JNCC Report No. 588

Community Analysis of Offshore MCZ Grab and Video Data (2014)

Chris Allen, Magnus Axelsson & Steven Dewey

April 2016

ISSN 0963 8901

For further information please contact:

Joint Nature Conservation Committee
Monkstone House
City Road
Peterborough PE1 1JY
http://jncc.defra.gov.uk

This report should be cited as:

Allen, C., Axelsson, M. & Dewey S. 2016. Community analysis of offshore MCZ grab and video data (2014). *A report to JNCC by Seastar Survey Ltd. JNCC Report No. 588*. JNCC, Peterborough.

Summary

The Marine and Coastal Access Act 2009 allows for the creation of a type of Marine Protected Area (MPA), called a Marine Conservation Zone (MCZ). MCZs are intended to provide protection to a range of nationally important marine wildlife, habitats, geology and geomorphology, and can be designated anywhere in English and Welsh inshore and UK offshore waters. Government policy dictates that establishment of MCZs should be based on the "best available evidence". The Marine Conservation Zone Project has identified a number of potential MCZs in English inshore and English, Welsh and Northern Irish offshore waters. A number of surveys have been undertaken to gather evidence on the composition of seabed habitats and communities within MCZ areas.

Seastar Survey Ltd. was contracted by JNCC in financial year 2013/14 to undertake statistical analysis on benthic community data collected from several offshore MCZs. The results of these analyses were then used to assign biotopes to the survey data based on both the Marine Habitat Classification for Britain and Ireland (Connor *et al* 2004) and EUNIS classification scheme. Data were supplied as faunal abundance counts from both benthic grab samples and from video footage and still images. Various different methodologies were used to rationalise data sets before undertaking multivariate statistical analyses using the PRIMER software package. Data from four offshore MCZs were analysed:

- South-West Deeps (West) MCZ
- North-East of Farnes Deep MCZ (formerly Rock Unique rMCZ)
- Swallow Sand MCZ
- East of Haig Fras MCZ

The following European Nature Information System (EUNIS)[1] biotopes were assigned after multivariate analysis of the survey data:

- **North East of Farnes Deep** – 4x level 4 habitats (SS.SCS.OCS; SS.SSa.OSa; SS.SMx.CMx and SS.SMx.OMx) and 3x level 5 biotopes (SS.SSa.CFiSa.EpusOborApri; SS.SSa.OSa.OfusAfil; SS.SSa.OSa.SpnMac; SS.SMx.OMx.PoVen)
- **East of Haig Fras** – 4x level 4 habitats (SS.SCS.OCS, SS.SSa.OSa; SS.SMu.OMu; SS.SMx.OMx) and 3x level 5 biotopes (CR.HCR.DpSp.(PhaAxi); SS.SSa.CFiSa.EpusOborApri; SS.SMx.OMx.PoVen)
- **South-West Deeps (West)** – 4x level 4 habitats (SS.SCS.OCS; SS.SSa.OSa; SS.SMu.OMu; SS.SMx.OMx) and 3x level 5 biotopes (SS.SSa.OSa.(Pex); SS.SSa.OSa.(Ech); SS.SMx.OMx.PoVen; SS.SMx.OMx.Csmi)
- **Swallow Sand** – 4x level 3 biotopes (SS.SSa.OSa; SS.SMu.CFiMu; SS.SMu.OMu; SS.SMx.CMx) and 4x level 4 sub-biotopes (SS.SSa.OSa.MalDef; SS.SSa.OSa.Dari; SS.SMu.CFiMu.SpnMeg; SS.SMu.OMu.PjefThyAfil)

New biotopes included 'Seapens and macrofauna on deep circalittoral fine sand' (**SS.SSa.OSa.SpnMac**), 'Deep circalittoral sand with heart urchins' (**SS.SSa.OSa.(Ech)**), 'Deep circalittoral sand with *Paraphellia expansa'* (**SS.SSa.OSa.(Pex)**), 'Deep circalittoral mixed sediment with *Caryophyllia smithii*' (**SS.SMx.OMx.Csmi**) and 'Deep circalittoral muddy sand with *Ditrupa arietina*' (**SS.SSa.OSa.Dari**).

The various limitations encountered during the project are discussed. The two principal limitations included a general lack of taxa present within the video/still data sets, and level of taxonomic identification that could be made from video/still data. The multivariate analysis

[1] http://eunis.eea.europa.eu/

methods employed were generally unable to reliably assign biotopes to video and still data based on faunal community data alone.

Contents

1 Introduction

The Marine and Coastal Access Act 2009 allows for the creation of a new type of Marine Protected Area (MPA), called a Marine Conservation Zone (MCZ). The establishment of MCZs are intended to protect a range of nationally important marine wildlife, habitats, geological and geomorphological features, and can be designated anywhere in English and Welsh inshore and UK offshore waters. Potential MCZs in English inshore and English, Welsh and Northern Irish offshore waters have been identified through the Marine Conservation Zone Project.

Government policy dictates that establishment of MCZs should be based on “best available evidence”. JNCC has therefore commissioned a range of research to collect information on the marine environment within offshore MCZs in order to provide the necessary evidence to underpin MCZ recommendations. Surveys undertaken to gather evidence for the MCZ Project involve collecting data to characterise the seabed habitats and their associated communities, enabling broad-scale mapping. The identification of biotopes within each MCZ will summarise the communities and habitats present, which in turn will help JNCC fulfil its role in providing advice for marine nature conservation.

Seastar Survey Ltd. was contracted in financial year 2013/14 to undertake statistical analysis on benthic community data collected from several offshore MCZs. The results of these analyses were then used to assign biotopes to the survey data based on both the Marine Habitat Classification for Britain and Ireland (Connor *et al* 2004) and the European Nature Information System (EUNIS)[2] classification scheme.

JNCC provided data collected from surveys of four offshore MCZs, consisting of both faunal data collected using benthic grabs and drop-down camera systems (both video footage and still images). All data supplied had been previously analysed by other contractors. Enumerated faunal counts were provided for each station sampled by benthic grab. The faunal communities within the video and still image data had been enumerated by a variety of methods, including SACFOR, percentage cover and counts. Particle Size Analysis (PSA) data accompanied all infaunal grab samples. Both benthic grab and dropdown camera data were supplied with appropriate metadata, such as time of sampling, sample depth, sample position *etc*.

Data from four offshore MCZs were analysed, with Figure 1.1 showing their locations around the British Isles. The four offshore MCZs were:

- South-West Deeps (West) MCZ
- North-East of Farnes Deep MCZ (formerly Rock Unique rMCZ)
- Swallow Sand MCZ
- East of Haig Fras MCZ

The aim of this contract was to examine the enumerated faunal data using various multivariate statistical techniques to elucidate the underlying faunal communities present within each MCZ. The assessments made on the faunal communities were then used to inform assignment of biotopes, summarising the communities and habitats present.

[2] http://eunis.eea.europa.eu/

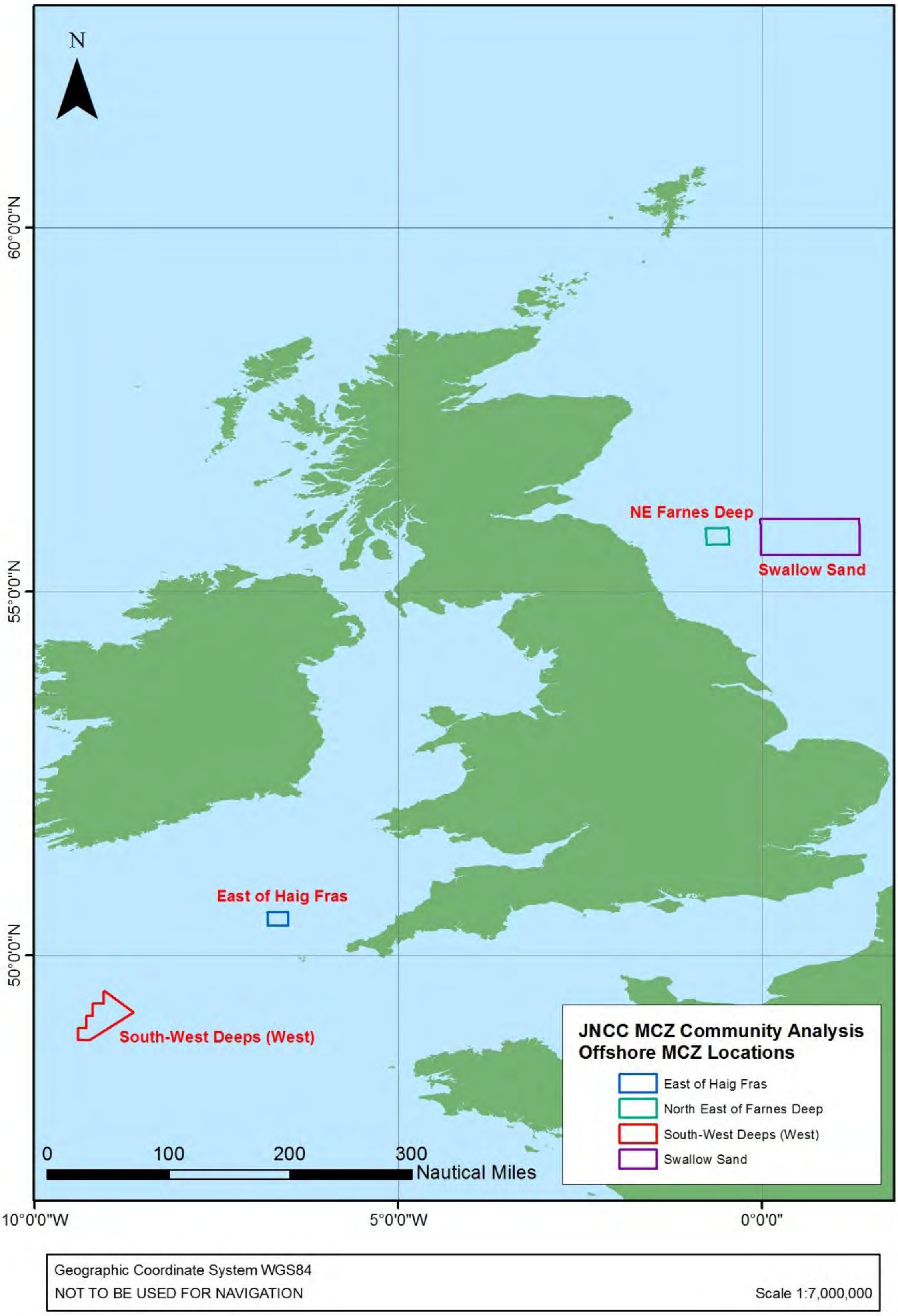


Figure 1.1. Map of offshore MCZ locations from which data sets were supplied for community analysis.

