THE INFLUENCE OF A HAWAIIAN SEAMOUNT ON A MESOPELAGIC MICRONEKTION COMMUNITY

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ABSTRACT

The distribution of mesopelagic micronekton (small fish, crustaceans and cephalopods) is not uniform throughout the oceans. Seamounts are a feature that can possibly influence the abundance, biomass, diversity and taxonomic composition of a community of mesopelagic micronekton by introducing a hard substrate and benthic predators into a realm normally devoid of these. Cross Seamount, located roughly 295 kilometers south of the island of Oahu, Hawaii, has a summit that is 330m below sea surface and has a diameter of approximately 8km. Using a large, modified Cobb trawl, samples were taken both directly over and away from the summit of Cross Seamount to sample the community of the deep scattering layer during the day and the shallow scattering layer during the night. Trawls were conducted during two cruises to Cross Seamount in the spring of 2005 and 2007. All organisms collected were identified to the lowest taxonomic level possible resulting in a description of the local mesopelagic micronekton community over and around Cross Seamount. Results from this study indicate that there is a significant decrease in total abundance of organisms and an absence of certain diel vertically migrating taxa directly over the summit as opposed to away. This may be due to increased predation by tunas and other pelagic and benthic predators or by active avoidance of the summit due to the shallow topography and to the presence of predators. The overall taxonomic composition of the community over the summit is dominated numerically by epipelagic juvenile fish and stomatopod larvae while away from the summit the community is dominated numerically by mesopelagic fish, mostly Myctophid fish with the epipelagic juvenile fish and stomatopod larvae contributing little to the overall taxonomic composition. The community over the summit also contains two
species that appear to be found in higher abundance over the summit as opposed to away and may be seamount associated species. These are a cranchiid squid, *Liocranchia reinhardtii*, and a myctophid fish, *Benthosema fibulatum*. The flanks of the seamount, at least at depth during the day, appear to have the largest abundance of fish and also potentially the highest species diversity of all areas sampled on and around Cross Seamount, however, this is based on a low sample size. Further sampling needs to be conducted over Cross Seamount and its flanks to fully determine the cause of the decrease in organisms over the summit as well as if the flanks of the seamount are a location of increased abundance. In addition, there is little to no information on the currents above and around Cross Seamount or the structure and characteristics of the phytoplankton and zooplankton communities above Cross Seamount. This seamount is known to impact the mesopelagic micronekton community and tuna community, but the mechanisms behind these impacts is largely unknown at this time.
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CHAPTER 1
INTRODUCTION

Mesopelagic micronekton are organisms generally between 2 to 20 cm in size and include such diverse taxonomic groups as crustaceans, fishes, and cephalopods (Brodeur and Yamamura 2005). This group of organisms is considered to be important in transferring the energy from epipelagic primary and secondary production. This transfer of energy can either be to higher trophic levels, as these organisms are an important food source for many marine predators such as tunas, whales, seabirds, and fur seals; or this transfer can be to the deeper regions of the ocean via respiration and excretion while these organisms are at depth (Pauly et al 1998; Hidaka et al 2001; Karpouzi et al 2007). A characteristic of all micronekton is the ability to maintain a position and swim against currents (Brodeur and Yamamura 2005). Additionally, many undergo diel vertical migration. Due to these characteristics, their distribution in the ocean is not dictated solely by physical forcing but also by behavior. Certain shallow features in the oceans, such as continental slopes, banks, and shelf-edges, may influence their abundance or community structure by altering the oceanic environment (Brodeur and Yamamura 2005). This alteration could either serve to increase or decrease the abundance of these organisms. Due to the importance of these organisms as a food source for many marine predators, this change in abundance could also impact the abundance and distribution of marine predators over and around certain features.

Seamounts are another shallow feature in the ocean that may influence mesopelagic micronekton abundance and distribution. Seamounts are defined as isolated submarine mountains that have an elevation more than 100 m above the seafloor with
most being of volcanic origin (Rogers 1994; Genin 2004). There are approximately
30,000 such features rising at least 1000 meters above the seafloor in the Pacific alone,
making seamounts relatively common features in the oceans (Smith and Jordan 1988).
By projecting at least 1000m into the water column, seamounts can generate a variety of
impacts on physical flow regimes, mostly by influencing and changing existing tidal
currents, and create a unique and different environment as opposed to the open ocean
(Gerin et al 1989; Noble and Mullineaux 1989; Mullineaux and Mills 1997; Mohn and
Beckmann 2002). Some documented seamount impacts are: generation of internal waves;
deflection, amplification, and distortion of existing internal waves; amplification of flow;
eddy formation; localized upwelling; and the possible formation of closed circulation
patterns called Taylor columns (Boehlert and Genin 1987; Rogers 1994). Not all
seamounts will generate the same effects. This is due to their different sizes, shapes and
depths of the summit below sea surface. For instance, Great Meteor Seamount, located in
the North Atlantic, is a large flat-topped seamount with steep slopes (often referred to as
a guyot) that has been documented to create many of the internal wave phenomenon and
closed circulation patterns previously mentioned due to tidal forcing over the seamount
(Mohn and Beckmann 2002). On the other hand, Cross Seamount is a smaller seamount
with a roughly flat and circular summit of only 8km in diameter as opposed to Great
Meteor’s 40km summit diameter. While there are strong currents generated by the
semidiurnal tides at Cross, the size of the summit is less than the shortest wavelengths of
internal tides in the area and thus any characteristics of internal waves detected at Cross
Seamount would not have been generated or greatly altered at the seamount itself but by
other processes in the area (Noble and Mullineaux 1989). This may lead to different physical flow patterns and different environmental conditions.

Due to the changes in physical flow regimes around seamounts, primary production in water either directly above or immediately downstream of seamounts has been shown to be elevated in comparison to the adjacent open ocean (Boehlert and Genin 1987; Rogers 1994). Mohn and Beckmann (2002) documented anomalies in the thickness of the mixed-layer due to uplift and compression of isotherms around the edges of Great Meteor seamount. This could be influential to phytoplankton production around the seamount by increasing the abundance of nutrients necessary for phytoplankton growth and production. Taylor columns and eddies that are generated downstream of seamounts are thought to aid in the retention of particles and planktonic organisms over and around a seamount (Boehlert and Mundy 1993; Mullineaux and Mills 1997). This retention could then lead to an increase in secondary productivity over seamounts by entraining both the concentration of food particles and the zooplankton over the seamount. However, direct evidence of increased zooplankton abundance over seamounts is complex mainly due to the increased predation of zooplankton over the summit of the seamount. This can lead to an overall decrease in abundance and the formation of gaps and patchiness in the distribution of zooplankton (Haury et al. 2000). Additionally, while Taylor columns are described as a possible mechanism for increased primary and secondary production, there remain few direct observations as to their occurrence and duration of occurrences (Genin 2004).

The abundance and production of top trophic levels has also been shown to be influenced by seamounts. Demersal and pelagic predators have been documented in both
commercial catch and scientific research as being higher in abundance around seamounts with the assumption that it is due to an increased concentration of their prey (Parin and Prut’ko 1985; Wilson and Kaufmann 1987; Rogers 1994; Fock et al 2002; Musyl et al 2003). These predators found in high abundance over seamounts do not feed largely on plankton or other epipelagic prey, but on mesopelagic micronekton. Fock et al (2002) found that four dominant benthic predators found over Great Meteor Seamount, *Macroramphosus* spp., *Capros aper*, *Antigonia capros*, and *Zenopsis conchifer*, had diets largely consisting of pelagic plankton and micronekton and that these predators were feeding primarily on the margins of the summit where they were more likely to encounter and catch their prey which undergo diel vertical migration. Parin and Prut’ko (1985) found elevated catches of various sharks, skates, tunas, billfish, and gempylids above Equator Seamount in the Western Tropical Indian Ocean, all with stomach contents largely consisting of a mesopelagic fish species of the family Myctophidae.

Despite evidence of increased foraging on mesopelagic micronekton over seamounts, as an entire group, they have been poorly sampled over and around seamounts. Many seamounts have summit elevations well within the depth ranges of the mesopelagic realm (approximately 300-1,000m below the sea surface) leading to possible interactions between these organisms and the seafloor. A few studies have found evidence that the mesopelagic micronekton community is different over seamounts in comparison to open ocean habitat. In particular, there are certain species that are considered to associate mostly with boundary regions, those regions located near land masses, which appear to also associate with seamounts (Reid et al 1991; Wilson and Boehlert 2004). Boehlert and Genin (1987) found that the sternoptychid fish *Maurolicus*
muelleri, the lophogastrid mysid *Gnathopahusia longispina*, and a small squid *Iridoteuthis iris* were all higher in abundance over Southeast Hancock Seamount (located on the Northern Hawaiian Ridge) but not in waters immediately surrounding the seamount. Parin and Prut’ko (1985) also found a species of myctophid fish that occurs in very high numbers over Equator seamount but is absent in waters away from the seamount.

