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Chatham-Challenger Ocean Survey 20/20 Post Voyage analyses: Objective 9 – Patterns in Species Composition

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O. Floerl
J. Hewitt
D. Bowden

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EXECUTIVE SUMMARY

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This report describes relationships, patterns and contrasts in benthic species composition, assemblages and habitats, both within and between sites and initial sampling strata across the Challenger Plateau and Chatham Rise. Data used came from four different fauna collection methods: DTIS video; seamount sled; still images taken along the DTIS video; and beam trawls.

Determination of assemblages is usually done using statistical clustering techniques, of which there are many. In order to ensure that the results did not depend on which technique was used, three clustering techniques were trialled on the DTIS video and seamount sled faunal data. The method chosen was average linkage clustering using a modified Gower distance measure for dissimilarities between samples.

Clustering was conducted on data from all four collection methods. Groups determined from the DTIS data alone were a reasonable surrogate for the other data sets and provided the most comprehensive spatial coverage. Therefore, the DTIS faunal groups were imposed on the other datasets and the taxa that characterised each group in each dataset were compared. The taxa that characterised these groups were then merged with information from Objective 6 on site biodiversity. However, the high degree of compositional dissimilarity found within each of these groups (generally more than 60%) precludes the use of the term "community". The use of the terms "biotopes" or "biocenoses" were explored but both of these terms imply uniformity of animal and plant life, and also in the case of biotopes the groups are expected to occur at small scales and in the case of biocenoses are expected to be uniform in environmental conditions. For this reason the groups are best defined as biotic habitats (BH).

Although two fewer biotic habitats were found on the Challenger Plateau than on the Chatham Rise, few biotic habitats were found in only one location: BH 3 was only found on the Challenger Plateau, while BH 2, 5 and 6 were only found on the Chatham Rise. In general the biotic habitats demonstrated spatial coherence on both the Chatham Rise and the Challenger Plateau, with nearby sites frequently belonging to the same biotic habitats. Differences between sites suggested that important drivers of biotic habitats will be depth, slope and productivity, although this will be analysed further in Objectives 10 and 14.

There was some correspondence between the biotic habitats and the sampling strata that had been predetermined from existing data prior to sampling; however, most biotic habitats were found in multiple strata. The number of strata that a biotic habitat was found in varied from one to six for the Challenger Plateau and from one to five for the Chatham Rise. This difference between the two locations suggests that determining biotic habitats from acoustic and environmental data is easier to do in an environment holding a number of strong environmental gradients. Its corollary suggests that environments lacking environmental and acoustic heterogeneity can still hold considerable variability in benthic biotic habitats. This information will be further explored in Objective 16.

This report describes the biotic habitats of the Challenger Plateau and Chatham Rise; Objectives 12 and 15 will determine environmental drivers of dominant species and overall community composition. Most importantly, the biotic habitats will be used directly in Objective 10 to determine vulnerability of different areas of the Challenger Plateau and Chatham Rise to disturbance; specifically trawling and mining.

OBJECTIVES

Project overall objectives:

1. To quantify in an ecological manner, the biological composition and function of the seabed at varying scales of resolution on the Chatham Rise and Challenger Plateau.
2. To elucidate the relative importance of environmental drivers, including fishing, in determining seabed community composition and structure.
3. To determine if remote-sensed data (e.g. acoustic) and environmentally derived classification schemes (e.g. Marine Environment Classification system) can be utilized to predict bottom community composition, function, and diversity.

Specific objective 9:

To elucidate the relationships, patterns and contrasts in species composition, assemblages, habitats, biodiversity and biomass (abundance) both within and between stations, strata and areas.

INTRODUCTION

The benthos of the New Zealand exclusive economic zone (EEZ) beyond the coastal and shallow shelf zones is known largely from commercial and scientific fisheries by catch records and from limited numbers of research voyages, many of which have been targeted at specific commercial fish species or habitats such as seamounts, canyons, and vent and seep sites. The OS 20/20 voyages to the Chatham Rise and Challenger Plateau represent the most comprehensive sampling initiative to date aimed at describing patterns of benthic habitat and biological diversity across extensive areas of the EEZ (Figure 1). A central goal of the OS 20/20 programme is to generate detailed quantitative descriptions of biodiversity across the EEZ. The role of Objective 9 is to determine how species composition varies across the two locations (Figure 1), and to determine whether distinct mappable biotic groups exist.

The study first evaluates a number of classification methods used to determine biotic groupings. The best of these methods is then used to determine biotic groups occurring in the data from video, still image, sea sled and beam trawl samples. Biotic groups are then integrated across collection methods and described in terms of their dominant taxa, within-group variability, biodiversity, and abundance, thus utilising information from Objective 6 of this project. This information is further utilised in Objective 10, where biotic groups will be translated into habitats, and their functionality, vulnerability and recoverability assessed. Finally, differences between the Challenger Plateau and the Chatham Rise and between the initial sampling strata (Figure 1) are described. These strata were determined prior to the biological sampling voyages, using depth and backscatter intensity from the multibeam transects, sea-surface temperature amplitude; surface chlorophyll *a* amplitude, and tidal and residual currents. This last analysis allows an assessment of the usefulness of the initial sampling stratification which will be further utilised in Objective 16: recommendations for future surveys of biodiversity.

Note that we originally intended to determine differences in biomass between and within locations, strata and classifications groups. However, this information was not collected during the voyages. The size of the organisms collected can be used as a surrogate for biomass and will be examined in Objective 10.

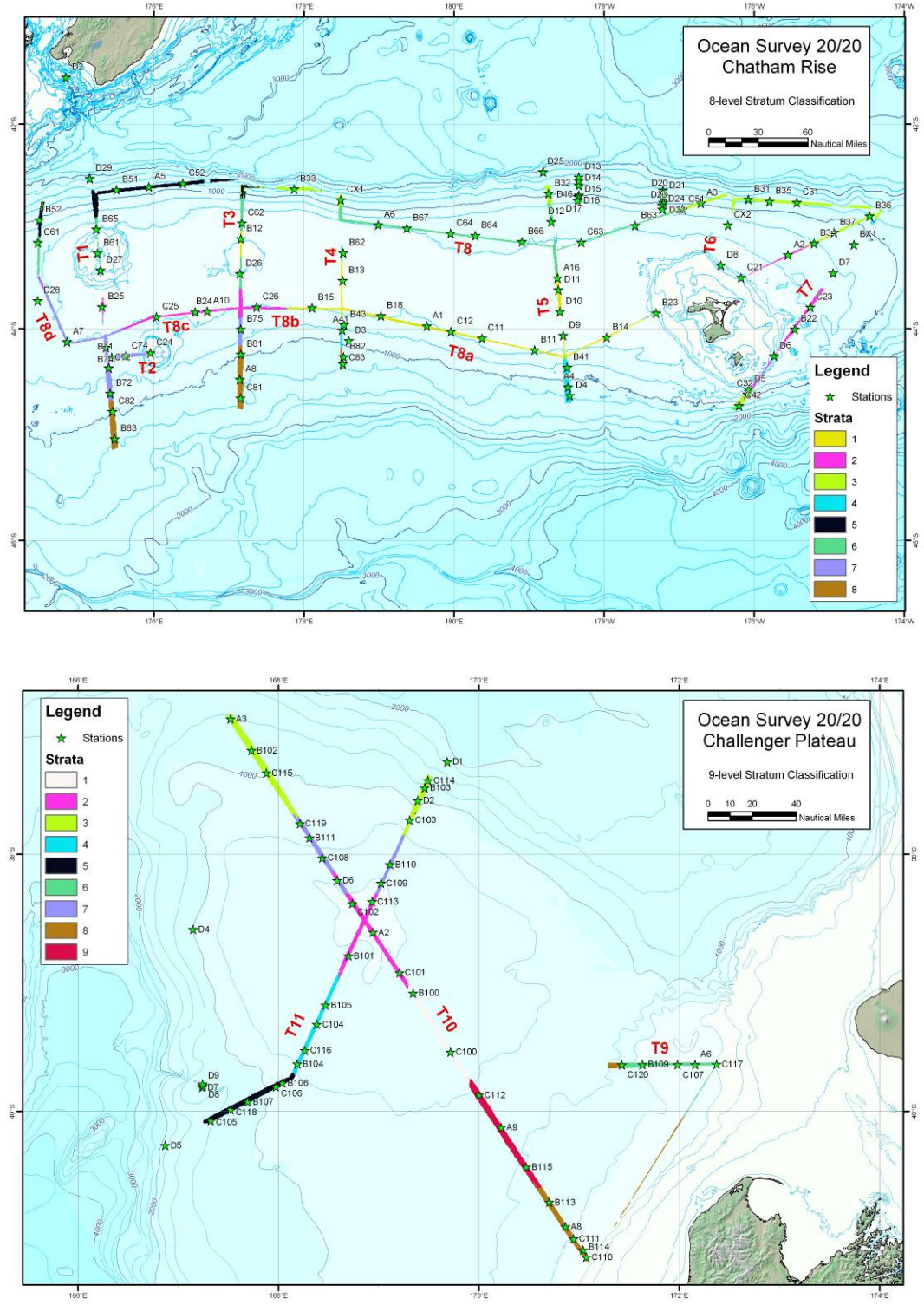

Figure 1: Chatham Rise (top) and Challenger Plateau (bottom) OS 20/20 surveys, showing acoustic multibeam transects (labelled red with 'T' prefix), *a priori* sampling strata (colour coded in legend), and sampling sites at which benthic invertebrates and sediments were collected (stars). Note, strata were classified separately for each location and thus the numbered strata do not represent the same environments in each.

METHODS

Datasets

Analyses to identify communities and their dominant or characterising species, and comparisons between communities, sampling locations and strata were performed on data from all four main collection methods: (1) video transects (DTIS); (2) photo quadrats (STILL); (3) sea mount sled (SEL) and (4) beam trawl (TB). Replication within and between locations (Chatham Rise vs. Challenger Plateau), initial sampling strata, and sites varied between the four collection methods. Highest replication was achieved for the DTIS and SEL data (131 and 117 sampling stations, respectively). Spatial coverage and replication were lower for STILL and TB data (see Objectives 1-5 and Table 1).

For all datasets, the abundances of the various taxa collected were standardised to numbers of individuals per 1000 m^2 of seabed. Only those taxa that were encountered in at least two samples across the overall dataset were included in the analyses. The seamount sled yielded the highest number of taxa (300), while the image-based sampling methods captured approximately half of this number (Table A3 and A4, and Objective 6 of this project).

Table 1: Datasets analysed in this objective. Sampling methods: video transects (DTIS); photo quadrats (STILL); sea mount epibenthic sled (SEL), and beam trawl (TB).

	Chatham Rise		Challenger Plateau	
Sampling method	No. of Sites	No. of stations	No. of Sites	No. of stations
DTIS	95	108	36	40
SEL	65	76	36	41
STILL	33	41	11	11
TB	27	29	14	14

Methods for determining community types

There were several methods available for determining biotic community types and unfortunately, different methods can give different results. For this reason we evaluated a number of different approaches, using DTIS and SEL data, before deciding on the method to use on all data.

Classification techniques

We evaluated the performance of two broad approaches to multivariate classification: (1) hierarchical and (2) non-hierarchical clustering. Hierarchical clustering using group-averaging was performed using the CLUSTER routine in PRIMER version 6.1 (www.primer-e.com). Non-hierarchical clustering using K-means was performed using the Vegan routine available in the R library of statistical tools (www.r-project.org).

Distance measures

We also evaluated the performance of three multivariate distance measures of faunal assemblage dissimilarity: Bray-Curtis similarity (on square-root transformed data); the modified Gower distance with a log transformation; and the Hellinger distance. The Bray-Curtis measure is based on species

abundances and has been used extensively in ecology due to its proven ability to identify patterns in complex multivariate datasets (Bray and Curtis 1957). The modified Gower measure was developed and evaluated only recently and has been shown to incorporate some attractive characteristics, most notably the ability to recognise both compositional differences between samples and order-of-magnitude differences in abundance (Anderson et al. 2006). Hellinger transformation of multivariate data prior to using partitioning techniques based on Euclidean distances is a powerful tool for identifying patterns of beta diversity (Legendre et al. 2001).

Methods for distinguishing clusters

The classification methods used here identify clusters of samples but do not define the level at which groups occur. For K-means, stopping techniques have been developed that indicate when global or local maxima in between-group variation have been reached (e.g. the Calinski-Harabasz pseudo-F statistic; Legendre et al. 2001). For group average linkage clustering no such technique exists; rather, a degree of multivariate similarity/distance between samples has to be specified. We examined the performance (i.e. ability to form clusters) of both measures at two dissimilarity/distance levels. For Bray-Curtis (fixed scale of 0¬ 100 %), dissimilarity levels of 40%, 60 % and 80 % were evaluated. The modified Gower distance scale is open-ended and varies depending on the data analysed. We evaluated two different distance levels for each dataset. For the video data we compared clusters of stations arising at modified Gower distances of 1.5 and 2.0. For the seamount sled data we evaluated clusters formed at distances of 1.0 and 1.5.

