

A STUDY OF THE DIVERSITY AND COMMUNITY STRUCTURE OF FAUNA AT HANNIBAL BANK BASED ON IMAGERY DATA

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Abstract

Hannibal Bank is a biodiversity hotspot off the Pacific coast of Panama. Using the AUV SeaBED, 12 photo-transects of the seafloor systematically captured over 21,712 images during a research cruise in 2015. A subset of the images was analyzed to characterize the benthic community by identifying and quantifying visible fauna based on morphology. In addition, the dominant substrate types within each image was also recorded. Additional multivariate analyses of the faunal assemblage data were performed to study the factors important in structuring the benthic community, including geography, substrate, and depth. A total of 5,606 images were analyzed identifying 137 morphospecies from the phyla Annelida, Arthropoda, Chordata, Cnidaria, Echinodermata, Mollusca, and Porifera.

Introduction

Seamounts are significant components of the seafloor. Their elevated topography mark the bottom of the ocean with their unique structure (Clark *et al.* 2012). The International Hydrographic Organization defines a seamount as a discrete, large isolated elevation greater than 1000 meters in relief above the seafloor, characteristically of cone form (Iyer *et al.* 2012). There are an estimated 100,000 seamounts in the world and 30% of those are located in just the Pacific

Ocean (Wessel *et al.* 2010). In addition, only a small fraction of these have been studied (Iyer *et al.* 2012). Seamounts typically occur in linear chains or clusters and are often the result of either volcanic or tectonic activity (Taranto *et al.* 2012). The morphology of seamounts vary, but they can have a conical shape with distinct topographies on different parts of the structure including the base, flank or sides of the seamount, and the peak.

As common features of the seafloor, seamounts may play important roles in marine ecosystems (Shank 2010). Seamounts often share similar features including forming isolated regions with suitable rocky habitats with higher levels of biodiversity than the surrounding areas (Cunningham *et al.* 2013). These high levels of biodiversity have made seamounts an important focus of study (Shank 2010).

Seamounts have the potential to interact with currents to cause upwelling and, as a result, bring nutrients from deep waters. This increased nutrient flow may lead to higher levels of primary productivity resulting in higher levels of biodiversity and biomass (Iyer *et al.* 2012). In addition, seamounts provide hard substrate for specific species to attach, such as corals, sponges, and other sessile organisms that require a hard surface to settle and attach to.

With these unique characteristics, seamounts form a unique environment for various organisms to come together and thrive. Seamounts are recognized areas that have provided habitat and nutrients for many different types of organisms (Iyer *et al.* 2012). In addition, there have been seamounts are thought to potentially play a role in the isolation of populations. With seamounts occurring in long chains, separated by significant distances of soft sediment, they may affect the distribution of some species. This isolation is thought to contribute to increased rates of speciation at seamounts (Shank 2010). Alternatively, seamounts have been proposed to serve as “stepping stones” for dispersal for various organisms as well (Shank 2010). Many seamounts

share similar origins and possibly even similar topography, but they are also unique with their own individual depth ranges, morphology, and other environmental factors that make each a potentially unique biodiversity hotspot (Shank 2010).

Several studies have tested the factors that influence the biodiversity and abundance of seamount fauna. Samadi *et al.* (2006) found little support for increased rates of endemism between the Norfolk ridge seamounts and the new Caledonia slope, seeming to counter the argument for increased isolation at seamounts. However, they also reported high numbers of species indicating the seamounts were biodiversity hotspots. Cho and Shank (2010) found varying patterns of gene flow among four ophiuroid brittle star species among seamounts in the North Atlantic. A study of invertebrates and algae from the continental margin and seamounts in the southwest Atlantic Ocean off the coast of Brazil found distinct faunal assemblages from seamount peaks versus the continental margin, with the factors of distance from shore, temperature, dissolved oxygen and particulate organic carbon identified as being important environmental predictors of assemblage composition for invertebrates (O'Hara *et al.* 2010). McClain *et al.* (2010) reported significant change in the composition of faunal assemblages over a ~1500 m depth range at Davidson seamount. A study at Hudson Canyon found that faunal assemblages varied dependent on seafloor morphology, with distinct fauna dominating the canyon margins and flanks which were dominated by coarse-grained sediments (sponges, zoanthids, and cup corals), muddy seafloor (sea pen assemblages), and sandy seafloor (sea star assemblages) (Pierdomenico *et al.* 2017).

The benefits of seamounts are not limited to marine ecosystems. They have the potential to be an economic boon for many people. The increased productivity often associated with seamounts may provide a means for economic prosperity as well, by providing fertile fishing

grounds (Taranto *et al.* 2012). With this benefit comes the potential for increased human impact on these unique ecosystems and contributes to the urgency to study these environments in order to understand potential to anthropogenic impacts.

