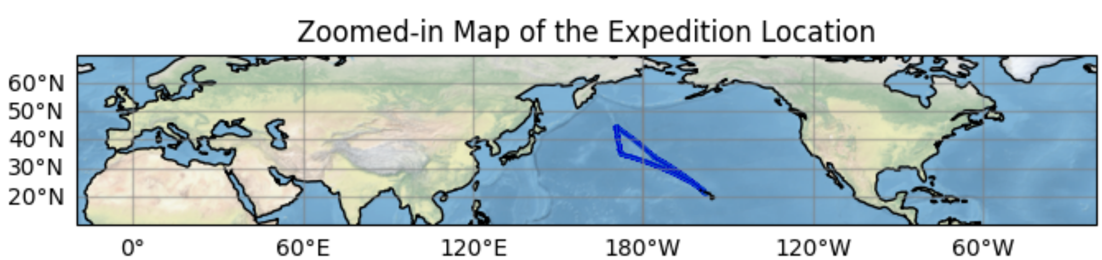




Figure 1: Map of Expedition Location

## 1.1 Expedition Overview

Most biogeographic boundaries are associated with water mass changes along coastlines. This expedition, however, sought to examine changes in water mass characteristics and associated benthic octocorals and sponges in the open sea. The goal of this project was to search for such a biogeographic boundary, thought to occur along the Emperor Seamount chain. The deep bathyal fauna of the Aleutian Ridge is completely different from that of the Hawaiian Ridge, so the science team hypothesized that the change in faunal makeup would occur close to the Main Gap in the Emperor Seamount chain, where the currents flow from west to east.

### 1.1.1 Authorizations and Permitting

No permits were needed for this expedition.

### 1.1.2 Expedition Timeline

The expedition commenced on July 26, 2019, departing from Honolulu, Hawaii, USA, and returned to Honolulu, Hawaii, USA, on August 26, 2019.

## 1.2 Project Description

The primary objective of the expedition was to explore and determine the nature, location, and extent of the biogeographic transition between the North Pacific and North Pacific Boreal bathyal provinces, that is, between the Aleutian Arc and the Northwestern Hawaiian Ridge, and to understand their phylogeographic connection. The expedition explored along the Emperor Seamount chain, as it is the only area between the Aleutian and Hawaiian Ridges where the seafloor is found at bathyal depths. That is, the seafloor is shallower than the abyss and at the same depths as the northern and southern ridges.

# 2 Expedition Accomplishments

This project was coupled with a science support grant from NOAA OER to sample the bathyal benthos along the Emperor Seamount chain in order to determine whether a biogeographic transition or boundary zone exists separating the North Pacific Boreal Province from the North Pacific Province.

## 2.1 At-sea Accomplishments

### 2.1.1 Science

Due to the remoteness of the Emperor seamounts, half of the expedition time was devoted to transiting to the research sites. Samples were obtained from seven (7) seamounts in the Emperor Chain and one unnamed seamount on Hess Rise over the course of eleven (11) ROV dives (Figure 2 & Figure 3). Samples and data collected included:

- 231 invertebrate specimens (not counting species growing on larger species),
- 32 fish species were identified from video and still images,
- DNA samples were taken from the collected octocorals,
- 38 water samples for eDNA analysis,
- 70 water samples encompassing 4570 L for radioisotope tracers,

- 31 rocks for geological analyses,
- 20,000 km2 of multibeam bathymetric and backscatter data,
- a gravimeter was continuously run,
- 10 magnetometer deployments over 7 seamounts, and
- ADCP surveys along the chain to determine current velocities and depths.

Due to COVID-19, many labs were closed following the expedition, which delayed sample analysis, yet a sufficient number of species have been identified. These identifications confirm the presence of a biogeographic break between the Jingu and Annei seamounts, most likely a consequence of the strong west to east current flowing through the 100 km gap between those seamounts.

Eight (8) bathymetric seamount surveys with the EM 302 multibeam system were carried out, some on transits between sites, and on the long transit from Honolulu to Hess Rise. Mapping statistics are as follows: 20,193 km2 total area mapped (8,824 km2 on eight (8) seamounts, 11, 369 km2 on transit from Honolulu to Hess Rise)

