The abundance and habitat use of demersal fishes on a rocky offshore bank using the ROPOS remotely operated vehicle

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Abstract

Offshore rocky banks are ecologically important refuge habitats for a number of U.S. commercial groundfish species. However, they are challenging to survey, and data on the abundance and ecology of fish populations at deep banks are limited. We used the remotely operated vehicle ROPOS to carry out visual surveys at two sites on Cherry Bank in the Southern California Bight, eastern Pacific Ocean. We observed differences in fish assemblages related to depth and habitat type and found that rockfishes (*Sebastes* spp) made up 65% of fishes recorded. Rockfishes and combfish (*Zaniolepis* spp) were associated with relatively shallow areas with hard substrate whereas flatfishes (Pleuronectiformes) and poachers (Agonidae) were found on unconsolidated sediments. Thornyheads (*Sebastolobus* spp) and hagfishes (Myxinidae) mainly occurred in areas of patchy habitat. Habitat and depth explained 52% of the variation in fish assemblages between transects with habitat explaining a greater proportion of the variation than depth. We observed large differences in the number of juvenile rockfishes and *Sebastomus* rockfishes between study sites with hard substrates and also had higher abundances of juvenile rockfishes versus sites characterized by mixed substrates. With the exception of unidentified *Sebastomus*, the current design had relatively low power to reliably detect observed differences for most taxa, so we report the number of additional transects that would be required to detect a 50% increase in densities. These data provide a baseline on groundfish densities and habitat associations at Cherry Bank and key information for the design of future work including Bayesian approaches to estimating coast-wide abundance.

Key Words: ROV, advanced technology, habitat use, groundfish, rockfishes

1. Introduction

Commercial and recreational fisheries are a key part of the U.S. economy contributing an estimated $97 billion to gross domestic product in 2015, providing jobs and contributing to maritime cultural heritage (NMFS, 2017). Effective monitoring of fish stocks is essential for sustainable fisheries management and an important component of the 1976 Magnuson-Stevens Fishery Conservation and Management Act. Assessments of fish populations can be based on fisheries dependent data such as catch information for target species, but these assessments can be biased due to differences in species catchability or selectivity of gear types (Murphy and Jenkins, 2010). In addition, advances in technology or the expansion of fishing grounds can mean population declines are not reflected in catch data (Miller et al. 2014). Monitoring methods such as experimental fishing, acoustics surveys or underwater visual census (UVC) by divers, are valuable sources of fishery independent information, and research trawl surveys have been used to monitor fish stocks in a number of regions (Bertrand et al., 2001; Doubleday and Rivard, 1981; Keller et al., 2017; Murphy and Jenkins, 2010). However, the need to acquire information on species that occur in deep untrawlable rocky habitats and marine protected areas where fishing restrictions apply has driven the development of alternative monitoring methods including underwater vehicles that enable visual surveys of fish stocks in ecologically important but challenging habitats (Barrett et al., 2010; Murphy and Jenkins, 2010)

Rocky banks on the continental shelf off the West Coast of the United States are important habitats for large aggregations of commercial groundfish species, but their high relief topography means they cannot be easily surveyed using traditional research trawls. Groundfishes off the West Coast are diverse (>90 species) and dominated by rockfishes, a group that includes a number of large species highly prized by commercial and recreational fishers (Love et al., 2002). Monitoring groundfish stocks is essential as they have been fished intensively for over 100 years and declines in abundance in the 1980s and 1990s led to nine groundfish species (including seven rockfish species) being declared overfished in 2001. Accurate assessments of groundfish populations are needed to track the effects of management measures introduced to allow stocks to recover such as harvest quotas, gear restrictions and marine protected areas (Fox et al., 2014). Surveys at offshore banks are particularly important as the pattern of fisheries expansion and depletion over time means that these relatively remote sites have the potential to act as refuge areas for targeted species (Miller et al., 2014).

The first visual surveys of a U.S. Pacific Coast offshore bank were carried out at Heceta Bank off Oregon using a manned submersible in the late 1980s (Pearcy et al., 1989). Since then, other banks off Oregon and California have been studied with various underwater vehicles (Hixon and Tissot, 2007; Love et al., 2009; Tolimieri et al., 2008; Yoklavich et al., 2007). A major benefit of these visual surveys is that in addition to information on fish assemblages, they also provide valuable ecological information such as associations between fishes, habitats and benthic invertebrates (Tissot et al., 2007; Tissot et al., 2006; Yoklavich et al., 2000). Studies have found that distinct groundfish assemblages are associated with particular depth ranges and habitats (Auster et al., 2003; Tissot et al., 2008; Tolimieri and Levin, 2006). Previous research has also provided density estimates (and an assessment) of some commercially important species at offshore banks (Yoklavich et al., 2007).

Cherry Bank is a rocky bank located in the Southern California Bight (SCB) (Yoklavich and Wakefield, 2015), an area extending from Point Conception in the north to just south of the U.S.-Mexican border (Dailey et al., 1993). The bathymetry of this region is relatively complex with numerous banks, islands and submarine canyons. Cherry Bank is in the western part of the

SCB associated with the Santa Rosa Ridge and is located inside the largest marine protected area (MPA) in California, one of two Cowcod Conservation Areas (CCA). This MPA was established by the Pacific Fishery Management Council in 2001 to promote the recovery of the once overfished cowcod (*Sebastes* levis) (Butler et al. 2003), which is no longer overfished and is presently in the last year of a 19-year rebuilding plan. The CCAs are closed to commercial and recreational fishing with three exceptions: 1) commercial and recreational fishing for 'other flatfish' using specific types of hook and line gear, 2) recreational fishing for various groundfishes shoreward of 73 m (40 fathoms), and 3) commercial fishing for rockfish and lingcod with limited-entry fixed gear and open access trawl gear, also in areas shoreward of 73 m (CFR §660.70). MPAs have been found to increase abundance, biomass and reproductive output of exploited species but regular monitoring is required to assess their effects on target species (Lester et al., 2009). Thus there is a need for more information on the assemblage structure of fishes, and other taxa such as deep-water corals (Salgado and Hoyt, 1996), for both monitoring and spatial planning in this complex region (Salgado et al., 2018; Yoklavich et al., 2007)

The primary aim of this study was to examine the relationship between habitat and demersal fish assemblage structure at Cherry Bank. We examined the effects of habitat on fish assemblage structure at two spatial scales. First, we investigate the influence of habitat on assemblage structure among locations made up of numerous habitat types. Second, we quantify differences in assemblage structure and fish abundance among individual habitat patches of uniform habitat type. In both cases we examine assemblage level patterns and those for individual species. A secondary aim of the study was to estimate the abundance of some groundfish on complex, hard substrata (untrawlable) versus soft sediments amenable to trawling with the goal of informing future stock assessments. We also examine the power of our sampling design to detect differences in abundance at different depths and habitats.

2. Methods

All sampling was carried out from 4-17 Oct 2004 on Cherry Bank (Fig. 1) using ROPOS (Remotely Operated Platform for Ocean Science, Shepherd and Juniper, 1997), a Canadian Remotely Operated Vehicle (ROV), aboard the R/V Thomas G. Thompson, operated by the University of Washington. Cherry Bank is a rocky bank located approximately 185 km west of San Diego and in the Southern California Bight. It is oriented NW-SE and is approximately 25 km long and 16 km wide at the center of the bank. Its depths extend from 110 m at the top to greater than 1500 m in the Tanner and San Nicolas Basins. Cherry Bank is representative of deep-water rocky-bank habitats that are home to a variety of commercially important fish species, including a diverse assemblage of rockfishes. Scientists from NOAA Fisheries Northwest and Southwest Fisheries Science Centers, in cooperation with geologists from Oregon State University, mapped a number of banks in the Southern California Bight in 2003 using an EM300 high-resolution multibeam sonar. This bathymetry survey identified Cherry Bank as a natural location for additional exploration due to its representative nature and because it had, at the time, received less attention than other rocky banks like Heceta Bank farther to the north (Hixon et al., 1991; Tissot et al., 2008) or submarine canyons in central California (Yoklavich et al., 2000; but see Yoklavich et al., 2007). Additional mapping of surrounding areas of Cherry Bank were mapped during the Thompson research cruise, creating a high-resolution map of the area that included the bank for depths shallower than 300 m. These surveys provided an excellent base map (Fig. 1) to plan ROV dives and overlay data sets as they became available.