Seamounts can be found in both deep ocean and off coastal shelves (Clark & Bowden 2015). Their proximity to land allows human impacts to occur. Fishing is one of the major impacts to seamount ecosystems, with disturbances to the coral and sponge aggregations a major threat to the ecosystem's longevity. Conservation of these areas is critical to ensure the survival of these valuable ecosystems found only on seamounts (Taranto *et al.* 2012).

Hannibal Bank is a geological feature located in the Gulf of Chiriquí. This bank has brought a lot of attention as it has become one of the world's largest regions for sports fishing. It is also considered a UNESCO World heritage site for its high levels of biodiversity and biomass. Although Hannibal Bank does not meet the technical criteria to be considered a seamount, it still shares similar qualities that a typical seamount would.

A research cruise in 2008 surveyed Hannibal Bank and found that it is composed of a combination of steep and gentle slopes, with multiple crests, rugose areas, gullies, and pinnacles (Cunningham *et al.* 2013). They also found that rocky substrate makes up 22.6km² of the bank and sediment 37.8km² and identified the rugose areas as primary targets for further research efforts as they may contain corals and their rigidity indicates that these should be some of the highest faunal diversity areas of the bank. A research cruise to Hannibal Bank in 2015 reported dense aggregations of the anomuran galatheid *Pleuroncodes planipes* at depths of 355-385 m along the flank of Hannibal bank in hypoxic waters (Pineda *et al.* 2016).

Hannibal Bank is a popular sports fishing area and also has artisanal fisheries. Therefore, the potential for human pressures to damage this unique ecosystem is high. The current study

will test the different factors that may be structuring the communities on the bank. It will contribute to a better understanding of the communities at Hannibal Bank, which can then help guide conservation efforts.

Material & Methods

Image Collection

A cruise onboard the M/V *Alucia* in spring 2015 was focused on Hannibal Bank. Images were collected by the Autonomous Underwater Vehicle (AUV) *SEABed*, in which the AUV was programmed to systematically take images along a photo transect to collect imagery of the benthos. Images of the seafloor were taken from a mean altitude of 3.5-4.5 meters above the bottom of a predefined path (Pineda *et al.* 2016). Each dive was unidirectional, meaning direction traveled linearly from north to south or east to west and dives were systematically planned in an attempt to obtain images from all aspects and topological regions of the bank. The AUV completed a total of 14 dives, 12 of which were analyzed for the current study (*see Figure 1*).

Image Analysis

Within a photo transect, every third image was analyzed in order to prevent overlap of area and the double-counting of organisms. In addition, as the AUV began taking pictures the moment it was beginning its descent to the seafloor, therefore we only analyzed images once the AUV had *Figure 1*. A map showing the dive tracks of the photo transects performed by the AUV SeaBED on Hannibal Bank. Each dive track is represented by a different color.