Decision criteria for selecting method

The following criteria were used:

- A technique's ability to partition the data into groups with relatively large memberships. When mapping, it is ideal to have groups with relatively large membership. Thus, the ability of a technique to result in a low number of excluded samples (i.e. single stations, or those in groups of two or three) was regarded as a positive characteristic.
- A technique's ability to partition the data into groups of high within-group similarity and high between-group dissimilarity. Analysis of Similarities (ANOSIM, Clarke 1993) was used to compare the groups identified by clustering. ANOSIM generates a global R statistic and R values for each pairwise comparison between clusters, larger values of R indicating greater separation between groups. Where ANOSIM returned a significant global test ($P<0.05$), Similarity Percentage analysis (SIMPER, Clarke 1993) was performed on the groups and the degree of multivariate dissimilarity among samples within groups was compared to that between groups. A substantially lower degree of within-group dissimilarity compared to between-group dissimilarity was interpreted as an indication of robust grouping.
- Consistency. Some sites on both the Chatham Rise and Challenger Plateau were sampled with more than a single station (i.e. there was replication of sampling). We examined sites with replicate sampling stations (generally n=2) and determined the frequency with which the classification technique assigned stations from the same site to different clustering groups. A low incidence of assigning stations from the same site to different cluster groups was regarded as an indication of meaningful grouping.

To decide on the final choice of classification technique, (hierarchical clustering using either the Bray-Curtisor the modified Gower measure, or non-hierarchical clustering by K-means on Hellinger-transformed data) we assigned performance scores to each technique for each of the criteria described above and derived a final value by summing the scores for each criterion. For each criterion, a score of 3 (performed best of the three techniques), 2 (moderate) or 1 (worst) was assigned. When two techniques performed similarly well (or poorly), the same score was assigned to both.

Defining epibenthic communities

Epibenthic communities could be defined for each of the collection methods. These would be expected to be different and probably would not show spatial congruence. This lack of spatial consistency in the location of communities determined by different collection methods is partly because communities are not just formed by species interactions as, over the scales sampled by this project, species will exhibit different responses to environmental drivers. The different resolutions of the collection methods and the number of stations sampled will also strongly affect the allocation of samples to groups and the within- and between-similarity of groups, based on species composition. For these reasons, and because the DTIS dataset incorporates the best spatial coverage of the sampling area (most stations and sites), we decided to impose the groups identified from the DTIS data on data collected by the other collection methods. We determined whether this decision was reasonable by examining differences between the groups defined by individual classification analyses for each collection method (SEL, STILL and TB) and those defined by the DTIS data.

We initially performed classification analysis for each collection method separately. ANOSIM and SIMPER were used to determine differences in assemblage composition between cluster groups (with more than three members). Then, each of the still image, beam trawl and sea mount sled datasets were partitioned using the classification groups determined for DTIS. ANOSIM and SIMPER were again performed to determine differences between imposed DTIS groups. Thus, for each sampling method, ANOSIM and SIMPER results were compared for (i) groups derived via individual classification analyses, and (ii) groups based on the DTIS classification.

Finally, the taxa collected by the different sampling methods that characterised the DTIS-classified groups were determined using SIMPER. These were defined as those that contributed to at least 50 % of the within-group Bray Curtis similarities, if mean abundances differed by more than 20% between groups.

Comparisons of assemblage composition, taxon abundance and diversity between and within communities

Permutational analysis of variance (PERMANOVA; Anderson 2001) was carried out on the dataset for each collection method to test for differences in assemblage composition between the sampling locations (Chatham Rise and Challenger Plateau) and the classification groups identified via cluster analysis. Groups were treated as a random factor nested within the Location term. PERMANOVA was performed on a resemblance matrix based on the modified Gower measure. Pseudo-variance components were calculated to examine the proportion of total variation in assemblage composition contributed by each term in the model and to determine the variance of community structure at the within-site, between-site, and within-location scales.

Univariate generalised linear models (McCullagh and Nelder 1989) were used to test for differences in the abundance and diversity of taxa between sampling locations and between classification groups. Comparisons were undertaken for the diversity measures evaluated and recommended in Objective 6: species richness (S), proportion of species rare in abundance (SRA5), proportion of species infrequently occurring (SRF), Pielou's evenness (J') and Simpson's Index. β-diversity (average Bray-Curtis dissimilarity among samples of a group) was calculated as an average value per group within each sampling location, and was thus not compared using statistical tests.

RESULTS:

Evaluation of methods for determining community types

Hierarchical clustering using square-root transformed Bray Curtis dissimilarities (BC) on DTIS data

The dendrogram based on BC dissimilarities between sites showed that at a 40% dissimilarity level there were very few groups with more than three members (Figure 2). Instead, most stations were not grouped with any other stations. At a 60% dissimilarity level, 30 groups of sampling stations were observed, and there were 43 single stations without group membership (Table 2, Figure 2). Eight groups (clusters) were identified that contained at least four stations and membership in these groups ranged from 4 to 10 stations. Overall, 62% of sampling stations were either in no groups (singletons) or in groups that did not qualify for further analysis. When clustering was done at a dissimilarity level of 80%, results improved markedly. Only 16.9 % of stations were not in groups (single) or in groups of less than four stations. There were 11 groups of at least four stations, the largest containing 27 stations.

Because of the large proportion of stations 'lost' at dissimilarity levels of 40% and 60%, these levels were not considered an adequate option for further analyses and the evaluation of Bray-Curtis based hierarchical clustering for DTIS data was restricted to a dissimilarity level of 80%.

There was a significant difference in the assemblage composition of clustering groups identified at 80% dissimilarity (ANOSIM global R = 0.864; P = 0.001). All pairwise comparisons between groups also resulted in high R-values (0.58 – 1.0), with significance levels of less than 0.05 (note that these are not adjusted for Type-I error inflation and should be interpreted with caution). On average, within-group dissimilarities were 31% lower than between-group dissimilarities (Table 3a).

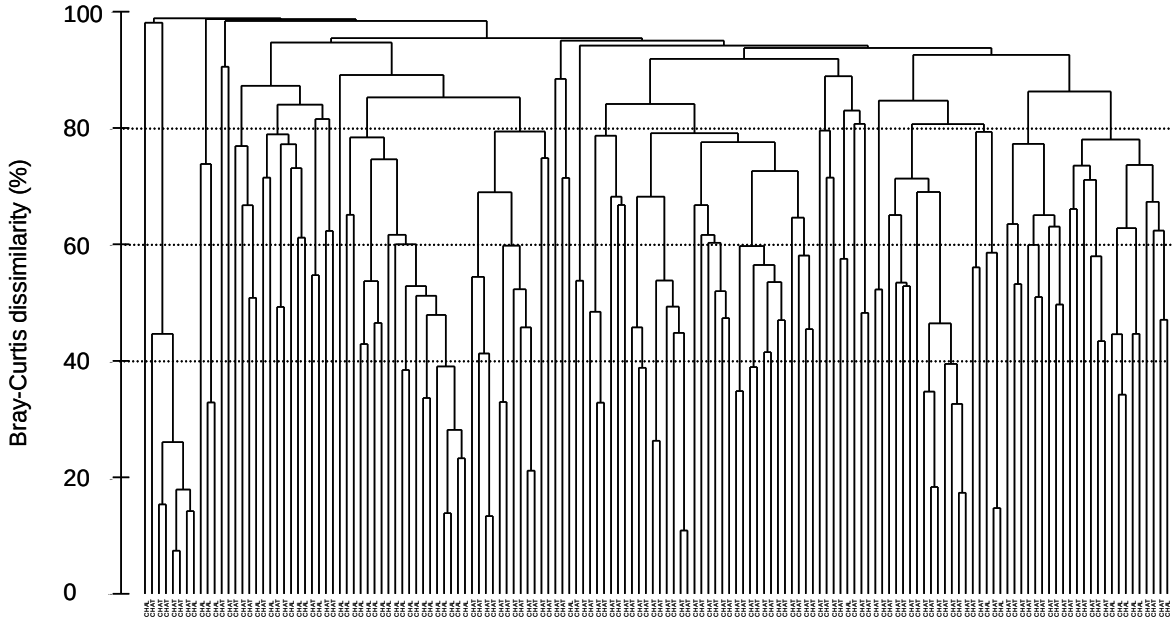

Figure 2: Cluster dendogram for video image (DTIS) derived via hierarchical clustering of square-root transformed data and Bray-Curtis dissimilarities. Dashed lines indicate the 40%, 60% and 80% dissimilarity levels at which clusters were identified.

Table 2: Summary of the results of classification approaches used on DTIS data. Hierarchical clustering was performed using Bray-Curtis dissimilarities (BC) or the modified Gower (MG) measure and groups were identified at 60% and 80% dissimilarity levels (BC), or at an MG distance of 1.5 and 2.0. Non-hierarchical classification was obtained via K-means clustering.

Group size (no. stations)	BC-60%	BC-80%	MG-1.5	MG-2.0	K-means
47					1
27		1		1	
21					1
18		1		1	
17				2	
16					1
15		1		1	1
14				1	
12		2		1	
11					1
10	1				
9		1	1		
8	1				1
7	2	2		1	1
6	2	1	1	1	2
5		1	1		1
4	2	1	2		1
3	9	2	8	1	
2	13	7	19	2	1
1	43	6	58	8	
Total groups (>1)	**30**	**20**	**32**	**12**	**12**
Total singles	**43**	**6**	**58**	**8**	**0**
Groups ≥4	**8**	**11**	**5**	**9**	**11**
No. stations not incl. in these groups	**96**	**26**	**120**	**15**	**2**
Percent stations excluded (groups ≤4)	**62%**	**17%**	**78%**	**10%**	**1.3%**
Percent stations from same site allocated to different groups		**13%**		**19%**	**25%**

Of the 131 sites sampled using DTIS, 16 sites were sampled at more than a single station (15 sites had two stations, one site had three stations). Overall, 13 % of the stations associated with these 16 sites, were allocated to a *different* clustering group than the other replicate station or stations from the same site using hierarchical clustering on the Bray-Curtis similarity measure.

Table 3: Results of SIMPER for DTIS data. Values are between-group Bray-Curtis dissimilarities identified by the various classification techniques. Values in bold are within-group dissimilarities. "av-DISS" (column 2) represents the average dissimilarity between the group in question (column 1) and all other groups in the data. Group numbering does not correspond to the same group number for another classification approach.

a) Bray Curtis 80%

Group	av-DISS	BC1	BC2	BC3	BC4	BC5	BC6	BC7	BC8	BC9	BC10	BC11
BC1	92.28	**66.41**										
BC2	93.26	93.51	**72.93**									
BC3	94.09	80.66	92.63	**60.09**								
BC4	94.32	95.16	84.13	93.61	**69.41**							
BC5	95.06	94.38	93.89	98.22	98.1	**66.03**						
BC6	94.47	92.03	95.72	94.48	96.86	94.77	**72.69**					
BC7	98.82	95.1	98.27	98.98	99.22	99.33	99.61	**27.86**				
BC8	92.61	88.31	90.51	89.61	92.79	93.51	86.26	99.55	**69.53**			
BC9	93.61	90.72	93.51	96.04	92.04	97.62	93.72	99.7	92.17	**69.16**		
BC10	96.34	99.02	96.51	99.19	93.35	95.56	99.35	99.54	98.72	87.02	**75.26**	
BC11	94.26	93.88	93.88	97.43	97.97	85.25	91.86	98.94	94.64	93.55	95.18	**64.05**

b) Modified Gower 2.0

Group	av-DISS	MG1	MG2	MG3	MG4	MG5	MG6	MG7	MG8	MG9
MG1	95.46	**61.8**								
MG2	93.15	93.02	**72.8**							
MG3	94.72	93.77	84.13	**69.41**						
MG4	95.04	98.13	93.89	98.1	**66.03**					
MG5	96.47	96.71	97.52	98.55	96.11	**78.56**				
MG6	93.16	88.91	90.72	92.57	93.86	90.86	**79.07**			
MG7	99.03	98.35	98.27	99.22	99.33	99.65	99.06	**27.86**		
MG8	95.80	97.35	93.8	93.42	95.64	98.55	95.4	99.4	**84.04**	
MG9	94.25	97.4	93.88	97.97	85.25	93.78	93.89	98.94	92.85	**64.05**

c) K-means (Hellinger)

Group	av-DISS	KM1	KM2	KM3	KM4	KM5	KM6	KM7	KM8	KM9	KM10	KM11
KM1	94.67	**87.9**										
KM2	95.59	93.65	**79.64**									
KM3	94.81	95.18	98.52	**62.7**								
KM4	95.11	94.37	95.78	97.28	**64.42**							
KM5	94.07	95.15	91.54	93.4	93.8	**78.5**						
KM6	95.39	96.14	95.52	95.43	88.9	92	**81.3**					
KM7	94.12	94.23	99.12	86.81	96.68	91.54	98.03	**63.5**				
KM8	97.37	97.76	96.55	96.51	97.5	93.88	97.53	97.8	**81.1**			
KM9	94.57	86.87	92	93.5	93.5	96.9	96.8	94.81	98.33	**65.7**		
KM10	93.99	94.73	95.27	92.12	95.28	92.95	95.76	83.12	97.93	94	**66.2**	
KM11	98.79	98.6	97.9	99.33	98.02	99.56	97.83	99.01	99.86	99.01	98.73	**27.9**

Hierarchical clustering using the modified log transformed Gower measure on DTIS data

Clustering at a modified Gower distance of 1.5 resulted in a total of 32 groups of sampling stations, and 58 single stations without group membership Table 2, Figure 3). Five groups were identified that contained at least four stations and membership in these groups ranged from four to nine stations. Overall, 78% of sampling stations were either in no groups or in groups that did not qualify for further analysis. When clustering was done at a distance level of 2.0, results improved markedly. Only 10% of stations were not in groups (single) or were in groups of less than four stations (Table 2, Figure 3). There were nine groups of at least four stations, the largest containing 27 stations.