ROPOS is a remotely operated vehicle designed to carry out various scientific tasks and exploration at depths up to 5000 m. The vehicle measures 1.75m x 2.6m x 1.45m and weighs approximately 2700 kg. An ORE Offshore TrackPoint II ultra-short baseline (USBL) navigation system was used to track ROPOS's position on the seafloor. The navigation data were piped to another computer, where ESRI ArcView Tracking Analyst was set up. Tracking Analyst allows display of the navigation data in real-time overlain on ArcView files such as topography, backscatter, trawl data and historical dive data. This enabled us to "drive over the topography", giving a visual comparison of the EM300 topography, ROPOS dive tracks, and the ROPOS video simultaneously and in real-time.

At the time of the study, ROPOS was equipped with two forward-looking video cameras: a forward-looking color camera, and lowlight Silicon Intensifier Target (SIT) camera. Video from both cameras was recorded on all dives along with a real time voice overlay of biotic and geologic observations by shipboard scientists. In order to provide a guide for estimating fish lengths (not included in the present analyses) and substrate size, such as for distinguishing between cobble and pebble-sized rocks, ROPOS is equipped with sizing lasers that projected two parallel beams 10 cm apart that produce reference light spots on objects within the field of view.

2.1 Sampling design and data collection

ROPOS dives were conducted at two sites (1 and 2) on Cherry Bank (Fig. 1) following a depth-stratified nested sampling design. This design allowed us to examine patterns among depths and at several spatial scales. Because of depth differences between the two sites, different depth zones were sampled at each site, although there was some overlap. We use 'location' to refer to a site*depth combination (e.g., site 1 in depth zone 150-200 m is a location). At site 1, we sampled in three depth zones: 150-200 m, 200-300 m, and 300-400 m for a total of 27 transects on two dives (R859 and R860, Fig. 1). At site 2, we sampled: the top of Cherry Bank at 100-125 m, and the slope of the bank at 150-200 m, 300-400 m, 500-600 m and 700-800 m depths on dives R861 and R862 (Fig. 1). Within each depth zone, we ran a total of nine 100-m transects divided into three randomized blocks (blocks nested within site*depth). Blocks were separated by 400-600 m (exact distance determined at random). Within each block, transects were oriented approximately as a triangle with the ends of each transect separated by ca. 20 m. The exact shape and orientation of the triangle as well as the distance between each transect was determined haphazardly to maximize the independence of the replicates (transects) and to ensure that transects did not overlap. This orientation was determined by logistical constraints of the ROPOS system and was developed to maximize the number of 100-m transects we could run over the course of a dive. Individual transects were run at a constant speed, although there was some variation among transects due to terrain (373 ± 125 seconds).

Video tapes were viewed post-cruise in the lab. We classified all observed fish to the lowest taxonomic unit possible. During data collection, each fish observation was given a time stamp allowing each individual fish to be associated with a habitat patch (see below). Rockfishes less than 20 cm were categorized as juvenile rockfish.

Habitat was classified according to a simplified version of habitat classification methods used by Stein(1992) and Green(1999). The primary habitat type that made up at least 50% of the area was first classified as either: ridge, boulder, cobble, sand, or unconsolidated sediment. If another habitat type made up at least 20% of the area in view it was designated as a secondary habitat type. We then converted the secondary habitat type to simply hard (ridge, boulder, cobble) or soft (sand, unconsolidated) to simplify the data. Thus, the designation boulder/soft indicates primarily boulder habitat with some soft sediments. We noted the start and stop times of habitat patches along each transect.

Because the height off the bottom of the ROV varied somewhat among transects, the actual 'swept area' (the area viewed on the tapes) differed among transects. To correct for this issue, we calculated a mean swath width by measuring swath width at 10 random points along each transect. Fish counts were then divided by swath width to produce density per 100 m2. Within-transect variance in swath width was small (coefficient of variation 22%).

We used time along a transect as a proxy for distance to calculate percent cover for each habitat type. The start and stop times of each large patch of habitat were recorded from the video tapes. Because transects were run at a constant speed and within-transect variation in width was small, we used percent time in a habitat type as an estimate of percent cover. Any vehicle stops were removed from these data.

2.2 Variation in assemblage structure among locations

To examine how assemblage structure varied among sites and depths, we used permutation-based multivariate analysis of variance, PERMANOVA (PERMANOVA v1.6, Anderson, 2001; Anderson, 2005). Because it is permutation based, this procedure does not require normally distributed data. However, the test is sensitive to differences in dispersion (the multivariate equivalent of heterogeneous variance). Therefore, we also tested for differences in dispersion in each case. We conducted three PERMANOVA analyses. Within each site, we conducted one PERMANOVA in which depth (fixed) was the main effect and block (random) was nested within depth. To examine variation among sites, we conducted a third PERMANOVA in which depth (fixed) and site (random) were the main effects, and block was nested within the depth*site interaction. This analysis included only the two depth zones that occurred at both sites (150-200 m and 300-400 m). In all cases, we used unrestricted permutation of the raw data with 4999 permutations.

To examine the relationship between fish assemblage structure and habitat characteristics, we used canonical analysis of principal coordinates with Bray-Curtis distance in a canonical correlation approach (CAP, Anderson and Willis, 2003). The procedure provides both an unconstrained (principal coordinates analysis) and constrained (canonical correlation) multivariate analysis of the data set. The unconstrained analysis examines fish assemblage structure without an a priori hypothesis and ordinates points based on the axis of greatest variation. The constrained analysis examines assemblage structure with an a priori hypothesis (in this case, the correlation with habitat characteristics) and seeks the axis that best addresses this hypothesis (Anderson and Willis, 2003). We chose m (the number of PCO axes used in the canonical portion of the analysis) based on the value of m resulting in the minimum residual sum of squares (Anderson and Willis, 2003).

For the CAP analysis, we used the abundance of each fish species on a 100-m transect and the percent cover of each habitat type along each transect. For the fish data, we used only those observations positively identified to species or some higher taxonomic level (generally genus or family), resulting in 45 taxa (Table 1).

Because depth and habitat covaried, we used multiple regression to partition the variance in assemblage structure of fishes between the two. To do so, we ran two analyses in which depth and the habitat matrix were alternatively used as main effects and covariates (based on their order in the model). The sums of squares for the covariate in each multiple regression gives the proportion of the total variance explained by that term independent of other terms in the model.

The sums of squares for the main effect gives the proportion of variance explained for said term given the covariate. The overlap (variance in common) for the two factors was given by subtracting the proportion of variance of one factor given the other from the total variance explained by the other. The analysis was done in DISTLM (Anderson, 2004) using a Bray-Curtis dissimilarity matrix derived from ln(y+1) transformed data. The fish data matrix included 45 taxa and the habitat matrix 10 categories. Depth was the absolute depth (not category) at the start of each transect.

2.3 Variation among locations in the abundance of selected taxa

We conducted a series of univariate analyses on the seven most abundant taxa to better characterize among-location differences. The seven taxa we examined were: bank rockfish (*Sebastes rufus*), *Sebastomus*, juvenile rockfishes, thornyheads, flatfishes, poachers and combfishes. Although presented on some figures, 'total rockfish' was not analyzed specifically as the results followed those for *Sebastomus*, which made up most of the rockfishes observed. We used log-linear models (general linear model, GLM, with log link, Poisson distribution) to compare abundance among sites and depths. In the analysis, site and depth were considered fixed effects since we were interested in making a number of specific comparisons. The natural log of swath width was used as an offset (McCullagh and Nelder, 1989). The block effect was ignored because it created model fitting problems due to blocks with zero individuals. Models were run in SAS 9.1 Proc Glimmix (when attempting to include the random block effect in a generalized linear mixed model) or Genmod (once random effects were excluded). The analysis included a number of missing level combinations (e.g., the depth zone 200-300 m did not occur at site 2), which both procedures handle by deleting the corresponding fixed effects parameters (SAS Institute Inc., 1999).

We calculated the effect size and power for a number of specific a priori comparisons between certain sites and depths (using the Estimate statement in Proc Genmod). These comparisons were made for two reasons. First, for certain comparisons, we were able to determine how much more abundant a taxon was at locations made up of primarily rocky habitat versus soft sediments at similar depths or vice versa (the effect size). For example, we compared the abundance of *Sebastomus* between sites at 150-200 m because these sites had substantially different habitat characteristics but were in the same depth zone (Figure 2). Second, by running power analysis on a range of comparisons, we were able to evaluate the performance of the sampling design for a range of potential dispersion values, effect sizes and means. In the power analysis, we used the overdispersion value for the overall model. Because the analyses use a log link, the effect sizes are interpreted as a multiplicative effect. Thus, one might compare how many times more fish there were on rocky habitat compared to sandy areas. As the goal of this exercise was to evaluate the potential performance of the sampling design, we did not make adjustments for multiple comparisons.