The impact of seamounts on mesopelagic micronekton communities goes beyond the presence of certain seamount or boundary layer associated species. Seamounts can also either attract certain species or perhaps discourage some species away from the seamount summit due to the shallow topography. If there is an aggregation or absence of mesopelagic micronekton over a seamount, it would not primarily be due to passive drifting in the current or possible entrainment over the summit, but to active behavior.

Behavioral reasons for aggregating in the vicinity of seamounts could be for reproductive reasons or an increased food supply near or over seamounts (Wilson and Boehlert 2004). Conversely, the mesopelagic micronekton community could be reduced or show no increase in abundance over the summit of a seamount due to predation or active avoidance of the shallow topography (Parin and Prut’ko 1985; Pusch et al. 2004).

Mesopelagic micronekton may instead aggregate around the flanks of the seamount, particularly while at depth during the day. This higher abundance of mesopelagic micronekton over the flanks is largely due to compaction. This effect occurs when the mesopelagic micronekton located directly above the summit of the seamount at night start to descend to depth as daylight approaches. As they descend they encounter the summit of the seamount but to avoid this hard substrate, and the demersal predators waiting there,
they move towards the flanks. The concentration of organisms around the flanks of the seamounts will then be greater due to the addition of organisms migrating from the summit (Parin and Prut’ko 1985). The next night, when the organisms migrate back up to shallower depths, the dense aggregation at the flanks can spread out over the summit again (Boehlert and Seki 1984; Parin and Prut’ko 1985). The differences in how mesopelagic micronekton may interact with a seamount could be a factor of the size, location, or other physical factors of the seamount itself. This implies that more seamounts should be studied as to their impact on mesopelagic micronekton communities to better understand the mechanisms that are most influential to this community of organisms.

South of the Big Island of Hawaii there is a rich tuna fishing ground located above Cross Seamount. The reason for this aggregation of tuna is unclear though one strong hypothesis is that there is increased foraging potential at the seamount as opposed to the open ocean. The tuna caught over the seamount are largely juvenile bigeye (Thunnus obesus) and yellowfin tuna (Thunnus albacares), with the bigeye tuna showing a longer residence time over the seamount than the yellowfin tuna (Holland et al 1999). Bigeye tuna caught over Cross Seamount typically have fuller stomachs containing a greater diversity of prey items and more mesopelagic prey items than individuals that were caught away from the seamount (Grubbs et al 2002). Yellowfin tuna also feed on mesopelagic micronekton but to a lesser extent than bigeye (Grubbs et al 2002). This evidence implies that Cross Seamount may be a desirable location for these tuna due to increased foraging potential.
While there is previous knowledge of the increased abundance of large pelagic predators and their diet at Cross Seamount, there is no previous knowledge of the mesopelagic micronekton community over and around the seamount. Evidence from tuna diet analysis suggests that there is an increased abundance of mesopelagic micronekton; however, no efforts have been previously made to directly test this hypothesis. The seamount itself has a summit that rises to a flat plateau that is a minimum depth of 330 meters below the sea surface. This structure may provide a large enough area to impact and change the community of mesopelagic micronekton. Preliminary analysis of acoustic surveys have shown dense aggregations of mesopelagic micronekton, or possibly other organisms, directly over the summit during the night and near the flanks of the seamount during the day (Reka Domokos unpublished data). Therefore, this study collected samples by trawling over and near Cross Seamount to determine the influence of Cross Seamount on the mesopelagic micronekton community and ask three main questions: (1) is the abundance and/or biomass of organisms different over the summit of the seamount as opposed to away; (2) is the diversity or taxonomic composition of the community different over the summit as opposed to away; and lastly (3) are there unique species located directly over the summit?
CHAPTER 2
METHODS

**Sampling**

Samples were collected from two cruises during late April of 2005 and late April and early May of 2007 aboard the NOAA research vessel Oscar Elton Sette. Sampling during both years was conducted when there was no eddy activity in the region surrounding Cross Seamount and during the full moon. A dual warp modified Cobb trawl with an open mouth area of approximately 140m$^2$ with a mesh size ranging from 152mm stretched at the mouth to a cod end lined with 3.2mm knotless nylon delta mesh netting was used for collection. In an attempt to reduce damage to specimens during the trawl, the cod end of the net was modified for the May 2007 cruise. A 1m diameter, 5m long plankton net with a mesh size of 1mm was added onto the end of the original cod end. At the end of the plankton net, a cod end bag constructed from plasticized canvas with dimensions of 30cm diameter by 61cm length was attached.

Two main types of trawls were conducted, day-deep and night-shallow. Day-deep trawls were conducted between 400-650m during the day and night-shallow trawls were conducted between 0-200m during the night. These depths were chosen based on concurrently conducted acoustic surveys which indicated the depths with the greatest density of sound scattering organisms. Each trawl was fished for 60 minutes at an average speed of 3 knots. This resulted in approximately $8.026\times10^5$ m$^3$ of water filtered per trawl. All organisms from each trawl were preserved on board the ship with 10% formalin buffered with Borax. In the lab all organisms from each trawl were sorted to the
lowest possible taxonomic level. For each taxonomic level, counts were made of individuals and a weight was taken of the group as a whole.

The trawls conducted around Cross Seamount can be divided into three main sample groups: summit, flank and away. Summit trawls are defined as those trawls conducted directly over the flat plateau summit of Cross Seamount and in waters no deeper than 500m. Away trawls are defined as those trawls conducted within the vicinity of Cross Seamount, no farther than 14 km from the summit, and in waters of depths greater than 1500m. Flank trawls are defined as trawls conducted on the slopes immediately surrounding the summit of Cross Seamount, and in waters between 500 and 1500m depths.

**Analysis**

Not all taxa captured and sorted from each trawl were used in the analysis portion of the study. Juveniles and some taxa that were smaller than 1cm were excluded from the analysis based on the criteria for micronekton size and inadequate quantitative sampling of organisms smaller than 1cm with the large net used. Lobster phyllosoma larvae were also excluded from the analysis, despite their large size, since they are considered as epipelagic organisms, not mesopelagic. Certain juvenile organisms were included in the analysis due to their size being larger than 1.5cm. These were: juvenile fish, stomatopod larvae, and eel leptocephalus larvae. While juvenile fish and stomatopod larvae are considered epipelagic, they are important in tuna diet and thus were used in the analysis. A few nektonic organisms that were larger than 30cm were excluded based on their ability to effectively evade the large net leading to inadequate quantitative sampling. All
gelatinous organisms, such as salps and scyphomedusa, were removed from the analysis due to inadequate sampling or inability to identify the organisms after fixation.

Abundance and biomass data, which was calculated as the count or weight of individuals per trawl, were compared using Mann-Whitney U-tests (Statistica 7.1). These comparisons were made at the specific, generic or familial level between the different trawl sample groups (i.e. night-shallow away vs. night-shallow summit). Initial comparisons were made between the 2005 and 2007 trawls of similar sample groups (i.e. between 2005 night-shallow away and 2007 night-shallow away) to determine if all trawls from similar sample groups could be pooled together. Next, comparisons were made between night-shallow summit (NSS) and night-shallow away (NSA), day-deep away (DDA) and NSA, and between day-deep flank (DDF) and DDA. All tests were reported as significant at a p-level ≤0.05.

The trawl groups were also compared to one another using diversity indices. These indices were species richness, diversity and evenness. The Margalef index of species richness, d, was calculated using the following equation:

\[
d = \frac{(S - 1)}{\log(N)}
\]

where S is the number of species and N is the total number of individuals. Species diversity was evaluated using Shannon's diversity index, H', with the following equation:

\[
H' = -\sum_{i=1}^{S} (P_i \cdot \ln(P_i))
\]
where $S$ is the number of species and $P_i$ is the proportion of $S$ made up of the $i$th species. Lastly, evenness was calculated by using Pielou's evenness index, $J'$, with the following equation:

$$J' = \frac{H'}{\log(S)}$$

where $H'$ is the Shannon's diversity index calculated with the previously mentioned equation and $S$ is the number of species.

Rarefaction curves were generated to further investigate the difference in taxonomic diversity between trawl groups with differing numbers of individuals sampled. This method estimates the number of different taxa that would be expected in a random sample of individuals taken from a larger sample group (James and Rathburn 1981). These estimations are then fit into a curve that depicts the increase in estimated taxa with increasing individuals until the total number of individuals and taxa present in the sample is reached. This would allow for a better comparison between large and small samples since taxonomic richness generally increases with increasing sample size (Hulpert 1971). For instance, the estimated taxonomic diversity of all samples could be compared to one another at a given number of individuals for which all samples have at least that many individuals.