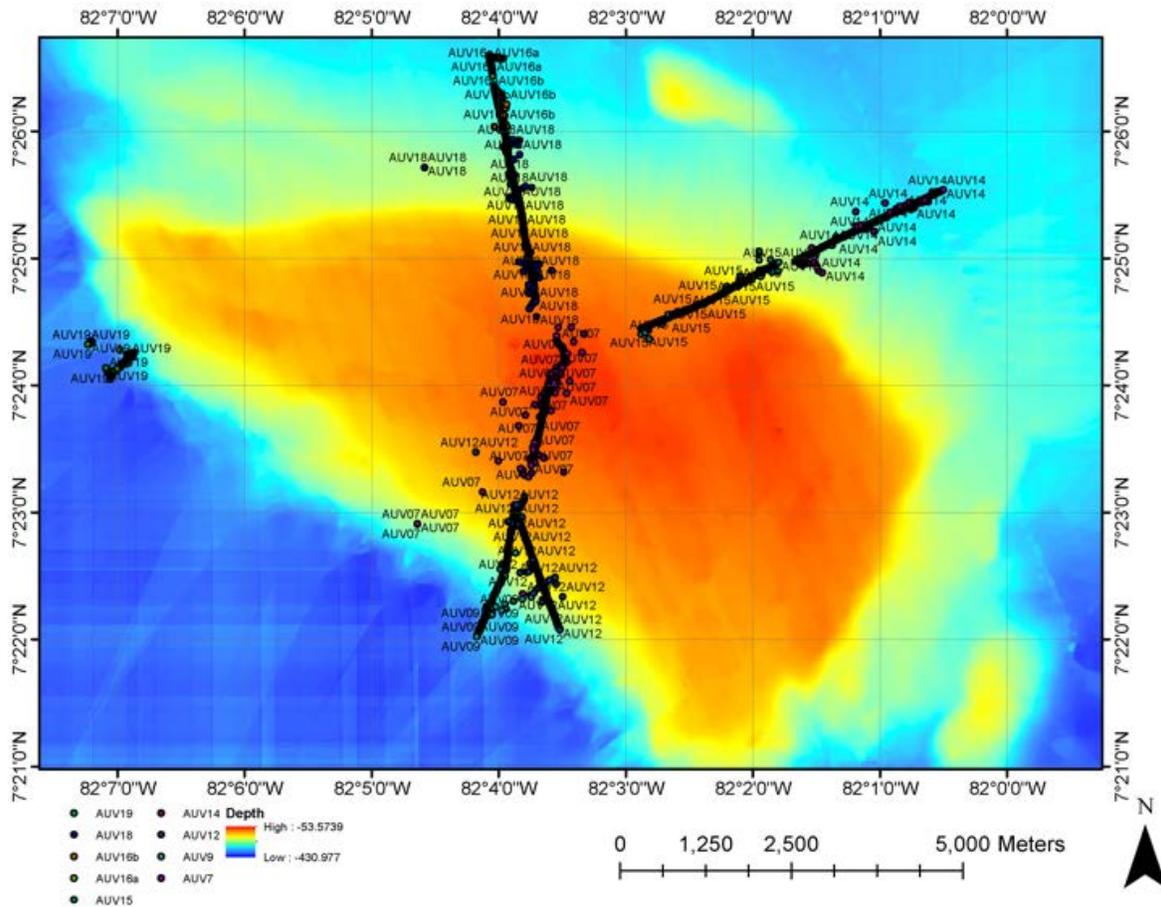


Figure 1. A map showing the dive tracks of the photo transects performed by the AUV SeaBED on Hannibal Bank. Each dive track is represented by a different color.

reached the seafloor. Therefore, although a total of 21,712 images were collected, of these, 5,606 images were included for analysis in the current study.

The image analysis included identification of all visible taxa to morphospecies, the quantity in which they occurred, and characterization of the dominant substrate types. During image analysis, a morphospecies image guide was compiled in order to ensure consistent identifications. This guide served as a reference when conservatively identifying similar organisms that appeared in the various dives and images. All “unknown” fauna that could not be

identified from the images were excluded from the analysis. The image analysis included the identification of all visible taxa to morphospecies, the quantity in which they occurred, and characterization of the dominant substrate types. During image analysis, a morphospecies image guide was compiled in order to ensure consistent identifications. This guide served as a reference when identifying, conservatively, similar organisms that reappeared in the various dives and images. All “unknown” fauna that could not be identified from the images were excluded from the analysis.

We also characterized the dominant substrate type in each image. Four categories were established: fine sediment, pebbles, cobbles, and boulders. Each type was identified within each image and the relative abundance was estimated.

Data Analysis

The abundance of each morphospecies was calculated for each image using methods similar to Pineda *et al.* 2016. Briefly, the area was calculated using image dimensions (pixels) from the camera and AUV altitude (meters). When AUV altitude data was missing from the vehicle metadata, the data gaps were filled in with average altitudes typically estimated from the altitude values 10 seconds prior and after the data gaps. We excluded observations when the data gaps for altitude were too large to estimate accurately. This resulted in an additional four percent of identifications that were removed from the analysis.

These modifications resulted in a final data set of 12,298 faunal observations included in our analysis. The area was used to calculate the abundance for each morphospecies per image. The abundance data were transformed by fourth root calculations in order to reduce the impact of very abundant and very rare taxa and used to make Bray-Curtis similarity matrices in PRIMER

v7 (Clarke *et al.* 2014). The resulting similarity matrices were then visualized by nonparametric multidimensional scaling (MDS) plots and the significance of differences among defined samples was assessed using analysis of similarity (ANOSIM) tests.

Multivariate analysis of faunal assemblage data using a Bray-Curtis similarity matrix has been widely used in ecological studies. Briefly, the MDS plots display relationships between variables and patterns of distribution (Clarke & Ainsworth 1993). The MDS plots can be considered to be a graphical representation of the Bray-Curtis similarity matrix. Therefore, the closer two sample points are to each other, the more similar the faunal assemblages are in those two samples based on community species composition. Conversely, the further apart two sample points are from each other in a MDS plot, the more dissimilar the faunal assemblages are from each other based on community species composition. These can then be used to identify potential patterns of community structure. The significance of this structuring can then be tested with an analysis of similarity (ANOSIM) test, which is an ANOVA-like hypothesis test that is used to evaluate a dissimilarity matrix instead of raw data (Clarke 1993).

Various multivariate analyses were performed to study community structure. The abundance data of each identified morphospecies was then binned into discrete samples in order to test the significance of multiple factors in determining faunal assemblage structure including: depth, dominant substrate type, and seamount topography.