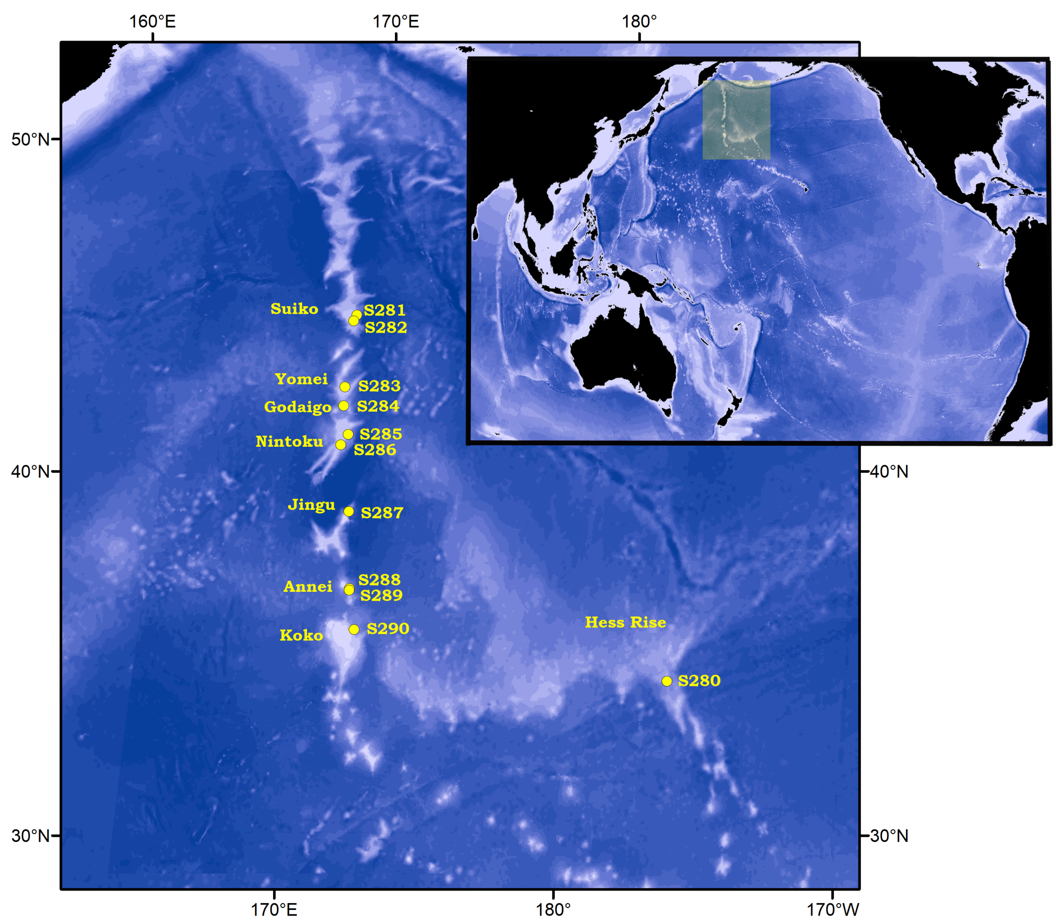



Figure 2: Composite map of the study sites (labeled) in the Emperor Seamounts and Hess Rise along with ship track (yellow line). Rectangular map is SRTM15+ bathymetry with FK190726 and preexisting multibeam data overlaid in brighter rainbow colors, all overlaid on Google

Earth imagery. For context, the Aleutian Trench lies to the north and the Hawaiian Ridge to the south and east.

### 2.1.2 ROV

Eleven (11) ROV dives on Hess Rise and then following the Emperor Seamounts from north to south, respectively took place: Suiko, Yomei, Godaigo, Nintoku, Jingu, Annei, Koko (Figures 3-9)