2 Methodology

The data provided from each survey was treated independently. Each MCZ survey was conducted by different staff at different times, whilst data sets had been analysed by different contractors. Benthic grab data and drop-down camera data were also analysed separately due to differences in sampling equipment. The methodologies employed during the multivariate data analysis are detailed below. In total nine data sets were examined:

- North East of Farnes Deep
  - grab data
  - video and still data
- East of Haig Fras
  - grab data
  - video and still data CEND0312 cruise
  - video and still data CEND0513 cruise
- South-West Deeps (West)
  - grab data
  - video and still data
- Swallow Sand
  - grab data
  - video and stills

Information on sample sites (survey station) within each survey area can be found in Appendix 1.

2.1 Benthic grab sample data

Four benthic grab sample data sets were analysed, one from each MCZ. Benthic grab samples were collected using a 0.1m^2 Hamon grab. Data were provided as a faunal data matrix detailing enumerated faunal counts at each survey station, with some presence/ absence records for epifaunal taxa. In addition to the faunal data, sediment PSA results were supplied for each station, along with relevant metadata regarding sample location and depth *etc*. The raw faunal data provided for each survey can be found in Appendix 2.

2.1.1 Rationalisation

Before any analysis was undertaken, the faunal data were rationalised. This step involved the examination of the data to identify any duplication of species data, occurrence of juveniles and inclusion of different data types (e.g. counts with SACFOR[3] or presence/ absence *etc*.). Data rationalisation was performed on a case-by-case basis, and the exact processes undertaken for each data set are detailed within the results section. Typical examples of rationalisation procedures undertaken included truncating data so that juveniles were included with adults, replicated species data combined, and non-specific identification converted to higher taxonomic levels where appropriate. Any fauna recorded as 'Present' were removed from the analysis since they could not be enumerated at the same level as those fauna actually counted. In order to ultilise these taxa all data would have to have been reduced to a presence/absence measure, reducing the power of the multivariate analyses. Rationalised faunal data matrices are included in Appendix 3.

As each data set was examined independently, no attempt was made to rationalise fauna between MCZ areas in order to make different data sets comparable. This was beyond the scope of this particular contract. Also, species identifications were kept as listed within the

[3] Marine Nature Conservation Review (MNCR) SACFOR abundance scale, http://jncc.defra.gov.uk/page-2684

raw data. For example, no attempts were made to correct unaccepted species nomenclature. It was felt that without access to the actual faunal material, no assumptions could be made to over-rule the identifications made by the original analysts based purely on the supplied faunal data matrix. Since no comparisons were being made between data sets, the need to correct faunal identifications was lessened. Since the software algorithms used only discriminate between lines of text, the main point of the rationalisation was to ensure species were not duplicated within the data set, and that all taxa had an abundance that was measured on a comparable scale. If future studies want to compare between data sets then more care would be required with respect to species nomenclature during rationalistion steps. See section 4.2 for a further discussion on the feasibility of comparing between data sets.

2.1.2 Data treatment

After rationalisation, the next step involved closer examination of the data to identify the need for any further data treatment. Univariate statistical analyses were undertaken using the DIVERSE function within PRIMER v.6 (Clarke & Warwick 2001) to assess various community measures for each grab sample. These included the total number of individuals (N), total number of species (S), species diversity as measured by the Shannon-Wiener (H'), Pielou's (J), Margalef's (d) diversity and Simpson's Dominance indices (see for example Gage & Tyler 1991; Fowler & Cohen 1992; Clarke & Warwick 2001). The Shannon-Wiener index was calculated using the natural log ($\log_e$). Each taxon was also examined to identify whether any were particularly abundant, and thus may potentially skew the data analyses. The requirements of any data transformation or further data set rationalisation were made based on these assessments. Data treatments were made on a survey by survey basis. The exact data treatments undertaken have been detailed in the results section for each particular data set.

2.1.3 Multivariate analyses

After data-treatment, resemblance matrices were constructed from each faunal data set using the Bray Curtis similarity measure. Cluster analysis was then undertaken, using group-averaged cluster mode, and the SIMPROF test applied to show evidence of structure within the groupings. The resultant dendrogram was then examined, and stations assigned to groups based on the pattern of clustering. Sediment PSA data was used as a factor to the data to show any trends between clustering patterns and the EUNIS sediment classification of samples. MDS ordination was also undertaken to examine the strength of the station grouping assigned from the dendrogram clusters. The SIMPER routine in PRIMER was then undertaken to assess which taxa were characteristic in the sample groups defined from the cluster analysis.

2.1.4 Biotope designation

The characteristic taxa for each faunal group derived from the SIMPER analysis were used as a basis for biotope designation. The characteristic species were checked against the various biotope descriptions with the MNCR v04.05 (Connor *et al* 2004), also taking into account the sediment type derived from the PSA results and the depth from which the sample was collected. Any biotopes that roughly matched the habitats and faunal communities identified from the samples were noted. This included highlighting any habitats that matched the sediment classification of the sample, and searching for matches between the characteristic species identified after SIMPER analysis of each sample with those listed within the biotope descriptions. A more in-depth assessment of the faunal abundance data then followed. This process was more subjective, relying on the experience of the analyst to identify trends in the faunal data. Typical patterns examined included looking at which species were present, and what this implied about the sedimentary environment of the habitat, whether certain combinations of species were present, or species that were indicative of other fauna (e.g. commensal species). These trends were used to refine the number of initially selected possible biotopes to the most appropriate fit to the sample data. Where no appropriate biotopes could be found, a new biotope was proposed, following guidelines issued by JNCC (Parry 2014). All MNCR biotopes were also recorded as their EUNIS habitat classification equivalents. The univariate data provided additional information about the faunal community at each station, such as dominance of certain taxa and overall diversity, which helped when assigning biotopes.

As mentioned, sample depth and sediment composition were considered when assigning biotopes. However, any trends within the faunal data that matched any existing biotopes were used to define samples over the physical environmental data. In these situations, depth or sediment composition mismatches to the assigned biotope were highlighted. Where insufficient faunal data was present to inform biotope designations, biotopes were assigned solely on sample depth and sediment classification.

Please note that designation of biotopes, even when based on the results of the multivariate analysis, involved a degree of subjectivity on the part of the analyst. Attempts have been made within the results section to explain the decisions made during biotope assignment, which should be borne in mind when considering the results of this contract.

2.2 Video footage and still image sample data

Five video and still image data sets were provided for analysis; one each for North East of Farnes Deep, Swallow Sand and South-West Deeps (West) respectively, and two for East of Haig Fras. The East of Haig Fras data was collected on two separate cruises (CEND0312 and CEND0513), and initially analysed by two different contractors. These data sets were therefore assessed independently from each other. The data sets were provided as completed proformas that detailed station metadata, descriptions of the habitats, and biotopes assigned from visual assessment of video and stills, alongside enumerated faunal data for each station. Faunal data was typically provided as SACFOR abundances.

Video footage and still images were acquired by either drop-down camera systems or towed camera systems. All survey methodolgies employed during the cruises followed MESH recommended operating guidelines for acquisition of underwater video and photographic images (Coggan *et al* 2007). During the original analysis of the video footage, video transects had been split into a number of segments where the analyst deemed changes in habitat occurred. Still images had been taken at approximately one minute intervals along each video transect. Appendix 4 details the survey proformas supplied, with Appendix 5 showing the faunal abundance matrices for each survey.

2.2.1 Rationalisation

Faunal data matrices were rationalised before any analyses were carried out. This process was largely the same as that outlined for the benthic grab sample data above. Any pelagic taxa found in the water column and therefore potentially independent of the seabed habitat were removed. Other examples included truncating data so that juveniles were included with adults, replicated species data combined, and non-specific identification converted to higher taxonomic levels where appropriate. Particular attention was paid to any qualifiers associated with taxa identifications, and taxa not combined where qualifiers indicated differences not reflected in the level of taxonomic differentiation (e.g. “Porifera, peach erect” and “Porifera, orange crust” were treated as different taxa.). SACFOR faunal abundances were converted into their numerical equivalent (i.e. Rare = 1, Occasional = 2 *etc.*). Data rationalisation was again performed on a case-by-case basis, and the exact processes undertaken for each data set are detailed within the results section. Rationalised faunal data matrices are included in Appendix 6.

2.2.2 Data treatment

Although there was a large quantity of still image data in terms of the number of images within each data set, each still image typically had very few taxa recorded. In order to account for this, still image data were combined for each parent video segment. The number of still images containing each taxon were calculated for each video segment, and expressed as a percentage of the total images taken on each video segment. This essentially amalgamated and translated SACFOR faunal abundances from each still image to a percentage occurrence for each video segment. The amount of still image data to examine was therefore reduced in terms of sample numbers, but each data point typically contained more information. Since adunbance of taxa was expressed as a frequency of occurance, this methodology also partly accounted for any samples where images were taken more frequently than one minute intervals.

Two points are worth noting about this particular treatment of the still image data. Any locally abundant taxa may be reduced in importance, whilst potential photographer basis to capturing ‘interesting’ fauna may skew the data sets. Therefore all results derived from the still image analysis were assessed alongside the results of the video footage analysis, with the video analysis providing a broader picture of the habitat, and the still images potentially revealing more about the taxa present.

Another disadvantage of this methodology was the potential to miss small-scale heterogeneity within the habitats that would not be visible from the video analysis. However, considering the general lack of visible epifauna on the soft sediment habitats, it was deemed that this method was necessary to produce sufficient varaibles for each station to make the multivariate analysis meaningful. The principal faunal components of soft sediment habitats are infaunal, so the benthic grab samples would provide a better picture of the actual faunal communities present at these sites, more effectively highlighting any habitat heterogeneity.

Both the video footage and still image faunal data were based on SACFOR or derived values rather than numerical counts. These data sets were therefore not suitable for univariate statistical analyses, and any standardisation or data transformations would not be appropriate.

2.2.3 Multivariate analyses

The multivariate analyses of the video footage and still data were similar to those outlined for the benthic grab sample data. Video footage data and still image data were examined separately. Faunal data were converted into resemblance matrices using the Bray Curtis similarity measure. Cluster analysis was then preformed, using group-averaged cluster mode and SIMPROF to test the structure of the resultant dendrogram. Stations were assigned to groups based on their clustering within the dendrogram. MDS plots were also constructed, and the clustering of stations compared to that seen in the dendrograms. SIMPER routines were then run to assess which taxa characterised the observed pattern of station groups within the dendrograms. Biotopes had been assigned during the original visual analysis of the video footage. SIMPER analyses were also undertaken to examine which fauna characterised each of the original designated biotopes, and whether these matched the biotope descriptions within the MNCR classification.