Finally, to investigate the relatedness of the communities sampled in each trawl group, a cluster analysis and similarity percentage procedure (SIMPER) was constructed using Primer E-5 software (Clarke and Warwick 2001). A Bray-Curtis similarity matrix
was computed using the abundance data for all taxa sorted from each trawl. This matrix was then used to construct a cluster analysis using group average linking. Due to the non-normal distribution in the abundance data and the large number of zeros (absences), a square-root transformation of the data was used to reduce the variability (Clarke and Green 1988). Main cluster groups were defined by the cluster analysis and then used in the similarity percentage procedure (SIMPER) analysis. SIMPER was used to determine more precisely which taxa contributed to the overall similarity, or dissimilarity, between cluster groups.
CHAPTER 3
RESULTS

This study resulted in 18 total trawl samples. There are 2 NSS, 3 NSA, and 3 DDA in 2005 and 3 NSS, 2 NSA, 1 DDA, 1 NSF and 3 DDF in 2007. Locations for each of the trawls are depicted in figure 1. No day-deep trawls were conducted directly over the summit of Cross Seamount due to the shallow topography. For all taxonomic categories used in the analyses there were no significant differences between the NSS trawls from 2005 and 2007 and the DDA trawls from 2005 and 2007. Between the 2005 and 2007 NSA trawls there was one taxonomic category that was significantly different (p<0.05). This category was *Myctophum* sp. with an abundance of 2 ind./trawl in 2005 and 1 ind./trawl in 2007. This group is relatively rare in catch rates and thus does not contribute considerably to overall community structure.

**Abundance and Biomass**

Away from the Seamount

A comparison of the NSA and DDA trawls was necessary in order to describe the community of mesopelagic micronekton away from the summit of Cross seamount and to allow for a brief comparison of this region to other studies that have described the mesopelagic micronekton community around the Hawaiian Islands. When comparing all organisms together, the NSA trawls have a higher total abundance of individuals than the DDA trawls (p<0.05, Table 1). The cephalopods (Table 2), *Chtenopteryx* sp., *Abraliopsis pacifica* (Enoploteuthidae), Onychoteuthidae, and *Pterygioteuthis giardi* (Pyroteuthidae) all had higher abundances in the NSA trawls (p<0.05). For crustaceans (Table 3),
Figure 1. Locations of the 18 trawls conducted over and around Cross Seamount: (a) day-deep trawls, (b) night-shallow trawls. Solid lines are away from summit trawls, dashed lines are flank trawls, and lines with perpendicular dash marks are summit trawls. The inset shows the approximate location of Cross Seamount (depicted as an *) off the Big Island of Hawaii.
Table 1. Diversity indices for the trawl groups used in statistics. The diversity indices are as follows: S=number of species/taxa, N=number of individuals, d= Margalef index of species richness, J'= Pielou’s evenness index, and H'= Shannon’s diversity index. Significance is denote by < or >, and is significant in the direction as indicated by the inequality sign (significance is at the p<0.05, Mann-Whitney U test).

<table>
<thead>
<tr>
<th></th>
<th>NSS (n=5)</th>
<th>NSA (n=5)</th>
<th>DDA (n=4)</th>
<th>DDF (n=3)</th>
</tr>
</thead>
<tbody>
<tr>
<td>S</td>
<td>30.40 ± 1.82</td>
<td>&lt; 50.20 ± 6.53</td>
<td>&gt; 30.50 ± 9.98</td>
<td>41.00 ± 16.09</td>
</tr>
<tr>
<td>N</td>
<td>279.60 ± 61.21</td>
<td>&lt; 1021.00 ± 273.15</td>
<td>&gt; 416.75 ± 122.80</td>
<td>435.67 ± 212.89</td>
</tr>
<tr>
<td>d</td>
<td>5.25 ± 0.52</td>
<td>&lt; 7.14 ± 1.03</td>
<td>&gt; 4.87 ± 1.43</td>
<td>6.58 ± 2.21</td>
</tr>
<tr>
<td>J'</td>
<td>0.75 ± 0.08</td>
<td>&lt; 0.74 ± 0.02</td>
<td>&gt; 0.63 ± 0.07</td>
<td>0.68 ± 0.07</td>
</tr>
<tr>
<td>H'</td>
<td>2.57 ± 0.21</td>
<td>&lt; 2.89 ± 0.13</td>
<td>&gt; 2.10 ± 0.27</td>
<td>2.47 ± 0.28</td>
</tr>
</tbody>
</table>
Sergestes sp. (Sergestidae), Hyperiidea amphipods, stomatopod larvae, and lobster phyllosoma larvae were all higher in abundance in the NSA trawls (p<0.05). The family Myctophidae resulted in ten different genera/species that are significantly higher in abundance in the NSA sample group than the DDA sample group (p<0.05, Table 4). These species/genera are: Benthosema suborbitale, Bolinichthys longipes, Ceratoscopelus warmingii, Diaphus fragilis, Diaphus schmidti, Hygophum proximum, Lampanyctus sp., Myctophum sp., Symbolophorus evermanni, and Triphoturus nigrescens (Table 4). The juvenile fish category, eel leptocephalus larvae and Vinciguerria sp. (Phosichthyidae) also showed a higher abundance in the NSA trawls than the DDA trawls (p<0.05, Table 4). In contrast to the majority of the results, the stomiiform group contained four groups that were higher abundance in the DDA trawls than the NSA trawls (p<0.05). These groups were: Cyclothone sp. (Gonostomatidae), Gonostoma atlanticum (Gonostomatidae), Danophos oculatus (Sternoptychidae), and Argyropelecus sp. (Sternoptychidae) (Table 4).

Most all the patterns in abundance between the NSA and DDA trawls were paralleled by biomass, though there was a small difference. All the cephalopod, Myctophidae and stomiiform groups that were different in abundance were also different in biomass between the two trawl types, with the trends previously described in the abundance comparison holding true for each of the groups (Tables 2-4). Of the crustaceans, Hyperiidea amphipods and Sergestes sp. do not have higher biomass in the NSA trawls despite being higher in abundance. It appears that these two groups may have larger individuals in the DDA trawls. For the Hyperiidea amphipods this can be explained by the presence of Cystosoma sp., a genus of larger individuals, which were
Table 2. Cephalopod abundance (average number per trawl ± standard deviation) and biomass (in parentheses following abundance, average grams per trawl ± standard deviation). Data for families are an average of all species within the family in addition to individuals only identified to the family level. Significance is denoted by > or < (abundance followed by biomass in parentheses), and is significant in the direction as indicated by the inequality sign (significant at p<0.05; Mann-Whitney U test).