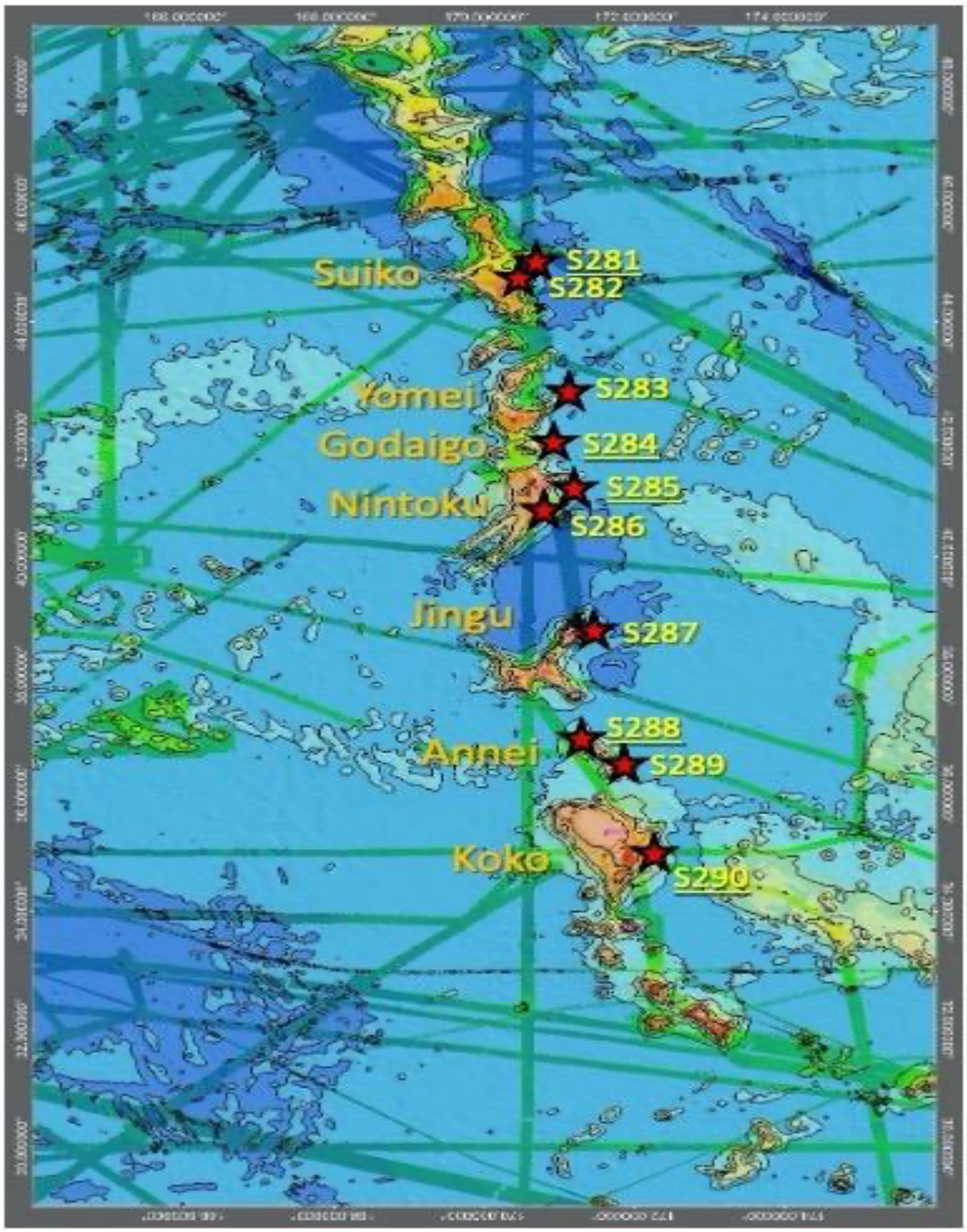



Figure 3: ROV SuBastian dive sites in the Emperor Seamount chain indicated by red stars and labels (e.g., S281). Hess Rise dive not shown. Same bathymetric presentation as in Figure 2.

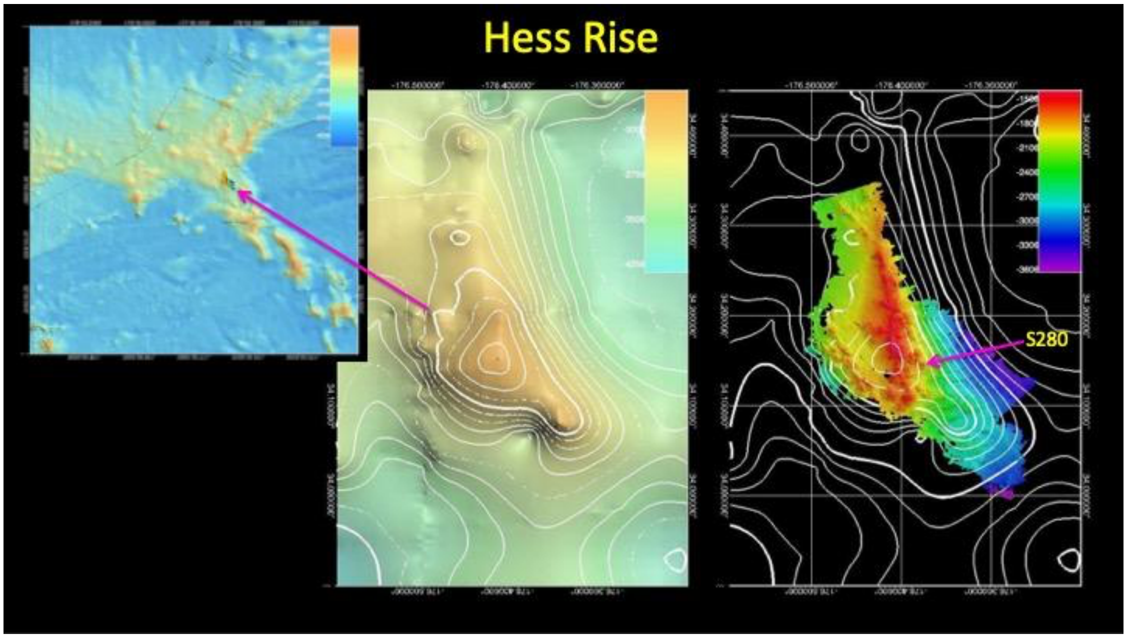



Figure 4: Location of Hess Rise (inset on left) and study site (center) using SRTM15+V2 global topography (Tozer et al., 2019). Dive site location and multibeam data collected (right) overlain on SRTM15+V2 200-m contours.

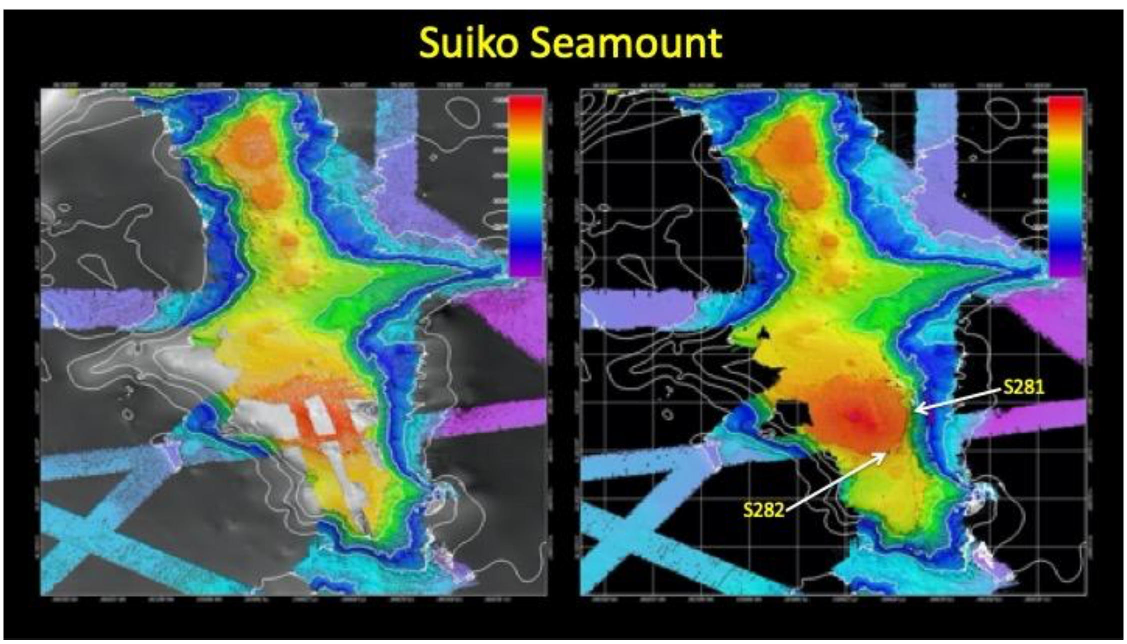



Figure 5: Suiko Seamount preexisting multibeam data on SRTM15+V2 (left) and after our surveys with dive sites annotated (right) overlain on SRTM15+V2 1000-m contours.