2.2.4 Biotope designation

Biotope designation of video and still image data followed the same procedure as for the benthic grab samples. The lack of PSA data for the video samples meant that sediment composition was based on estimates and descriptions made by the original analysts as recorded on the survey proformas. Biotopes for each video segment were assessed based on the SIMPER results from both the video and still image analyses.

2.3 Limitations

There were several limitations encountered during the course of this contract. Many limitations were particular to specific data sets, and have been discussed in more detail in the results section under the relevant surveys. Below is a summary list of the problems and potential limitations encountered during analysis:

- Transcription errors and typing mistakes in station identifiers.
- Fauna recorded as counts and present/absent within the same data matrix.
- Out-dated/no longer accepted species nomenclature according to WoRMS (2014) within data sets.
- Potential double counting of taxa under different taxonomic levels.
- Lack of faunal taxa within data sets to inform analyses.
- Identifications made to dubiously low taxonomic levels based solely on video and still images.
- Limited numbers of still images originally analysed from video segments.
- Taxa recorded at only at high taxonomic levels, resulting in data being dominated by relatively ubiquitous taxa (e.g. Serpulidae, Hydrozoa, Bryozoa *etc*.).

In general, limitations were more pronounced with the video and still data sets compared to the benthic grab sample data. Some of these limitations reflected the nature of the equipment employed. For example, faunal identifications can be more certain when material is collected by a grab compared to that seen in a still image or within video footage.

3 Results

The results of the community analysis of each data set are presented separately below, with benthic grab samples reported first, followed by the results of the video and still analyses.

3.1 North East of Farnes Deep MCZ – grab data

3.1.1 Data rationalisation

The raw faunal data matrix was rationalised according to the methodology. For this particular data set, fauna recorded as 'Present' were removed prior to analysis. These fauna were mainly a variety of encrusting bryozoans. Species records for juveniles were merged with their adult counterpart where appropriate, and the 'Enteropneusta (?)' taxon was also removed. The rationalised data were then imported into PRIMER for statistical analysis.

3.1.2 Univariate statistical analysis

The results from the species diversity analysis of the North-East of Farnes Deep MCZ grab data are given in Table 3.1. The total numbers of individuals present within the 46 sediment grab samples ranged from 19 individuals to 298 individuals per sample. The total number of taxa ranged from 16 to 68 per sample, indicating that there are some differences between the different locations. Across all stations, the mean number of species/taxa per station was 37 ± 1.83 (±1 SE), and the mean number of individuals was 92 ± 9.04 (±1 SE). The samples showed a relatively high degree of evenness, with all samples having a J' value of 0.82 or higher, except station 211 (evenness = 0.77). This indicated that the samples were not dominated by any particular taxa, with records for individuals spread evenly across the taxa present in each sample.

Table 3.1. Summary of infaunal community univariate statistics, North East of Farnes Deep MCZ grab data. Total number of individuals (N), number of species (S), Margalef's species richness (d), Pielou's equitability index (J'), Shannon-Wiener diversity index (H') and Simpson's Dominance Index.

Station	S	N	d	J'	H'(log_e)	Simpson's
166	49	143	9.67	0.85	3.32	0.95
168	42	99	8.92	0.90	3.38	0.96
169	68	274	11.94	0.89	3.76	0.97
170	25	49	6.17	0.91	2.92	0.95
172	46	105	9.67	0.90	3.46	0.96
173	34	75	7.64	0.91	3.21	0.96
174	45	93	9.71	0.93	3.53	0.97
176	17	36	4.47	0.92	2.60	0.93
179	50	138	9.95	0.87	3.39	0.95
180	47	130	9.45	0.89	3.44	0.96
181	45	155	8.72	0.82	3.13	0.93
183	40	104	8.40	0.87	3.21	0.94
184	53	145	10.45	0.84	3.35	0.95
185	68	298	11.76	0.82	3.46	0.95
187	53	186	9.95	0.82	3.24	0.93
190	47	203	8.66	0.85	3.27	0.95
191	29	62	6.78	0.91	3.05	0.95
193	16	19	5.09	0.97	2.70	0.98

Station	S	N	d	J'	H'(log_e)	Simpson's
194	32	64	7.45	0.92	3.20	0.96
196	42	96	8.98	0.92	3.43	0.96
197	41	73	9.32	0.93	3.45	0.97
198	25	41	6.46	0.92	2.97	0.95
200	49	156	9.51	0.87	3.38	0.95
202	35	60	8.30	0.94	3.35	0.97
204	54	156	10.50	0.86	3.45	0.95
208	27	42	6.96	0.95	3.12	0.97
209	28	49	6.94	0.94	3.13	0.97
210	22	38	5.77	0.94	2.91	0.96
211	43	141	8.49	0.77	2.89	0.87
212	32	54	7.77	0.96	3.31	0.97
213	45	86	9.88	0.90	3.42	0.95
214	31	69	7.09	0.88	3.02	0.94
215	35	97	7.43	0.83	2.96	0.91
216	31	60	7.33	0.94	3.22	0.97
217	42	66	9.79	0.94	3.53	0.98
218	32	74	7.20	0.87	3.02	0.94
219	22	38	5.77	0.93	2.87	0.95
220	24	44	6.08	0.92	2.91	0.95
222	21	35	5.63	0.89	2.70	0.92
223	25	43	6.38	0.95	3.07	0.97
224	28	46	7.05	0.92	3.06	0.95
225	33	51	8.14	0.96	3.37	0.98
226	25	34	6.81	0.96	3.10	0.98
227	53	113	11.00	0.93	3.71	0.98
229	30	54	7.27	0.95	3.25	0.97
230	33	59	7.85	0.95	3.32	0.97

3.1.3 Multivariate statistical analysis

A resemblance matrix using non-standardised, untransformed data was created using Bray Curtis similarity. A dendrogram was then plotted using this resemblance matrix. The raw data was then square root transformed, before a second resemblance matrix constructed, again using Bray Curtis similarity. The resulting dendrogram was plotted, and compared to the untransformed data. Both dendrograms showed similarities, with two large groupings of stations, and a third small group comprised of stations 169 and 190. The stations within each grouping remained consistent between the transformed and non-transformed data, with only one station (209) switching between the main two groups. There were some small changes within the sub-grouping structure between each dendrogram plot. The square root transformed data was chosen to lower the importance of the few taxa that were recorded in relatively high numbers compared to the rest of the data set. Appendix 7 shows the dendrogram plots for the North East of Farnes Deep MCZ grab data.

Figure 3.1 shows the dendrogram for the North East of Farnes Deep MCZ grab data split into cluster groups. The samples were split into three main groups, A, B and C. Samples within group A were separated from the remaining samples at ~39% similarity. Samples from group B were ~44% similar, and group C separated out at ~27% similarity. Station 209 was an outlier for group A (A*), whilst sample 193 was an outlier for group C (C*). No stations were more than 58% similar, suggesting discrete differences between the faunal communities identified from each sample. In order to examine the main clusters in more detail, group A was split into two sub-groups, A1 and A2, whilst group C was split into four sub-groups (C1 – C4).

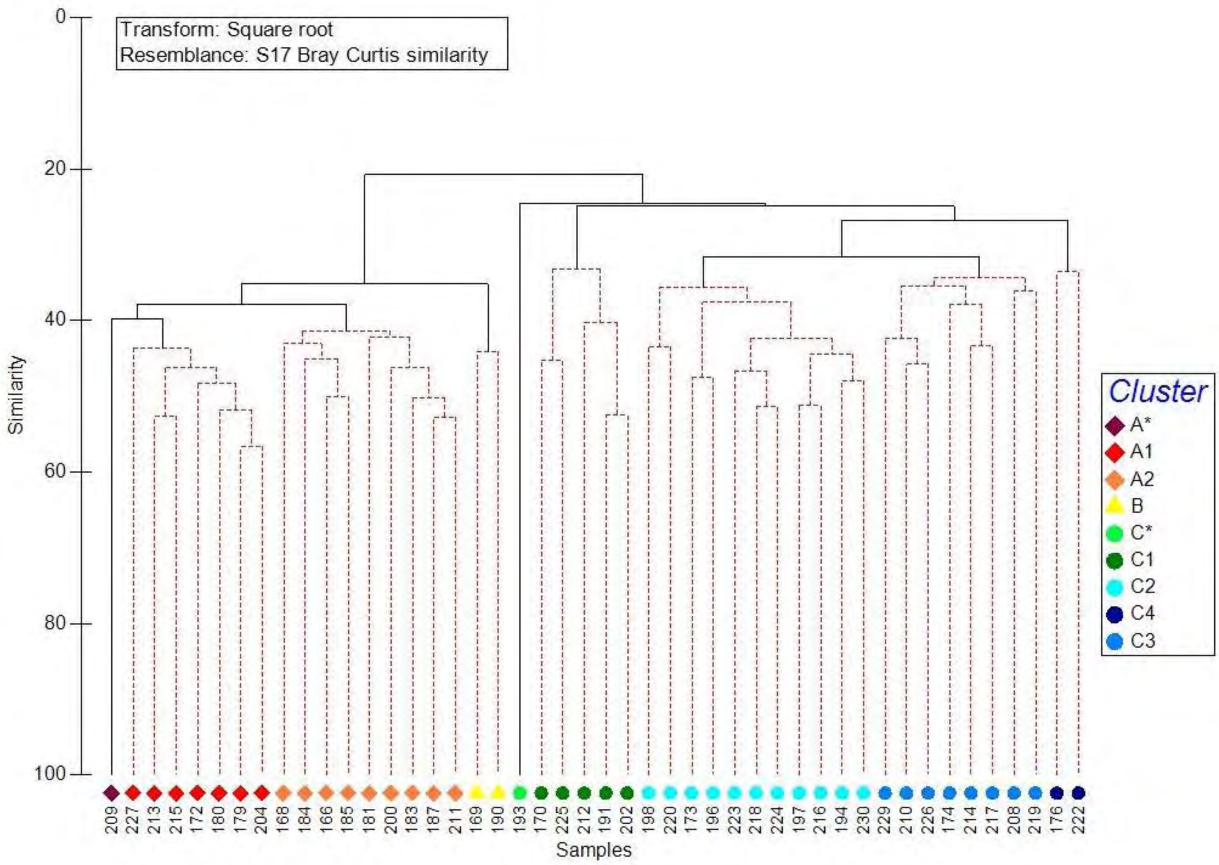


Figure 3.1. Dendrogram plot following cluster analysis of macrofaunal abundance counts, North East of Farnes Deep MCZ grab data. Samples coloured according to assigned cluster groups.