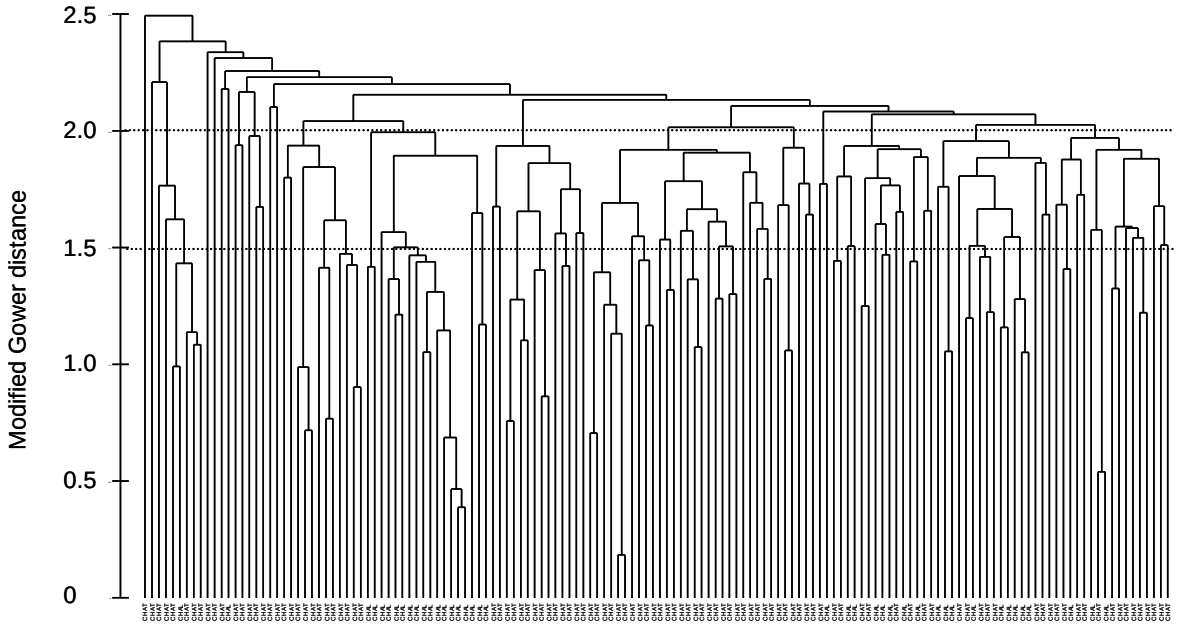

Figure 3: Cluster dendogram for video image (DTIS) derived via hierarchical clustering using the modified Gower distance measure. The two dashed lines indicate the 1.5 and 2.0 distance levels at which clusters were identified.

Similar to clustering using Bray Curtis dissimilarities, because of the large proportion of stations 'lost' at a distance level of 1.5, this level was not considered an adequate option for further analyses. The evaluation of hierarchical clustering for DTIS data based on modified Gower distance was restricted to a distance of 2.0.

There was a significant difference in the assemblage composition of clustering groups identified at a modified Gower distance of 2.0 (ANOSIM global R = 0.759, P = 0.001). All pairwise comparisons also resulted in high R-values (0.49 – 0.98), with significance levels of less than 0.05 (not adjusted for Type-I error). On average, within-group dissimilarity among samples was 29% lower than between-group dissimilarity (Table 3b). Overall, 19% of the stations associated with sites containing multiple stations were allocated to a different clustering group as the other replicate station or stations from the same site.

Non-hierarchical K-means clustering on Hellinger transformed DTIS data

K-means cluster analysis on Hellinger transformed DTIS data resulted in a best-fit model of 12 clusters, associated with a Calinski-Harabasz pseudo-F statistic of 7.25. Lower or higher values of K

resulted in a lower pseudo-F statistic (e.g. 6.81 for K=11; 6.91 for K=13), indicating that between-group dissimilarity was maximised at K=12. Of the 12 groups identified by the analysis, 11 had a membership of at least four stations and membership in these groups ranged from 4 to 47 stations (Table 2). Only two stations (1.3% of total) were not included in these groups and were excluded from further analysis.

ANOSIM identified significant differences in assemblage composition between the 11 clusters (global $R = 0.492$, $P = 0.001$). The R-values of pairwise comparisons between groups varied widely, however, (-0.05 – 1.0) and were not all significant. On average, within-group dissimilarity among samples was 27% lower than between-group dissimilarity (Table 3c). Overall, 25% of the stations associated with sites containing multiple stations were allocated to a *different* clustering group as the other replicate station or stations from the same site.

Hierarchical clustering using square-root transformed Bray Curtis dissimilarities on SEL data

Clustering at a dissimilarity level of 60% resulted in a total of 24 groups of sampling stations, and 55 single stations without group membership (Table 4, Figure 4). Three groups were identified that contained at least four stations and membership in these groups ranged from four to six stations. Overall, 87% of sampling stations were either in no groups or in groups that did not qualify for further analysis. Better results were obtained for clustering done at a dissimilarity level of 80%. At this level, 48% of stations were not in groups (single) or in groups of less than four stations. There were nine groups of at least four stations, the largest containing 14 stations.

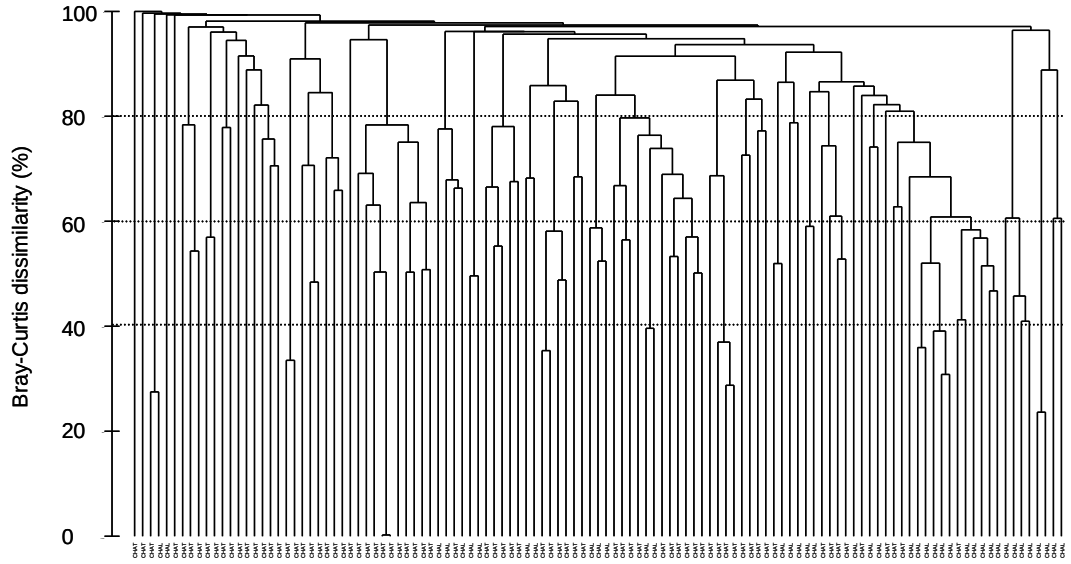

Figure 4: Cluster dendogram for sea mount sled (SEL) derived via hierarchical clustering of square-root transformed data and Bray-Curtis dissimilarities. The two dashed lines indicate the 40%, 60% and 80% dissimilarity levels at which clusters were identified.

Because of the large proportion of stations excluded at a dissimilarity level of 60%, this level was not considered an adequate option for further analyses and the evaluation of Bray-Curtis based hierarchical clustering for DTIS data was restricted to a dissimilarity level of 80%.

There was a significant difference in the assemblage composition of clustering groups identified at 80% dissimilarity (ANOSIM global $R = 0.890$, $P = 0.001$). All pairwise comparisons also resulted in high R-values (0.63 – 1.0), with significance levels of less than 0.05 (not adjusted for Type-I error inflation). On average, within-group dissimilarity among samples was 33% lower than between-group dissimilarity (Table 5a). Of the 101 sites sampled using the sea mount sled, 16 sites were sampled at more than a single station (all of these sites had two stations). Overall, 56% of the stations associated

with these 16 sites were allocated to a *different* clustering group as the other replicate station from the same site.

Table 4: Summary of the results of classification approaches used on SEL data. Hierarchical clustering was performed using Bray-Curtis dissimilarities (BC) or the modified Gower (MG) measure and groups were identified at 60% and 80% dissimilarity levels (BC), or at an MG distance of 1.0 and 1.5. Non-hierarchical classification was obtained via K-means clustering.

Group size (no. stations)	BC-60%	BC-80%	MG-1.0	MG-1.5	K-means
47					1
36				1	
23				1	
17					1
15				1	1
14		1			
12		1			1
10		1			
9					1
7					1
6	1				1
5	1	1		2	
4	1	5		3	
3	5	5	3	1	1
2	16	15	6	4	
1	55	11	96	10	1
Total groups (>1)	**24**	**29**	**9**	**13**	**8**
Total singles	**55**	**11**	**96**	**10**	**1**
Groups ≥4	**3**	**9**	**0**	**8**	**7**
No. stations not incl. in these groups	**102**	**56**	**117**	**21**	**4**
Percent stations excluded (groups ≤4)	**87%**	**48%**	**100%**	**18%**	**3.4%**
Percent stations from same site allocated to different groups		**56%**		**19%**	**25%**

Table 5: Results of SIMPER for SEL data. Values represent between-group Bray-Curtis dissimilarities identified by the various classification techniques. Values in bold represent within-group dissimilarities. "av-DISS" (column 2) represents the average dissimilarity between the group in question (column 1) and all other groups in the data. Group numbering does not correspond to the same group number for another classification approach.

a) Bray Curtis 80%

Group	av-DISS	BC1	BC2	BC3	BC4	BC5	BC6	BC7	BC8	BC9
BC1	93.31	**73.15**								
BC2	91.58	87.13	**62.94**							
BC3	96.32	95.6	93.6	**52.78**						
BC4	93.09	86.12	85.76	92.74	**51.47**					
BC5	98.08	95.53	97.78	100	99.75	**70.69**				
BC6	93.53	94.35	84.51	94.6	95.58	97.69	**66.32**			
BC7	95.93	97.34	93.03	99.18	96.14	97.28	86.42	**72.5**		
BC8	96.55	95.15	93.71	98.19	94.03	96.64	96.24	98.98	**72.43**	
BC9	97.62	95.24	97.13	96.68	94.56	100	98.88	99.03	99.45	**52.39**

b) Modified Gower 1.5

Group	av-DISS	MG1	MG2	MG3	MG4	MG5	MG6	MG7	MG8
MG1	95.43	**76.42**							
MG2	93.55	90.79	**76.46**						
MG3	95.24	94.82	92.74	**68.03**					
MG4	96.70	97.88	97.72	90.66	**71.29**				
MG5	97.63	96.44	96.37	98.53	97.85	**85.08**			
MG6	97.13	97.27	91.85	98.01	98.68	97.79	**82.38**		
MG7	95.51	94.61	88.32	97.05	95.92	97.15	96.61	**66.32**	
MG8	97.73	96.19	97.07	94.86	98.18	99.25	99.7	98.88	**52.39**

c) K-means (Hellinger)

Group	av-DISS	KM1	KM2	KM3	KM4	KM5	KM6	KM7
KM1	93.58	**74.25**						
KM2	96.95	94.48	**92.01**					
KM3	95.61	87.86	97.43	**83.05**				
KM4	95.31	89.29	96.73	94.68	**92.07**			
KM5	98.60	98.66	98.69	99.53	97.08	**95.89**		
KM6	97.09	96.03	95.93	98.47	97.16	98.5	**89.42**	
KM7	96.95	95.16	98.41	95.68	96.92	99.11	96.43	**86.51**

Hierarchical clustering using the modified log transformed Gower measure on SEL data

Clustering at a modified Gower distance of 1.0 resulted in a total of nine groups of sampling stations, and 96 single stations without group membership (Table 4, Figure 5). However, none of these groups contained at least four stations. Given this result, a distance level of 1.0 this level was not considered an option for further analyses and the evaluation of hierarchical clustering for SEL data based on modified Gower distance was restricted to higher distance levels.

Clustering at a modified Gower distance of 1.5 resulted in 13 groups and 10 single stations without group membership. Of the 13 groups, 8 contained 4 or more stations (Table 4). Overall, 19% of stations were either without group membership or in groups of less than four stations. There was significant variation in assemblage composition of the eight groups (ANOSIM: global $R = 0.650$; $P = 0.001$). All pairwise comparisons resulted in high R-values (0.48 – 1.0), with significance levels

of less than 0.05 (not adjusted for Type-I error). On average, within-group dissimilarity among samples was 27% lower than between-group dissimilarity (Table 5b). Overall, 19% of the stations associated with sites containing multiple stations were allocated to a *different* clustering group as the other replicate station or stations from the same site.