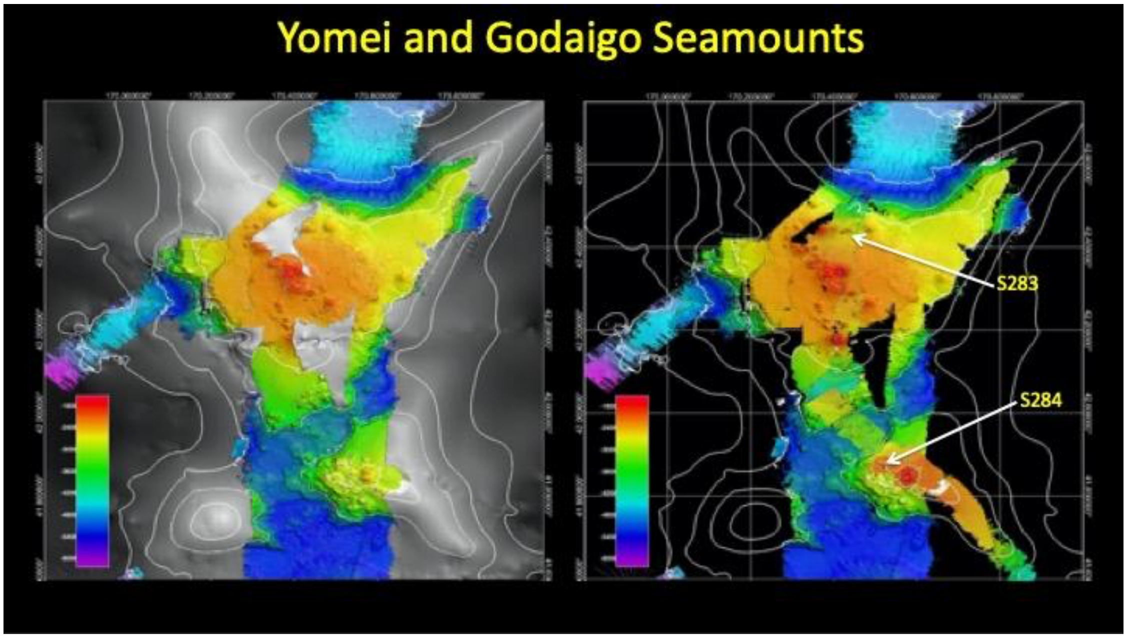



Figure 6: Yomei and Godaigo Seamounts preexisting multibeam data on SRTM15+V2 (left) and after our surveys with dive sites annotated (right).

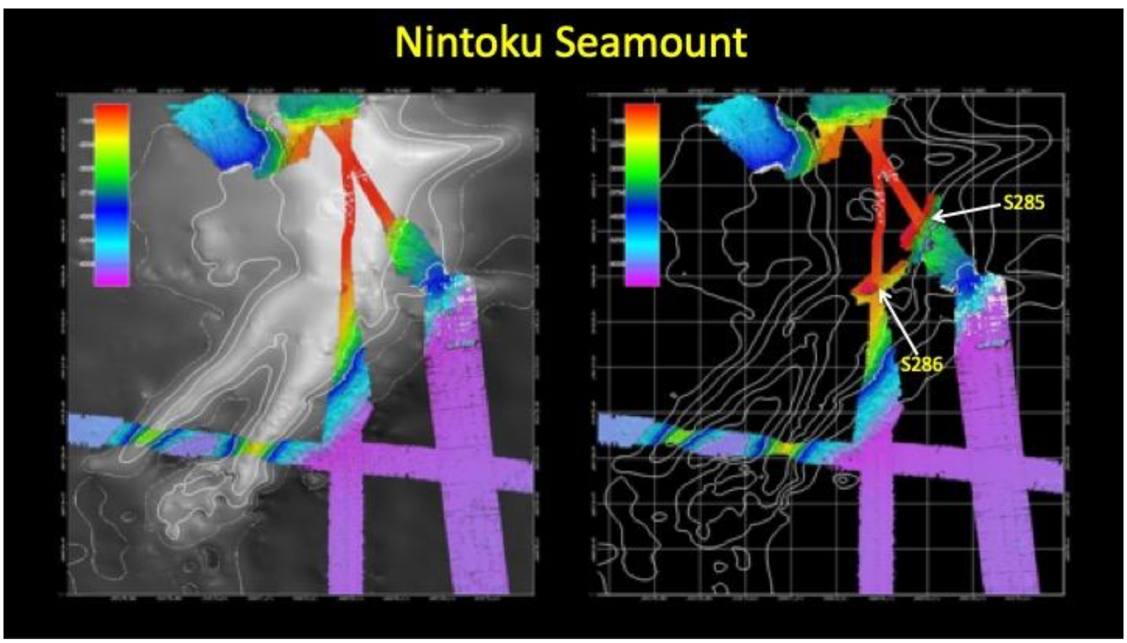



Figure 7: Nintoku Seamount preexisting multibeam data on SRTM15+V2 (left) and after our surveys with dive sites annotated (right).