Figure 3.2 shows a 2D MDS ordination plot of the cluster analysis. The MDS plot largely supported the dendrogram, with sub-groups A1 and A2 separated away from sub-groups C1 – C4. Sub-group C4 appeared to be poorly supported. The MDS plot had a moderate stress value of 0.17.

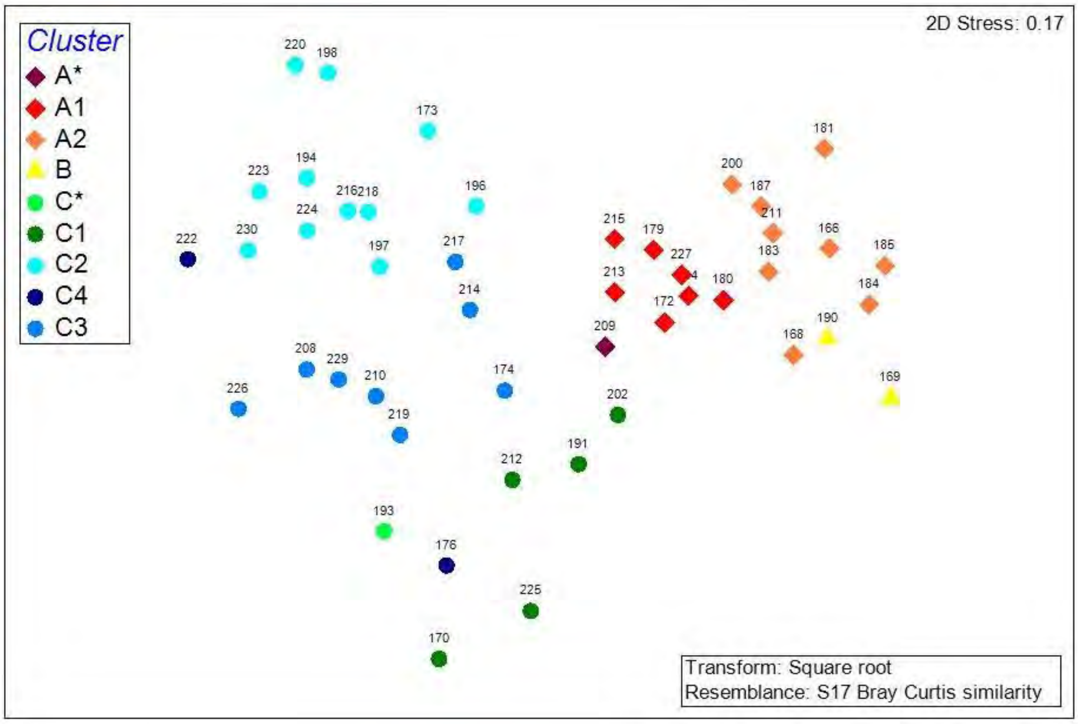


Figure 3.2. MDS ordination plot of North East of Farnes Deep MCZ grab data

Figure 3.3 shows the dendrogram with the EUNIS sediment classification derived from the PSA results for each sample displayed. Group A1 was characterised by mixed sediments, with groups A2 and B characterised by coarse and mixed sediments. All the sub-groups within group C were composed of a variety of mixed, coarse, and sand and muddy sand sediments. Examining the raw PSA data, samples from sub-groups A1, A2 and group B tended to have more significant gravel and sand fractions, whilst the sediment from sub-groups C1 – C4 tended to be dominated more by sand and mud fractions.

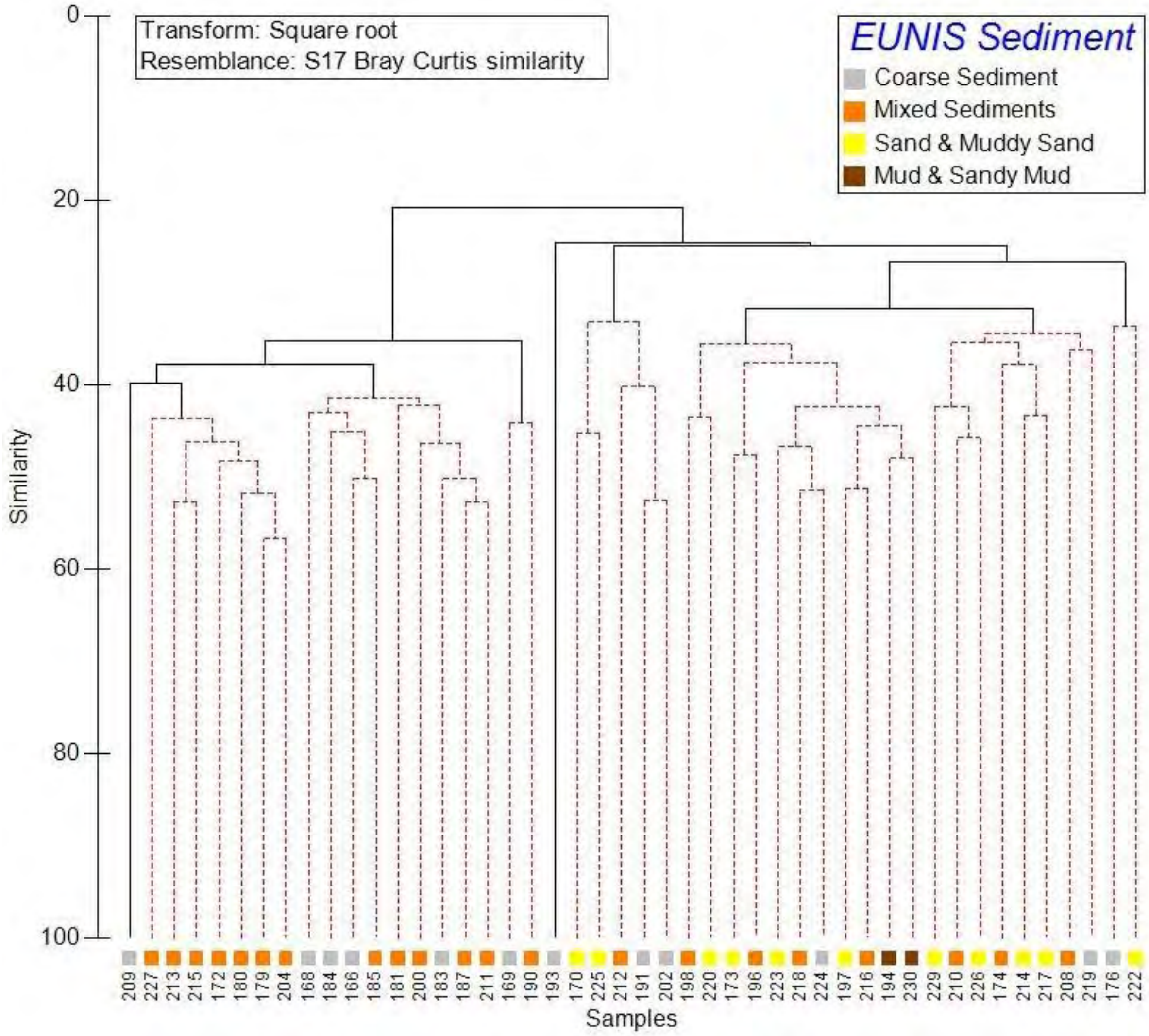


Figure 3.3. Dendrogram plot following cluster analysis of macrofaunal abundance counts, North East of Farnes Deep MCZ grab data. Samples coloured according to EUNIS sediment classification based on PSA data.

SIMPER analysis was undertaken to assess which species were characteristic for each of the sub-groups identified from the cluster analysis. Table 3.2 outlines the characteristic taxa for each sub-group, listing those taxa that contributed at least 70% similarity for each sub-group. Full SIMPER results showing all contributing species for each sub-group can be found in Appendix 7.

Groups A1 and A2 had many of the same characterising species, including *Leptochiton asellus*, *Paradoneis lyra*, *Galathowenia oculata*, *Echinocyamus pusillus*, *Hydroides norvegica* and Serpulidae polychaetes. The list of characterising fauna was predominantly composed of various polychaete species. However, the amount these species contributed to each sub-group varied. For example *Galathowenia oculata* contributed 9.5% to the similarity between samples in group A1, but only 2.95% in group A2. The data suggested that the faunal communities present in sub-groups A1 and A2 were relatively similar, and differences probably represented local patchiness in habitats rather than different environments.

Group B had some similar species to group A (e.g. *Leptochiton asellus, Verruca stroemia, Hydroides norvegica etc.*). Most notable were the relatively high contributions of *Chone* sp. (a sabellid polychaete), *Laonice bahusiensis* (a spionid polychaete) and *Phisidia aurea* (a terebellid polychaete) in group B, which were absent from the list of characterising fauna from groups A1 and A2. These differences probably reflect some environmental variance between samples from group B and group A, although the similarity between the other fauna meant that it was unlikely to represent an entirely different broadscale habitat.

Sub-groups C1 – C4 were also characterised by a pre-dominance of polychaetes, but also generally had more echinoderms and bivalve molluscs contributing to the similarity between stations than seen in groups A and B. Although sub-groups C1 – C4 showed some endemic fauna that were present across all the sub-groups, each sub-group had certain fauna that characterised it alone.

The fauna that characterised sub-group C1 was mostly similar to groups A and B, with many of the same characterising species listed for groups A and B such as *Galathowenia oculata*, *Echinocyamus pusillus*, and *Paradoneis lyra*. However, other taxa such as *Spiophanes bombyx, Aricidea cerrutii, Nephtys longosetosa* and *Ophelia borealis* were present only on the list of contributing species for sub-group C1. Some of these species are commonly found in coarse sandy sediments (e.g. *Ophelia borealis* and *Spiophanes bombyx*).

Sub-group C2 showed some large differences in the contributing species compared to groups A and B, with only *Galathowenia oculata, Owenia fusiformis* and nemerteans common between the groups. *Thyasira flexuosa, Trichobranchus roseus, Phoronis* sp. and *Diplocirrus glaucus* were characteristic of sub-group C2, along with amphiurid brittlestars and synaptid holothurians. The combination of fauna was suggestive of muddier sediments.

Sub-group C3 was characterised by a combination of fauna that were common in part to both sub-groups C2 and A1 - A2. Certain polychaete species, *Echinocyamus pusillus* and Nemertea present in C2 were similar to sub-groups A1 and A2, whilst the presence of bivalve molluscs and Amphiuridae were more similar to sub-group C2.

The list of contributing fauna to sub-group C4 contained bivalves, polychaetes, nemerteans and *Phoronis* sp., many of which were characteristic of sub-group C3. The samples within sub-group C4 appeared to be relatively faunally sparse compared to the other samples, and probably represented slightly impoverished versions of sub-group C3.