For the factor of depth, observations were placed into samples of 25 m depth ranges ranging from 50 m depth to 425 m. The samples were then grouped into bins of: Very Shallow (50-75 m), Shallow (75-100 m, 100-125 m, and 125-150 m), Middle (150-175 m, 175-200 m, 200-225 m, 225-250 m, and 250-275 m), Deep (275-300 m, 300-325 m, 325-350 m, 350-375 m, and 375-400 m), and Very Deep (400-425 m). The significance of the dissimilarity between the

bins was then tested using an ANOSIM test. In order to investigate the factor of depth in more detail, a depth profile of the abundance of each phylum was also constructed to discern bathymetric patterns of distribution.

For the factor of dominant substrate type, observations were placed into samples where the dominant substrate type had >50% relative abundance using the categories Boulder, Cobbles, Pebbles, and Fine sediment. When no one substrate occurred in >50% relative abundance, the observations were categorized as multiple mixed categories: Mixed – Boulders, Mixed – Cobbles, Mixed – Pebbles, Mixed – Fine sediment, Mixed – Boulders/Cobbles, Mixed – Boulders/Fine sediment, Mixed – Cobbles/Pebbles, Mixed – Cobbles/Fine sediment, and Mixed – Pebbles/Fine sediment. The samples were then grouped into bins of substrate size: Large substrate types (Boulders, Cobbles, Mixed – Boulders, Mixed – Cobbles, and Mixed – Boulders/Cobbles), Small substrate types (Pebbles, Fine sediment, Mixed – Pebbles, Mixed – Fine sediment, Mixed – Cobbles/Pebbles, and Mixed – Pebbles/Fine sediment), and Mixed substrate types (Mixed – Boulders/Fine sediment and Mixed – Cobbles/Fine sediment). The significance of the dissimilarity between the bins was then tested using an ANOSIM test.

For the factor of topography, observations were first separated into dives and then the dives were partitioned into where they occurred on the bank: peak, flank (or side of the bank), and base. The samples were then grouped into bins of Peak (AUV_07_Peak, AUV_09_Peak, AUV_12_Peak, AUV_15_Peak, and AUV_18_Peak), Base (AUV09_Base, AUV14_Base, AUV16a_Base, and AUV19_Base) and Flank (AUV_09_Flank, AUV_12_Flank, AUV_14_Flank, AUV_15_Flank, AUV_16b_Flank, AUV_18_Flank, and AUV_19_Flank). The significance of the dissimilarity between the bins was then tested using an ANOSIM test.

Results

There was a total of 137 morphospecies identified from 6 different phyla (see Table 1). The phylum chordata had the highest number of identified morphospecies at 39, dominated by fish species. The next most diverse phylum was the arthropods with 35 morphospecies, dominated by brachyuran crabs, caridean shrimp, and anomuran galatheid squat lobsters. This was followed by the phylum cnidaria with 27 morphospecies, dominated by sea anemones and corals.

Table 1. A table showing the number of morphospecies identified in each phylum. There was a total of 137 morphospecies.

| Phylum | Morphospecies |
|---------------|----------------------|
| Chordata | 39 |
| Arthropoda | 35 |
| Cnidarian | 27 |
| Echinodermata | 21 |
| Porifera | 10 |
| Annelida | 5 |

The multivariate analysis testing the importance of the factor of depth in structuring communities found significant structuring of the communities based on depth regions when and Very Deep (400-425 m) ($p=0.001$, see Figure 2). Within the MDS plot, each of these depth regions are well observations were binned into 25 meter increments. The analysis identified 5