<table>
<thead>
<tr>
<th>Cephalopod Family</th>
<th>NSB (µg)</th>
<th>NSA (µg)</th>
<th>DDA (µg)</th>
<th>DDF (µg)</th>
<th>NSF (µg)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Ctenopsideidae</td>
<td>10.2±0.4 (3.8±0.2)</td>
<td>12.4±0.7 (5.2±0.6)</td>
<td>1.6±0.1 (0.3±0.1)</td>
<td>6.6±0.2 (0.5±0.1)</td>
<td>7 (0.01)</td>
</tr>
<tr>
<td>Heteroteuthidae</td>
<td>2.4±0.3 (3.2±0.2)</td>
<td>-</td>
<td>-</td>
<td>-</td>
<td>6 (0.01)</td>
</tr>
<tr>
<td>Lycoteuthidae</td>
<td>9.6±0.8 (4.5±0.7)</td>
<td>1.9±0.9 (0.8±0.1)</td>
<td>-</td>
<td>-</td>
<td>2 (0.05)</td>
</tr>
<tr>
<td>Onychoteuthidae</td>
<td>0.2±0.1 (3.1±0.3)</td>
<td>2.6±0.6 (3.5±0.5)</td>
<td>-</td>
<td>-</td>
<td>-</td>
</tr>
<tr>
<td>Majoidea</td>
<td>3.8±0.6 (2.7±0.6)</td>
<td>-</td>
<td>-</td>
<td>-</td>
<td>-</td>
</tr>
<tr>
<td>Dactylochita</td>
<td>0.9±0.1 (0.1±0.1)</td>
<td>-</td>
<td>-</td>
<td>-</td>
<td>1 (0.05)</td>
</tr>
<tr>
<td>Euphausiidae</td>
<td>3±0.8 (3.2±0.2)</td>
<td>11.4±1.2 (12.9±2.1)</td>
<td>1.9±0.1 (0.3±0.1)</td>
<td>6 (0.05)</td>
<td></td>
</tr>
<tr>
<td>Abdallopida sp.</td>
<td>0.6±0.1 (0.1±0.1)</td>
<td>11.2±1.2 (12.3±2.0)</td>
<td>0.6±0.1 (0.3±0.1)</td>
<td>-</td>
<td>6 (0.05)</td>
</tr>
<tr>
<td>Abdallopida sp.</td>
<td>0.2±0.1 (0.1±0.1)</td>
<td>3.2±0.8 (2.2±0.2)</td>
<td>-</td>
<td>-</td>
<td>-</td>
</tr>
<tr>
<td>Abdallopida sp.</td>
<td>2.2±0.1 (2.3±0.1)</td>
<td>11.8±1.4 (12.7±2.0)</td>
<td>0.2±0.1 (0.3±0.1)</td>
<td>-</td>
<td>2 (0.05)</td>
</tr>
<tr>
<td>Abdallopida sp.</td>
<td>1.4±0.5 (2.3±0.3)</td>
<td>-</td>
<td>-</td>
<td>-</td>
<td>1 (0.05)</td>
</tr>
<tr>
<td>Abdallopida sp.</td>
<td>-</td>
<td>0.5±0.1 (0.3±0.1)</td>
<td>-</td>
<td>-</td>
<td>-</td>
</tr>
<tr>
<td>Abdallopida sp.</td>
<td>0.4±0.1 (0.4±0.1)</td>
<td>2.9±0.5 (3.5±0.5)</td>
<td>-</td>
<td>-</td>
<td>2 (0.05)</td>
</tr>
<tr>
<td>Pyroteuthidae</td>
<td>2.4±0.3 (1.4±0.1)</td>
<td>10.6±1.6 (10.5±0.8)</td>
<td>1.6±0.1 (0.4±0.1)</td>
<td>6 (0.05)</td>
<td></td>
</tr>
<tr>
<td>Pteropelmatidae</td>
<td>1.8±0.5 (0.9±0.1)</td>
<td>7.2±0.8 (3.7±0.1)</td>
<td>-</td>
<td>-</td>
<td>2 (0.05)</td>
</tr>
<tr>
<td>Pteropelmatidae</td>
<td>0.2±0.1 (0.1±0.1)</td>
<td>2.3±0.3 (1.8±0.3)</td>
<td>-</td>
<td>-</td>
<td>-</td>
</tr>
<tr>
<td>Pyroteuthidae</td>
<td>0.2±0.1 (0.2±0.1)</td>
<td>1.0±0.1 (0.7±0.1)</td>
<td>-</td>
<td>-</td>
<td>-</td>
</tr>
<tr>
<td>Chonoplagidae</td>
<td>-</td>
<td>-</td>
<td>-</td>
<td>-</td>
<td>-</td>
</tr>
<tr>
<td>Octopodidae</td>
<td>3±0.8 (3.2±0.2)</td>
<td>9.6±1.8 (9.3±2.3)</td>
<td>1.6±0.1 (0.4±0.1)</td>
<td>-</td>
<td>-</td>
</tr>
<tr>
<td>Octopodidae</td>
<td>3±0.8 (3.2±0.2)</td>
<td>9.6±1.8 (9.3±2.3)</td>
<td>1.6±0.1 (0.4±0.1)</td>
<td>-</td>
<td>-</td>
</tr>
<tr>
<td>Octopodidae</td>
<td>3±0.8 (3.2±0.2)</td>
<td>9.6±1.8 (9.3±2.3)</td>
<td>1.6±0.1 (0.4±0.1)</td>
<td>-</td>
<td>-</td>
</tr>
</tbody>
</table>
Table 3. Crustacean abundance (average number per trawl ± standard deviation) and biomass (in parentheses following abundance, average grams per trawl ± standard deviation). Data for families are an average of all species within the family in addition to individuals only identified to the family level. Significance is denoted by > or < (abundance followed by biomass in parentheses), and is significant in the direction as indicated by the inequality sign (significant at p<0.05; Mann-Whitney U test).

<table>
<thead>
<tr>
<th>Family</th>
<th>NBS</th>
<th>NSA</th>
<th>ODA</th>
<th>DOF</th>
<th>NDF</th>
</tr>
</thead>
<tbody>
<tr>
<td>Ophiopholis</td>
<td>25.80±28.47 (0.88±1.06)</td>
<td>23.83±21.04 (13.33±11.68)</td>
<td>44.24±48.83 (12.44±7.00)</td>
<td>18.34±18.02 (14.02±26.25)</td>
<td>28 (0.56)</td>
</tr>
<tr>
<td>Ophiophorus</td>
<td>2.40±5.37 (2.04±6.58)</td>
<td>8.20±9.73 (4.68±9.93)</td>
<td>20.75±31.29 (10.23±4.49)</td>
<td>8.02±6.57 (12.11±1.74)</td>
<td>4 (0.55)</td>
</tr>
<tr>
<td>Jurididae</td>
<td>23.40±26.80 (7.9±3.75)</td>
<td>23.00±16.68 (3.4±2.35)</td>
<td>13.25±10.17 (2.3±2.71)</td>
<td>6.33±6.69 (2.1±2.05)</td>
<td>22 (0.51)</td>
</tr>
<tr>
<td>Scolopopida sp</td>
<td>-</td>
<td>1.20±0.66 (0.73±1.86)</td>
<td>0.75±1.50 (2.08±2.71)</td>
<td>3.67±5.51 (2.3±2.49)</td>
<td>-</td>
</tr>
<tr>
<td>Acanthephyra sp</td>
<td>-</td>
<td>0.40±0.65 (0.4±0.83)</td>
<td>0.50±1.00 (0.1±0.32)</td>
<td>3.23±2.84 (0.8±1.52)</td>
<td>-</td>
</tr>
<tr>
<td>Pandalidae</td>
<td>-</td>
<td>2.80±4.62 (0.8±2.03)</td>
<td>8.75±4.64 (1.5±2.07)</td>
<td>0.30±0.85 (0.1±0.18)</td>
<td>-</td>
</tr>
<tr>
<td>Sargitidae</td>
<td>6.40±5.03 (3.27±0.13)</td>
<td>&lt;1</td>
<td>53.40±28.21 (7.6±7.94)</td>
<td>&gt;</td>
<td>12.00±6.85 (2.1±2.68)</td>
</tr>
<tr>
<td>Sargita sp</td>
<td>0.25±0.45 (0.02±0.05)</td>
<td>10.80±13.54 (3.5±2.71)</td>
<td>0.25±0.50 (0.07±0.14)</td>
<td>-</td>
<td>-</td>
</tr>
<tr>
<td>Sargitidae sp</td>
<td>8.25±4.22 (0.25±0.12)</td>
<td>&lt;1</td>
<td>42.03±20.24 (2.1±2.71)</td>
<td>&gt;</td>
<td>11.75±9.29 (2.1±2.78)</td>
</tr>
<tr>
<td>Benthegoeidae</td>
<td>-</td>
<td>3.60±5.22 (0.6±0.87)</td>
<td>-</td>
<td>0.33±0.56 (0.1±0.21)</td>
<td>-</td>
</tr>
<tr>
<td>Gomphidae sp</td>
<td>-</td>
<td>-</td>
<td>-</td>
<td>-</td>
<td>-</td>
</tr>
<tr>
<td>Lophogastidae</td>
<td>1.28±1.84 (0.04±0.06)</td>
<td>-</td>
<td>1.28±1.84 (0.04±0.06)</td>
<td>-</td>
<td>1.75±2.22 (0.5±0.08)</td>
</tr>
<tr>
<td>Lophogaster sp</td>
<td>-</td>
<td>-</td>
<td>-</td>
<td>-</td>
<td>-</td>
</tr>
<tr>
<td>Hyperiidae</td>
<td>9.06±7.31 (0.38±0.28)</td>
<td>8.69±3.13 (0.5±0.38)</td>
<td>&gt;</td>
<td>3.93±1.71 (0.2±0.23)</td>
<td>(&gt;)</td>
</tr>
<tr>
<td>Statopoda</td>
<td>55.08±1.35 (0.56±0.83)</td>
<td>77.68±1.24 (2.9±3.37)</td>
<td>-</td>
<td>-</td>
<td>-</td>
</tr>
</tbody>
</table>
Table 3. Fish abundance (average number per trawl ± standard deviation) and biomass (in parentheses following abundance, average grams per trawl ± standard deviation). Data for families are an average of all species within the family in addition to individuals only identified to the family level. Significance is denoted by > or < (abundance followed by biomass in parentheses) and is significant in the direction as indicated by the inequality sign (significant at p≤0.05; Mann-Whitney U test)