Examining the univariate statistics, samples within sub-groups A1 and A2 typically all had over 40 taxa identified and over 100 individuals counted. Group B showed similar numbers of taxa recorded, but over 200 individuals per sample. Samples from sub-groups C1 – C4 typically had over 20 taxa recorded, but the majority had less than 40 in total. Numbers of individuals in samples from sub-groups C1 – C4 were all less than 100.

Table 3.2. Results of SIMPER analysis of the sub-groups identified from cluster analysis of macrofaunal abundance counts, North East of Farnes Deeps MCZ grab data

Group / Cluster	% Contribution of characterising species	
	Taxa / species	**Contribution (%)**
A1	*Galathowenia oculata*	9.5
	Leptochiton asellus	6.93
	Paradoneis lyra	6.54
	Echinocyamus pusillus	5.84
	Hydroides norvegica	4.94
	Owenia fusiformis	4.63
	Scoloplos armiger	4.44
	Serpulidae	4.43
	Paramphinome jeffreysii	4.26
	Myriochele danielsseni	4.14
	SIPUNCULA	3.71
	Notomastus	3.55
	Spiophanes kroyeri	3.04
	Phoronis	2.53
	NEMERTEA	2.09
A2	*Hydroides norvegica*	9.63
	Leptochiton asellus	9.12
	Verruca stroemia	8.04
	Serpulidae	6.6
	Paradoneis lyra	5.3
	Echinocyamus pusillus	5.15
	SIPUNCULA	3.89
	Spiophanes kroyeri	3.53
	Tridonta montagui	3.44
	NEMERTEA	3.34
	Notomastus	3.12
	Galathowenia oculata	2.95
	Paramphinome jeffreysii	2.93
	Mediomastus fragilis	2.86
	Nucula nucleus	2
B	*Chone*	9.08
	Leptochiton asellus	7.94
	Phisidia aurea	6.61
	Echinocyamus pusillus	6.23
	Laonice bahusiensis	5.39
	Notomastus	5.39
	NEMERTEA	4.92
	Paramphinome jeffreysii	4.92
	Hydroides norvegica	4.92
	Eteone longa (agg)	4.4
	Glycera lapidum	4.4
	Mediomastus fragilis	3.11
	Verruca stroemia	3.11
	Atylus vedlomensis	3.11

Group / Cluster	% Contribution of characterising species	
	Taxa / species	Contribution (%)
C1	*Echinocyamus pusillus*	9.14
	NEMERTEA	8.42
	Notomastus	7.84
	Spiophanes bombyx	6.8
	Paradoneis lyra	6.31
	Ophelia borealis	5.87
	Nephtys longosetosa	4.2
	Aricidea cerrutii	4.11
	Galathowenia oculata	3.68
	Paramphinome jeffreysii	3.36
	Abra prismatica	3.02
	Edwardsiidae	2.42
	Owenia fusiformis	2.37
	Cerianthus lloydii	2.28
	Spiophanes kroyeri	2.2
C2	*Thyasira flexuosa*	8.19
	Galathowenia oculata	8.02
	Trichobranchus roseus	7.75
	Owenia fusiformis	7.59
	Phoronis	6.89
	NEMERTEA	5.76
	Diplocirrus glaucus	5.19
	Notomastus	3.84
	Amphiura filiformis	3.28
	Scoloplos armiger	2.76
	Labidoplax buskii	2.33
	Chaetoderma nitidulum	2.18
	Astrorhiza	2.15
	Terebellides stroemi	2.07
	Amphiuridae	1.95
	Arctica islandica	1.91
C3	*Notomastus*	9.18
	Scoloplos armiger	8.52
	Phoronis	8.42
	NEMERTEA	8.12
	Echinocyamus pusillus	7.56
	Owenia fusiformis	5.91
	Amphiuridae	4.99
	Chaetozone setosa	4.5
	Glycera alba	4.23
	Paradoneis lyra	4.2
	Anobothrus gracilis	4.09
	Diplocirrus glaucus	3.89
C4	*Arctica islandica*	21.26
	Owenia fusiformis	17.36
	NEMERTEA	12.28
	Paradoneis lyra	12.28
	Galathowenia oculata	12.28
	Tellimya ferruginosa	12.28
	Phoronis	12.28

3.1.4 Spatial distribution of samples

Figure 3.4 shows the spatial distribution of the sample sites within the survey area. Although there did not appear to be a particular pattern between the sub-groups, samples from groups A and B tended to be found in the south east of the survey area on predicted coarse sediments, whilst samples from group C were found more on predicted sand sediments.

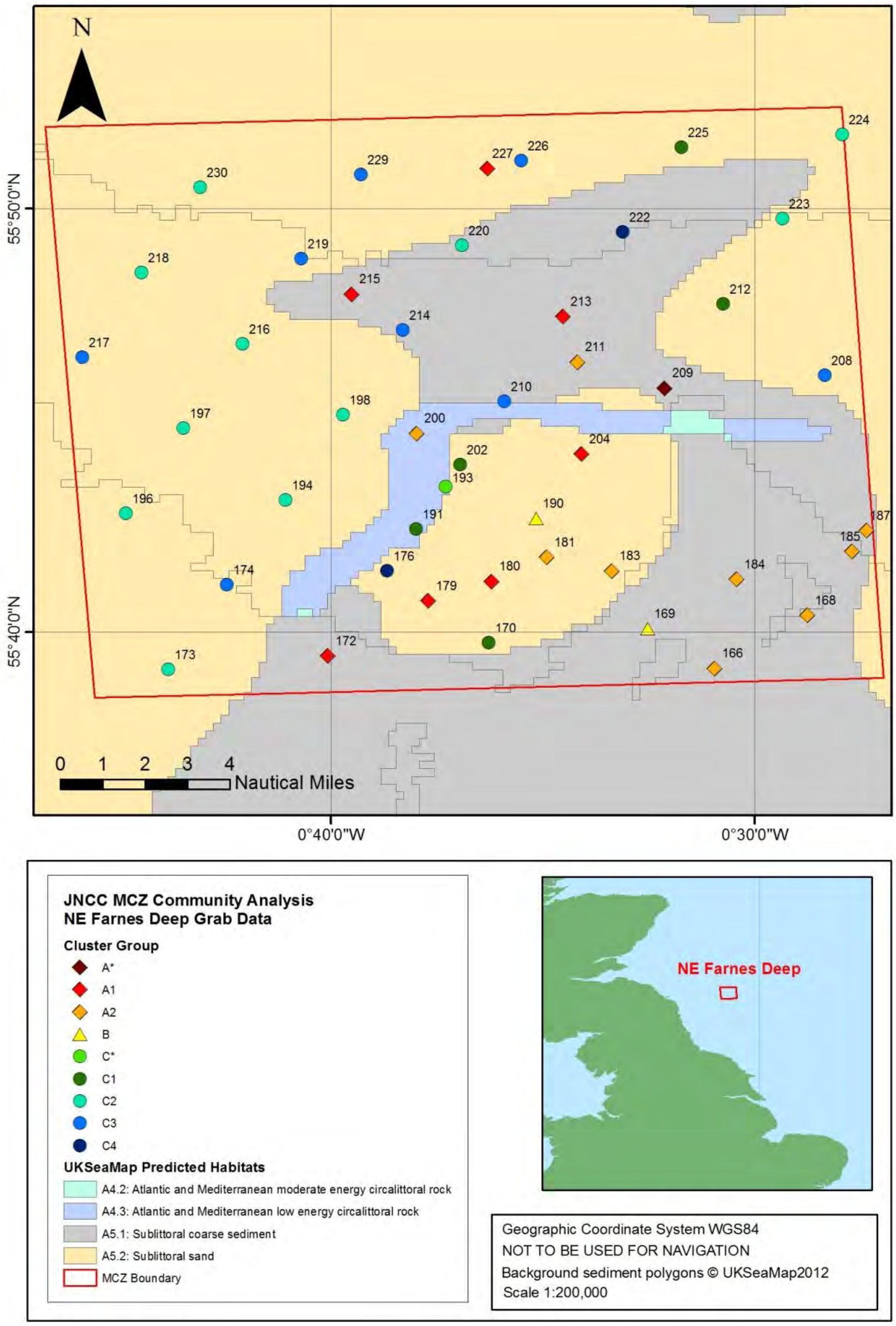


Figure 3.4. Geographical distribution of samples, North East of Farnes Deep grab data.

3.1.5 Biotope designation

The faunal communities that characterised sub-groups A1 and A2 were sufficiently similar to suggest that these samples probably represented the same habitat, with some small-scale variation due to localised patchiness. Examining the faunal matrices in more detail showed that a variety of polychaetes were common across these samples, including *Hydroides norvegica, Paramphinome jeffreysii, Galathowenia oculata, Paradoneis lyra, Mediomastus fragilis* and *Verruca stroemia.* Other common fauna within these samples included *Echinocyamus pusillus*, *Leptochiton asellus*, Nemertea and sipunculids. Many of these species appear on the list of characterising fauna for the **SS.SMx.OMx.PoVen** biotope, although were absent for the list of species within the biotope description. Some of the species present in the sample were more characteristic of shallower waters (e.g. *Galathowenia oculata*). The large number of species and individuals support the assignment of a mixed sediment biotope, as these tend to be more species rich and diverse.

The faunal community that characterised group B was largely similar to sub-groups A1 and A2. The slight differences between the faunal community present between group B and sub-groups A1 and A2 were not sufficient to justify separating these samples into a different biotope.

Sub-group C1 was characterised by species that closely resembled those listed within the description for the biotope **SS.SSa.CFiSa.EpusOborApri**, with *Ophelia borealis, Spiophanes bombyx, Aricidea cerrutii, Abra prismatica* and *Echinocyamus pusillus* all present within the samples.

The presence of the polychaetes *Owenia fusiformis* and *Diplocirrus glaucus,* the echinoderms *Amphiura filiformis* and *Labidoplax buskii* suggested a close relationship between the faunal communities present from samples in sub-group C2 and the biotope **SS.SSa.OSa.OfusAfil**. However, the presence of large numbers of *Thyasira flexuosa* together with some *Astrorhiza* foraminiferans, suggested some affinity with the biotope **SS.SMu.OMu.ForThy**. On balance, the majority of the faunal community within the samples was a better match for the **SS.SSa.OSa.OfusAfil** biotope, with the presence of the foraminifera perhaps suggesting a slightly higher level of silt in the habitat. The community that characterised sub-group C3 was similar to sub-group C2, with many of the fauna suggesting a match with the **SS.SSa.OSa.OfusAfil** biotope. However, some of the polychaete species present (e.g. *Scoloplos armiger* and *Chaetozone setosa*) were more representative of the biotope **SS.SSa.CFiSa.** The samples suggested a mosaic of both biotopes within this sub-group. The fauna within sub-groups C2 and C3 were sufficiently different from C1 to assign different biotopes.