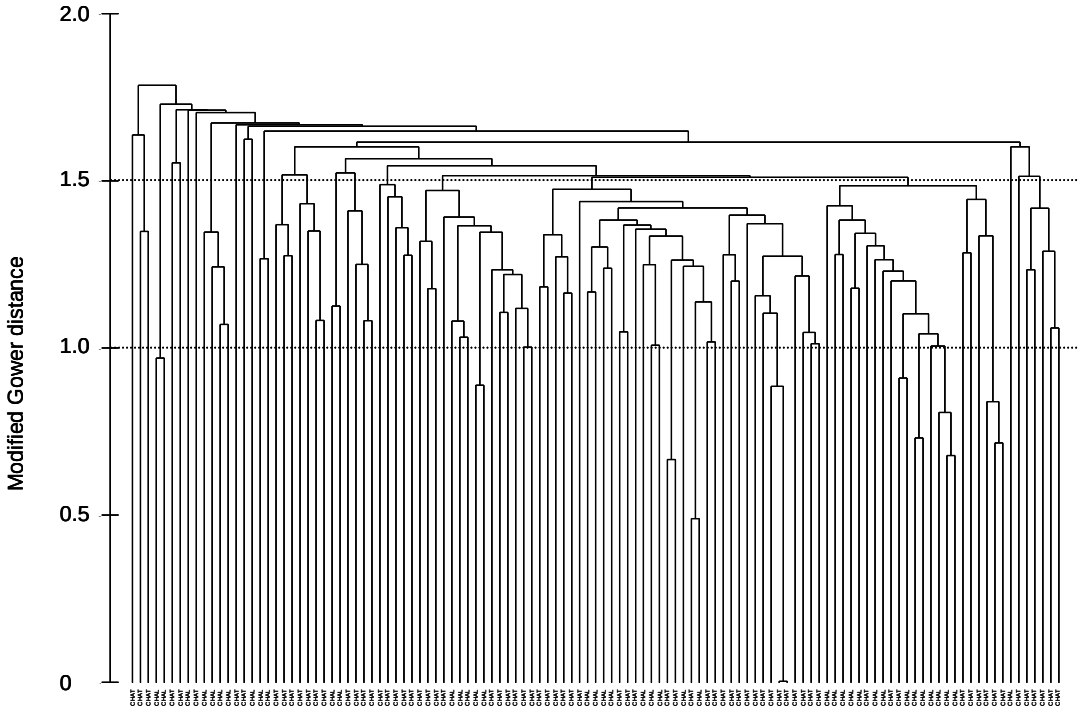

Figure 5: Cluster dendogram for sea mount sled (SEL) derived via hierarchical clustering on modified Gower distances. The two dashed lines indicate the 1.0 and 1.5 distance levels at which clusters were identified.

Non-hierarchical K-means clustering on Hellinger transformed SEL data

K-means cluster analysis on Hellinger transformed SEL data resulted in a best-fit model of nine clusters (K), associated with a Calinski-Harabasz pseudo-F statistic of 3.62. Lower or higher values of K resulted in a lower pseudo-F statistic (e.g. 3.43 for K=8; 3.37 for K=10), indicating that between-group dissimilarity was maximised at K=9. Of the nine clusters identified by the analysis, seven had a membership of at least four stations, ranging from 6 to 47 stations (Table 4). Only four stations (3.4% of total) were not included in these groups and were excluded from further analysis.

ANOSIM identified significant differences in assemblage composition between the seven groups (global R = 0.282; $P = 0.001$). The R-values of pairwise comparisons between groups varied widely (-0.10 – 0.78) and were not all significant. On average, within-group dissimilarity among samples was 9% lower than between-group dissimilarity (Table 5c). Overall, 25% of the stations associated with sites containing multiple stations were allocated to a *different* clustering group as the other replicate station or stations from the same site.

Deciding on a final classification approach

Following examination of the results described above, scores were allocated to each of the classification approaches to evaluate overall performance and suitability. Hierarchical classification using group-average clustering and the modified Gower distance measure yielded the highest total

score (19), while the same technique using Bray Curtis dissimilarities was allocated a score of 17. The particular strength of the modified Gower measure was its ability to separate the station data into groups with low within-group dissimilarity and high between-group dissimilarity, the resulting high R-values returned by ANOSIM, and its consistency in allocating stations from the same site (i.e. nearby sampling location) to the same clustering groups (Table 6).

Non-hierarchical classification using K-means clustering achieved the lowest score (14). While the k-means clustering routine resulted in the lowest number of 'solitary' stations or those in groups of less than four, it performed less well in creating groups of high multivariate dissimilarity (indicated by low R-values) and in allocating stations from the same sampling site to the same clustering group (Table 6).

Table 6: Decision table for selecting a classification approach based on a set of a-priori criteria.

Data	Criterion	Bray Curtis	Modified Gower	Kmeans
DTIS	Stations not in groups with ≥4 members	1	2	3
	Separation by ANOSIM	3	2	1
	Within vs. between group dissimilarities	2	3	2
	Stations from same site allocated to same group	3	2	1
SEL	Stations not in groups with ≥4 members	1	2	3
	Separation by ANOSIM	3	3	1
	Within vs. between group dissimilarities	3	2	1
	Stations from same site allocated to same group	1	3	2
	Overall score	**17**	**19**	**14**

Evaluation of the use of DTIS-based groups

Classification analyses (group-average clustering based on modified Gower measure) performed for SEL, STILL and TB datasets individually resulted in a smaller number of groups than the classification by DTIS, as per section 3.1.6 (Table 7). This was especially apparent for the still image data, where the use of DTIS-based groups resulted in twice as many clusters than when groups based on still image data were used. Despite this, there was a reasonable correspondence between the classification groups derived through individual cluster analyses for each collection type and the imposed DTIS groups. While the use of DTIS groups for the other collection types generally reduced the R-value of ANOSIM comparisons; all global tests were still highly significant ($P = 0.001$), as were pairwise comparisons ($P < 0.05$; Table 8).

Table 7: Classification group sizes when individual classification analyses are carried out for STILL, SEL and TB data, or when DTIS groups are imposed onto these datasets.

	Classification groups	DTIS groups imposed
Still images (STILL)	4	9
Sea mount sled (SEL)	8	9
Beam trawl (TB)	6	8

Table 8: Results of ANOSIM and SIMPER on assemblage composition within and between classification groups (i) identified for each collection type individually, or (ii) DTIS groups imposed on the other collection types (SEL, STILL, TB). [a]comparison statistically significant at P <0.05. [b] comparison not significant.

	Classification groups	DTIS groups imposed
Sea mount sled (SEL)		
ANOSIM	R=0.650; *P*=0.001	R=0.275; *P*=0.001
Within-group dissimilarity (av. ± SD)	73.5 ± 12.5	86.7 ± 10.5 [a]
Between-group dissimilarity (av. ± SD)	96.1 ± 1.4	96.4 ± 1.0 [b]
Still images (STILL)		
ANOSIM	R=0.641; *P*=0.001	R=0.535; *P*=0.001
Within-group dissimilarity (av. ± SD)	75.8 ± 3.8	74.3 ± 8.5 [b]
Between-group dissimilarity (av. ± SD)	86.1 ± 0.5	85.1 ± 2.1 [b]
Beam trawl (TB)		
ANOSIM	R=0.809; *P*=0.001	R=0.642; *P*=0.001
Within-group dissimilarity (av. ± SD)	71.8 ± 6.3	79.6 ± 9.4 [b]
Between-group dissimilarity (av. ± SD)	90.1 ± 1.3	89.5 ± 1.9 [b]

Imposition of DTIS groups on SEL data significantly increased the average within-group dissimilarity (by approximately 13%). However, the use of DTIS groups for STILL and TB data resulted in no change to the average within-group dissimilarities, nor did it affect between-group dissimilarities for any of the datasets (One-way ANOVAs Table 8).

Given these results, it was decided to determine species composition using the groups derived from cluster analysis of DTIS data, for all collection methods.

Associations of taxa with the DTIS-classified groups

Higher taxonomic resolution of the SEL and TB data was utilised to better define the DTIS and STILL characterising taxa. Thus, data from the SEL suggests that the onuphid (quill worm) characterising biotic habitat 5 is actually Hyalinoecia longibranchiata and the ophuroid in biotic habitat 9 is Ophiura ooplax.

Varying numbers of taxa were determined to define the different groups using data collected by different methods (Table 9). Generally the TB data had higher numbers of taxa required to define groups, probably due to the number of smaller taxa collected by this method. Groups 1, 3 and 7 generally were well defined by between one and three taxa from each collection method.

Characterising taxa for a number of the groups were similar between collection methods (Table 9), especially for Groups 1, 3, 4 and 5. Group 1 was defined predominantly by the ophuroid, *Ophiomusium lymani*, using DTIS, STILL and SEL data. Similarly, the echinoid, *Gracilechinus multidentatus*, was important in defining Group 4 with data from all four methods. As expected, some

differences between collection methods were observed. The finer resolution of the STILL data resulted in differences between the DTIS and STILL data. Differences between the DTIS, SEL and TB data were driven by differences in the relative proportion of smaller epibenthos and infauna collected by the two methods (DTIS mainly detecting larger epibenthos).

Locational and biodiversity differences between groups

The identified groups showed some separation associated with the Chatham Rise and Challenger Plateau. Groups 2, 5 and 6 were only observed from the Chatham Rise data, while Group 3 was only observed from the Challenger Plateau data. Sites from both Chatham Rise and Challenger Plateau were contained in Groups 1, 4, 7, 8 and 9, although Groups 1 and 4 had only one to two sites from the Challenger Plateau.

For each of the four collection methods, there were significant differences in the overall assemblage composition between the cluster groups in each of the two sampling locations (Groups(Location) term P = 0.001, Table 10). Generally, the proportion of the variation in multivariate dissimilarity explained by sampling location was very small (0–8%). Variation among cluster groups explained 11–32% of the total variation. For all collection methods, the largest proportion of variation was associated with residual variation among sites within groups (68–88% of variation, Table 10).

Table 9: Taxa contributing the most to within-group similarities for the 9 DTIS-classified groups with percentage contribution in brackets. L, M or H indicate whether the taxon had low, medium or high density. Asterisks (*) indicate that the abundance of a taxon in this group was significantly different to that of other groups (see Appendix Table A1 for statistical details).

Group	Video images (DTIS)	Still images (STILL)	Sea mount sled (SEL)	Beam trawl (TB)
1	*Ophiomusium lymani* (94, H)*	*O. lymani* (50, H)* Holothurians (23, H)*	*O. lymani* (81, H)*	Single station sampled – permutations impossible.
2	*Radicipes* spp. (35, H)* *Anthoptilum* (30, H)*	Cladhorizidae (16. M) * Shrimps (*Pycnoplax victoriensis, Campylonotus rathbue)* (16, M)* *Anthoptilum* (15, M)	*Pycnoplax victoriensis* (85, H)*	*Laetmogone violacea* (16, H)* *Anthoptilum* (8, H)* *C. rathbue* (8, H) * *Munida gracilis* (8, M)* Oedicerotidae (7, H)* *P. victoriensis* (7)
3	Hydroids (79, H)*	Holothurians (55, M) * Galatheidae (15, H)*	*Hyalinoecia longibranchiata* (37, H)* Sipunculidea (30, H)*	*Munida gracilis* (35, H)* *Philocheras acutirostratus* (27, H)*
4	*Gracilechinus multidentatus* (83, H)*	*G. multidentatus* (37, H)* Ophiuroidea (19, H)*	*G. multidentatus* (54, H)* *Paracaudi chilensis* (18, H)	*G. multidentatus* (67, H)*

Group	Video images (DTIS)	Still images (STILL)	Sea mount sled (SEL)	Beam trawl (TB)
5	*Sympagurus dimorphus* (41, H)* *Hyalinoecia longibranchiata* (11, H)*	Cladhorizidae (50, H)*	*H. longibranchiata* (33, H)* *Falsilutia powelli* (10, H)* Foraminifera (8, H)	Serolidae (6, H)* Foraminifera (6, H)* *H. longibranchiata* (6, H) *S. dimorphus* (6, H)* *Munida gracilis* (5, H)* *Flabellum knoxi* (5, H)* *Ypsilothuria bitentaculata* (5, H)* *Campylonotus rathbue* (4, H)* *Fusitriton laudandus* (4, H) * *Comitas onokea vivens* (4, H)*
6	Paguridae (27, H) Spatangidae (26, H)*	Cladhorizidae (40, H)* Shrimp (20,M)*	*Pseudarchaster garricki* (26, H)* *Fissidentalium zelandicum* (17, H)* *Austrofusus glans* (17, H)*	No stations
7	*Munida gracilis* (76, H)*	*Notopandalus magnoculus* (46, H)* *M. gracilis* (11, H)*	Chaetopteridae (30, H)* *Hyalinoecia longibranchiata* (21, M)* *M. gracilis* (9, H) *	*N. magnoculus* (55, H)* *M. gracilis* (17, H)*
8	*Nematocarcinus* sp. (35, H)* *Enypniastes eximia* (31, H)*	*Parapagurus latimanus* (26, H)* Gastropoda (*Nassarius ephamillus, Fusitriton laudandus)* (17, H)* Foraminifera (giant) (14, H)	*Nassarius ephamillus* (45, H)* Sipunculidea (17, H)*	Sipunculidea (10, H)* *P. latimanus* (9, H)* *F. laudandus* (6, M)* Actiniaria (6, M)
9	*Fusitriton laudandus* (21, H)* Shrimp (17, H)* *Ophiura ooplax* (12, L)	Paguridae (23, H)* Shrimp (12,M)* Hydroids (12, M)	*Ophiura ooplax* (46, H)* *Kinbergonuphis proalopus* (11, M)	*F. laudandus* (33, M)*

Table 10: Results of PERMANOVA on assemblage composition in the two study locations (Chatham Rise and Challenger Plateau) and the groups within each location. Shown are the P values of the effects of the PERMANOVA test, and the proportion of the overall variation (pseudo-variance components) explained by each model term (see Appendix Table A2 for full details).