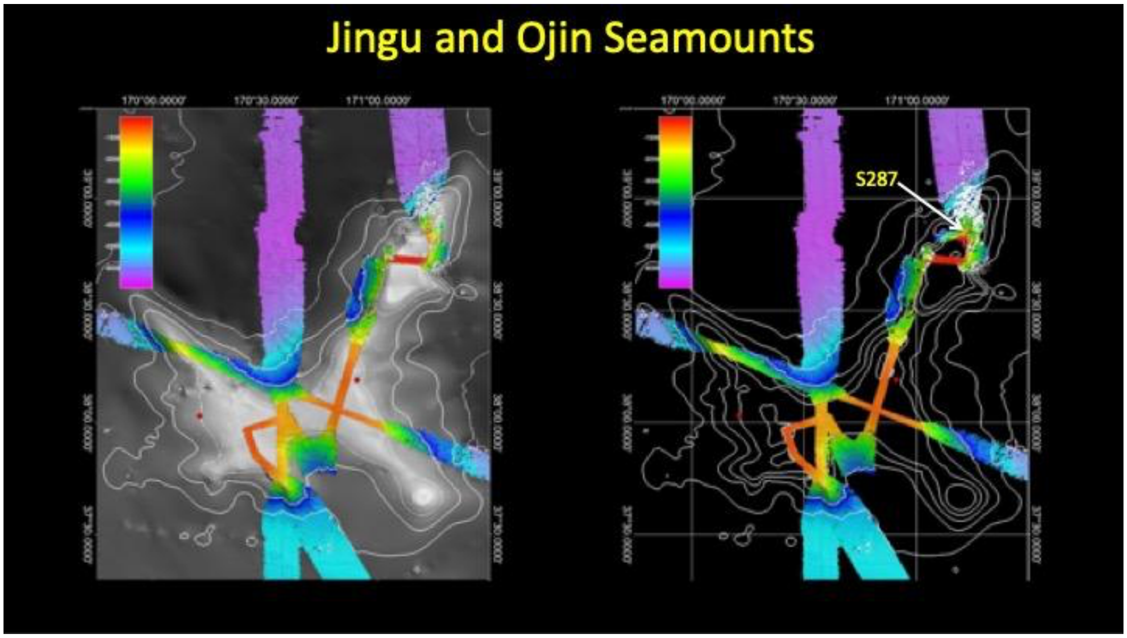



Figure 8: Jingu and Ojin Seamounts preexisting multibeam data on SRTM15+V2 (left) and after our surveys with dive site annotated (right).

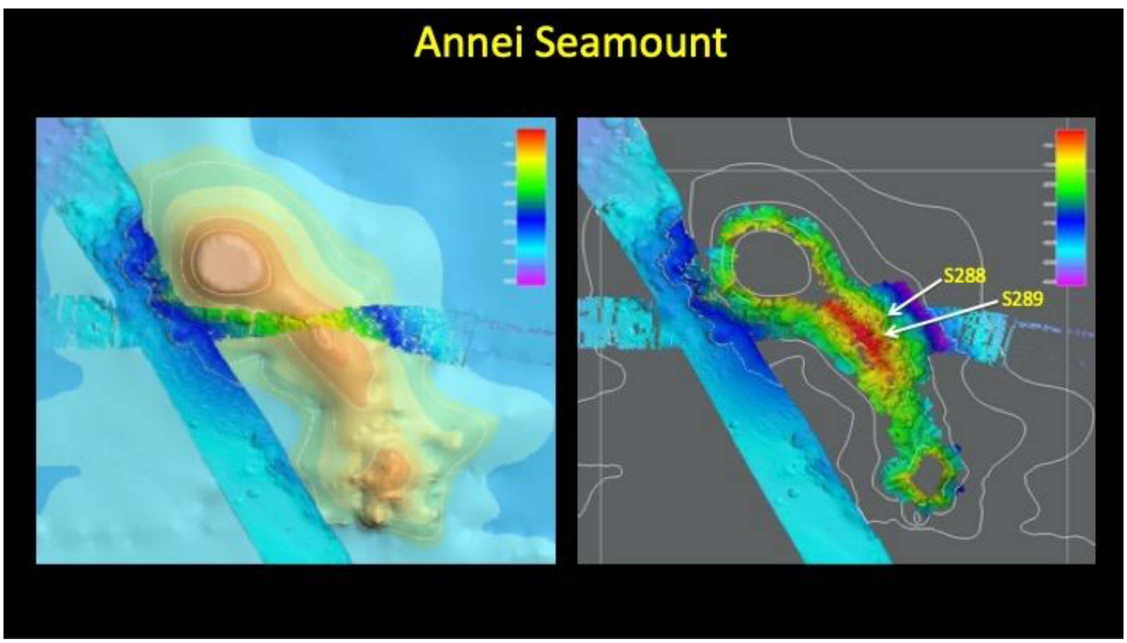



Figure 9: Annei Seamount preexisting multibeam data on SRTM15+V2 (left) and after our surveys with dive sites annotated (right).