<table>
<thead>
<tr>
<th>Family</th>
<th>NSB (avg)</th>
<th>NSA (avg)</th>
<th>DDA (avg)</th>
<th>DDF (avg)</th>
<th>NBF (avg)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Myctophidae</td>
<td>58.40±2.74 (78.02±2.74)</td>
<td>82.20±0.85 (96.90±0.85)</td>
<td>53.05±0.61 (59.26±0.61)</td>
<td>117.67±20.77 (117.22±20.77)</td>
<td>72.36±0.36</td>
</tr>
<tr>
<td>Diagonichthyidae</td>
<td>12.00±4.32 (12.50±4.32)</td>
<td>4.20±0.95 (3.80±0.95)</td>
<td>1.50±0.65 (1.50±0.65)</td>
<td>0.25±0.15 (0.25±0.15)</td>
<td>0.80±0.20 (0.80±0.20)</td>
</tr>
<tr>
<td>Sternoptychidae</td>
<td>3.00±0.45 (2.35±0.45)</td>
<td>1.00±0.15 (1.00±0.15)</td>
<td>1.00±0.15 (1.00±0.15)</td>
<td>0.25±0.05 (0.25±0.05)</td>
<td>0.80±0.20 (0.80±0.20)</td>
</tr>
<tr>
<td>Exocoetidae</td>
<td>2.00±0.40 (2.00±0.40)</td>
<td>25.20±0.61 (25.20±0.61)</td>
<td>10.40±0.20 (10.40±0.20)</td>
<td>0.25±0.05 (0.25±0.05)</td>
<td>10.80±0.60 (10.80±0.60)</td>
</tr>
<tr>
<td>Oxyopidae</td>
<td>3.00±0.45 (6.10±0.45)</td>
<td>10.60±0.80 (10.60±0.80)</td>
<td>0.25±0.05 (0.25±0.05)</td>
<td>0.25±0.05 (0.25±0.05)</td>
<td>7.00±0.20 (7.00±0.20)</td>
</tr>
<tr>
<td>Cetorhynchidae</td>
<td>2.00±0.40 (2.00±0.40)</td>
<td>25.00±0.60 (25.00±0.60)</td>
<td>10.40±0.20 (10.40±0.20)</td>
<td>0.25±0.05 (0.25±0.05)</td>
<td>10.80±0.60 (10.80±0.60)</td>
</tr>
<tr>
<td>Engraulidae</td>
<td>2.00±0.40 (2.00±0.40)</td>
<td>10.60±0.80 (10.60±0.80)</td>
<td>0.25±0.05 (0.25±0.05)</td>
<td>0.25±0.05 (0.25±0.05)</td>
<td>7.00±0.20 (7.00±0.20)</td>
</tr>
<tr>
<td>Clupeidae</td>
<td>2.00±0.40 (2.00±0.40)</td>
<td>10.60±0.80 (10.60±0.80)</td>
<td>0.25±0.05 (0.25±0.05)</td>
<td>0.25±0.05 (0.25±0.05)</td>
<td>7.00±0.20 (7.00±0.20)</td>
</tr>
<tr>
<td>Engraulidae</td>
<td>2.00±0.40 (2.00±0.40)</td>
<td>10.60±0.80 (10.60±0.80)</td>
<td>0.25±0.05 (0.25±0.05)</td>
<td>0.25±0.05 (0.25±0.05)</td>
<td>7.00±0.20 (7.00±0.20)</td>
</tr>
<tr>
<td>Clupeidae</td>
<td>2.00±0.40 (2.00±0.40)</td>
<td>10.60±0.80 (10.60±0.80)</td>
<td>0.25±0.05 (0.25±0.05)</td>
<td>0.25±0.05 (0.25±0.05)</td>
<td>7.00±0.20 (7.00±0.20)</td>
</tr>
</tbody>
</table>

**Significance:**
- Significance follows abundance followed by biomass in parentheses.
- Significant in the direction as indicated by the inequality sign (significant at p≤0.05; Mann-Whitney U test).
found in the some of DDA trawls but not in the NSA trawls. The eel leptocephalus larvae also did not have higher biomass in the NSA trawls despite having a higher abundance, again implying that larger individuals are residing at depth.

Seamount Summit and Away

Overall, there are fewer organisms over the summit of Cross Seamount than away, with the summit having approximately 2/3 fewer individuals (p≤0.05, Table 1). In the cephalopod category (Table 2), the family Pyroteuthidae as a whole and the genus Chteneteryx sp., were both higher in abundance in the NSA trawls than the summit trawls (p≤0.05). In contrast, the Cranchiidae squid, Liocranchia reinhardtii, was higher in abundance in the NSS trawls than the NSA trawls (p≤0.05). Of the crustacean category, (Table 3), only one group, Sergestes sp. (Sergestidae), was found to be higher in abundance in the NSA trawls (p≤0.05). Nine species of the family Myctophidae are significantly more abundant in the NSA sample group, with five of these species not occurring at all in the NSS sample group (p≤0.05, Table 4). Bolinichthys longipes, Ceratoscopelus warmingii, Diaphus schmidti, and Symbolophorus evermanni all occurred in both the NSA and NSS sample groups with a higher abundance away from the summit (p≤0.05). Diaphus fragilis, Diaphus rolbolini, Lampadena urophaos, Lampanyctus sp., and Triphoturus nigrescens are all quite abundant in the NSA sample group but completely absent from the NSS sample group. The only stomiiform group that was found to be different between the two trawl groups was Vinciguerria sp with a higher abundance in the NSA sample group (p≤0.05, Table 4).
All of the taxonomic groups that were different between the NSS and NSA trawls based on abundance data were also found to be different based on biomass data. However, six additional taxonomic groups had higher biomass in the NSA trawls than the NSS trawls without being higher in abundance (Tables 2-4). As a whole the family Cranchiidae has a higher biomass in the NSA trawls \((p<0.05)\), despite the individual species within the family not differing greatly in biomass between the two trawl types. Within the family Myctophidae four species were found to be higher in biomass in the NSA trawls without being higher in abundance \((p<0.05)\). These species are: *Benthosema suborbitale*, *Diaphus mollis*, *Hygophum proximum*, and *Myctophum* sp.

**Community Composition**

Of all the trawl groups, the NSA trawls appear to have the highest species diversity \((H')\) and abundance of organisms than the other trawl groups \((p<0.05, \text{ Table 1})\). In comparison, the DDA, DDF and NSS trawls have lower species diversity \((H')\); however this may be due to the fact that these trawl groups also have low numbers of total individuals \((N)\). On average, the NSS trawls have 60% less individuals and 40% less taxa than the NSA trawls \((\text{Table 1})\). Despite these differences in number of individuals and species diversity, the NSS and NSA trawl groups both have a relatively even distribution of individuals amongst taxa present as indicated by a Pielou’s evenness index \((J')\) close to one \((\text{Table 1})\). The DDF and DDA trawl groups both have evenness indices \((J')\) that are similar and lower than the night-shallow trawl groups, indicating a less even distribution of individuals amongst the taxa present in these groups.
The use of rarefaction curves allowed for a better comparison between trawl groups that have different numbers of individuals and/or sample sizes. When each of the trawl groups were compared to one another at a potential sample size of only 979 individuals (the total number of individuals sampled from the smallest trawl group, NSF) the DDF trawl group has the highest number of estimated taxa of all the trawl groups at 62 estimated taxa (Fig. 2). The NSA trawl group, which has the highest species diversity when its total number of individuals sampled (4,659 total individuals) is taken into account, has slightly less estimated taxa at this smaller potential sample size. This implies that while the DDF group has a lower species diversity index (H') than the NSA group, this may be a result of this group having a low number of total individuals sampled. The DDF group may have the highest species diversity of all the trawl groups.

The three main trawl types, NSA, NSS, and DDA, separate into distinct clusters based on a Bray-Curtis similarity matrix constructed using the abundance data from the lowest possible taxonomic units sorted from each trawl (Fig. 3). The flanks trawls were included in the cluster analysis. All night-shallow trawls are separated from the day-deep trawls at approximately the 27% similarity level. Amongst the night-shallow trawls, the NSS trawls separate out from the NSA trawls at approximately the 40% similarity level. The DDA cluster splits into two additional clusters at approximately the 42% similarity level, however, these clusters are still all strongly dissimilar to all night-shallow trawls and can be used as a whole cluster group for comparison purposes. The flank trawls did not separate into distinct clusters from the other trawl away types. The one NSF trawl was grouped within the NSA trawls and the DDF trawls within the DDA trawls.
Figure 2. Rarefaction curves for the five different trawl groups. The individual trawls within each trawl group were summed together to create the curve for each group.
indicating that the taxonomic composition of these trawls were not to dissimilar from the away trawls.

The NSA and DDA cluster groups were compared and the NSS and NSA cluster groups were compared using the SIMPER analysis. No direct comparison was made between NSS and DDA due to their difference in location and water depth. Additionally, the flank trawls were not included in the NSA and DDA groups used in the SIMPER analysis. While the flank trawls were clustered with the NSA and DDA trawls respectively, they are considered a different locality and for the SIMPER analysis were excluded.

The DDA cluster as a whole has an average of 48.55% similarity with the largest contributor to the overall similarity being Cyclothone sp. (Gonostomatidae) which contributes to 34.3% of the similarity. This genus is also has the highest abundance in all trawls with an average abundance of 182 individuals per trawl (Table 4). Diaphus mollis, Vinciguerria sp. and Oplophorus gracilirostris, together with Cyclothone sp., contribute to the top 50% of the overall similarity within the DDA community (Fig 4). Fourteen taxonomic groups account for 90% of the overall similarity within the DDA cluster group. These groups include five Gonostomatidae fishes, two Myctophidae fishes, one Sternoptychidae fish, five crustaceans, and eel leptocephalus larvae.