We estimated the statistical power of the GLM tests following Willis et al. (2003) who provide a conversion from standard power analysis, which assumes homogeneity of variance, to the Poisson situation where variance equals the mean and the data may also be overdispersed such that $\sigma^2 = \phi\mu$, where ϕ is the overdispersion parameter. An approximate upper bound on type II error rate is given by the value β obtained as the probability of having standard-normal quantile z_β given by:

$$z_\beta = \frac{\log(k)}{\sqrt{\frac{\phi}{n\mu_1}\frac{k+1}{k}}} - z_{\alpha/2} \qquad (1)$$

where k is the ratio of the two means $k = \mu_2/\mu_1$ and μ_1 is the smaller of the two means. The lower bound on power is then 1- β. As usual, n is the sample size. The standard normal quantile exceeds the value z_β with probability β. The value α is the type I error rate (here 0.05) such that $z_{\alpha/2} = z_{0.025} = 1.96$. It is relevant to note that overdispersion and low mean abundance in the smallest of the means being compared reduces power. It follows that for a given overdispersion, the number of samples (n) required to achieve a desired power is determined by the size of the smallest mean (μ_1). Thus we do not present all possible comparisons.

2.4 Variation in assemblage structure among patches of habitat

The above analyses examine variation in assemblage structure among locations. We also wanted to determine whether we could distinguish different assemblages in patches of specific types of habitat. Along each transect the start and stop times of sections of habitat were noted during data collection. These individual habitat patches within transects were used as replicates in the analysis with the data being the counts of each taxa within these patches. We calculated the area of each section by converting time to linear distance (% of total transect time * 100 m) and multiplying by the mean swath width. We then conducted a discriminant function type CAP analysis to determine whether assemblage structure varied among specific habitat types. We also used multiple regression to partition the variance among habitat type and depth as noted above. Habitat was coded as a dummy variable to allow it to be used as a covariate in the analysis.

We used generalized linear mixed models (GLMM) to determine whether the abundance of the seven aforementioned taxa (see above) varied among habitat types and to see if we could distinguish preferred substrata. Since the data were counts, we used a Poisson distribution and log link (McCullagh and Searle, 2001; McCullagh and Nelder, 1989). In the analysis, habitat type was a fixed, class variable and the depth a covariate. The natural log of the patch area was used as an offset to account for differences in overall area sampled among the habitat patches. Site and block within site*depth were included as random effects where block was the set of three transects. Obviously, habitat patches within transects were not randomly sampled and are potentially spatially autocorrelated. Therefore, we modeled spatial autocorrelation within transects using a spatial power covariance structure (Littell et al., 1996), where the sequential rank of a habitat patch along each transect was the location variable. Samples outside the observed depth range of individual taxa were not included in the analyses.

3. Results

Seventy-two 100-m transects were completed over three days of ROPOS dives. Transects averaged 2.38 m (± 0.797 s.d.) in width resulting in a total area surveyed of 17,143 m2. We observed 1893 fishes from 45 taxa across the two sites (Table 1). Of these, 19% were identified to species, and 92% were identified to family. Rockfishes (*Sebastes*) accounted for 65% of all fishes observed. Considering only rockfishes, the majority (~60%) of all rockfishes were classified as *Sebastomus* complex (genus *Sebastes*, subgenus *Sebastomus*). The *Sebastomus* complex (hereafter *Sebastomus*) includes ten species off of California, which are difficult to identify without close scrutiny (Chen, 1971; Love et al., 2009; Love et al., 2002). Only 20% were identified to species. The seven most abundant taxa overall were: Bank rockfish (*Sebastes* rufus), *Sebastomus* rockfishes, juvenile rockfish (juv *Sebastes* spp), thornyheads (*Sebastolobus* spp), Flatfishes (Pleauronecitidae), poachers (Agonidae) and combfishes (*Zaniolepis* spp).

Habitat varied considerably among locations (Fig. 2).The shallower areas of site 1 were almost exclusively hard substrata. The top of Cherry Bank and the deeper sections of site 2 were more mixed, while the remaining locations were primarily soft sediment habitat types.

3.1 Variation in assemblage structure among locations

At site 1, groundfish assemblage structure varied among depths (PERMANOVA, $F_{2,6} = 9.907$, $p = 0.0034$), and there was significant variation within depths as well (PERMANOVA, $F_{6,18} = 2.0753$, $p = 0.017$). Likewise, at site 2, assemblage structure varied among depths (PERMANOVA, $F_{4,10} = 8.2499$, $p = 0.0002$), and there was significant variation within depths (PERMANOVA, $F_{10,30} = 2.6837$, $p = 0.0002$). Given that we conducted three multiple comparisons (additional one below), the results should be considered significant at $p < 0.017$. At site 1, dispersion values were homogeneous for both depth and block within depth ($p > 0.44$ for both). For site 2, however, there was some indication of unequal dispersion among depths ($p = 0.022$) suggesting that significant results might be caused by different multivariate dispersions as well as variation in the location of the multivariate centroid. Essentially, differences in variability within sites may have caused the significant result not differences in assemblage structure among sites. This result is analogous to the violation of homogeneity of variance in an ANOVA leading to a significant result.

When the two sites were compared across common depth zones, there was a depth* site interaction indicating that depth related patterns were not consistent at different sites (Table 2). This depth*site interaction was likely caused by habitat structure which differed among locations (Fig. 2). At 150-200 m, site 1 was comprised of primarily hard, complex substrata while site 2 was primarily soft substrata. For the analysis comparing the two sites at two depths, only the site effect showed some indication of heterogeneous dispersion ($p = 0.0492$) although the significance level is greater than the adjusted p-value.

The unconstrained (PCO) and constrained (canonical) portions of the CAP analysis produced similar ordinations (though reversed) indicating that the axis of greatest variation in fish assemblage structure was the same as the axis related to the correlation with habitat structure and depth (Fig. 3). The first three PCO axes explained 60.4% of the variation in fish assemblage structure and were used in the canonical correlation portion of the CAP analysis. Fish assemblage structure was strongly correlated with habitat structure (canonical correlations: $\delta_1 = 0.97$, $\delta_2 = 0.92$, $\delta_3 = 0.48$, $p = 0.0002$). Note that in this case the habitat matrix also included depth. Examination of component loadings (correlations between canonical axes and original fish or habitat variables) showed that depth was positively correlated with axis 1 and negatively correlated with axis 2. Hagfishes and thornyheads were found in deeper areas at site 2 in what might be considered patchy habitat (Fig. 3b & c), as “Unconsolidated, hard” and “Rocky, soft” habitats were also assigned to this same region (Fig. 3d). Flatfishes, Dover sole (*Microstomus pacificus*) specifically, and poachers were found primarily on unconsolidated sediments (Fig. 3b, c & d). Several rockfish taxa, as well as combfishes, were associated with shallower areas and hard substrata.

The combination of depth and habitat explained 52% of the variation in fish assemblage structure among transects (Fig 4). Habitat explained 29.4% of the variation, while depth explained only 7.7% of the variation. The two factors held 15.1% of the variation in common with 47.7% unexplained.

3.2 Abundance with depth and habitat type

Rockfishes in general and *Sebastomus*, bank rockfish, and juvenile rockfishes in particular were most common at shallower locations with complex, hard substrata (Fig. 5). Thornyheads were most abundant below 500 m on soft sediments. Flatfish distribution among sites was the opposite of that of rockfish, being most common at locations with unconsolidated sediment. Poachers inhabited intermediate depths (300-400 m) with soft sediment, while combfishes were most abundant in the shallower areas of Cherry Bank.

Bank rockfish were only found in the two shallower depths zones at site 1 but did not differ in abundance between depths (Table 3). *Sebastomus* were 1.59 times more numerous at site 1 in the 150-200 m depth zone than on the top of Cherry Bank (site 2 100-125 m), which was shallower and contained somewhat less hard substratum. There were substantial differences between sites at 150-200 m. Site 1, where the habitat was primarily cobble and ridge, contained 165 times as many *Sebastomus* rockfishes per 100 m2 as at site 2. Juvenile rockfishes were more than eight times more common at site 1 in the 150-200 m depth zone than site 2 at 100-125 m. Thornyheads were more abundant in deeper waters with 1.94 times as many individuals at 700-800 m than at 500-600 m at site 2. Poachers were 3.64 times more abundant at site 1 versus site 2 at 150-200 m, while combfishes were 4.79 times more abundant at site 1 at 150-200 m than at 100-125 m at site 2.