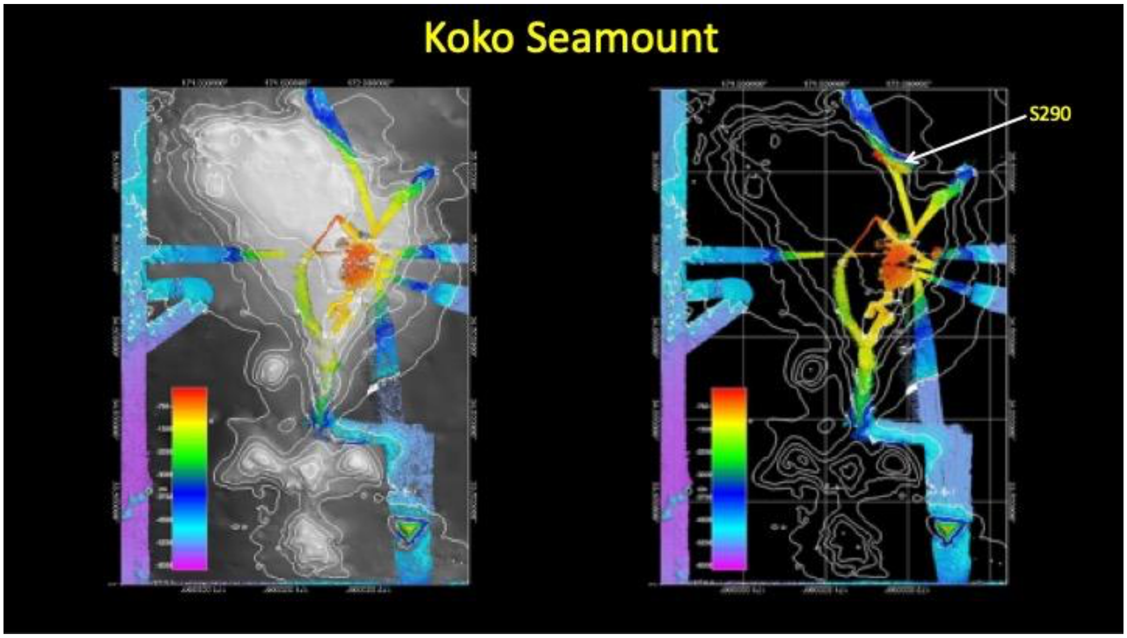



Figure 10: Koko Seamount preexisting multibeam data on SRTM15+V2 (left) and after our surveys with dive site annotated (right).

### 2.1.3 Innovative Technologies

Samples were collected to study microbial films on octocorals, microbial components of the seamount sediment, and eDNA was collected via water samples. A standard chemistry method was developed and adapted for seawater analysis; the process included concentrating radium, thorium, and actinium isotopes from the water column using MnO-coated acrylic fibers, using 45-75 L water samples collected from Niskin bottles or the ship's seawater intake. To capture the isotope ratios at the benthic boundary, MnO-fiber were mounted in a sealable bottle on ROV SuBastian. The bottle housing the fiber was fabricated so that the fiber was sealed on the descending and ascending part of the dive and opened only during bottom time, capturing only the boundary layer isotope signatures. Samples for cesium isotope measurement were collected from Niskin bottles or the ship's seawater intake and were filtered through a KNiFC ion exchange resin; this method was recently developed and adapted for seawater analysis.

### 2.1.4 Software Used

For the geophysics and acoustical oceanography work:

- Schmidt Ocean Institute's (SOI), marine technicians and science team members processed the EM 302 multibeam bathymetric data while at sea using QPS Qimera and MB-System software (Caress & Chayes, 1996).
- Dr. Fabio Tontini of the Institute of Geological and Nuclear Sciences (GNS) in New Zealand processed marine gravimetric data after the cruise by using internally developed code scripts and equations. He also provided the marine gravimeter.
- Dr. John Smith processed the marine magnetic data d after the cruise by using the Generic Mapping Tools (GMT) software (Wessel et al., 2019).

- The University of Hawaii Data Acquisition Systems (UHDAS) group at the University of Hawai'i processed the ADCP data after the cruise using software they developed. The UHDAS suite is run on NOAA and UNOLS vessels.

## 2.2 Post expedition activities and accomplishments

Geological sample cutting and descriptions were carried out by colleagues in the UH Earth Sciences Department, Dr. Aaron Pietruszka and Professor Michael Garcia, after the cruise. Thin sections for petrographic microscope studies were also ordered and supported by funds from the NOAA OER award.

# 3 Impact to date

## 3.1 Overview

In 2007, Dr. Watling attended a meeting in Mexico City to help provide an assessment of deep-sea benthic biogeography. However, it became clear that there were not enough biological samples to provide distribution information on a global basis. Instead, using theories about water masses and the evolution of fauna over time, the meeting group proposed the existence of a series of biological provinces at bathyal, abyssal, and hadal depths, which they published in 2009 (Vierros et al., 2009) and revised in 2013 (Watling et al., 2013).
In the intervening years, remotely operated vehicles, such as ROV SuBastian, were built with vastly improved imaging capabilities, making it possible to map the distribution of species over wide areas of the ocean. These images provided data that could be used to test some of the province ideas proposed in the 2013 paper (Watling et al., 2013).
As such, Dr. Watling and the science team hypothesized that a biogeographic boundary was likely to be present separating the Central Pacific benthic fauna from the North Pacific. The one place where a boundary might be found, they suggested, was along the Emperor Seamount chain, which they proposed to visit with *R/V Falkor.* The expedition yielded the finding of a boundary at a place called the Main Gap, that separates Jingu seamount from Annei Seamount. At the Main Gap, there is a strong and deep current that runs from west to east and seems to limit the movement of the fauna from the Hawaiian Ridge to the Emperor seamounts.
Knowledge of the biogeography of the benthos in the deep sea is an important aspect of conservation management. If protected areas are to be designed and located on the high seas, it is important that all biogeographic areas and their disparate faunas be included in the protection. Thus, knowing where the biogeographic boundaries or transition zones are, is a critical aspect of that decision-making process. This expedition revealed that a boundary that was predicted to occur in the area of the Main Gap, did, in fact, occur at that location. Therefore, the theoretical approach of using water mass distributions to predict biogeographic boundaries might help identify other biogeographic boundaries in the future.