As mentioned previously the DDA cluster groups divides into two additional clusters. The first cluster consists of trawls 05-22 and 05-27 (Group 1) and the second consists of trawls 05-28 and 07-08 (Group 2). In both groups the highest contributor to similarity within the individual groups is Cyclothone sp. accounting for 32.66% of the
Figure 3. Cluster analysis constructed using the Bray-Curtis similarity matrix with square root transformation of the data. The similarity is reported in percentages. * denotes the flank trawls, with the three day-deep flanks located within the DDA cluster group and the one night-shallow flank trawl located within the NSA cluster.
overall similarity for Group 1 and 28% of the overall similarity for Group 2. The taxon that is the main cause of dissimilarity between Group 1 and 2 (contribute 7.47% to the overall dissimilarity) is the caridean shrimp *Oplophorus gracilirostris*. This species was found to be higher in abundance in Group 1 with an average of 51.5 individuals per trawl. Group 2 only had an average of 2 individuals per trawl. The next taxon that accounts for the greatest amount of dissimilarity between the two groups is *Cyclothone* sp. This genus was higher in Group 2 (average abundance of 252.5 individuals per trawl) than in Group 1 (111.5 individuals per trawl). Additionally, several species were only caught in the trawls of Group 2. These species were *Diaphus schmidti*, *Bolinichthys distofax*, Pandalidae shrimps, *Serrivomer* sp., and *Hygophum proximum*. Since none were caught in the trawls of Group 1 these taxa accounted for much of the difference between the two groups. Possible causes for the dissimilarity between these two groups may be that the trawls in Group 1 sampled slightly shallower depths (481-539m) than the Group 2 trawls (518-560m). However, the precision of the netmind data used to approximate the depth of the trawl in the water is not great enough to determine if these differences are truly significant. There are no other apparent differences, such as trawl location or time of day, between these two groups to explain the cause of dissimilarity. The differences between the two years may be due to inter-annual differences.

The NSA cluster group has an average similarity of 60.94% and is the most diverse cluster group with 25 taxonomic groups contributing to 90% of the overall similarity within the cluster group. The taxa accounting for the majority of the overall similarity within the group is the Myctophid species *Diaphus schmidti* at 10.14% overall similarity and an average of 163.2 individuals per trawl. The taxa that contribute to the
top 50% of the overall similarity within the NSA cluster are listed in Figure 4 and consists of more taxa than the other two trawl groups. The top 90% of the overall similarity contains: twelve Myctophidae fish, one Gonostomatidae fish, eel leptocephalus larvae, four crustaceans, stomatopod larvae, and five cephalopods. The taxonomic composition of the NSA community is numerically dominated by Myctophid fish, followed by crustaceans and then cephalopods (Fig 5b). When the epipelagic juvenile categories are eliminated from the analysis there is little change to the overall taxonomic composition (Fig 5d)

Within the NSA cluster groups, the 2005 and 2007 years divided into two separate clusters with an average similarity of 54.83%. The main contributor to the difference the two years is stomatopod larvae (6.26% overall dissimilarity) with an average abundance of 165.5 individuals per trawl in 2005 and 19 individuals per trawl in 2007. The cause for the difference between the two years may be due to inter-annual differences or possibly the time of night the net was fished. The two 2005 trawls were fished approximately one hour earlier than the 2007 trawls, this could result in a difference due to timing of nightly vertical migration. The netmind data, as previously mentioned, was not very precise and no information regarding the depth of the net in the water was available for the two 2005 trawls on one of the 2007 trawls.

The NSS cluster group has an overall average similarity of 57.46% with the highest contributor to the overall similarity being juvenile fish at 20.56% of the overall similarity. The juvenile fish are also the most abundant group within the NSS cluster with an average abundance of 156.4 individuals per trawl. Juvenile fish together with stomatopod larvae, leptocephalus larvae, Janicella spinacauda (Caridean: Oplophoridae),
<table>
<thead>
<tr>
<th>Taxa</th>
<th>Abundance (ind./trawl)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Unidentified Juvenile Fish</td>
<td>55</td>
</tr>
<tr>
<td>Stomatopoda Larvae</td>
<td>55</td>
</tr>
<tr>
<td>Leptocephalus Larvae</td>
<td>55</td>
</tr>
<tr>
<td>Jannexia spinacea- laevis</td>
<td>55</td>
</tr>
<tr>
<td>Diaphus asinoides</td>
<td>55</td>
</tr>
<tr>
<td>Hydromedus amphipod-</td>
<td>55</td>
</tr>
<tr>
<td>Centropagopus waringsi</td>
<td>55</td>
</tr>
<tr>
<td>Vignaqua sp.</td>
<td>55</td>
</tr>
<tr>
<td>Sargassella sp.</td>
<td>55</td>
</tr>
<tr>
<td>Hypophum proximum</td>
<td>55</td>
</tr>
<tr>
<td>Phyllosoma larva</td>
<td>55</td>
</tr>
<tr>
<td>Lepidodonta nitidifrons</td>
<td>55</td>
</tr>
<tr>
<td>Botanthermorphinales</td>
<td>55</td>
</tr>
<tr>
<td>Phylloglottis girard-</td>
<td>55</td>
</tr>
<tr>
<td>Diaphus mali-</td>
<td>55</td>
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</tbody>
</table>

**Figure 4. A schematic of Cross Seamount listing the taxa that contribute to the top 50% of the overall similarity within the three major trawl groups. The numbers next to the taxa are the average abundance (ind./trawl) within the trawl group.**
and *Diaphus schmidtii* contributes to the top 50% of overall similarity within the cluster group (Fig 4). A total of 15 taxonomic groups contribute to the top 90% of the overall similarity within the NSS cluster group. These groups are: five species of Myctophidae, one species of Gonostomatidae, three crustaceans, two cephalopods, juvenile fish, stomatopod larvae, and eel leptocephalus larvae. The taxonomic composition of the NSS community is numerically dominated by epipelagic juvenile fish followed closely by stomatopod larvae, and then mesopelagic fish, crustaceans and cephalopods (Fig 5a). When the epipelagic juvenile categories are excluded the composition of the community changes dramatically and is dominated by mesopelagic fish (mostly of the family Myctophidae) followed closely by crustaceans and finally cephalopods (Fig 5c).

Within the NSS cluster there is a separation of the two different years into different clusters. The overall average similarity between the 2005 and 2007 year clusters is 53.54%. Unidentified juvenile fish contribute the highest percentage of overall dissimilarity at 13.97%, with an average abundance of 41.5 individuals per trawl in 2005 and 233 individuals per trawl in 2007. Causes for the difference between the two years may be the maximum depth the net was fished in the water, with the 2005 trawls having a shallower maximum depth (average of 120.5m) than the 2007 trawls (average of 181.3m). Another cause for the difference may simply be inter-annual differences. There was no difference in the time of night the trawls were fished and no differences based on the location of the trawls on the summit.

The DDA and NSA cluster groups have an overall average similarity of 25.81%. The highest contribution to the overall dissimilarity is from *Cyclotheme* sp.
Figure 5. The taxonomic composition of the night-shallow summit (a. and c.) and night-shallow away (b. and d.) communities based on the abundance of broad taxonomic groups. a-b includes the epipelagic juvenile groups of juvenile fish and stomatopod larvae in addition to the mesopelagic categories. c-d only includes mesopelagic micronekton groups.
(7.41 % dissimilarity) with a much higher abundance in the DDA trawls than in the NSA trawls. Of the 14 taxonomic groups that contribute to 50% of the dissimilarity 12 occur in higher density in the NSA cluster and two, *Cyclothone* sp. and *Oplophorus graciliostris*, occur in higher density in the DDA cluster group.

The overall average similarity between the NSA and NSS cluster groups is 39.64%. *Diphys schmitii* is the largest contributor to the difference at 6.81% of the dissimilarity followed next by *Lampanyctus* sp. (6.19% dissimilarity) and *Ceratoscopelus warmingii* (5.46% dissimilarity). These top three contributors are all from the family Myctophidae and were all in much higher abundance in the NSA trawls than in the NSS trawls. Fourteen taxonomic groups contribute to 50% of the dissimilarity, of which three occur in higher abundance in the NSS trawls while the other eleven have higher abundance in the NSA trawls. The three that are higher in abundance in the NSS trawls are: juvenile fish, *Benthosema fibulatum* and *Janicella spinacauda*.

**Flanks**

Over the flanks of the seamount, only one night-shallow trawl was conducted. This prevents robust statistical comparisons of biomass and abundance to other night-shallow trawls, but a few qualitative comparisons can be made. There appears to be a large abundance of fish and a lower abundance of crustaceans in the NSF trawl when compared to the NSA and NSS trawl groups (Fig 6). The large abundance of fish, mostly of the family Myctophidae, would appear to make the NSF trawl similar to the NSA sample group; however the low abundance of crustaceans and cephalopods are more characteristic of the NSS sample group (Fig 6). The NSF trawl had no *Sergestes* sp, very
Figure 6. Bar graph depicting the average abundances with standard deviation for the NSA, NSF, and NSS trawl groups.
little *Sergia* sp. and a markedly lower abundance of stomatopod larvae and Hyperiidea amphipods (Table 3). The cephalopod families Enoploteuthidae and Onychoteuthidae were also very low in abundance in comparison to the night-shallow away trawls (Table 2).