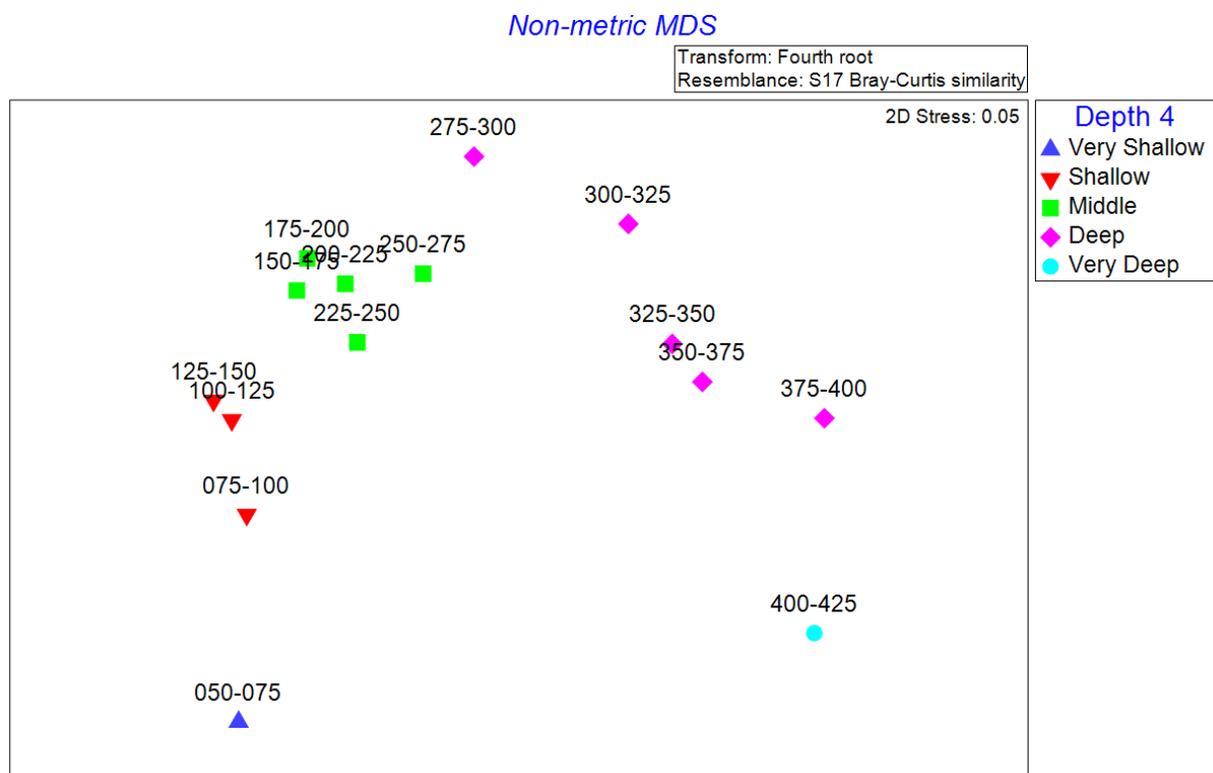


Figure 2. MDS Plot of morphospecies abundance placed into samples of 25 m depth ranges and samples binned into five depth regions: Very Shallow, Shallow, Middle, Deep, and Very Deep. $R = 0.832$, $p = 0.001$

distinct depth regions: Very Shallow (50-75 m), Shallow (75-150 m), Middle (150-275 m), Deep (275-400 m), clustered together and spaced out evenly between the rest of the groups. This indicates similarity within the groups which is also indicated by the high R -value of 0.832 and low p -value of 0.001 obtained from the ANOSIM.

In order to study the factor of depth in more detail, a depth profile of the abundance of the different phyla was constructed (see Figure 3). There is wide variation in the distribution of the abundance of the different phyla throughout the bathymetric range of Hannibal Bank. There is overlap between the phylum but there is greater abundance of arthropods found at the deeper ranges between 300 to 400 m. This is unique due to its comparison to other phyla who show