## 3.2 New Discoveries & New Species

A total of 231 specimens were collected by the ROV SuBastian during the expedition. While the taxonomic work is still ongoing, some taxa have now been identified, including some specimens representing small species removed from the surfaces or interiors of larger species such as octocorals or sponges.
Among the hydroids collected, one new genus and two new species have been described and published in Zootaxa (Calder and Watling, 2021). Sea urchins collected were two new records for the area. Sponges and octocorals have so far been identified to genus level or determined to be new to science. Bamboo and other corals from Jingu seamount and further north seem to all be new species (not yet described). Some of the bamboo coral specimens were used in a paper

reviewing the genus *Lepidisis*, noting that most species have been incorrectly assigned to that genus, and several specimens from the northern Emperor seamounts are new *Lepidisis* species (Watling & France, 2021).

Figure 11: *Hydractinia galeai* - hydrozoan. Photo Credit: Dr. Les Watling

Figure 12: *Latebrahydra schulzei* - hyodrozoan. Photo Credit: Dr. Les Watling

In addition to the collected specimens, the imaging capabilities of the ROV were used to document other taxa. Chief among those were the benthopelagic fishes, crabs, and one benthopelagic hydromedusa. With help from several fish taxonomists at the Pacific Biological Station in Nanaimo, B.C., Canada, 32 fish taxa were identified, most to species level. Dr. Dale Calder, from the Royal Ontario Museum, identified the hydromedusa, a species that seems to lurk in the deep cold waters of the global ocean.

**Octocorals:** Among the 89 octocoral samples taken for genetic sequencing, 41 specimens have been identified with previously unknown sequences, likely representing newly described species. The DNA sequences revealed two at-sea misidentifications at the family level, for example, an Acanthogorgiidae (Acanthogorgia sp.) identified at sea as a Plexauridae, and an encrusting Alcyoniidae (Alcyonium nr roseum) that was misidentified as a stoloniferous octocoral.

**Bamboo corals:** Twenty-three bamboo coral colonies were sampled, and the genetic sequences reveal eleven unique species present. Among the bamboo corals analyzed, are three species with individuals distributed across multiple seamounts; two of these were north of the biogeographic gap, one species was collected from both Suiko and Nintoku and another was collected from Godaigo, Nintoku and Jingu. The third species (Isidella kerI1a) crossed the gap, being found on Suiko, Jingu and Annei. Bamboo corals with the Isidella kerI1a genetic barcode (based on the combined mtMutS-5’, mtMutS-3’, igr4) are geographically widespread; previously identified in Hawaii, New Caledonia, New Zealand, the western North Atlantic, and the Caribbean. The family Primnoidae were the next most abundant octocoral sampled (n=15 colonies). Eight (8) specimens were identified as Parastenella ramosa and were collected on all five seamounts north of the gap, but not farther south; no other primnoids species were sampled across multiple seamounts. Finally, eleven (11) specimens in the Family Chrysogorgiidae were collected. All specimens taken north of the gap were new and are awaiting description whereas those from south of the gap belong to previously described species, some of which are known from the NW Atlantic.

**Sea Pens:** A phylogenetic analysis that included rock pens sampled during the expedition is the first to suggest that the adaptation of sea pens to live on solid rock has evolved just once.

**Microbes**: Most studies of microbial diversity focus only on the bacteria (Archaea and Bacteria) through a single method approach, generally that of high-throughput sequencing (HTS) of 16S rRNA gene fragments. Coral, sediment and seawater samples collected from depths of ~1300 to 2000 m on seven seamounts in the Emperor chain north of Hawai’i were subject to a biphasic analysis of all three domains by culturing and HTS. Bacteria from thirteen phyla were cultivated from all samples, but according to HTS those in the Proteobacteria, Actinobacteria, and Tenericutes were most common in corals, sediments, and seawater, respectively. Cultivated Eucarya comprised yeasts, fungi, and a nanoflagellate, Cafeteria sp. HTS analysis of coral mucus and tissue detected a range of predatory flagellates and photoheterotrophic bacteria, plus Mycoplasma-like organisms. Bacteria communities in corals varied markedly and lacked an obvious “core” microbiome, but the number of samples was low. Bacteria communities in sediments did not differ significantly between locations and were dominated by Gammaproteobacteria, Actinobacteria, and Acidobacteria, but they did differ significantly from those in adjacent seawater and corals. Taxa related to bacteria detected in sediments are anaerobes involved in reduction of nitrite and ammonium oxidation, and sulfur cycling. Preliminary results of this work, the first all-domain analysis of microbial communities in different sample types on the Emperor Seamounts, shows over 5000 unique features, and affirm findings of broad taxonomic diversity and novelty among microbial eukaryotes in the ocean.

**Video**: The videos for all the dives were annotated by the University of Hawai'i School of Ocean and Earth Science and Technology (SOEST) Deep-sea Animal Research Center (DARC) through a separate NOAA contract. Those data are now available and an analysis of the taxa present at each dive site using hierarchical cluster analysis produced two main groups of sites:

1) those from Suiko to Jingu seamount; and
2) Annei, Koko and Hess Rise seamounts.