Statistical analysis could be conducted on the DDF sample group (n=3) for comparison with the DDA sample group. Both trawl groups have relatively the same number of species and number of individuals (Table 1). The DDF trawl group has an average number of 435.67 individuals and the DDA trawl group has an average number of 416.75 individuals. When the abundance and biomass of taxa are analyzed between the two trawl groups few differences are found. This would corroborate the Cluster analysis which showed the DDF trawls intermixed within the cluster of the DDA trawls. Several taxa were found to have higher biomass in the DDF group without having a higher abundance, implying that perhaps the individuals found in the DDF group are larger. These taxa include: Hyperiidea amphipods, *Hygophum proximum*, *Lampanyctus* sp., and other fish (Tables 3-4). The “other fish category” of DDF group consisted of Paralepidids, which were quite large in size and absent from the DDA group, and Serrivomeridae eels which are large in size and more abundant in the DDF group. In the DDA group, the “other fish category” consisted of a higher abundance of a Gempylid fish species, *Nealotus tripes*, of which the individuals were relatively small in size. The family Stomiidae is the only taxon that has both a higher abundance and higher biomass in the DDF trawl group. Lastly, one genus, *Vinciguerria* sp. was found to have both a higher abundance and biomass in the DDA trawl group (Table 4).
CHAPTER 4
DISCUSSION

This current study has resulted in a description of the local mesopelagic micronekton community surrounding Cross Seamount that does not differ greatly with previous studies from the region around Hawaii despite the use of a very large Cobb trawl. Previous descriptions of the mesopelagic micronekton communities in the open ocean around Hawaii by Maynard et al (1975) and Reid et al (1991) have both used Isaacs-Kidd midwater trawls (IKMT) which had 3m and 2m wide square mouths respectively. In addition to the IKMT, Reid et al (1991) also used a large Cobb trawl with an approximate 200m$^2$ mouth opening, though collected fewer samples with this larger net. Studies at other seamounts have also used nets all quite a bit smaller than the one used in this study, ranging from small 2m wide IKMT to a Young Fish Trawl with an 80m$^2$ mouth opening (Boehlert and Seki 1984; Pusch et al 2004; Wilson and Boehlert 2004). The advantage to using a larger net is that many of the mesopelagic micronekton species, such as most squids and larger myctophids, are known to successfully avoid smaller nets (Clarke 1983; Reid et al 1991). These organisms are the main diet of many benthic and pelagic predators and thus are important to this study. In this study the net had very large mouth opening (approximately 140m$^2$) and large mesh size which allowed for a faster towing speed, both of which would help to reduce the ability of these organisms to avoid the net. Unfortunately, these characteristics reduced the ability of the net to adequately sample the catch of small and delicate organisms. However, the addition of the modified cod end in 2007 did result in a greater catch of juvenile and smaller organisms, though these organisms were still excluded from the analysis to
remain consistent with the 2005 samples. Lastly, large nets with non-rectangular mouth openings, such as the net used in this study, can result in an inability to precisely calculate the volume of water filtered for each trawl and prevents the use of calculations to estimate the number or biomass of organisms per area of ocean (Kashkin and Parin 1983; McClatchie et al 2000).

Despite the differences in the nets used in previous studies, the community structure of mesopelagic micronekton described away from the seamount in this study is comparable to past studies in the area and can be considered representative of the open ocean community. This is important due to the relatively close proximity of the trawls conducted off the seamount summit to the summit itself (Fig 1). Maynard et al (1975) described the night-shallow micronekton community as largely consisting numerically of Panaceid shrimps followed by myctophid fish, euphausids, caridean shrimps, and gonostomatid fish. The main structure of the night-shallow community away from the seamount summit is very similar and is largely dominated by fishes of the family Myctophidae followed by crustaceans (mainly caridean shrimps and stomatopod larvae), Vinciguerria sp. and then squids. Euphausids were not reported in this study due to inadequate sampling. Reid et al (1991) also had a description of the night-shallow community surrounding the Hawaiian Islands, and reported this community as largely numerically dominated by fishes (mostly Myctophid fish), followed by shrimps (largely Sergestid shrimps) and very few cephalopods. The day-deep community described in this paper is also very similar to Maynard et al (1975) with Cyclothone sp. by far dominating the community in abundance followed by a myctophid species (Diaphus mollis), several shrimps and other species of the family Gonostomatidae. A comparison
can be made of the myctophid fish community away from the seamount summit to a past study near the Hawaiian Islands. Clarke (1973) used a combination of 2 and 3m IKMT and a large modified Cobb trawl to sample the myctophid fish community. The most abundant species from this past study were, in decreasing order: *Ceratoscopelus warmingii*, *Lampanyctus steinbecki*, *Triphoturus nigrescens*, and *Lampanyctus niger* (Clarke 1973). In the present study, the top four most abundant myctophid species away from the seamount summit were: *Diaphus schmidtii*, *Ceratoscopelus warmingii*, *Lampanyctus* sp., and *Hygophum proximum*. The slight difference in the most abundant myctophid species from this present study to the Clarke (1973) study could be due to only using a large Cobb trawl instead of three different nets of different sizes.

**Is the abundance or biomass different over the summit?**

Directly over the summit of Cross Seamount the average abundance and biomass of organisms is drastically less than away from the summit. The overall abundance of organisms in the NSS community is approximately one-third of the abundance of the NSA community, largely as a result of the absence or reduced abundance of certain taxa (Tables 2-4). Pusch et al (2004) in their study of Atlantis and Great Meteor Seamount in the Atlantic Ocean found similar results in which the abundance of mesopelagic fish above the seamount was considerably less than adjacent waters. Haury et al (2000) also found similar results regarding zooplankton community at seamounts in the North Pacific. Reasons for this reduction in overall abundance may be due to increased predation of mesopelagic micronekton over the summit. As migrating micronekton descend to their daytime depths, those that were located above the summit of the seamount will come into
close proximity to the summit or flanks before reaching their normal daytime depths. This could compact the organisms and make them readily available to both benthic and pelagic predators by preventing the organisms from descending to depths where they can effectively hide from predators. Many seamounts have documented increased abundance of both pelagic and benthic predators (Parin and Prut'ko 1985; Holland et al. 1998; Sibert et al. 2000; Fock et al. 2002). At Cross Seamount, not only is there a high abundance of tunas over the summit, but diet analysis of bigeye and yellowfin tuna caught over the summit showed that these individuals had fuller stomachs containing large amounts of mesopelagic shrimps, fishes and squids than individuals caught in the open ocean (Grubbs et al. 2002). The taxa that bigeye consume heavily over the summit are Oplophorid shrimps, followed by Sergestid shrimps, Myctophid fish, and cephalopods (Grubbs et al. 2002). All of these taxa, except for the Oplophorid shrimps, showed decreased abundance over the summit as opposed to away from the summit (Tables 2-4). This evidence supports predation causing the decrease in abundance over the summit for most taxa except for the oplophorid shrimps.

In addition to predation decreasing the number of individuals over the summit, the mesopelagic micronekton may also be actively avoiding the summit of the seamount. Mesopelagic micronekton tend to avoid coming close to either the seafloor or sea surface, areas where they cannot hide and escape from predators as effectively (Benoit-Bird and Au 2004). Instead of being located over the summit, many of the organisms may instead be found over the flanks of the seamount at all times or perhaps only during the daytime. Results from trawls conducted by Pusch et al. (2004) over the slopes of Great Meteor and Atlantis Seamounts indicated that there was a decrease in density of organisms and
number of species over the slopes as opposed to the open ocean; however this decrease is not as large as that found over the summit of both seamounts. Boehlert and Genin (1984) and Parin and Prut'ko (1985) both found high concentrations of mesopelagic organisms along the seamount flanks during the day and a more diffuse scattering of organisms above the flank and summit during the night as indicated by acoustic transects.

Horizontal migrations have been documented in mesopelagic micronekton around the main Hawaiian Islands in which the organisms resided at depths greater than 400 m during the day and migrated horizontally and vertically to shallow, near-shore waters off the islands (Benoit-Bird and Au 2004). This could also potentially happen around seamounts. Organisms may migrate horizontally and vertically to the shallower waters over the summit but migrate back to deeper waters over the flanks for the daytime in order to avoid the shallow topography and predation. However, there is little evidence to suggest that this occurs at Cross Seamount. There is a low abundance of organisms over the summit at night, which does not indicate that organisms are migrating over the summit at night from the flanks. In addition the flanks of Cross Seamount were sampled, though not adequately enough to indicate if there is a large community of mesopelagic micronekton residing along the flanks. The day-deep flank trawls do not appear very different from the day-deep away trawls with regards to abundance of organisms and taxonomic composition of the community. The one night-shallow flank trawl suggests a very high abundance of fishes (Fig 6), however this was a result from only one trawl sampled. Additional sampling and analysis of the flanks would result in a better description and understanding of the impact of Cross Seamount on the mesopelagic micronekton community. In addition, analysis of acoustic transects over the flanks and
summit of the seamount, with particular emphasis during times of maximum migration in the evening and pre-dawn, would aid in describing where the majority of the organisms are during different parts of the day and potentially their migration patterns.