The fauna that characterised sub-group C4 did not match any biotope in particular. The presence of *Galathowenia oculata, Owenia fusiformis* together with *Tellimya ferruginosa,* nemerteans and *Phoronis* suggested that the **SS.SMx.CMx** biotope was the best fit for this sub-group, rather than **SS.SSa.OSa** as indicated by the sediment data.

Of two outliers, sample 209 (A*) was largely similar to sub-group A1, so was classified as the biotope **SS.SMx.OMx.PoVen**. Sample 193 (C*) was the most faunally poor sample, with few species with which to match to biotope descriptions. This sample was assigned the biotope **SS.SCS.OCS** based on the sediment description and depth of the sample.

Table 3.3 summarises the biotopes designated to the North East of Farnes Deep MCZ grab data. A geographical spread of the assigned biotopes is displayed in Figure 3.5. There appeared to be some correlation between sand biotopes and UK SeaMap predicted sandy sediments (McBreen *et al* 2011), and mixed biotopes and coarse sediments.

Table 3.3. Summary of biotopes assigned to faunal abundance counts from North East of Farnes Deep MCZ grab data.

Biotope	Description	Cluster Groups	Samples	Depth Range
A5.15 : Deep circalittoral coarse sediment **SS.SCS.OCS**	**Uncertain match**. Biotope based solely on sample depth and sediment classification	C*	193	73m
A5.251 : *Echinocyamus pusillus, Ophelia borealis* and *Abra prismatica* in circalittoral fine sand **SS.SSa.CFiSa.EpusOborApri**	Characteristic fauna included *Ophelia borealis, Spiophanes bombyx, Aricidea cerrutii, Abra prismatica* and *Echinocyamus pusillus.* Substratum from stations included sand and muddy sand, mixed sediments and coarse sediments. Potential depth mismatch	C1	170, 191, 202, 212, 225	70 – 74m
A5.272 : *Owenia fusiformis* and *Amphiura filiformis* in deep circalittoral sand or muddy sand **SS.SSa.OSa.OfusAfil**	**Uncertain match.** Characteristic fauna included polychaetes *Owenia fusiformis* and *Diplocirrus glaucus,* the echinoderms *Amphiura filiformis* and *Labidoplax buskii,* and the bivalve *Thyasira flexuosa.* Substratum for stations included coarse sediment, sand and muddy sand, mixed sediments and mud and muddy sand	C2	173, 194, 196, 197, 198, 216, 218, 220, 223, 224, 230	75 – 90m
A5.272 : *Owenia fusiformis* and *Amphiura filiformis* in deep circalittoral sand or muddy sand / A5.25 : Circalittoral fine sand **SS.SSa.OSa.OfusAfil / SS.SSa.CFiSa**	**Uncertain match.** Some species characteristic of **OfusAfil** included *Owenia fusiformis, Diplocirrus glaucus* and Amphiuridae, whilst polychaetes *Scoloplos armiger* and *Chaetozone setosa* characteristic of **CFiSa.** Substratum from stations included sand and muddy sand, mixed sediments and coarse sediments	C3	174, 208, 210, 214, 217, 219, 226, 229	69 – 87m
A5.44 : Circalittoral mixed sediments **SS.SMx.CMx**	**Uncertain match.** Characteristic fauna included *Galathowenia oculata* and *Owenia fusiformis* together with *Tellimya ferruginosa,* nemerteans and *Phoronis.* Substratum included sand and muddy sand, and coarse sediments. Potential depth mismatch	C4	176, 222	75 – 78m
A5.451 : Polychaete-rich deep *Venus* community in offshore mixed sediments **SS.SMx.OMx.PoVen**	**Uncertain match**. Characteristic fauna included *Hydroides norvegica, Paramphinome jeffreysii, Galathowenia oculata, Paradoneis lyra, Mediomastus fragilis* and *Verruca stroemia.* Other common fauna within these samples included *Echinocyamus pusillus*, *Leptochiton asellus*, Nemertea and sipunculids. Substratum included mixed and coarse sediments	A*; A1, A2 and B	209, 172, 179, 180, 204, 213, 215, 227, 166, 168, 181, 183, 184, 185, 187, 211, 169, 190	61 – 74m

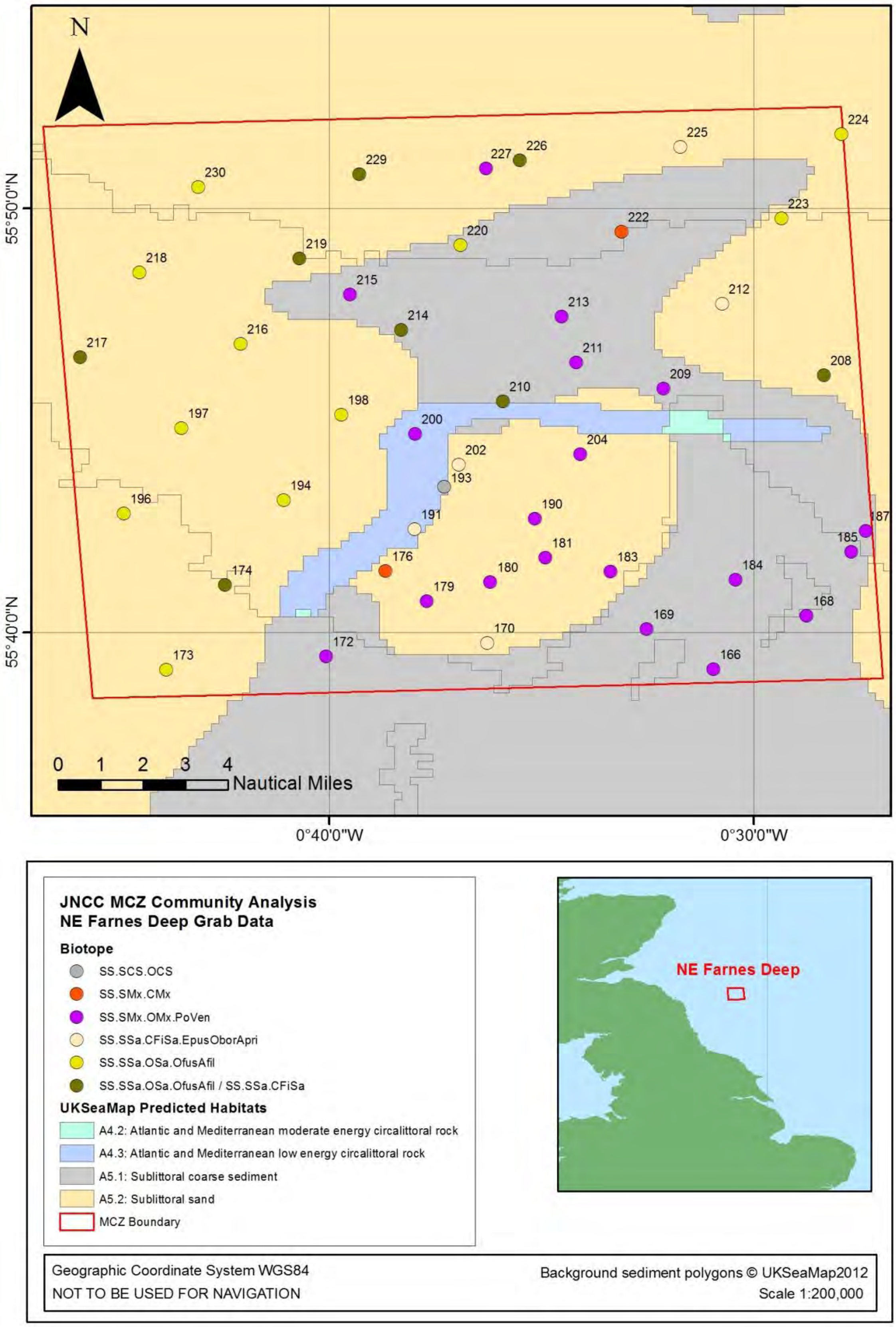


Figure 3.5. Geographical distribution of biotopes assigned to North East of Farnes Deep grab data following multivariate analysis.

3.2 East of Haig Fras MCZ – grab data

3.2.1 Data rationalisation

The raw faunal data matrix was rationalised according to the methodology. For this particular data set, fauna recorded simply as 'Present' were removed prior to analysis. These fauna mainly represented fragments of individuals, the majority of which were only identified to family level, and some hydroids. Species recorded as juvenile were merged with adults where appropriate. Some pelagic taxa (Copepoda, Chaetognatha and Ostracoda) were removed, as was the meiofaunal Nematoda. The rationalised data were then imported into PRIMER for statistical analysis.

3.2.2 Univariate statistical analysis

Table 3.4 summarises the results of the species diversity analysis of the East of Haig Fras MCZ grab data. The total numbers of individuals present within the 48 sediment grab samples ranged from 15 individuals to 162 individuals per sample. The total number of taxa ranged from 8 to 49 per sample, indicating that there are some differences between the different locations. Across all stations, the mean number of species/taxa per station was 26 ± 1.51 (±1 SE), and the mean number of individuals was 51 ± 4.22 (±1 SE). The samples showed a relatively high degree of evenness, with all samples having a J' value of 0.77, indicating that the samples were not dominated by any particular taxa, with records of individuals spread evenly across the taxa present in each sample.

Table 3.4. Summary of infaunal community univariate statistics, East of Haig Fras MCZ grab data. Total number of individuals (N), number of species (S), Margalef's species richness (d), Pielou's equitability index (J'), Shannon-Wiener diversity index (H') and Simpson's Dominance Index.