The power of the tests was moderate or low for the specific comparisons, being highest for the contrast of *Sebastomus* rockfish numbers between sites at 150-200 m (Table 3). In most cases, only a modest increase in the number of transects (from 9 to 27) would be required to reliably detect the observed differences. However, to have adequate power ($1-\beta = 0.8$) to detect a 50% increase (effect size of 1.5) in density, the present sampling design required a substantial number of replicates for most comparisons and related combinations of abundance and dispersion (Fig. 6).

3.3 Variation in assemblage structure among patches of habitat

Assemblage structure differed among habitat patches (PERMANOVA, F9,286 = 3.86, p <0.001). The discriminant-type CAP (categorical habitat variables) showed that poachers and flatfishes were primarily associated with habitat patches such as sand/soft and uconsolidated/soft that lacked hard substrata of any type ($\delta_1 = 0.84$, $\delta_2 = 0.64$, $\delta_3 = 0.55$, $p < 0.001$, Fig. 7). Thornyheads were associated with areas of mixed hard and soft substrata including ridge/soft, unconsolidated/hard, and boulder/soft habitats suggesting a positive association with patchy areas. *Sebastomus* and unidentified rockfishes were associated with areas with complex, hard substrata such as ridge/hard, boulder/hard, and cobble/hard, although they also utilized more patchy areas as well. Partitioning of the variance showed that depth and habitat explained 7.5% and 8.6% of the variation in groundfish assemblage structure respectively, with 11.7% of the variance held in common. Over 70% of the variance was unexplained.

All of the seven taxa examined varied in their abundance in specific habitat patches (Fig. 8). While a number of taxa were absent on some substrata, only bank rockfish, *Sebastomus*, juvenile rockfishes and thornyheads showed variation among habitats on which they were present (GLMM, $p < 0.05$ for all). Bank rockfish were more common on ridge/hard and boulder/hard than on the less complex cobble/hard, but did not use other substrata. For *Sebastomus* and juvenile rockfishes, this was primarily a distinction between hard and soft substrata. Neither taxon showed variation in abundance among the various hard habitat types (Tukey's test, $p > 0.05$ for all) with similar densities in ridge, boulder and cobble habitat regardless of whether the secondary habitat was hard or soft. There were more fishes on these hard habitats than on unconsolidated or sand habitats (Tukey's test, $p < 0.05$ for all) except for the sand with hard substrata which had similar density of fish to the primarily hard substrata. Within the primarily soft substrata, the presence of some hard substrata did result in higher numbers of rockfishes and *Sebastomus* rockfish ($p < 0.05$ for unconsolidated/hard vs. unconsolidated soft, and sand/hard vs. sand/soft). Overall, *Sebastomus* rockfishes were 7.29 (95% CL: 1.03 - 15.18) times as various on patches of hard substrata (ridge, boulder and cobble) as they were on primarily soft sediments (sand and unconsolidated).

Flatfishes, poachers and combfishes showed no variation in abundance among habitat types where they were present to some extent (GLMM, $p > 0.05$ for all three). None of these fishes were found on ridge/hard habitat patches, and flatfish also avoided boulder/soft, cobble/hard, cobble/soft and sand/hard habitat patches.

4. Discussion

Understanding assemblage structure in relation to habitat and depth provides a baseline for spatial and ecosystem-based management, and quantifying essential fish habitat. Here, we observed differences in deep groundfish assemblages related to habitat type and depth. Rockfishes and combfishes inhabited relatively shallow areas with hard substrate whereas flatfishes and poachers were found on unconsolidated sediments. Thornyheads and hagfishes were found primarily in areas of patchy habitat. Together, habitat and depth explained 52% of the variation in fish assemblages between transects with habitat explaining a greater proportion of the variation than depth. In terms of abundance, we observed large differences in the number of rockfish in the sub-genus *Sebastomus* between study sites with 165 times more per 100 m2 at site 1 than at site 2. Site 1 was predominantly made up of hard substrates and also had higher abundances of juvenile rockfishes than site 2, which was characterized by mixed substrates. Thornyheads were most abundant in the deepest depth zone surveyed. This habitat-level information on especially rockfish abundance can help to inform estimates of coast-wide abundance, especially through Bayesian statistical approaches.

4.1 Vehicle effects: attraction and avoidance

While visual surveys have many advantages over traditional sampling methods for fishes, these methods have their own inherent biases such as those associated with avoidance, attraction, and detection. Underwater survey platforms generate a variety of visual, auditory, and mechanical stimuli (e.g., light, sound, water displacement/pressure waves (McIntyre et al., 2015; Ryer et al., 2009; Somerton et al., 2017; Trenkel et al., 2004). Stoner et al. (2008) reviewed observations of fish responses to survey platforms from 22 studies across a range of locations (both qualitative and quantitative). In the quantitative studies, thirteen of 25 fish taxa showed avoidance or neutral responses, nine taxa showed attraction to or avoided platforms, and two taxa were either attracted or neutral. Sixteen of the 22 studies summarized by Stoner et al. (2008) were located in the eastern North Pacific and share a number of species or taxa with the current study, including rockfishes, thornyheads and flatfishes. Studies of sampling bias in visual surveys fall into different categories including quantifying fish behavioral reactions to a vehicle (Adams et al., 1995; Lorance and Trenkel, 2006; Yoklavich et al., 2007) comparing the relative abundance between different vehicles (Laidig et al., 2013), and laboratory experiments to quantify responses to individual stimuli (Ryer et al., 2009). Yoklavich et al. (2007) assessed the biomass of cowcod (*S. levis*) off southern California, using direct counts from an HOS and applying line-transect methods. Their detailed quantification and analyses showed that cowcod, a large sedentary rockfish, did not exhibit attraction or avoidance to the HOS. In a comparable line-transect based survey employing the same HOV of another large sedentary rockfish (yelloweye, *S. rubberimus*) in southeastern Alaska, O'Connell et al. (1993) observed no avoidance or attraction. Working off central California, Laidig et al. (2013) compared the response of 28 taxa of eastern North Pacific fishes to an ROV and HOS and observed 57 % and 11% of fishes reacted to the ROV and submersible, respectively. Fishes that were benthopelagic (>1 m above the seafloor) reacted at higher rates to both the ROV (73%) and HOS (22%) than fishes that that occurred on the seafloor. Under laboratory conditions, Ryer et al. (2009) examined reactions in seven eastern North Pacific fishes to a looming light source that simulated the approach of a mobile survey platform. They observed a range of responses with the more active species showing the greatest tendency to move away from the source of illumination, including two benthopelagic species of rockfish. Overall, there is a range of biases in visual surveys that varies by species, survey platforms and their associated stimuli, habitat and conditions and likely many other factors. There is a critical need for further research to quantify species-specific responses to survey platforms and to quantify sampling efficiency to support accurate abundance estimates.

4.2 Assemblage structure and habitat relationships

We noticed fairly small-scale variation in assemblage structure among locations at the level of blocks within depths. Partitioning the variance suggested that much of this small-scale variation could be ascribed to habitat characteristics at the level of the individual transect.

In general, rockfishes were found at locations with rocky substrata such as ridge, boulder and cobble. Flatfishes and poachers were more common at locations with sand or unconsolidated sediments. Thornyheads were common at deeper depths and associated with what might be considered patchy habitats composed of both soft and hard sediments.

Our results differ to some extent from previous work regarding rockfish habitat use patterns. At Cherry Bank, all rockfish species that showed some pattern of differential habitat use were more common on hard, complex substrata. Other researchers have noted associations of some rockfishes with less complex, trawlable soft sediments. For example, Pacific Ocean perch (*Sebastes alutus*), splitnose (*S. diploproa*), greensstriped (*S. elongatus*), and bocaccio (*S. paucispinus*) rockfish were all more common on trawlable habitats than in untrawlable ones around Vancouver Island, British Columbia (Matthews and Richards, 1991). Similarly, Krieger and Ito (1999) found shortraker rockfish (*S. borealis*) to be more common on soft substrata than on hard ones. Greenstriped abundance was higher on fine sand and mud versus more complex, hard substrata in a number of studies (Matthews and Richards, 1991; Murie, 1994; Richards, 1986). Here, greenstriped, like all other rockfish, were more abundant at locations with hard substrata like ridge, boulder and cobble (in the multivariate analysis). We observed only 14 greenstriped rockfish, but at the level of habitat patches, they were evenly distributed over primarily hard (7) and primarily soft substrata (7). However, ten out of the 14 fishes were in patches with at least some hard substrata. This difference in outcomes may also be due in part to the scale at which habitat was defined, as the above studies used fairly broad definitions of habitat compared to ours. Stein et al. (1992), who used a habitat classification system upon which ours is based, also noted higher densities of greenstriped rockfish in mud-cobble habitat patches and sandy-ridge areas supporting the conclusion that this species uses patchy habitats, not uniformly sandy or muddy ones.