**Is the diversity or taxonomic composition of the community different over the summit?**

The composition of the community over the summit of the seamount is quite different than the community away from the summit. Results from the cluster analysis (Fig 3), show that all of the trawls conducted over the summit of Cross Seamount cluster into a distinct group from the trawls conducted away from the summit. The diversity indices indicate that the species diversity is lower over the summit. Even though there are fewer total numbers of individuals sampled over the summit, the rarefaction curve shows the summit community also has fewer numbers of taxa per any given number of individuals than away from summit community (Fig 2). A look at the taxonomic composition of the mesopelagic micronekton community over the summit reveals that while fish, in particular Myctophid fish, numerically dominate the community, crustaceans are also quite abundant and numerically contribute to a larger portion of the overall taxonomic composition of the community than away from the summit (Fig 5c-d). However, when the epipelagic juveniles are included in the taxonomic composition of the community, the summit of the seamount is dominated numerically by juvenile fishes and stomatopod larvae while away from the seamount there appears to be little change in the taxonomic composition with the addition of the epipelagic juveniles (Fig 5a-b). This may imply that over the summit of the seamount the dramatic decrease in abundance and
biomass of organisms may largely be due to a large decrease in mesopelagic micronekton but not epipelagic micronekton. Either avoidance or higher rates of predation on mesopelagic micronekton rather than epipelagic micronekton may be the cause. However, further analysis of tuna diet over and away from the summit of Cross Seamount concurrent with sampling of mesopelagic micronekton and trawls that sample the day-deep community over the summit should be conducted to fully determine the cause of this shift towards epipelagic juvenile micronekton over the summit. Looking at the taxonomic composition of the mesopelagic micronekton community over the summit in finer detail may help to determine if it is predation or avoidance or possibly both that causes the decrease in organisms over the summit.

Interestingly, all of the mesopelagic micronekton taxa that are absent over the summit have daytime depths which are greater than the summit depth (>500m) while the taxa that are lower in abundance over the summit have daytime depths that are approximately equal to the depth of the summit. For instance, the myctophid genus *Lampamyctus*, which is completely absent over the summit (Table 4), has average daytime depths between 590 and 1,200 meters, well below the depth of the summit (Clarke 1973). This is also true for many shrimps. *Gennadas* sp., *Acanthephyra* sp., and *Systellaspsis* sp. are completely absent over the summit and all have daytime depths which are greater than 500 meters (Table 3; Omori 1974). In contrast, those vertically migrating taxa which are still present over the summit of the seamount, but in reduced abundance compared to away trawls, have daytime depth ranges that range from above to slightly below the depth of the summit. Many cephalopods, such as *Pterygioteuthis giardi* and *Abraliopsis* sp., have daytime depths between 300 and 600 m (Roper and Young
1975). Other taxa that follow this trend are the myctophid fish *Diaphus schmidti* with
daytime depths between 490 to 625 meters (Clarke 1973) and the shrimps *Sergestes* sp
and *Sergia* sp., with daytime depths between 200 and 700m (Omori 1974).

Despite the many differences in abundance of certain taxa, the summit community
does not appear to differ greatly from the community away from the summit regarding
size of organisms. In this study the size of organisms is estimated by comparing the
biomass recorded for each taxa. In the few taxa that did appear to differ in size, they all
appeared to have larger sizes away from the summit of the seamount as opposed to over
the summit. The family Cranchiidae, as a whole, appears to have larger individuals away
from the summit. This is mainly due to the fact that a number of the larger species of
cranchiid squids are absent in summit trawls. One species in particular, *Helicocranchia*
*beebei*, is one of the larger squids in the family and is completely absent over the summit
(Table 2). In the family Myctophidae, four species were found to have larger individuals
off the summit as opposed to on. These four are: *Benthosema suborbitale*, *Diaphus mollis*,
*Hygophum proximum* and *Myctophum* sp. There was however large variation in the catch
of these four myctophids leading to large standard deviations in the abundance and
biomass averages. A cause for the apparent absence of some larger individuals over the
summit could be due to avoidance of this area. Many larger individuals tend to reside at
deeper depths during the day than smaller individuals in order to more effectively hide
from visual predators (Clarke 1973; Hays et al 1994). The summit would prevent these
individuals from reaching these deep depths making them more vulnerable to predation.
Are there unique species over the summit?

Over the summit there appears to be one definite and one possible summit associated species. The definite species is the cranchiid squid *Liocranchia reinhardtii*. This species was found to be significantly higher in abundance over the summit than away (Table 2). This species however does not appear to be exclusive to the summit as one was caught in a trawl away from the summit. The possible summit associated species is the myctophid fish *Benthosema fibulatum*. While this species was not statistically more abundant over the summit due to highly variable catch rates, none were caught away from the summit (Table 4). Reid et al (1991) describes both species as part of the Hawaiian mesopelagic boundary community, which is defined as species that are associated with the flanks of the main Hawaiian Islands. The other species listed by Reid et al (1991) as being of the boundary-layer community were not found to be significantly higher in abundance over the summit. Of the other species listed as belonging to the Hawaiian boundary community, five were not caught in any of the trawls in this present study and three were caught in relatively low abundances both over and away from the summit. The three that were caught in low abundance in comparison to the Reid et al (1991) study both over and away from the summit were *Diaphus trachops*, *Oplophorus gracilirostris*, and *Abralia trigonura*. The summit of Cross Seamount is in the 400 to 700 meter depth range which is listed in Reid et al (1991) as being the day time depth of the boundary layer, yet these species were not higher in abundance over the summit. One possible explanation could be that many near shore communities often show increased concentrations of primary and secondary (zooplankton) productivity and mesopelagic micronekton are known to consume large amount of zooplankton (Maynard et al 1975;
Currently there is not much information regarding the primary and secondary productivity at Cross Seamount. Studies focusing on primary and secondary production are needed to further understand the dynamics of the mesopelagic micronekton community over and around Cross Seamount. In particular, a determination of whether or not there is an increased forage base for the mesopelagic micronekton over, or perhaps immediately away, from the seamount would help to explain the distribution and composition of the mesopelagic micronekton community over and around Cross Seamount. Additionally, Cross Seamount may not actively retain larvae of possible seamount associated organisms through circulation patterns and due to its relatively small size in comparison to the Main Hawaiian Islands. This may not encourage the recruitment of larvae of seamount or island associated organisms to Cross Seamount. Many seamounts, such as Southeast Hancock Seamount and Great Meteor Seamount, have not been found to actively retain larvae of seamount associated species and in fact the larvae of most organisms were found to be lower in abundance over the seamount as opposed to away (Boehlert and Mundy 1993)

**Conclusion**

Seamounts can provide a unique habitat for many species and can help describe the patchy distribution of many organisms throughout the world’s oceans. Understanding the dynamics that lead to this patchiness will aid in better management for not only these organisms but also for the commercially important species that prey on these organisms. Mesopelagic micronekton have an important role as both prey for many marine predators and in the flux of organic matter to the deep sea. Cross Seamount is a site of increased
tuna relative to the adjacent open ocean. A proposed reason for this increased abundance is that there is an increased forage base over the seamount. This study has shown that Cross Seamount does have an impact on the abundance and community structure of the local mesopelagic micronekton community. Even though there is a large decrease in abundance of organisms over the summit when compared to the nearby described away community, this decrease may be due to predation by tunas and perhaps other seamount associated predators, in addition to active avoidance of the seamount summit by deeper migrating taxa. Additionally, there is preliminary evidence that the flanks of the seamount may contain a very high abundance of organisms, particularly myctophid fish. The rarefaction curve generated for the day-deep flank community indicates that despite having a low total number of individuals sampled there is high species diversity. Future work should focus more on the flanks of the seamount to better understand its influence on the mesopelagic micronekton community. While the summit is the site of high concentrations of pelagic predators, it may be the flanks that have the largest positive impact on their forage base, mesopelagic micronekton. Another area of future work is constructing a detailed description of the presence and distribution of phytoplankton and zooplankton over and around the summit along with a description of the physical flow patterns over and around the summit. There is strong evidence that Cross Seamount is influencing large marine predators and mesopelagic micronekton, but the mechanisms behind this influence are unknown and cannot be fully determined without further studies at this seamount.
LITERATURE CITED


Clarke, T.A. 1983. Comparison of abundance estimates of small fishes by three towed nets and preliminary results of the use of small purse seines as sampling devices. Biological Oceanography 2: 311-340


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