	Location	Group(Location)	Residual
Video images (DTIS)	*P* = 0.524	***P* = 0.001**	
	0 %	32 %	68 %
Still images (STILL)	***P* = 0.038**	***P* = 0.001**	
	8 %	12 %	80 %
Sea mount sled (SEL)	*P* = 0.181	***P* = 0.001**	
	1 %	11 %	88 %
Beam trawl (TB)	*P* = 0.405	***P* = 0.001**	
	1 %	23 %	76 %

Biodiversity and abundance

DTIS video: Significant differences between the groups were detected for all the biodiversity indices, but no differences between locations were found (Table 11, Figure 6). By far the largest number of individuals was encountered at sampling stations associated with Group 1 which was dominated by dense populations of the ophiuroid *Ophiomusium lymani* (e.g. 44 600 individuals 1000 m^{-2} at one site on Challenger Plateau and an average of 17 900 individuals 1000 m^{-2} across 5 stations on Chatham Rise, Figure 6g). Differences in other biodiversity indices were less distinct. Number of species exhibited a significant interaction between location and groups but, for both, Group 9 had the highest number of species. SRA5 (proportion of species rare in abundance at a site) also had a significant interaction between location and groups but, for both, Groups 1 and 9 were highest. Simpson diversity and Pielou's evenness were significantly lower in Group 1 than all the others (Figure 6). While no statistical tests could be run on beta diversity (the within group Bray-Curtis dissimilarity), this was generally high for all except Group 1, although the highest values were found in Group 7.

Table 11: Differences between groups and locations found for total abundance of organisms (number of individuals) and diversity measures identified in Objective 6: species richness (S), species rare in abundance (SRA5), species rare in frequency (SRF), Pielou's evenness (J') and the Simpson Index.

	No. individuals	S	SRA5	SRF	J'	Simpson
DTIS						
Location	P = 0.800	P = 0.889	P = 0.752	P = 0.522	P = 0.562	P = 0.587
Group	**P <0.001**	**P <0.001**	**P <0.001**	P = 0.074	**P <0.001**	**P <0.001**
Location*Group	P = 0.143	**P = 0.006**	**P = 0.013**	P = 0.103	P = 0.794	P = 0.864
STILL						
Location	P = 0.177	**P <0.001**	P = 0.503	P = 0.145	**P = 0.003**	P <0.001
Group(Location)	**P <0.001**	P = 0.129	P = 0.315	P = 0.968	**P = 0.025**	P = 0.054
	P = 0.13	P = 0.691	P = 0.407	P = 0.598	P = 0.165	P = 0.195
SEL						
Location	P = 0.132	P = 0.416	P = 0.217	P = 0.102	P = 0.293	P = 0.086
Group(Location)	P = 0.248	**P = 0.007**	**P = 0.048**	P = 0.463	**P = 0.011**	**P = 0.008**
	P = 0.222	P = 0.798	P = 0.360	P = 0.085	P = 0.420	P = 0.169
TB						
Location	P = 0.991	P = 0.356	P = 0.150	P = 0.637	P = 0.139	P = 0.229
Group(Location)	**P = 0.006**	**P = 0.008**	P = 0.057	**P = 0.008**	P = 0.222	P = 0.111
	P = 0.361	P = 0.288	P = 0.215	P = 0.800	**P = 0.004**	**P = 0.007**

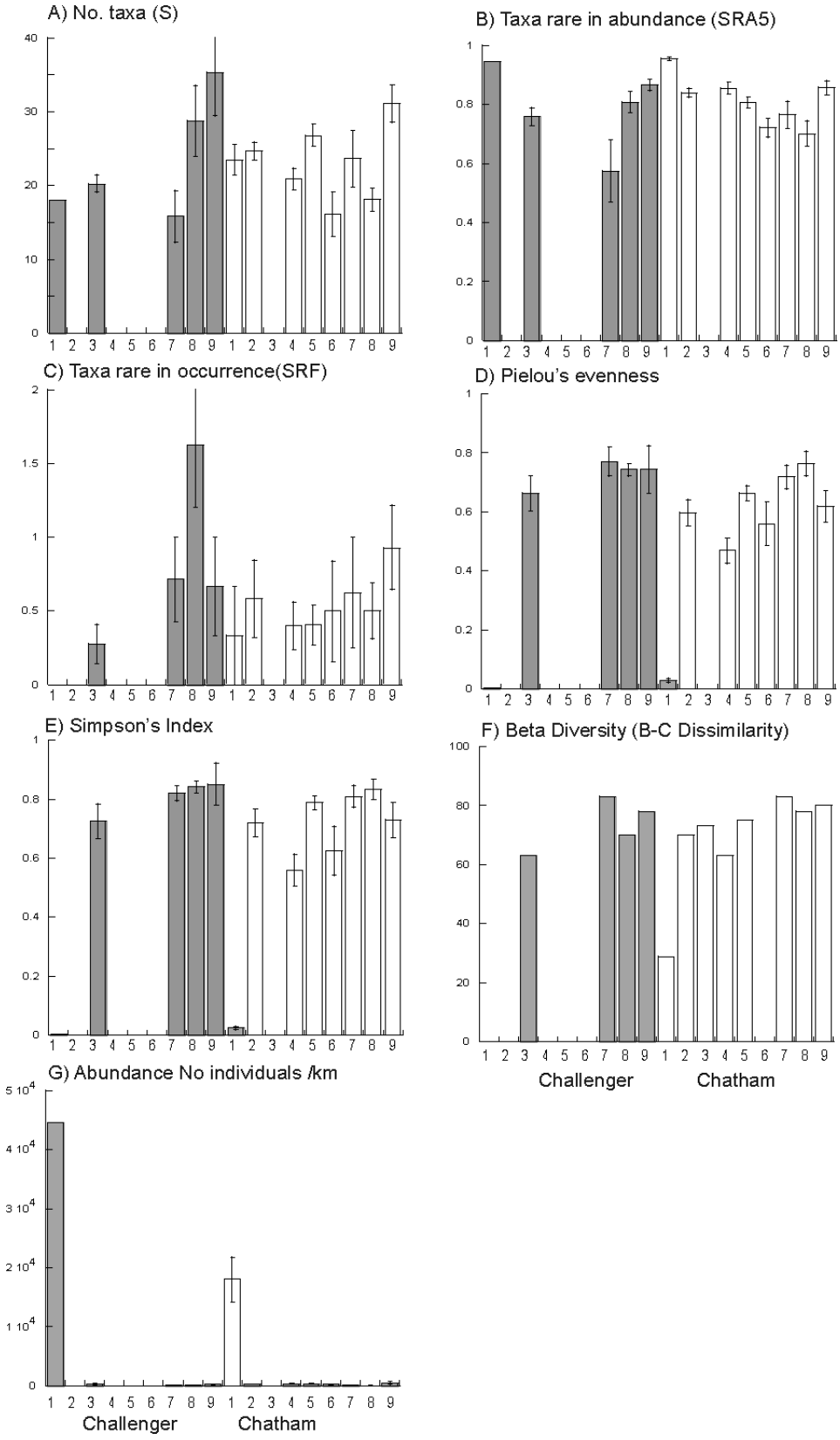

Figure 6: Abundance and diversity measures for DTIS data. Numbers on x-axis refer to Groups 1–9, filled bars Challenger Plateau, open bars, Chatham Rise.

DTIS stills: Abundance and diversity patterns for the STILL data were not consistent (Figure 7). No effects of group or location were observed for SRF or SRA5. A significant interaction term was found

only for abundance data with Group 1 having highest abundance in the Chatham data and Group 9 being highest in the Challenger. For Pielou's evenness and Simpson's index, there were overall differences between the locations, however Group 4 had the highest values in both locations (Table 10, Figure 7).

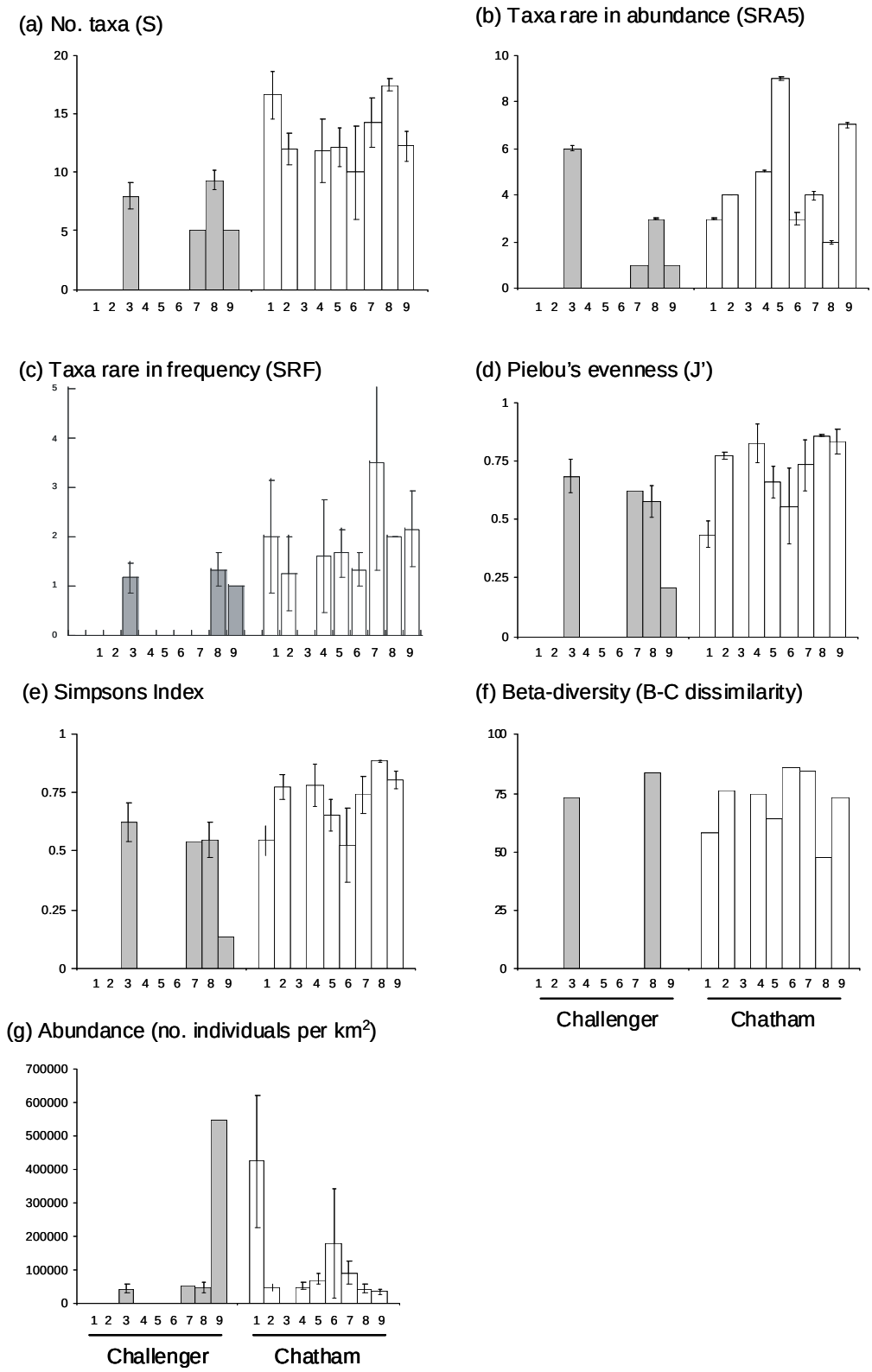

Figure 7: Abundance and diversity measures for STILL data. Numbers below x-axis refer to Groups 1–9. Note that too few data points were available for Groups 7 and 9 in the Challenger Plateau for calculation of beta diversity.

Seamount sled: Abundance and diversity patterns were more consistent for the SEL data (Figure 8). No differences were observed between locations and no interaction terms were significant (Table 10). For Pielou's evenness and Simpson's index, Group 1 had the lowest values. For SRA5 and abundance, Group 1 had the highest values. No significant effects were observed for the total number of taxa or for SRF.