An observation that is somewhat difficult to interpret is the correlation between rockfish (total, juvenile and *Sebastomus*) abundance and the sand/hard substratum. While this may represent an association for patchy habitat, it is also possibly an artifact of the distribution and abundance of the sand/hard substratum among locations. This substratum was found only at the location on the top of Cherry Bank and was not particularly abundant there. The correlation seen in the CAP analysis may, therefore, be an artifact of a correlation with hard substrata which made up most of the site. The examination of habitat use by individual fishes (abundance within patches of habitat) does show total rockfish abundance to be fairly high within sand/hard patches. However, the relationship may be reliant to some extent on the other habitat types present at this specific location. The top of Cherry Bank was made up of almost 60% hard substrata. Individual fishes within the sand/hard patches may have been in transit to other adjacent patches or utilizing partly sandy sections of an otherwise untrawlable location. At present, the data do not allow for conclusive interpretation.

At the level of habitat patches, all species varied in their abundance in different types of habitat patches, but the differences were largely limited to presence/absence type conclusions. Thornyheads, flatfishes, poachers and combfishes showed no variation in density among habitat types in which they were present to some extent. For unidentified rockfishes, juvenile rockfishes and *Sebastomus*, the only differences were between primarily hard (ridge/hard, boulder/hard, boulder/soft, cobble/hard, cobble/soft) versus entirely soft (unconsolidated/soft and sand/soft) substrata. Abundance of fishes in habitat patches with at least some hard substrata (unconsolidated/hard, sand/hard) was similar to habitat patches with primarily hard substrata.

The lack of discrimination among habitat types may be the result of ‘averaging’ the habitat use patterns of multiple species within the multi-specific taxa like ‘total rockfish’ or *Sebastomus*. For example, bank rockfish, the only individual identifiable species common in reasonable numbers, showed strong differences among habitat patches, being found only on entirely hard, complex habitat patches and in greater abundance on ridge/hard and boulder/hard than on the less complex cobble/hard habitat. Likewise, while yelloweye rockfish (*S. ruberrimus*) in southeastern Alaska are found on cobble, continuous rock, broken rock and boulder habitats, they are most abundant on the last two substrata and below 108 m (O'Connell and Carlile, 1993). On Heceta Bank, Stein et al. (1992) were also able to more precisely define habitat use by a number of rockfishes.

4.3 Power analysis

The power of the current design was not particularly good in most cases; this is true for a number of reasons. First, overdispersion reduces the power of the test, and many species showed some sign of overdispersion. Second, the size of the smaller of the two means also strongly affects the power. This consequence is most easily seen in the case of *Sebastomus* when contrasting the results from the comparison (1) between the top of Cherry Bank (100-125 m) and site 2 at 150-200 m versus (2) that of site 1 and site 2 at 150-200 m. There were very few *Sebastomus* at site 2 in the 150-200 m depth range and more than 3000 transects would be needed to reliably detect a 50% difference in density (effect size of 1.5 times as many fish). When *Sebastomus* densities were much higher at both locations, just under 30 transects would provide adequate power to detect a 50% difference between areas with densities similar to the top of Cherry Bank and site 1 at 150-200 m.

The results of the power analysis are not entirely worrisome, however. For example, there were vast differences in *Sebastomus* density between site 1 and site 2 at 150-200 m, one of which was dominated by complex, hard substrata and the other by soft substrata. Only 14 transects would be required to attain acceptable power given the observed effect size, and the general approach would be acceptable for comparing trawlable and untrawlable habitats given a modest increase in sampling effort of five transects. In fact, for most comparisons, an increase to 25-30 transects would provide adequate power given the current means and over-dispersion parameters. We were able to complete 30 transects in one dive (day) when focusing on one site, indicating that a site could be adequately characterized for the more common taxa in one day of sampling.

4.4 Conclusions

Population assessment for West Coast fisheries, and many fisheries world-wide, relies heavily on fishery-independent trawl surveys to provide an index of abundance to the stock-assessment process. However, the trawl surveys typically cannot sample in complex rocky habitat, which may bias estimates of abundance for those species most commonly found in such habitats like rockfishes. This problem has motivated the development of methodologies that can survey such areas. While they surely have their own biases, technologies like ROVs (including drop cameras, towed cameras, and autonomous underwater vehicles) can survey in untrawlable habitat and have the added advantage in that they are non-destructive making them useful for the collection of data on overfished or at risk species or for surveying areas closed to fishing like MPAs. Increasingly Bayesian techniques and spatial modeling provide a way to incorporate visual surveys from complex habitat and habitat information with trawl surveys to produce better estimates of coast-wide abundance (Shelton et al., 2014; Thorson et al., 2015; Tolimieri et al., 2015).

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Table 1. Taxa observed at Cherry Bank.

Family	Species	Common name	Number	Length (cm)	SE
Myxinidae	*Eptatretus* spp.	unknown hagfish	19	32.3	2.0
Chimaeridae	*Hydrolagus colliei*	spotted ratfish	4	20.0	0.0
Scliorhinidae	catshark	catshark	1	30.0	0.0
Rajidae	*Raja* spp.	skate, unidentified	2	35.0	0.0
Rajidae	*Raja inornata*	California skate	1	22.0	0.0
Rajidae	*Raja rhina*	longnose skate	2	65.0	5.0
Alepocephalidae	*Alepochephalus tennebrosus*	California slickhead	4	18.8	0.8
Alepocephalidae	*Talismania bifurcata*	Threadfin slickhead	1	23.0	0.0
Macrouridae	*Albatrossia pectoralis*	giant grenadier	3	25.0	5.8
Macrouridae	*Coryphaenoides acroliepis*	Pacific grenadier	3	30.0	7.6
Moridae	*Antimora microlepis*	Pacific flatnose	2	35.0	-
Merlucciidae	*Merluccius productus*	Pacific hake	28	24.4	0.9
Scorpaenidae	unknown *Sebastomus*	*Sebastomus* rockfish	732	14.0	0.1

Scorpaenidae	*Sebastolobus* spp.	thornyhead, unidentified	202	13.3	0.3
Scorpaenidae	*Sebastes* spp.	rockfish, unidentified	163	16.5	0.5
Scorpaenidae	*Sebastes* spp. Juv.	juvenile unknown rockfish	89	7.6	0.3
Scorpaenidae	*Sebastes rufus*	Bank rockfish	62	23.5	0.8
Scorpaenidae	*Sebastes wilsoni*	pygmy rockfish	35	10.4	0.2
Scorpaenidae	*Sebastes diploproa*	splitnose rockfish	34	18.8	1.1
Scorpaenidae	*Sebastes jordani*	shortbelly rockfish	28	14.4	0.3
Scorpaenidae	*Sebastes ensifer*	swordspine rockfish	23	15.4	0.2
Scorpaenidae	*Sebastes elongatus*	greenstriped rockfish	14	18.8	0.8
Scorpaenidae	*Sebastes paucispinis*	bocaccio	10	38.1	2.1
Scorpaenidae	*Sebastolobus altivelas*	longspine thornyhead	7	19.7	2.1
Scorpaenidae	*Sebastes levis*	cowcod	6	27.7	6.1
Scorpaenidae	*Sebastes rosaceus*	rosy rockfish	6	20.3	3.0
Scorpaenidae	*Sebastes melanostomus*	blackgill rockfish	5	24.4	1.7
Scorpaenidae	*Sebastes zacentrus*	sharpchin rockfish	7	17.7	1.0
Scorpaenidae	*Sebastes miniatus*	vermilion rockfish	3	40.0	0.0