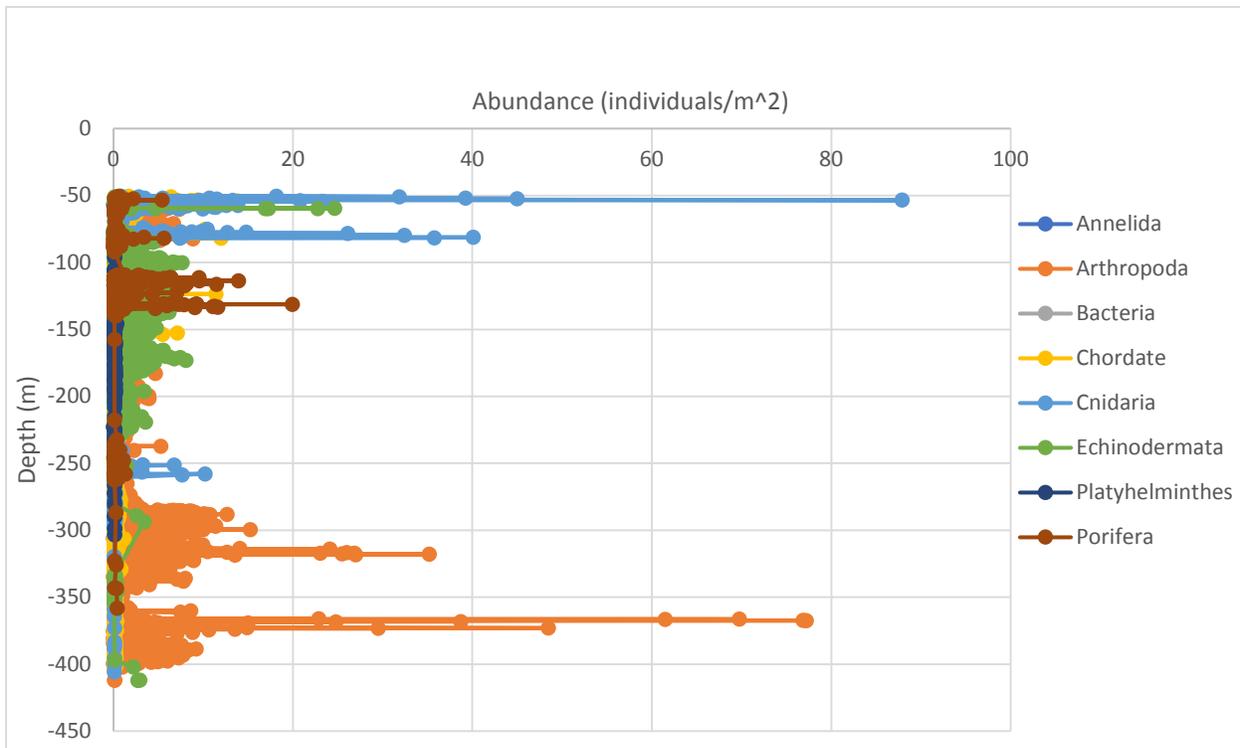


Figure 3. Abundance distribution of phyla by depth. The different phyla are represented by different colors.

limited presence in the deeper depth ranges. There is a greater abundance of cnidarians at the shallower depths, above 100 m. The echinoderms showed a mid-depth range abundance having a high abundance at shallow depths, but also showing a strong presence between 100 to 200 m. They were not limited as they were seen in all ranges of depth. Porifera also had high abundance around the 125 m depth range. The chordates were present at all depth ranges but not in relatively high abundances in any particular depth range.

The multivariate analysis testing the importance of the factor of substrate type found significant structuring of the communities when observations were grouped into samples by dominant substrate which were then binned into categories of size. The analysis identified 4 distinct substrate types: Boulder, Cobble, Pebble, and Fine Sediment ($p=0.001$, see Figure 4).

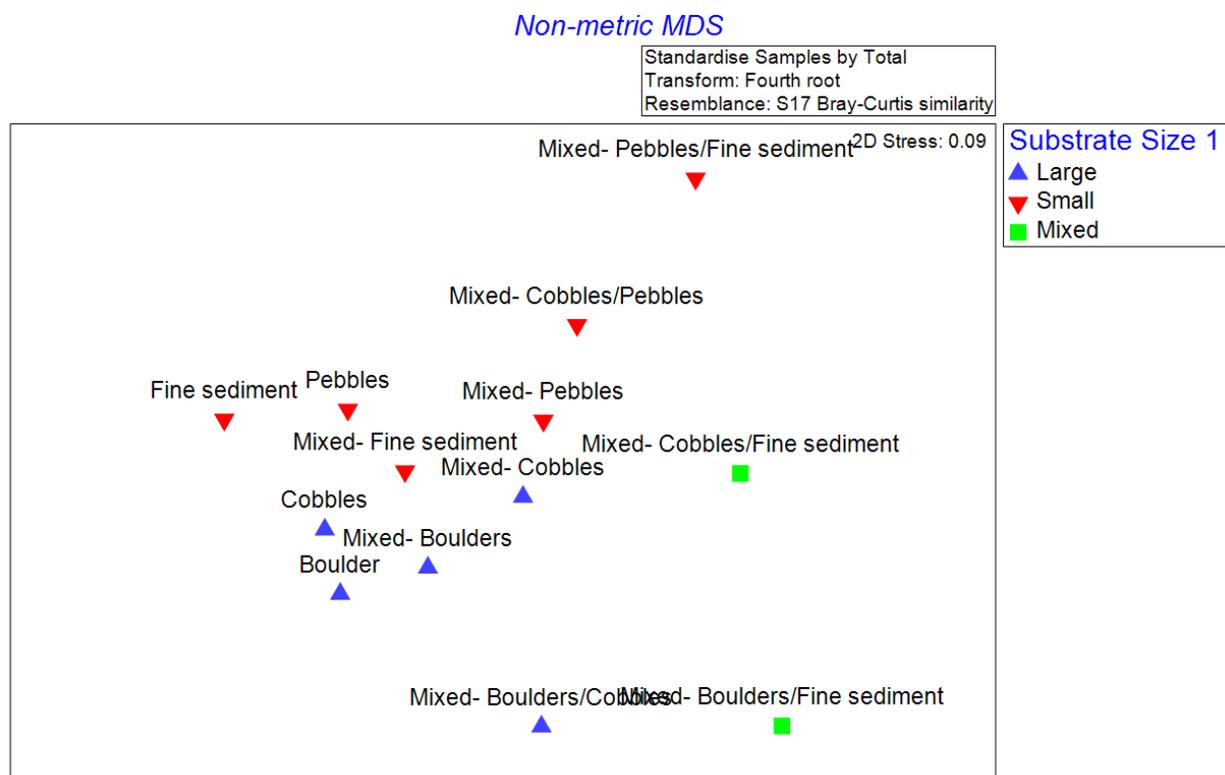


Figure 4. MDS Plot of morphospecies abundance placed into samples of substrate type (Boulders, Cobbles, Pebbles, Fine sediment, and multiple mixed categories) and samples then binned into bins of substrate size: large, small, and mixed. $R = 0.37$, $p = 0.001$