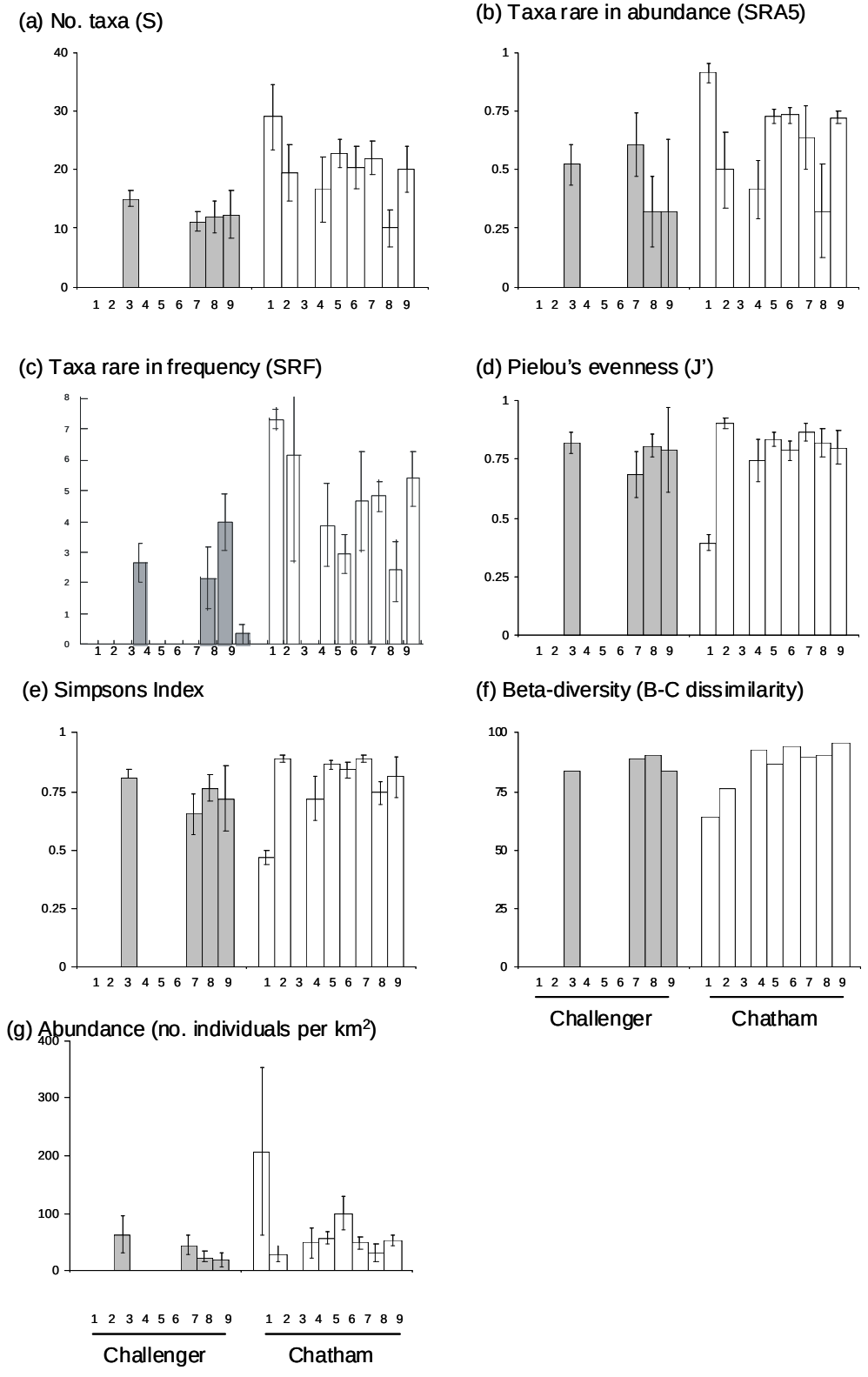

Figure 8: Abundance and diversity measures for SEL data. Numbers below x-axis refer to Groups 1–9.

Beam trawl: The very unequal sampling effort between locations for the TB technique suggests that the significant interactions between group and location found for Pielou's evenness and Simpson's Index should not have undue weight placed on them (Table 10). Abundance was highest in Group 1 (Figure 9); this was probably true for SRA5 as well. Number of species and SRF was highest in Group 5.

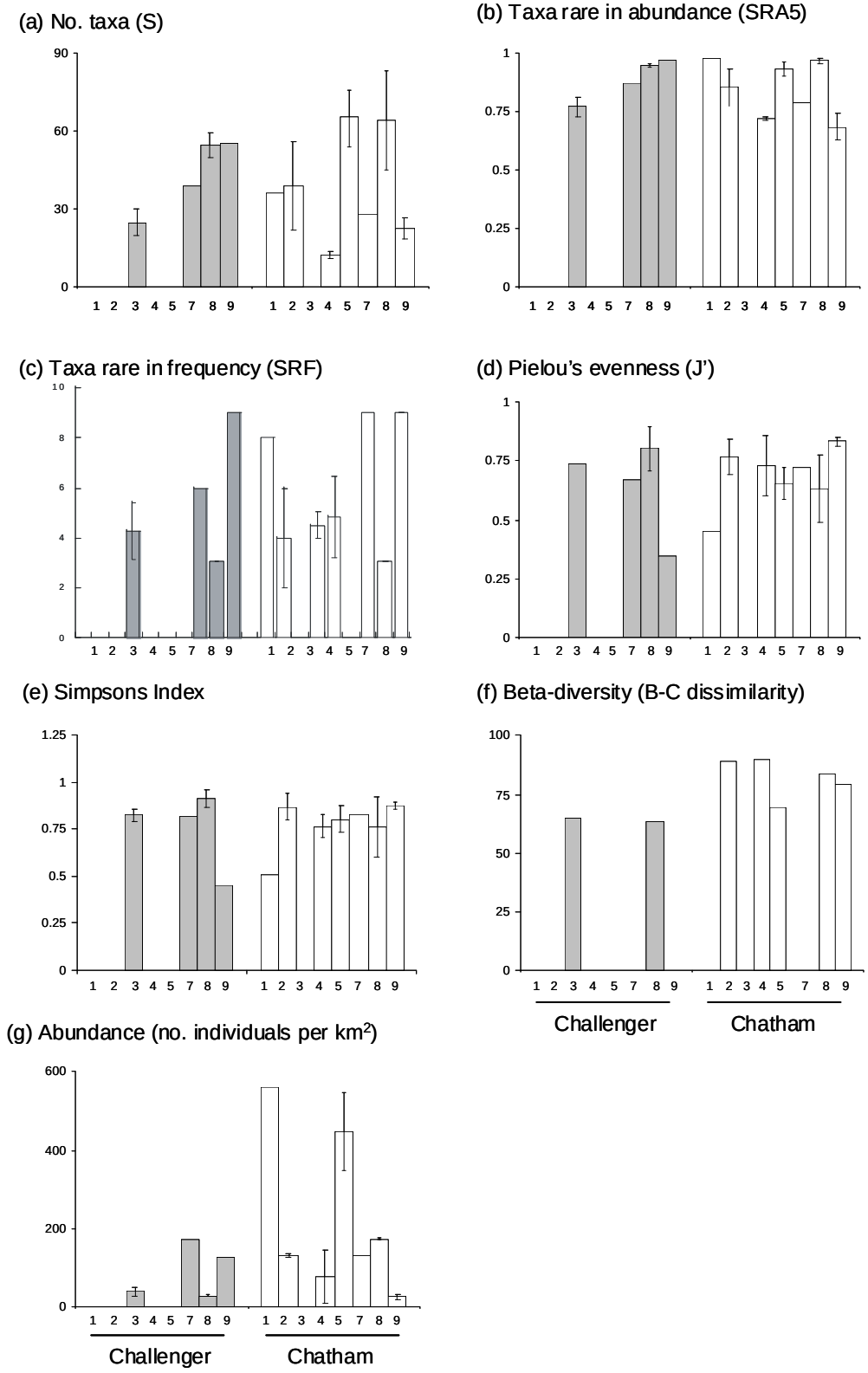

Figure 9: Abundance and diversity measures for TB data. Numbers below x-axis refer to Groups 1–9. Note no samples were taken within Group 6.

DISCUSSION

Clustering techniques

While the clustering technique used in the final assessment of groups was average linkage clustering of a modified Gower distance measure based on a log transformation, the comparison between cluster techniques run on the DTIS and SEL data did not show strong differences between techniques. Sampling stations were generally assigned to the same groups by all methods and the species defining the groups were generally similar. The number of groups with more than three members varied across techniques from 9 to 11. The major reason for selecting the modified Gower technique was the high percentage (90 %) of sampling stations that occurred in groups with four or more members. Average group linkage clustering of Bray-Curtis dissimilarities tended to split stations into very small groups, while the K-means clustering on Hellinger distances retained very disparate stations in one group.

Groups determined from the DTIS data seemed a reasonable surrogate for the other data sets and provided the most comprehensive coverage. Interestingly few groups were found in only one location, although two fewer groups were found on the Challenger Plateau than on the Chatham Rise. Group 3 was only found on the Challenger Plateau, while Groups 2, 5 and 6 were only found on the Chatham Rise.

However, the degree of compositional dissimilarity found within each of these groups (generally more than 60%) precludes the use of the term "community". The use of the terms "biotopes" or "biocenoses" were considered but both of these terms imply uniformity of animal and plant life, and also in the case of biotopes the groups are expected to occur at small scales and in the case of biocenoses are expected to be uniform in environmental conditions. For this reason the groups are best defined as biotic habitats and this term will be used throughout the rest of the text.

Biotic habitats observed in the Challenger Plateau and Chatham Rise locations

Taxa characterising these biotic habitats were defined as those that contributed to at least 50% of the within-group Bray Curtis similarities for each collection method. Characterising taxa for a number of the groups were similar between collection methods, although, as expected, some differences were observed. These differences were most likely based on differing sampling resolutions and relative proportions of epibenthos to infauna collected. For example, the STILL technique allowed counts of smaller organisms, but was likely to underestimate the effect of large taxa unless they were exceptionally dense. Differences between the DTIS and the TB data were generally greatest, with TB collecting more infauna and much smaller sizes of organisms than either the DTIS or SEL.

Merging the characterising taxa from all methods, together with the biodiversity characteristics, the following nine major biotic habitats can be described:

- B1. An ophiuroid (*Ophiomusium* lymani) habitat containing six members and exhibiting high abundance, low beta diversity and a high proportion of infaunal species that were rare, with low evenness and Simpsons diversity.
- B2. A mixed habitat of Anthozoa (*Radicipes*, *Anthioptilum*), Sponges (Cladhorizidae) and Decapods (*Pycnoplax victoriensis*, *Campylonotus rathbue*) with 12 members, containing a varied community sampled by the TB method (presumably small infauna).
- B3. A mixed habitat of Hydroids, Holothurians, Decapods (Galathiedae and Crangnoidae), Sipunculids and an Onuphid, with 17 members.
- B4. Predominantly the echinoid, *Gracilechinus multidentatus*, with some Ophiuroids and a Holothurian, containing 12 members and exhibiting a low epifaunal Simpson's index and evenness.
- B5. A mixed habitat of Parapaguridae, Sponges, Onuphids and Gastropods, with a very varied community sampled by TB, of 12 members.

- B6. A habitat dominated by Parapaguridae and Spatangidae, with Sponges, Shrimps and two infaunal Gastropods. with six members.
- B7. A habitat dominated by decapods (*Munida gracilis* and *Notopandalus magnoculus*) with patches of small tube-dwelling polychaetes (Chaetopterids and Onuphids), containing 14 members and exhibiting high epifaunal beta diversity.
- B8. A mixed habitat dominated by a Caridea decapod and a Holothurian with Parapaguridae, Gastropods, and an infaunal Sipunculid, containing 15 members.
- B9. A mixed Gastropod, Shrimp, and Ophiuroid habitat, with small Hydroids, Paguridae and an infaunal Polychaete. It has high epifaunal species richness and contains 17 members.

Other Biotic habitats with very few members were observed:

(m10) Anemones- 3 members, (m11) Zoroasteridae/Asteriidae, Crabs, Anemones and Asteroidea- 2 members, (m12) Holothurians and Shrimps- 2 members, (m13) Polychaetes, Encrusting Sponges, Bryozoans and Anemones- 1 member, (m14) Holothurians and Ophiuroids- 1 member, (m15) Sponges- 1 member, (m16) *Spatangus* sp.- 1 member, (m17) *Astropecten*/*Lithosoma*- 1 member, (m18) *Teratomaia richardsoni*/Halichondrid- 1 member and (m19) Desmophyllum/Caryophyllia/Scaphopoda-1 member.

In general, the biotic habitats demonstrated spatial coherence on both the Chatham Rise (Figure 10) and the Challenger Plateau (Figure 11). Figures 10 and 11 suggest that important drivers of faunal composition will be depth, slope and productivity, although this will be analysed further in Objectives 10 and 14.

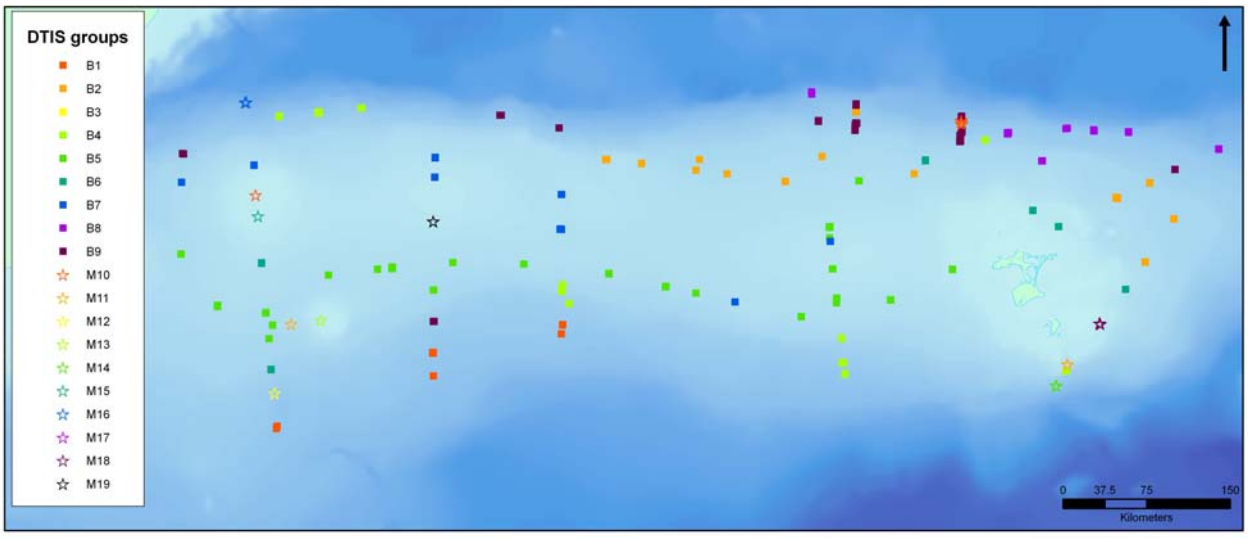

Figure 10: Distribution of biotic habitats across the Chatham Rise.