Scorpaenidae	*Sebastes saxicola*	stripetail rockfish	3	15.0	0.0
Scorpaenidae	*Sebastes rubrivinctus*	flag rockfish	2	21.5	3.5
Scorpaenidae	*Sebastolobus alascanus*	shortspine thornyhead	2	40.0	0.0
Scorpaenidae	*Sebastes ruberrimus*	yelloweye rockfish	1	40.0	0.0
Hexagrammidae	*Zaniolepis* spp.	combfishes	52	13.0	0.4
Hexagrammidae	*Zaniolepis frenata*	shortspine combfish	7	13.5	2.0
Agonidae	unknown agonidae	poacher, unidentified	91	12.9	0.3
Zoarcidae	eelpout	eelpout	20	13.3	1.1
Zoarcidae	*Lycodes cortezianus*	bigfin eelpout	8	20.4	0.8
Zoarcidae	*Lycodes pacificus*	blackbelly eelpout	7	13.0	0.6
Zoarcidae	*Lycodapus mandibularis*	pallid eelpout	6	11.3	1.0
Zoarcidae	*Bothrocara brunneum*	Twoline eelpout	2	42.5	7.5
Gobiidae	*Coryphopterus nicholsii*	blackeye goby	3	9.0	0.8
(Pleuronectiformes)	flatfish	flatfish	48	16.3	0.1
Pleuronectidae	*Microstomus pacificus*	Dover sole	30	23.3	1.6
Pleuronectidae	*Errex zachirus*	rex sole	5	19.0	1.9

Unidentified fish	fish	110	9.9	0.8

Table 2. Results of PERMANOVA comparing two sites at two depths.

Source	df	Mean Square	F	p
Site	1	14678	4.0497	0.006
Depth	1	36000	1.5766	0.294
Site*Depth	1	3626	6.2971	0.0004
Block (Site*Depth)	8	22834	3.5007	0.0002
Residual	24	1035		

Table 3. Results of *a priori* contrasts from generalized linear models (log link and Poisson distribution) comparing abundance of the seven most common fish taxa. ϕ is the overdisperion parameter (deviance/df) from the full model. CL = 95% confidence limits. *n* is the sample size required for a power of 0.8 given the current data. Site 2 100-125 m was the top of Cherry Bank.

Taxon	Common name	Comparison	χ^2	p	Effect size	95% CLs	ϕ	Power	*n*
Sebastes rufus	Bank rockfish	Site 1 150-200 vs. Site 1 200-300	0.59	0.443	1.59	0.22-5.23	5.17	0.07	293
Sebastomus spp.	Unidentified rockfishes	Site 1 150-200 vs. Site 2 100-125	6.76	0.009	1.59	0.22-2.25	4.63	0.37	27
		Site 1 150-200 vs. Site 2 150-200	11.21	<0.001	165.34	23.29-3289.11	4.63	0.62	14
Juv. *Sebastes* spp.	Juvenile rockfish	Site 2 150-200 vs. Site 2 100-125	7.23	0.007	8.33	1.17-59.14	8.85	0.26	25
Sebastolobus spp.	Thornyheads	Site 1 300-400 vs. Site 2 300-400	0.07	0.787	1.42	0.20-18.38	3.41	0.04	2673
		Site 2 700-800 vs. Site 2 500-600	5.66	0.017	1.94	0.27-3.34	3.41	0.39	26
Pleuronectidae	Flatfishes	Site 1 150-200 vs. Site 2 100-125	0	0.948	1.08	0.15-11.74	1.48	0.03	>10000
		Site 1 150-200 vs. Site 2 150-200	1.69	0.194	3.63	0.51-25.41	1.48	0.17	107
		Site 1 300-400 vs. Site 2 300-400	0	0.992	1.01	0.14-1.75	1.48	0.03	>10000
Agonidae	Poachers	Site 1 150-200 vs. Site 2 150-200	9.81	0.002	3.64	1.62-8.18	3.07	0.44	22
Zaniolepis spp.	Combfishes	Site 1 150-200 vs. Site 2 100-125	8.9	0.003	4.79	0.68-13.42	1.58	0.45	21
		Site 1 150-200 vs. Site 2 150-200	1.89	0.169	2.25	0.32-7.12	1.58	0.14	94

Figure Legends

Figure 1. Location of the study sites at Cherry Bank. Inset panes show ROV dive locations in detail. Bottom pane shows the location of Cherry Bank relative to Los Angeles, San Diego and the Channel Islands. Triangles show locations of data collection for this study.

Figure 2. Percent cover of ten habitat types under a binary classification system across locations. R = rocky ridge, B = boulder, C = cobble, S = sandy, U = unconsolidated, h = hard (includes R, B and C), s = soft (includes U and S). The first digit indicates the substratum that made up at least 50% of the bottom. The second digit indicates a substratum that made up at least 20%.

Figure 3. Results of canonical correlation type canonical analysis of principal coordinates. (a) results of principal coordinates analysis of fish assemblage structure, (b) results of the canonical correlation portion of the analysis. (c) correlations between individual species and the canonical axes. Overlapping text in the lower left corner includes: cowcod, greenstriped, shortbelly, swordspine and juvenile rockfishes. (d) correlations between percent cover of habitat types, including depth, and the canonical axes. Overlapping text in lower left corner includes Bh and Ch, in the lower right corner Uh and Rs. Habitat classification Follows figure 2. Data are centroids ± 1 S.E.

Figure 4. Results of partitioning of variance in fish assemblage structure among habitat type and depth. Y-axis is the proportion of variance explained by habitat and depth for (a) among locations (b) among patches of habitat.

Figure 5. Density of eight taxa among locations. Error bars are ± 1.0 s.e.

Figure 6. Sample size required for a given multiplicative effect size for a number of comparisons. S1 and S1 are for site 1 and site 2 respectively.

Figure 7. Results of canonical analysis of principal coordinates, discriminant type. (a) results of principal coordinates analysis of fish assemblage structure (b) results of canonical analysis showing both the ordination of habitat types and correlations between individual species and canonical axes. Data are centroids ± 1 S.E.

Figure 8. Abundance of eight taxa on ten different habitat patches. Habitat classified as in Figure 2. ‘nd’ indicates no data. This result occurs when the habitat type was not present within the depth range observed for that species. Error bars represent ± 1.0 s.e.