Station	S	N	d	J'	H'(log_e)	Simpson's
350	13	16	4.33	0.97	2.48	0.97
353	17	41	4.31	0.77	2.18	0.83
355	18	36	4.74	0.90	2.59	0.92
357	30	72	6.78	0.89	3.02	0.94
360	28	48	6.98	0.93	3.10	0.96
362	19	29	5.35	0.95	2.79	0.96
364	34	62	8.00	0.94	3.30	0.97
367	42	66	9.79	0.95	3.56	0.98
369	46	129	9.26	0.82	3.14	0.92
371	33	52	8.10	0.94	3.27	0.97
373	17	20	5.34	0.97	2.76	0.98
376	16	20	5.01	0.96	2.65	0.96
378	40	83	8.83	0.93	3.44	0.97
380	16	41	4.04	0.82	2.28	0.87
381	26	43	6.65	0.93	3.03	0.96
384	15	23	4.47	0.92	2.49	0.93
386	33	66	7.64	0.92	3.23	0.96
388	26	33	7.15	0.98	3.19	0.98
391	9	16	2.89	0.79	1.73	0.77
396	25	43	6.38	0.91	2.91	0.94

Station	S	N	d	J'	H'(log_e)	Simpson's
398	12	18	3.81	0.89	2.22	0.90
400	28	45	7.09	0.95	3.17	0.97
402	8	15	2.59	0.82	1.71	0.79
405	35	56	8.45	0.96	3.40	0.98
407	12	26	3.38	0.79	1.95	0.79
410	36	59	8.58	0.95	3.41	0.98
412	34	73	7.69	0.90	3.16	0.95
415	16	29	4.46	0.92	2.56	0.94
417	23	51	5.60	0.86	2.69	0.91
420	18	31	4.95	0.91	2.63	0.94
422	18	26	5.22	0.97	2.81	0.97
425	28	54	6.77	0.88	2.93	0.93
427	49	162	9.44	0.86	3.35	0.95
430	42	73	9.56	0.96	3.58	0.98
433	26	50	6.39	0.89	2.92	0.94
436	18	34	4.82	0.89	2.57	0.92
438	30	71	6.80	0.89	3.04	0.95
441	19	27	5.46	0.96	2.81	0.97
443	40	76	9.01	0.95	3.51	0.98
446	29	70	6.59	0.94	3.16	0.96
448	31	53	7.56	0.91	3.13	0.95
451	30	65	6.95	0.93	3.15	0.96
453	46	104	9.69	0.92	3.53	0.97
458	17	33	4.58	0.90	2.56	0.93
461	35	83	7.69	0.86	3.06	0.93
463	15	24	4.41	0.94	2.53	0.94
466	24	63	5.55	0.89	2.83	0.94
468	25	42	6.42	0.96	3.09	0.97

3.2.3 Multivariate statistical analysis

The highest abundance of any single taxa within a sample was 29 individuals, so it was not deemed appropriate to apply any transformation to the rationalised data. A resemblance matrix using non-standardised, untransformed data was created using Bray Curtis similarity. Cluster analysis was then performed, and the resulting dendrogram plotted (Figure 3.6).

The dendrogram showed that overall the similarity of the faunal communities between samples was relatively low, with all stations at least less than 60% similar to their closest neighbour. The dendrogram showed a small cluster of outliers composed of four stations (sub-groups A1 and A2) splitting off from the other stations at ~20% similarity. Station 373 (B*) was an outlier of a large cluster of stations that were subdivided into 3 groups (B – D), which were then split into further sub-groups.

Group B split away from groups C and D at around ~22% similarity. Group B was split into sub-groups B1 and B2 (each containing three stations) which had ~30% similarity. Group C split from group D at ~27% similarity, and was sub-divided into two sub-groups (C1 and C2). Sub-groups C1 and C2 split at ~ 30% similarity and both consisted of five stations.

Group D contained three sub-groups (D1 – D3), consisting of three, six and six stations respectively. Group E split from the other stations at ~20% similarity. Group E contained a sub-group of outliers (E2), composed of three stations that separated out from the rest of the group at ~22%. Station 388 (E*) was an outlier from sub-group E1, splitting off at ~27% similarity. Sub-group E1 contained eight stations.

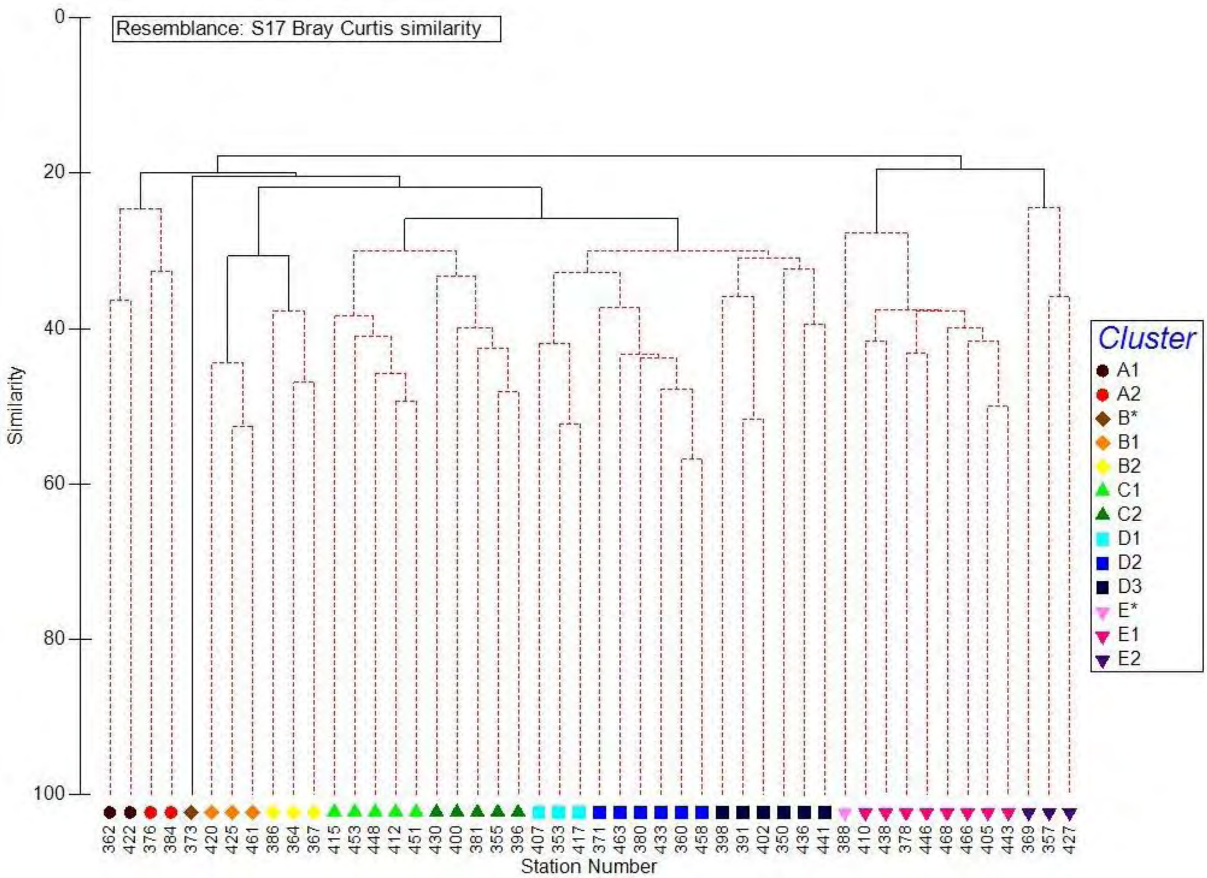


Figure 3.6. Dendrogram plot following cluster analysis of macrofaunal abundance counts, East of Haig Fras MCZ grab data. Stations coloured according to assigned cluster groups.

Figure 3.7 shows a 2D MDS ordination plot of the cluster analysis. The stress value of 0.22 suggests that not too much reliance should be placed on the detail of the plot. The MDS plot showed the separation of groups B and E, but the separation between groups C and D were less well defined.

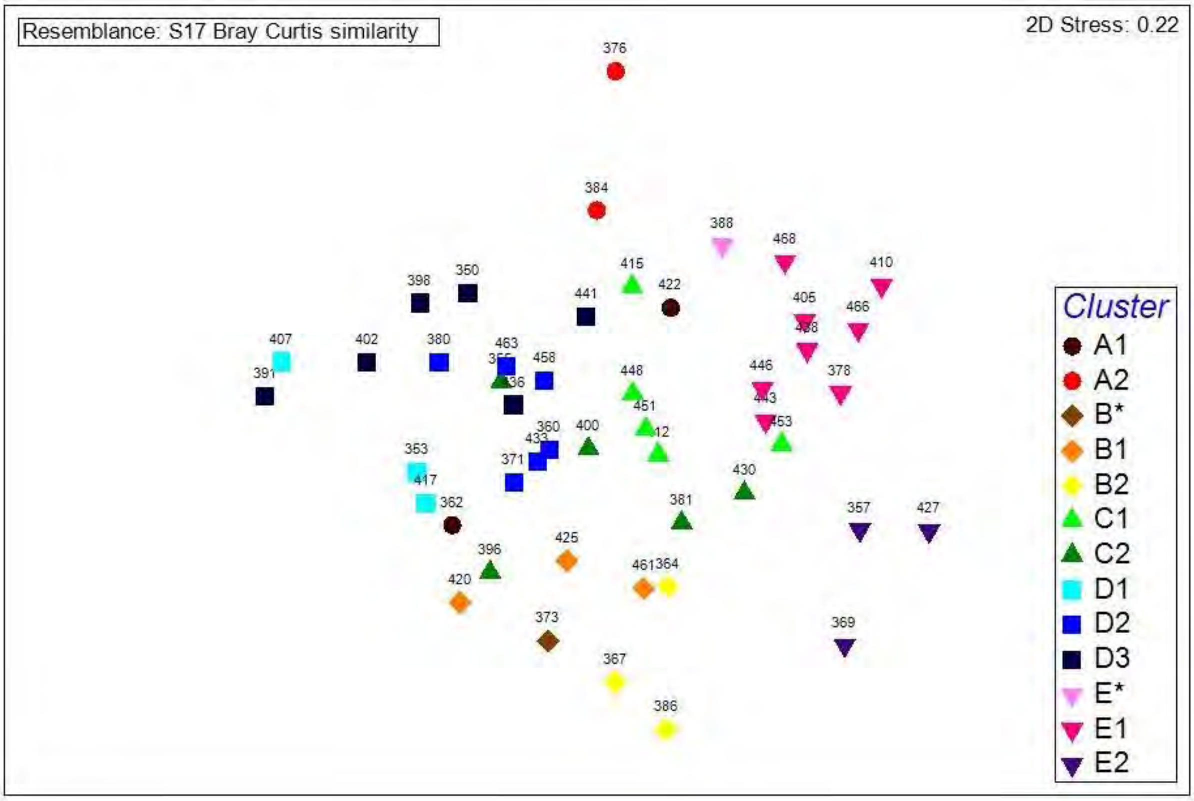


Figure 3.7. MDS ordination plot of East of Haig Fras MCZ grab data.

Figure 3.8 shows the dendrogram with the EUNIS sediment classification derived from the PSA results for each sample displayed. There appeared to be some patterns in the station groupings that were supported by the sediment data. For example, sub-group E2 was all mixed sediments, whilst E1 was all sand and muddy sand or mud and sandy mud. Group D was mainly sand and muddy sand, with the sub-groups containing occasional stations of either mixed or coarse sediments. Group C contained stations classified as mainly mixed or coarse sediments. The sub-groups B1 and B2 contained stations with different sediment classifications.