Although the clustering is not as distinct as for the depth analysis (apparent also with the lower R value of 0.37), the larger-sized substrate types cluster together and separate from the smaller-sized substrate types. The mixed substrate types are also distinct from within the large and small substrate sized bins. This is a highly significant result with $p = 0.001$.

The multivariate analysis testing the importance of the factor of topography found significant structuring of the communities based on where the observations were made relative to position on the bank. The analysis identified 3 distinct topographic regions: the peak, base, and the flank ($p=0.007$, see Figure 5). The peak and the base appear to be distinct from each other while the flank seems to be transitional between these two regions, with certain flank samples being more to peak samples and other flank samples being more similar to base samples. This

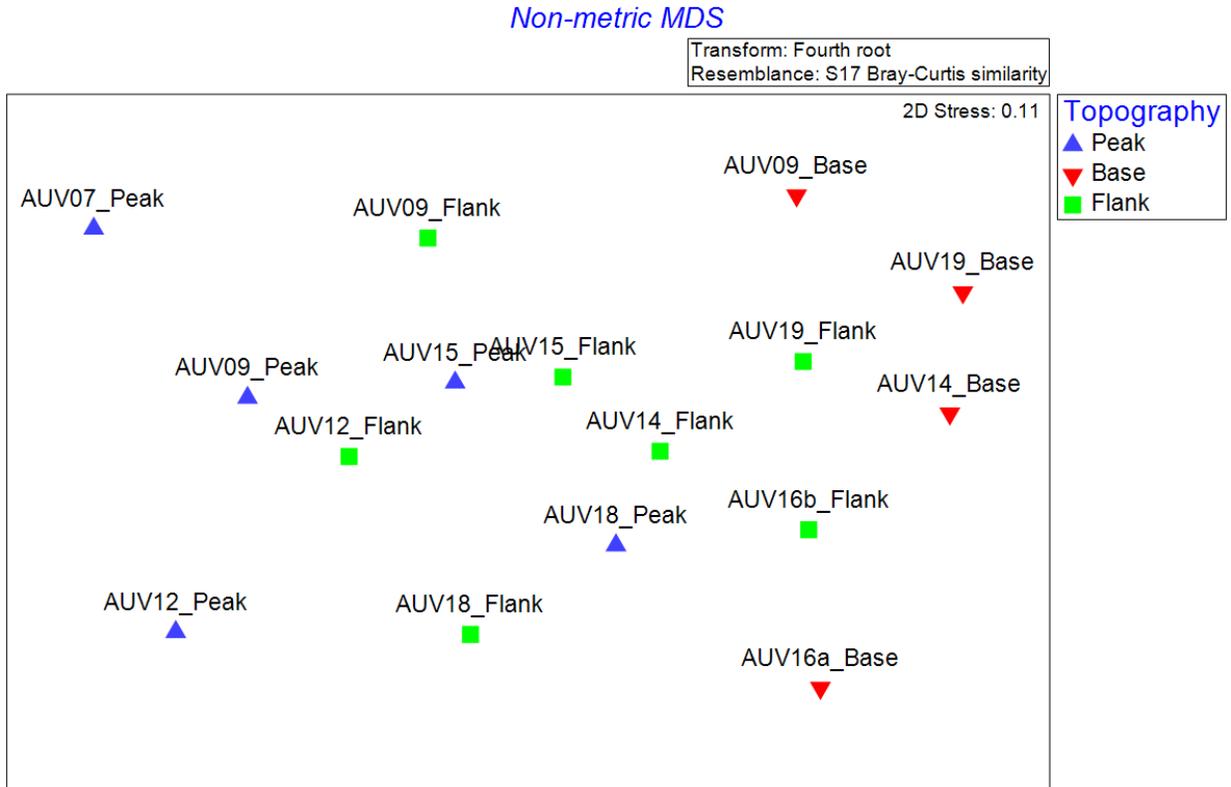


Figure 5. MDS Plot of morphospecies abundance placed into samples of dives partitioned into positions on the bank (peak, flank, and base) and samples then binned into bins of topography: peak, base, and flank. $R = 0.329$, $p = 0.007$

is reflected in the lower R value of 0.329.