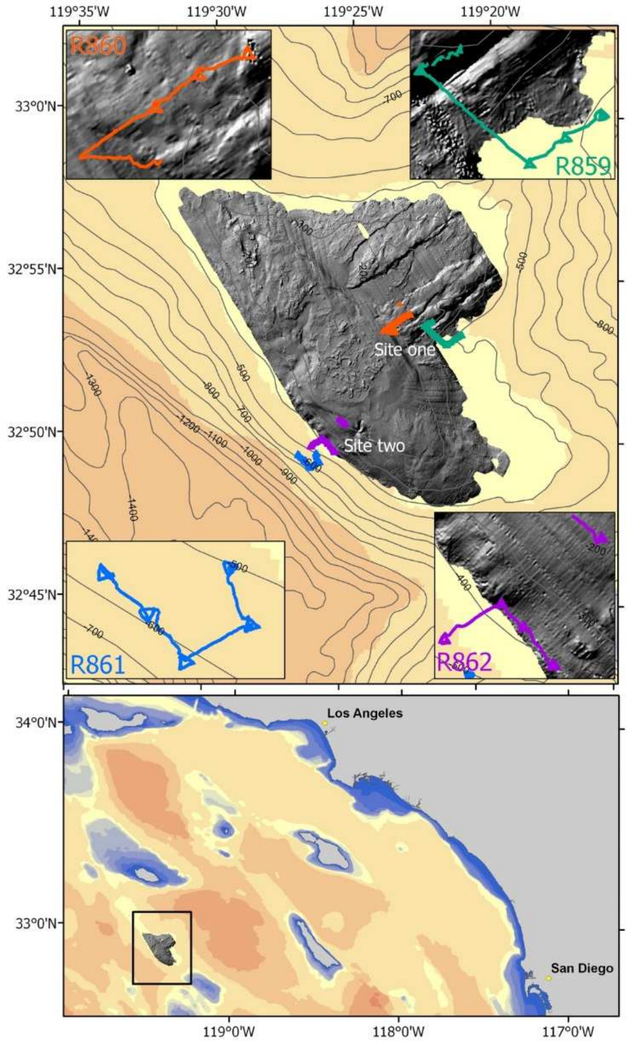


Figure 1 – Single column

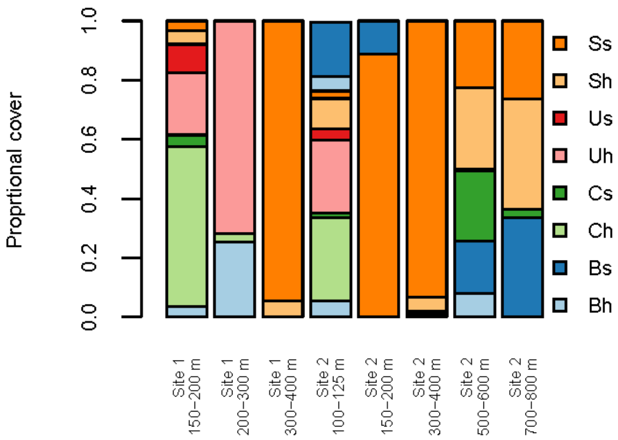


Figure 2 – Single column

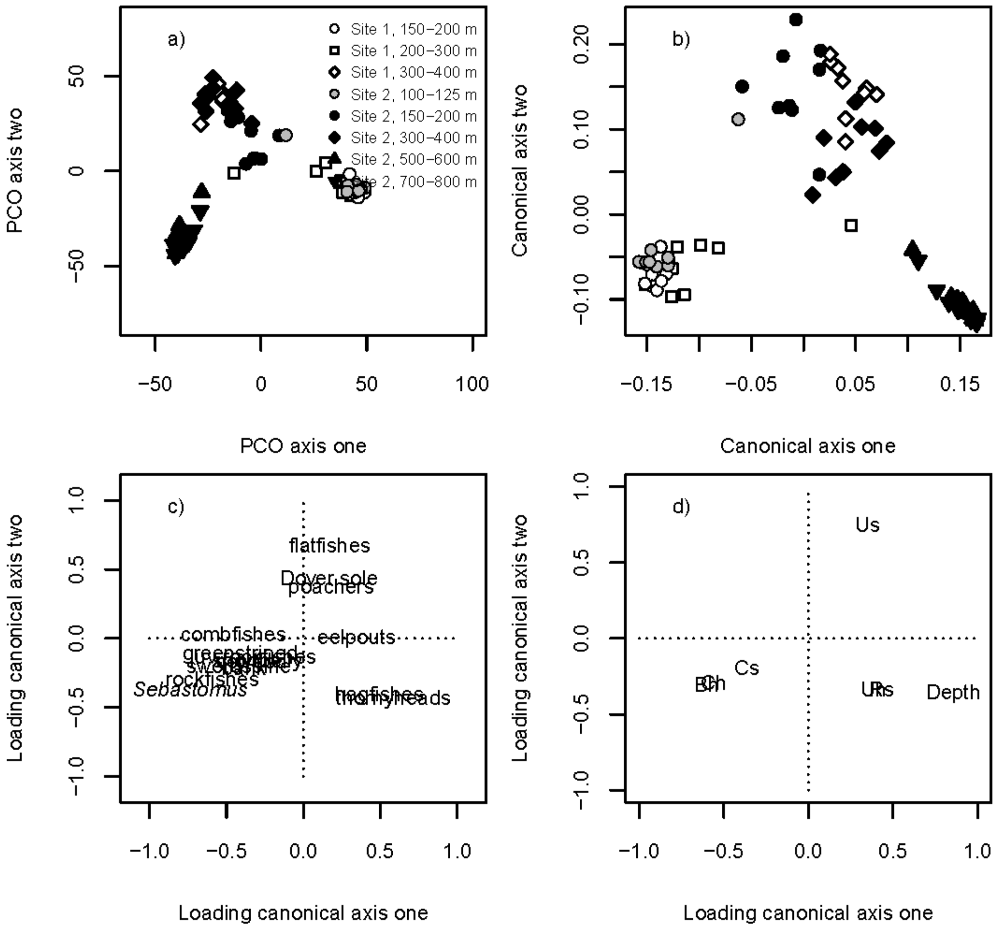
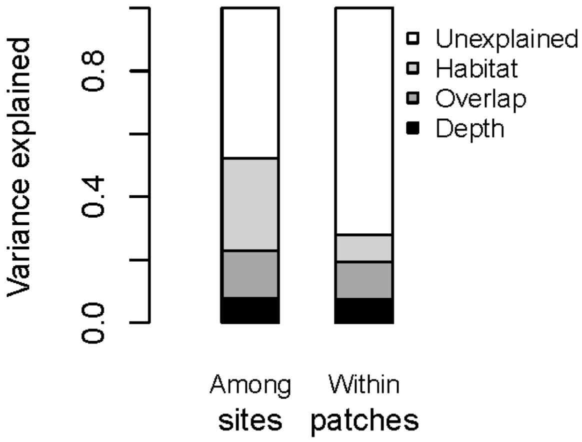


Figure 3 – 1.5 Column



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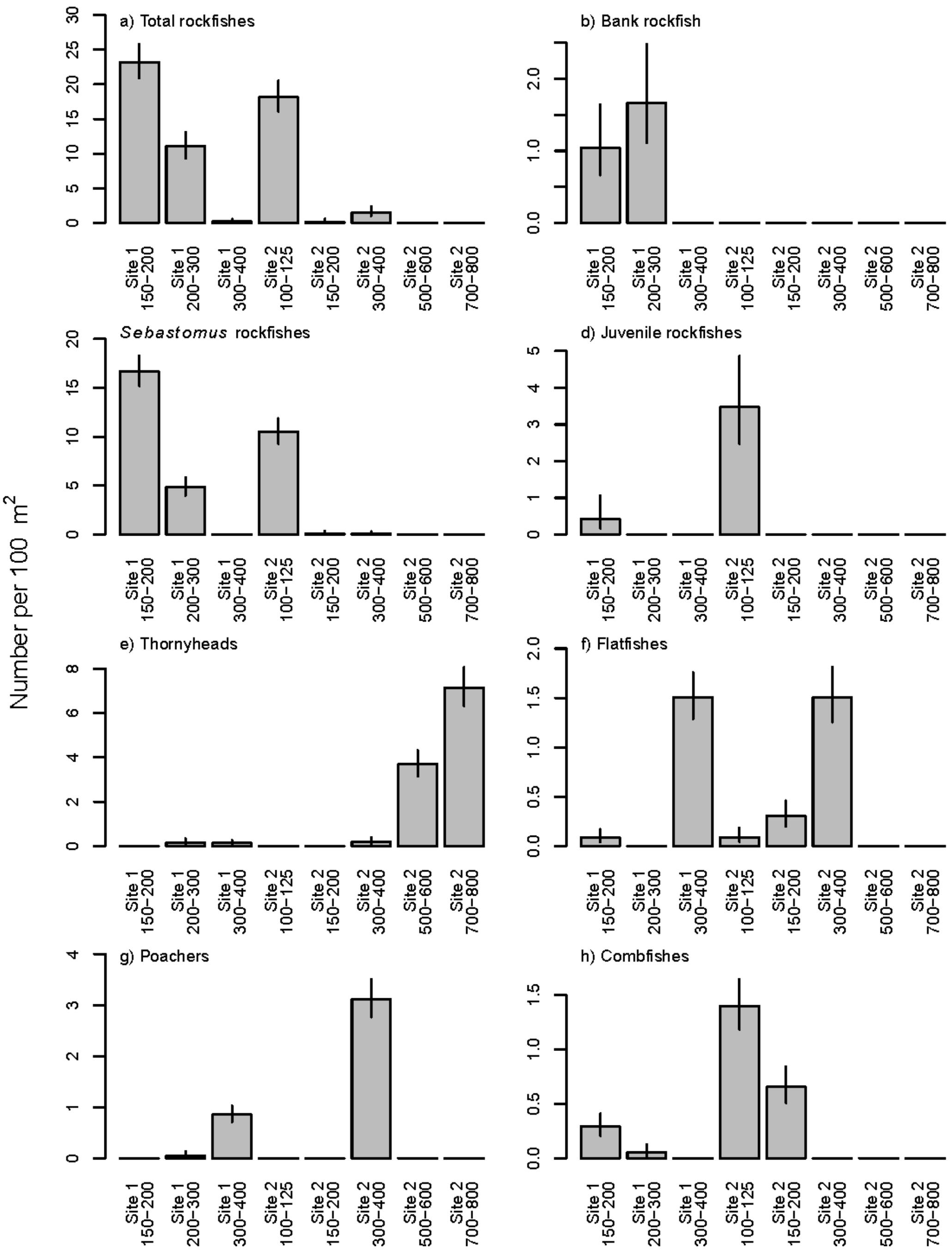