The first group can be subdivided into the shallow dives vs. the deeper dives. That is, the fauna of the dives that started at about 1500 m was distinct from the fauna at the dives that started around 2000 m. A similar, but not as distinct, division seemed to be present at the southern dive sites. Jingu and Annei seamounts are separated by a relatively short distance, about 200 km. So, for the attached fauna, the flow through the deep part of the Main Gap definitely seems to form a Current Wall, much as the science team hypothesized. On the other hand, the small amount of data that was obtained for benthopelagic fauna suggests that there is a larger transition area, from Nintoku to Koko seamounts, a distance of about 600 km.

## 3.3 Data

| Data Type | Curator | Completed |
|---|---|---|
| Environmental sensor data collected by *R/V Falkor* | Rolling Deck to Repository | Y |
| ADCP data | University of Hawaii | Y |
| Field magnetometer | MGDS | Y |
| High resolution bathymetry and backscatter | MGDS | Y |
| Radium fibers and resins holding cesium isotopes | Dulai lab at the University of Hawaii<br>Data is available upon request | Y |
| Specimen Images | MGDS | Y |
| Annotated imagery | Squidle+ | Y |
| Molecular genetic samples | Stored at France Lab at the University of Lousiana Lafayette and Baco-Taylor lab at Florida State University | |
| Rock samples | University Hawaii Geological Sample Facility samples request link | Y |
| Taxon details of the newly discovered *Genus Latebrahydra* | World Register of Marine Species | Y |
| Taxon details of the newly discovered hydrozoan species *Latebrahydra schulzei* | World Register of Marine Species | Y |
| Taxon details of the newly discovered hydrozoan species *Hydractinia galeai* | World Register of Marine Species | Y |
| Water Chemistry Data | | N |
| Geochemical vertical distribution data (including Radium, Cesium isotopes, and corresponding salinities) | | N |
| Genetic analysis data from octocoral specimens and other fauna samples | GenBank | N |

| Data Type | Curator | Completed |
|---|---|---|
| DSC ages and growth rates | | N |
| Complete Paleontological Specimens | | N |

### 3.4 Publications

Calder, Dale R., and Les Watling. 2021. "Report on Hydrozoans (Cnidaria), Excluding Stylasteridae, from the Emperor Seamounts, Western North Pacific Ocean." Zootaxa 4950 (2): 201–47. https://doi.org/10.11646/zootaxa.4950.2.1.

Ganguly, Upasana, and Scott C. France. 2020. "Role of Depth and Substrate in the Evolution of Sea Pens (Pennatulacea, Octocorallia): A Phylogenetic Study." In. AGU. https://agu.confex.com/agu/osm20/meetingapp.cgi/Paper/653649.

Raineault, Nicole, and NOAA Office of Ocean Exploration and Research. 2020. "New Frontiers in Ocean Exploration: The e/v Nautilus, NOAA Ship Okeanos Explorer, and r/v Falkor 2019 Field Season." Edited by Ocean Exploration Trust and Joanne Flanders. Oceanography 33 (1): 1–122. https://doi.org/10.5670/oceanog.2020.supplement.01.

Watling, Les. 2020. Raw Video Frame Grab Images Acquired with ROV SuBastian During r/v Falkor Expedition FK190726 (2019). https://doi.org/10.1594/IEDA/327032.

Watling, Les, Amy Baco-Taylor, Sarah Bingo, Glenn S. Carter, Henrietta Dulai, Scott France, Becca Lensing, et al. 2020. "Finding Biogeographic Boundaries in the Deep Sea: Alaska, Hawaii, and the Emperor Seamount Chain." In. AGU. https://agu.confex.com/agu/osm20/meetingapp.cgi/Paper/650037.

## 4 References

Caress, D. W., & Chayes, D. N. (1996). Improved processing of Hydrosweep DS multibeam data on the R/V Maurice Ewing. *Marine Geophysical Researches*, *18*(6), 631–650. https://doi.org/10.1007/BF00313878

Vierros, M., Cresswell, I., Escobar Briones, E., Rice, J., & Ardron, J. (2009). *Global open oceans and deep seabed (GOODS): Biogeographic classification—UNESCO Digital Library* (IOC. Technical Series, p. 96) [Programme and meeting document]. UNESCO. https://unesdoc.unesco.org/ark:/48223/pf0000182451

Watling, L., & France, S. C. (2021). Toward a Revision of the Bamboo Corals: Part 2, Untangling the Genus Lepidisis (Octocorallia: Isididae). *Bulletin of the Peabody Museum of Natural History*, *62*(2), 97–110. https://doi.org/10.3374/014.062.0202

Watling, L., Guinotte, J., Clark, M. R., & Smith, C. R. (2013). A proposed biogeography of the deep ocean floor. *Progress in Oceanography*, *111*, 91–112. https://doi.org/10.1016/j.pocean.2012.11.003

# 5 Appendix

## 5.1 Cruise Blogs

- A series of Cruise Log Videos are available.
- ROV SuBastian performed dives 280-290. Livestream Dive List.

## 5.2 Science party information

Scientists aboard *R/V Falkor:*

| Scientist | Institution |
|---|---|
| Les Watling | University of Hawaiʻi - Mānoa |
| Sarah Bingo | University of Hawaiʻi - Mānoa |
| Glenn Carter | University of Hawaiʻi - Mānoa |
| Henrietta Dulai | University of Hawaiʻi - Mānoa |
| Scott C. France | University of Louisiana at Lafayette |
| Becca Lensing | University of Hawaiʻi - Mānoa |
| Nicole Morgan | Florida State University |
| Brendan Roark | Texas A&M University |
| John R. Smith | University of Hawaiʻi - Mānoa |
| Natalie Summers | University of Hawaiʻi - Mānoa |

## 5.3 Media

There was a range of media engagements and outreach activities carried out during this expediton. For further information, please contact SOI.