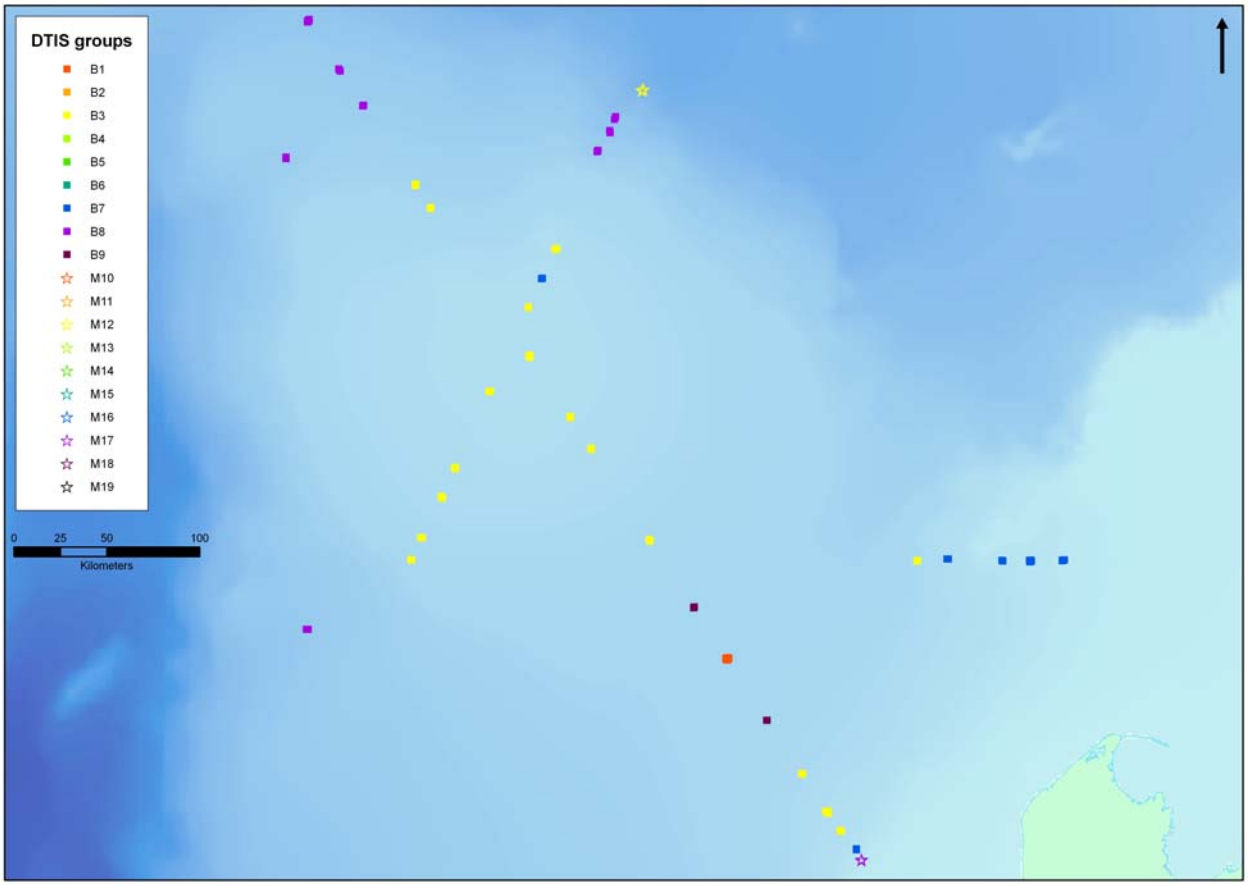

Figure 11: Distribution of biotic habitats across the Challenger Plateau.

Do biotic habitats reflect initial sampling strata?

There was some correspondence between the biotic habitats and the initial sampling strata. For example, Biotic habitat 1 was located within stratum 8 in the Chatham Rise and stratum 9 in the Challenger Plateau, and Biotic habitat 9 in the Challenger Rise was also located within stratum 9 (Table 12). While most sites assigned to Biotic habitat 8 (containing stations from both Chatham Rise and Challenger Plateau) were located in sampling stratum 3, those from the other biotic habitats were found in multiple strata (Table 12).

The number of strata that a biotic habitat was found in varied from one to six for the Challenger Plateau and from one to five for the Chatham Rise. This difference between the two locations suggests that determining biotic habitats from acoustic and environmental data is easier to do in a region encompassing a number of strong environmental gradients. This finding is not unexpected, however its corollary is important. That is, environments lacking environmental and acoustic heterogeneity can still hold considerable variability in benthic biotic habitats. Moreover Chatham Rise strata were more likely to contain more than three biotic habitats, suggesting that even in environmentally heterogeneous areas, relating biotic habitats to environmental and acoustic data is difficult.

Table 12: Number of sampling sites in each of the major and minor biotic habitats determined in this study (B and m prefix values, respectively, at left) and the initial sampling strata in which they occurred (S1-9, top). The 'Maximum' column shows the highest percentage of a group observed in a single sampling stratum (these values have no meaning in cases where a habitat occurred at only a single site and therefore are not given).

	S1	S2	S3	S4	S5	S6	S7	S8	S9	Maximum
Challenger										
B1									1	
B3	2	4		4		1	3	3		24
B7						4	1	1		67
B8			7		1					88
B9									3	100
m12			1							
m17								1		
Chatham										
B1								5		100
B2		3	1			6			2	50
B4			1	4	4				3	25
B5	9	6				1	5		4	36
B6		3				1	1		1	50
B7	3					4			1	50
B8			6						1	88
B9			4		1			1	8	57
m10						1			2	67
m11							1		1	50
m12								1		
m13		1								
m14				1						
m15									1	
m16									1	
m18									1	
m19									1	

SUMMARY

This report describes relationships, patterns and contrasts in species composition, assemblages and habitats, within and between sites, initial sampling strata and locations. This was achieved by focussing on defining groups of sites that were more similar to each other than to other sites. The groups were determined from DTIS video data because these were the most spatially comprehensive. However, there was considerable concordance between data from the four collection methods in the taxa that characterised the groups. The taxa that characterised these groups were then merged with information from Objective 6 on site biodiversity to develop descriptions of biotic habitats.

While biotic habitats of the Challenger Plateau and Chatham Rise have been described in this report, reports on other objectives will expand this work. Canonical ordination and regression tree techniques are being used in Objectives 12 and 15 to determine environmental drivers of dominant species and overall community composition. The relationships found (or not found) between the biotic habitats and location (Chatham vs Challenger) and the initial sampling strata will be utilised in Objective 16 to inform future sampling strategies. Most importantly, the biotic habitats developed will be used directly in Objective 10 to estimate vulnerability of different areas of the Challenger Plateau and Chatham Rise to disturbance. Determining which taxa define how similar communities are between sites is essential to this task, as the life history characteristics of these organisms provide important

information on how the community functions and whether there are any historic patterns of physical disturbance.

ACKNOWLEDGEMENTS

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Data Storage

Data from the analyses presented here have been lodged with the Ministry of Fisheries Data Manager at NIWA for loading in to the Ministry of Fisheries Marine Biodiversity and Biosecurity Database (BIODS) where they will be referenced to the raw data from which they are derived.

APPENDIX

Table A 1: ANOVA summary results for defining taxa for each classification group (biotope) as identified by SIMPER. Results for each species represent comparisons of density per 1000 m^2 between biotic habitats.

Taxon	Mean Square	F-ratio	*P*
DTIS			
Ophiomusium lymani	16355	150.4	0.000
Radicipes spp.	69.65	25.96	0.000
Hydroids	46.13	9.7	0.000
Gracilechinus multidentatus	280.87	60.27	0.000
Paguridae	98.15	19.54	0.000
Hyalinoecia longibranchiata	51.30	4.75	0.000
Spatangidae	41.8	8.736	0.000
Munida gracilis	25.04	11.97	0.000
Nematocarcinus sp.	11.25	13.63	0.000
Enypniastes eximia	12.32	13.24	0.000
Gastropod	12.22	5.96	0.000
Shrimp	13.78	7.03	0.000
Ophiura ooplax	0.25	0.91	0.511
STILL			
Ophiomusium lymani	63966.00	24.28	0.000
Holothurians	37065.229	4.539	0.001
Cladhorizidae	36315.525	3.572	0.003
Shrimp	2068.189	3.884	0.002
Hydroids	2386.618	1.149	0.354
Galatheidae	1366.308	2.266	0.043
Gracilechinus multidentatus	2669.193	15.522	0.000
Ophiura ooplax	4359.465	2.468	0.029
Munida gracilis	848.411	2.615	0.022
Paguridae	2974.069	3.077	0.009
Gastropoda	1857.340	2.981	0.011
Foraminifera (giant)	1718.022	1.119	0.372
SEL			
Ophiomusium lymani	70.329	38.251	0.000
Pycnoplax victoriensis	2.948	13.805	0.000
Hyalinoecia longibranchiata	7.253	2.352	0.023
Sipunculidea	2.744	2.450	0.018
Gracilechinus multidentatus	6.292	5.222	0.000
Paracaudi chilensis	0.615	1.943	0.062
Falsilutia powelli	2.127	3.063	0.004
Foraminifera	2.500	1.755	0.095
Pseudarchaster garricki	3.579	5.093	0.000
Fissidentalium zelandicum	2.549	4.790	0.000
Austrofusus glans	1.617	3.906	0.000
Chaetopteridae	3.001	1.997	0.055
Munida gracilis	1.088	3.520	0.001
Nassarius ephamillus	1.450	2.973	0.005
Ophiura ooplax	2.048	3.053	0.004
Kinbergonuphis proalopus	0.639	1.275	0.265
TB			
Laetmogone violacea	2.037	7.234	0.000
Anthoptilum	0.545	4.193	0.003
Campylonotus rathbue	3.585	5.162	0.001
Munida gracilis	11.799	5.141	0.001
Oedicerotidae	0.196	3.256	0.012
Pycnoplax victoriensis	1.459	1.697	0.150
Philocheras acutirostratus	4.040	5.102	0.001
Gracilechinus multidentatus	2.417	2.580	0.035
Serolidae	6.430	4.880	0.001
Foraminifera	36.111	2.395	0.047

Hyalinoecia longibranchiata	9.538	1.497	0.209
Sympagurus dimorphus	5.287	3.328	0.010
Flabellum knoxi	9.100	5.047	0.001
Ypsilothuria bitentaculata	6.783	7.525	0.000
Fusitriton laudandus	4.446	2.633	0.032
Comitas onokea vivens	3.186	9.411	0.000
Notopandalus magnoculus	4.676	2.961	0.019
Sipunculidea	2.301	2.561	0.036
Parvamussium maorium	4.935	1.900	0.107
Parapagurus latimanus	0.637	4.353	0.002
Fusitriton laudandus	4.446	2.633	0.032
Actiniaria	0.479	1.743	0.139

Table A 2: Full PERMANOVA output: Comparison of assemblage composition between sampling locations (Chatham Rise and Challenger Plateau) and groups identified by classification analysis of DTIS.

Term	d.f.	Sums of Squares	Mean Square	F-ratio	P
DTIS					
Location	1	3.964	3.964	0.871	0.524
Group(Location)	11	93.542	8.503	5.415	0.001
Residual	120	188.44	1.570		
Total	132	296.7			
STILL					
Location	1	12.763	12.763	1.756	0.038
Group(Location)	10	88.141	8.814	1.576	0.001
Residual	36	201.23	5.589		
Total	47	305.68			
SEL					
Location	1	2.511	2.511	1.212	0.181
Group(Location)	10	22.444	2.244	2.019	0.001
Residual	95	105.59	1.111		
Total	106	131.3			
TB					
Location	1	1.001	1.001	1.051	0.405
Group(Location)	9	10.456	1.1618	1.808	0.001
Residual	25	16.064	0.642		
Total	35	28.571			

Table A 3: Epibenthic megafaunal taxa identified from seamount sled (SEL) and Beam Trawl (TB) samples collected during voyages TAN0705 and TAN0707 to Chatham Rise and Challenger Plateau.