Discussion

This study attempted to test factors thought to be important in structuring biological communities at seamounts and seamount-like structures. It identified the factors of depth, substrate, and topography as all playing significant roles in structuring the communities at Hannibal Bank based on community composition.

As seen in Figure 2, the observations partitioned into 25 m intervals clustered together forming five distinct faunal assemblages. The bin clustering indicates that there are specific communities being found in each depth region that is unique in itself, with samples within the cluster more similar to each other than to samples in other clusters. Figure 3 also supports this conclusion and provides additional insight to explain this result. There is a distinct bathymetric pattern of dominant abundances changing from different phyla with increasing depth (see Figure 3). The shallow depth regions are dominated by the phylum cnidaria with high abundances, which could be an explanation of why the very shallow and shallow regions are distinct from other depth regions on Hannibal Bank. The majority of cnidarians here are corals which are often found in shallower waters due to the need for sunlight for the zooxanthellae to photosynthesize. They are also often filter feeders and the peak of seamount features often have increased flow (Boehlert & Genin 1987). Cnidarians, like specific corals, have been found to provide habitats for various fish species and live in symbiotic relationships with echinoderms (Evans *et al.* 2016). Their presence in the peak and very shallow depths may have a significant influence on community structure.

The arthropods were very abundant in deeper waters, but not limited to those depths. Their presence might explain why the very deep and deep depth regions were distinct from other depth regions. It is possible that the type of substrate and availability of nutrients in that area attract such large densities of arthropod, such as arthropod swarms that have been identified there previously (Pineda *et al.* 2016). In addition, Cunningham *et al.* (2013) indicated that the flanks of Hannibal Bank had rocky habitat, that may attract arthropods in this particular depth region.

Sponges from the phylum Porifera made an appearance around 125 meters, which could be the beginning slopes of the flank. Chordates, primarily fish, were also relatively evenly distributed throughout the bank at all depths. The phylum Echinodermata was relatively evenly distributed in all depth regions, which could also contribute to the communities in each depth region. Although we observed this distinct bathymetric pattern at the phylum level, further analysis at the species level depth may show further faunal turnover with depth. Depth has also been shown to be correlated with species distributions in other studies (Clarke & Ainsworth 1993; Evans *et al.* 2016). These studies covered a wider range in depth, however similar patterns were observed at Hannibal Bank as well, despite the smaller depth range.

Substrate size was also found to be significant in structuring distinct faunal assemblages (see Figure 4). The samples in the larger rocky sediment types of boulders and cobbles had a distinct faunal composition with similarities within this substrate size while also being dissimilar to the samples in the smaller sized substrate types of pebbles and fine sediment. The mixed sample types were also distinct from both the large and small sized substrate types.

Topography was also found to be significant in structuring distinct faunal assemblages (see Figure 5). It appears that there are unique environments between the peak, base, and flank of the bank. The clustering of samples binned by topography is not as distinct as the other two factors. This is also reflected in the lowest R-value of 0.329 and highest p-value of 0.007 for topography. However, some clustering of the samples is observed, indicating that they are forming unique communities at these different topographic locations. The samples at the base and the peak locations did not cluster within each location, however they are different and distinct from each other. The flanks appear to be intermediary between the peak and the base. The flanks of Hannibal Bank are recognized to have larger, rocky sediment types which can be

beneficial for the communities formed on the steep edges, which could explain the abundance of arthropods at these depth and these regions (Cunningham *et al.* 2013). Pierdomenico *et al.* (2017) found similar results in a study of Hudson Canyon, where distinct faunal assemblages were associated with different substrate types.

It was found that the factors of depth, location, and substrate significantly structure the biological communities at Hannibal Bank. These results are similar to what has been found in other seamount and canyon areas. Understanding the factors that are important in creating faunal assemblages at Hannibal Bank allows us to assess the different communities that exist there and understand how they may be impacted with increasing human impacts. These results provide us insight into how to protect and care for this unique feature.

Acknowledgments

I would like to thank my mentor Dr. Walter Cho for all his support and guidance these past few years, and members of my committee, Dr. Mike Mooring and Professor Kerri Sevenbergen, for their contributions as well. I would also like to acknowledge Point Loma Nazarene's Summer Research Program and the Research Associates for the opportunity and funding to begin this experience in the field of science. In addition, the Captain and crew of the M/V Alucia, pilots and crew of submarines Nadir and DeepRover2, and the AUV SeaBED team for their important contributions to this data. Special thanks to Dr. Jesús Pineda, Chief Scientist of the cruise and finally Dr. Mark Mann for the opportunity to be a part of the Honors Humanities Program.

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