Figure 5 – 2 column

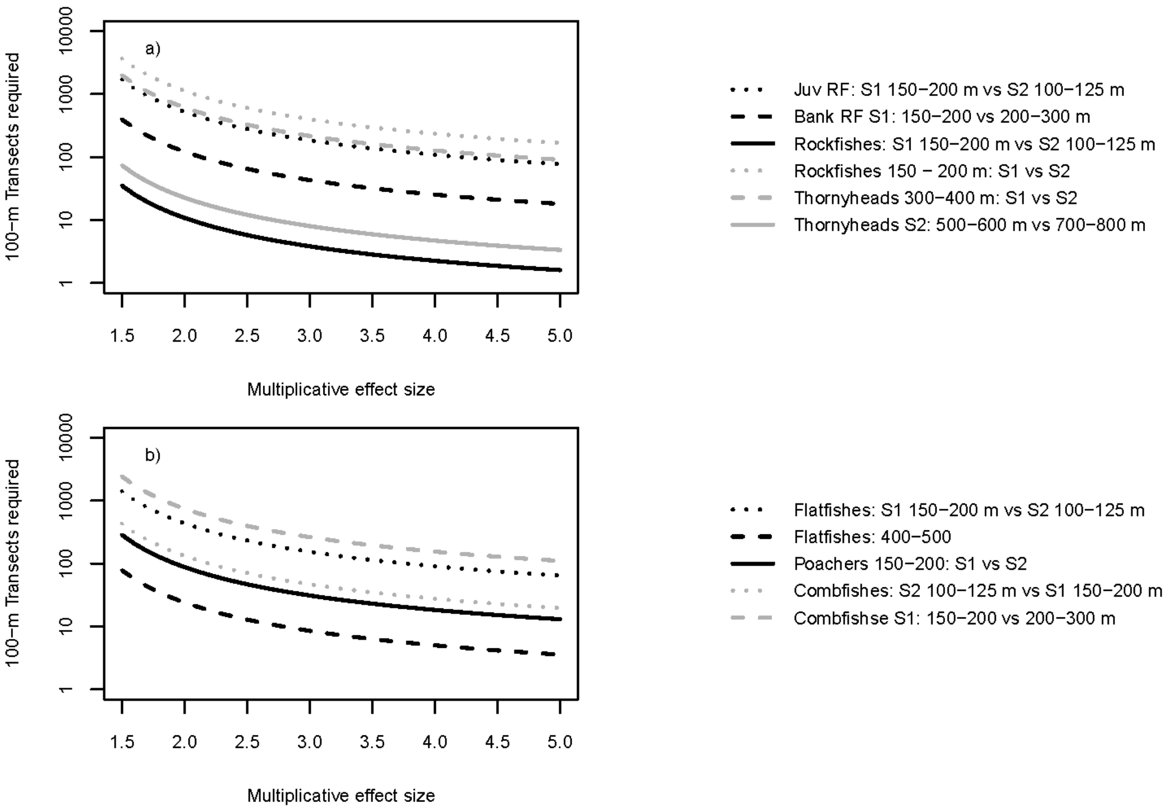

Figure 6 – 2 column

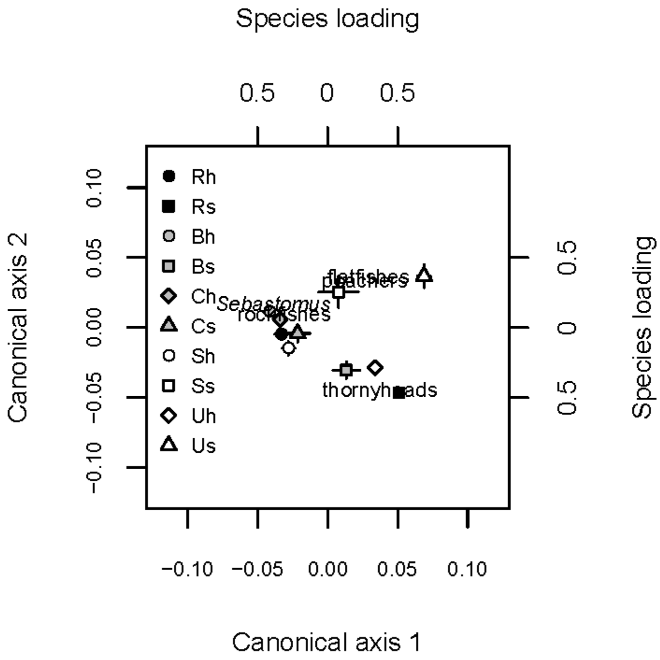

Figure 7 – Single column

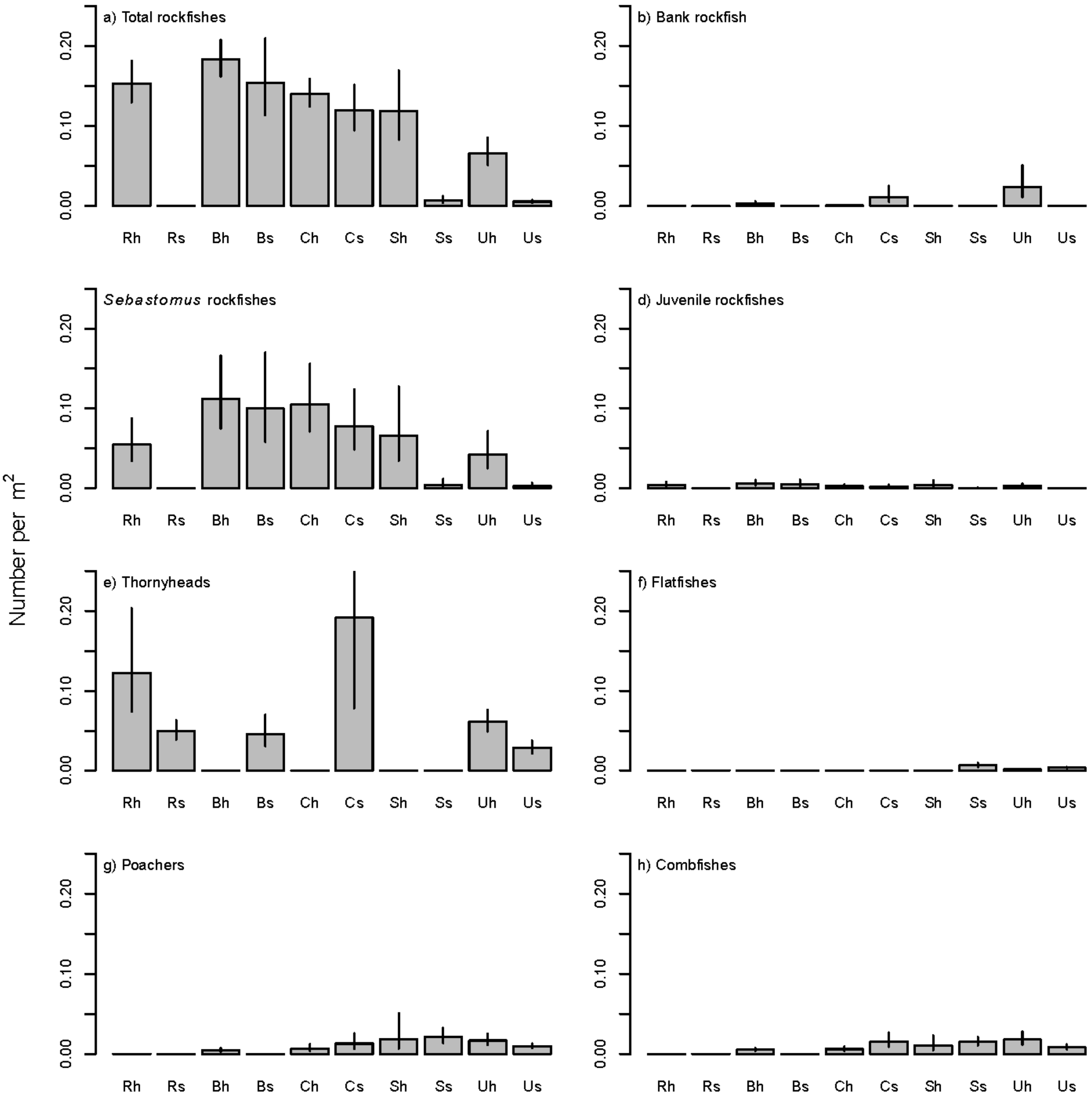

Figure 8 – 2 column