Phylum	Class	Order	Number of taxa (species or higher level)
Foraminifera	Xenophyophorea		1
Porifera	Demospongiae	Astrophorida	8
		Dendroceratida	1
		Dictyoceratida	3
		Hadromerida	11
		Halichondrida	6
		Haplosclerida	8
		Poecilosclerida	21
		Spirophorida	6
	Hexactinellida	Amphidiscosida	5
		Hexactinosida	2
		Lyssacinosida	6
Cnidaria	Anthozoa	Actiniaria	15
		Alcyonacea	7
		Antipatharia	2
		Corallimorpharia	2
		Gorgonacea	10
		Pennatulacea	14
		Scleractinia	12
		Telestacea	2
		Zoanthidea	4
	Hydrozoa	Anthoathecata	8
		Hydroida	1
		Leptothecata	11
	Scyphozoa		1
Mollusca	Aplacophora	Aplacophora	1
	Bivalvia	Arcoida	4
		Dimyidae	1
		Limoida	1
		Myoida	9
		Mytiloida	1
		Nuculoidea	13
		Ostreoida	4
		Pholadomyoida	2
		Pterioida	2
		Veneroida	5
	Cephalopoda	Octopoda	2
		Sepiida	1
		Sepiolida	1
		Spirulida	1
		Teuthida	2

Phylum	Class	Order	Number of taxa (species or higher level)
	Gastropoda	Kapala	1
		Speoides	1
	Gastropoda Opisthobranchia	Cephalaspidea	4
		Nudibranchia	1
	Gastropoda Prosobranchia	Archaeogastropoda	10
		Cocculiniformia	1
		Heterostropha	1
		Mesogastropoda	18
		Neogastropoda	31
		Neotaenioglossa	6
		Stenoglossa	29
		Vetigastropoda	2
	Polyplacophora	Neoloricata	1
	Polyplacophora Neoloricata	Ischnochitonida	2
	Scaphopoda	Dentaliida	3
	Solenogastra		1
Nemertea	Nemertea	Nemertea	1
Echiura			1
Priapulida	Priapulida	Priapulida	1
Sipuncula	Sipunculidea		1
Annelida	Polychaeta	Amphinomida	3
		Eunicida	22
		Phyllodocida	11
		Phyllodocida Aphroditiformia	13
		Phyllodocida Nereidiformia	3
		Sabellida	13
		Scolecida	19
		Spionida	5
		Terebellida Cirratuliformia	2
		Terebellida Terebelliformia	6
Brachiopoda	Articulata	Terebratulida	6
	Rhynchonellida		1
Bryozoa	Gymnolaemata	Cheilostomata	70
		Ctenostomata	1
	Stenolaemata	Cyclostomata	5
Arthropoda Chelicerata	Pycnogonida	Pycnogonida	2
Arthropoda Crustacea	Malacostraca	Amphipoda	20
		Decapoda	87
		Euphausiacea	1
		Isopoda	18
		Mysidacea	2

Phylum	Class	Order	Number of taxa (species or higher level)
		Stomatopoda	1
		Tanaidacea	1
	Maxillopoda	Pedunculata	11
		Sessilia	2
	Ostracoda		1
Echinodermata	Asteroidea	Brisingida	6
		Forcipulatida	5
		Notomyotida	9
		Paxillosida	18
		Spinulosida	4
		Valvatida	16
		Velatida	9
	Crinoidea	Articulata	4
		Bourgueticrinida [aka Millericrinida]	3
		Cyrtocrinida	1
	Echinoidea	Cidaroida	5
		Echinoida	3
		Echinothurioida	5
		Pedinoida	1
		Spatangoida	9
	Holothuroidea	Aspidochirotida	6
		Dactylochirotida	1
		Dendrochirotida	9
		Elasipodida	6
		Holothuroidea	1
		Molpadiida	8
	Ophiuroidea	Euryalinida	3
		Ophiurida	48
Chordata	Ascidiacea [Tunicates]	Enterogona Aplousobranchia	2
		Pleurogona Stolidobranchia	7
	Thaliacea [Salps]		1

Table A 4: DTIS video and still images: operational taxonomic units (OTU) for mega-epibenthic fauna identified from seabed still images.

Phylum	Class	Order	OTU
Annelida	Echiura		Echiuran
	Polychaeta	Aciculata	Hyalinoecia
		Canalipalpata	Sabellid
			Errant polychaete
			Polychaeta
			Worm indet.
Arthropoda	Malacostraca	Decapoda	Agononida nielbrucei
			Atelecyclidae
			Brachyura
			Campylonotus rathbunae
			Chirostylidae
			Galatheidae
			Galatheoidea
			Gastroptychus novaezelandiae
			Glyphocrangon
			Goneplacidae
			Haliporoides sibogae
			Ibacus alticrenatus
			Inachidae
			Leptomithrax longipes
			Lithodes cf. longispinus
			Lithodes murrayi
			Lithodidae
			Majidae
			Metanephrops challengeri
			Munida gracilis
			Natant decapod
			Nematocarcinus sp.
			Neolithodes brodiei
			Neommatocarcinus huttoni
			Nephropidae
			Paguridae
			Paralomis zealandica
			Platymaia maoria
			Plesionika sp.
			Polycheles spp.
			Polychelidae
			Pycnoplax victoriensis
			Scyllaridae
			Teratomaia richardsoni
			Trichopeltarion fantasticum
			Vitjazmaia latidactyla
		Isopoda	Acutiserolis spp
			Isopods
			Serolidae
			Peracida
	Pycnogonida	Pantopoda	Collossendeis sp
			Pycnogonid indet
			Pycnogonids

Phylum	Class	Order	OTU
Brachiopoda			Brachiopoda
Bryozoa (Ectoprocta)	Gymnolaemata	Cheilostomata	Bryozoan
			Bryozoan - antler form
			Bryozoan - bushy form
			Bryozoan - erect cheilostome
			Bryozoan - feather form
			Bryzoan - branched form
			Bryzoan - branched white
			Bryzoan - encrusting cheilostome
			Bryzoan - lace form
Chordata	Ascidiacea		Ascidian
Cnidaria	Anthozoa	Actiniaria	Anemone (hermit)
			Anemone (large columnar)
			Anemone (mauve)
			Anemone (small red)
			Anemone indet.
			Anenome 10
			Anenome 11
			Anenome 12
			Anenome 13
			Anenome 14
			Anenome 15
			Anenome 16
			Anenome 17
			Anenome 18
			Anenome 19
			Anenome 4
			Anenome 5
			Anenome 6
			Anenome 7
			Anenome 8
			Anenome 9
			Anenome 1
			Anenome 2
			Anenome 3
			Anenome indet.
		Alcyonacea	Alcyonacea
			Alcyoniidae
			Anthomastus 3
			Anthomastus sp.
			Clavularia sp
			Taiaroa tauhou
			Telesto sp
		Antipatharia	Antipatheria
			Antipathes
			Bathypathes
			Dendrobathypathes
			Leiopathes
			Parantipathes
			Trissopathes
		Ceriantheria	Ceriantharia spp

Phylum	Class	Order	OTU
		Corallimorpharia	Corallimorpharia
			Corallimorpharia 1
			Corallimorpharia 2
			Corallimorpharia 3
		Gorgonacea	Callogorgia sp.
			Chrysogorgiidae
			Coralliidae
			Corallium sp.
			Gorgonacea
			Isididae
			Lepidisis sp.
			Paragorgia sp.
			Paragorgiidae
			Primnoella sp.
			Primnoidae
			Primnoidea/Callogorgia
			Radicipes sp.
			Sibogagorgia spp
			Thourella sp.
		Pennatulacea	Acanthoptilum sp.
			Anthoptilum grandiflorum
			Anthoptilum sp.
			Distichoptilum gracile
			Funiculina quadriangularis
			Gyrophyllum sibogae
			Halipteris sp.
			Kophobelemnon sp.
			Kophobelemnon stelliferum
			Pennatula aculeata
			Pennatula inflata
			Pennatula sp.
			Pennatulacea
			Pennatulacea 1
			Pennatulacea 2
			Pennatulacea 3
			Pennatulacea 4
			Pennatulacea 5
			Stylatula sp.
		Scleractinia	Cup coral
			Enallopsammia spp.
			Flabellum
			Flabellum 1
			Flabellum 3
			Flabellum knoxi
			Flabellum loure kexeii
			Flabellum rubrum
			Goniocorella dumosa
			Madrepora oculata
			Madrepora sp.
			Scleractinia
			Scleractinia (thicket)

Phylum	Class	Order	OTU
			Solenosmillia variabilis
			Solitary coral
		Stolonifera	Rhodelina sp
		Zoanthidea	Epizoanthidea
			Coral indet.
	Hydrozoa	Anthoathecatae	Athecate hydroid 1
			Errina sp.
			Stylasteridae
		Leptothecatae	Hydroid
			Hydroid 2 branches
			Hydroid A
			Hydroid orange
Echinodermata	Asteroidea	Brisingida	Brisinga chathamica
			Brisinga tasmani
			Brisingid 1
			Brisingid 2
			Brisingid 3
			Brisingid 4
			Brisingidae
			Hymenodiscididae
		Forcipulatida	Asteriidae
			Cosmasterias dyscrita
			Pseudechinaster rubens
			Zoroaster sp
			Zoroasteridae
			Zoroasteridae/Asteriidae
		Notomyotida	Benthopecten sp
			Benthopectinidae
		Paxillosida	Astropectinidae
			Dipsacaster magnificus
			Dipsacaster sp
			Paxillosida?
			Radiaster sp
			Radiasteridae
		Spinulosida	Crossaster multispinus
			Crossaster sp.
			Echinasteridae
			Henricia sp.
			Hymenaster sp
			Pterasteridae
			Solaster torulatus
			Solasteridae
		Valvatida	Ceramaster sp
			Goniasteridae
			Hippasteria sp
			Lithosoma novazealandiae
			Lithosoma/Pseudarchaster
			Mediaster sp
			Pillsburiaster sp
			Valvatida
		Velatida	Myxaster?
			Asteroids

Phylum	Class	Order	OTU
	Crinoidea	Bourgueticrinida	Crinoidea (stalked)
		Comatulida	Crinoidea (motile)
			Crinoids
	Echinoidea	Cidaroida	Cidaridae
			Cidaroida
			Goniocidarinae
			Goniocidaris parasol
			Goniocidaris sp
			Histocidaridae
			Ogmocidaris benhami
			Stereocidaridae
		Clypeasteroida	Peronella hinemoae
		Echinoida	Dermechinus horridus
			Echinidae
			Echinoida
			Gracilechinus multidentatus
		Echinothurioida	Echinothuriidae
			Echinothuriidae/Phormosomatidae
			Phormosoma bursarium
			Phormosomatidae
			Sperosoma sp.
		Pedinoida	Caenopedina
			Caenopedina spp
			Pedinidae
		Spatangoida	Paramaretia peloria
			Spatangidae
			Spatangus sp
		Temnopleuroida	Pseudechinus flemingi
			Temnopleuridae
			Echinoids
	Holothuroidea	Aspidochirotida	Bathyplotes moseleyi
			Bathyplotes sp.
			Bathyplotes sulcatus
			Benthodytes incerta
			Pseudostichopus mollis
			Pseudostichopus peripatus
			Pseudostichopus sp
			Stichopodidae
			Stichopus mollis
			Synallactidae
		Elasipodida	Elasipoda
			Elasipoda 1
			Elasipoda 2
			Enypniastes eximia
			holothurian indet < 25 mm (Pale)
			Laetmogone violacea
			Pannychia sp
			Pelagothuridae
			Psychropotidae
			holothurian indet < 25 mm (Pale)
			holothurian indet.
			holothurian uni 1
			holothurian uni 2

Phylum	Class	Order	OTU
			holothurian uni 3
			holothurian uni 4
			Holothurians
	Ophiuoroidea	Euryalinida	Euryalinida
			Gorgonocephalidae
		Ophiurida	Amphiuridae
			Ophiacanthidae
			Ophiomusium lymani
			Ophiomyxa brevirima
			Ophiurida (apricot small)
			Ophiurida (Mauve small)
			Ophiurida unspecified
			Ophiuridae
			Unknown ophiurida 0
			Ophiuoroids
Echiura			Echiuran
Foraminifera (Protozoa)	Foraminifera	Foraminiferida	Foram (giant)
			Foraminifera
	Granuloreticulosea	Foraminiferida	Bathysiphon
Mollusca	Bivalvia	Ostreoida	Delectopecten fosterianus
		Pholadomyoida	Euciroa galatheae
			Bivalve indet.
			Bivalvia
	Cephalopoda	Octopoda	Bathypolypodinae
			Benthoctopus sp
			Cirroteuthididae/Luteuthididae
			Enteroctopus zealandicus
			Graneledone sp
			Graneledoninae
			Octopodinae
			Opisthoteuthididae
			Opisthoteuthis sp
			Pinnoctopus cordiformis
			Cephalopoda
	Gastropoda	Archaeogastropoda	Calliostoma alertae
			Callostomatidae
		Neogastropoda	Aeneator recens
			Amalda sp
			Austrofusus glans
			Buccinidae
			Coluzea sp
			Comitas onokeana vivens
			Muricidae
			Olividae
			Pagodula sp
			Penion sp
			Turbinellidae
			Turridae
			Volutidae
			Volutomitira banksi
			Volutomitridae

Phylum	Class	Order	OTU
		Neotaenioglossa	Cassidae
			Fusitriton magellanicus
			Naticidae
			Ranellidae
		Nudibranchia	Opisthobranchia
			Gastropoda
			Opisthobranchia
	Scaphopoda		Scaphopoda
Porifera	Calcarea	Leucosolenida	Leucosolenia
			Calcarea
	Demospongiae	Astrophorida	Astrophorid
			Geodia regina
			Geodinella vestigifera
			Pachastrellidae
			Tethyopsis n. sp.
			Thenea sp.
		Hadromerida	Hadromerid
			Suberites affinis
		Halichondrida	Axinella or Pararaphoxya
			Axinella spp
			Halichondrid
		Haplosclerida	Haplosclerid
			Petrosia
		Lithistida	Awhiowhio sepulchrum
			Costifer wilsoni
			Lithistid
			Neoaulaxinia persicum
		Poecilosclerida	Cladhorizidae
			Cladhorizidae sp. nov.
			Latrunculia spp
			Poecilosclerid
		Spirophorida	Spirophorida
			Tetilla leptoderma
			Demonspongiae
			Encrusting sponges
	Demspongiae		Demospongiae
	Hexactinellida	Amphidiscosida	Hyalonema sp.
			Pheronema sp.
		Hexactinosida	Farreidae
			Hexactinosida
		Lyssacinosida	Euplectella regalis
			Hyalascus n. sp
			Hexactinellida
			Demospongiae
			Sponge (mauve)
		Amphipoda	Amphipoda
		Euphausiacea	Euphausiacea
		Mysida	Mysida
			Buccinidae/Ranellidae
			Galatheidae (white)