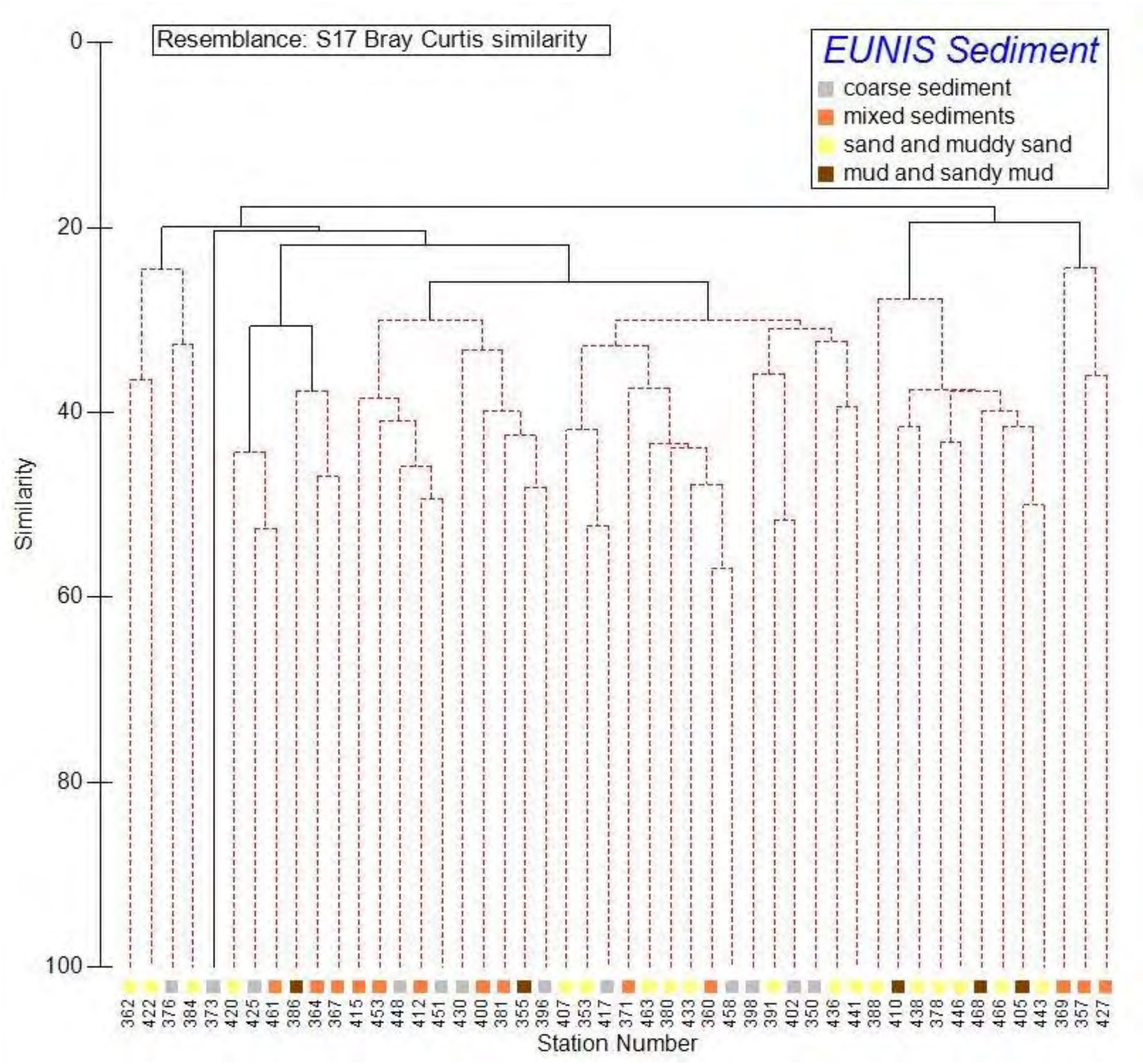


Figure 3.8. Dendrogram plot following cluster analysis of macrofaunal abundance counts, East of Haig Fras MCZ grab data. Stations coloured according to EUNIS sediment classification based on PSA data.

SIMPER analysis was undertaken to assess which species were characteristic for each of the sub-groups identified from the cluster analysis. Table 3.5 outlines the characteristic taxa for each sub-group, listing those taxa that contributed at least 90% similarity for each sub-group. Full SIMPER results showing all contributing species for each sub-group can be found in Appendix 8.

Sub-group A1 was characterised by Nemertea, polychaetes including *Aponuphis bilineata, Lumbrineris cingulata, Laonice bahusiensis, Spiophanes bombyx, Notomastus latericeus* and *Galathowenia oculata*, and phoronids. Two of the polychaete species were also characteristic of sub-group A2 (*Lumbrineris cingulata* and *Laonice bahusiensis*), which was also characterised by *Ampharete falcate* and *Echinocyamus pusillus*. Sub-group A1 had slightly higher species diversity than sub-group A2.

Sub-groups B1 and B2 had some similar characteristic species such as *Aponuphis bilineata, Galathowenia oculata, Spiophanes kroyeri* and nemerteans. Stations within sub-group B2 had a higher species diversity compared to those within B1. The presence of *Ophelia borealis* as a characteristic species for B1 indicated an element of sand within the sediment, whilst the presence of *Lumbrineris cingulata, Notomastus latericeus, Mediomastus fragilis* characterising B2 suggested a coarser or mixed sedimentary environment.

Juvenile Ophiuroidea, *Galathowenia oculata, Aspidosiphon muelleri, Echinocyamus pusillus,* and *Lumbrineris cingulata* were all present on the characterising fauna lists for sub-groups C1 and C2. *Amphiura filiformis* and *Urothoe elegans* were both characteristic of sub-group C1, whereas juvenile Nephtyidae, *Owenia fusiformis, Aonides paucibranchiata* and *Lucinoma borealis* were all characteristic of sub-group C2.

The characterising species *Echinocyamus pusillus* and *Galathowenia oculata* were common across sub-groups D1 – D3. The grouping of the stations within these clusters was mainly driven by the high occurrence of *Echinocyamus pusillus* in all the samples. Sub-groups D2 and D3 also had characterising species such as juvenile Ophiuroidea, *Amphiura filiformis* and nemerteans in common. Stations within sub-group D2 had higher species diversity than those from sub-groups D1 and D3.

Sub-groups E1 and E2 had several characterising species of polychaetes that were absent from the SIMPER analysis of the other sub-groups. These included *Amphictene auricoma*, *Magelona minuta* and *Euclymene* (Type A). Important contributing species in sub-group E1 that did not characterise E2 included *Amphiura filiformis*, *Urothoe elegans* and *Diplocirrus glaucus*. Species that contributed highly to E2 but did not characterise E1 included *Owenia fusiformis* and *Spiophanes kroyeri*.

The SIMPER analysis identified some taxa that appeared to be relatively ubiquitous across all clusters, such as Nemertea, *Galathowenia oculata* and *Echinocyamus pusillus*. However, the relative abundance of these taxa within each sample appeared to be important to some of the clustering structure (e.g. sub-groups D1 – D3 had the highest counts of *E. pusillus*). The relative species diversity also appeared to play a role in the structuring of the sub-groups, as discussed above. Most stations had relatively few taxa with more than one individual recorded. The presence of many species on several sub-groups' lists of characteristic fauna suggested that there may not have been large scale differences between many of the stations. The different faunal communities probably represented small scale patchiness or slightly differences in proportions of mud, sand and gravel fractions within the sediment.

Table 3.5. Results of SIMPER analysis of the sub-groups identified from cluster analysis of macrofaunal abundance counts, East of Haig Fras MCZ grab data.

Group / Cluster	% Contribution of characterising species	
	Taxa / species	**Contribution (%)**
A1	NEMERTEA	20.00
	Aponuphis bilineata	10.00
	Lumbrineris cingulata	10.00
	Laonice bahusiensis	10.00
	Spiophanes bombyx	10.00
	Notomastus latericeus	10.00
	Galathowenia oculata	10.00
	Phoronis	10.00
A2	*Lumbrineris cingulata*	57.14
	Laonice bahusiensis	14.29
	Ampharete falcata	14.29
	Echinocyamus pusillus	14.29
B1	*Aponuphis bilineata*	27.81
	Galathowenia oculata	22.83
	Echinocyamus pusillus	11.83
	NEMERTEA	4.98
	Glycera (juv)	3.94
	Ophelia borealis	3.94
	Paramphitrite birulai	3.94
	ECHINOIDEA (juv)	3.94
	Spiophanes kroyeri	3.1
	Goniadidae (juv)	2.49
	Cirrophorus branchiatus	1.24
B2	Goniadidae (juv)	12.67
	NEMERTEA	11.4
	Aponuphis bilineata	8.88
	Polycirrus	7.64
	Spiophanes kroyeri	7.6
	Galathowenia oculata	7.6
	Edwardsiidae	3.8
	Aspidosiphon muelleri	3.8
	Lumbrineris cingulata	3.8
	Aonides paucibranchiata	3.8
	Mediomastus fragilis	3.8
	Grania	3.8
	Echinocyamus pusillus	3.8
	Eulalia mustela	2.56
	Notomastus latericeus	2.56
	Chaetozone setosa	2.48
	Aglaophamus rubella	1.28

Group / Cluster	% Contribution of characterising species	
	Taxa / species	**Contribution (%)**
C1	OPHIUROIDEA (juv)	22.28
	Echinocyamus pusillus	12.17
	Galathowenia oculata	10.49
	Amphiura filiformis	7.71
	Lumbrineris cingulata	7.16
	Urothoe elegans	6.37
	Aspidosiphon muelleri	5.06
	Spiophanes kroyeri	4.89
	Pseudonotomastus southerni	3.92
	NEMERTEA	2.69
	Antalis entalis	2.37
	Terebellides stroemi	2.28
	Chaetozone zetlandica	1.83
	Astrorhiza	1.44
C2	*Aspidosiphon muelleri*	30.37
	Echinocyamus pusillus	11.65
	NEMERTEA	10.59
	Galathowenia oculata	8.52
	Lumbrineris cingulata	5.78
	OPHIUROIDEA (juv)	4.84
	Chaetozone zetlandica	3.91
	Nephtyidae (juv)	3.12
	Owenia fusiformis	2.24
	Aonides paucibranchiata	1.92
	Glycera lapidum	1.78
	Lucinoma borealis	1.56
	Minuspio cirrifera	1.5
	Cirrophorus branchiatus	1.48
	Clymenura	1.48
D1	*Echinocyamus pusillus*	70.08
	Galathowenia oculata	8
	Chaetozone zetlandica	5.71
	Aponuphis bilineata	3.2
	Nephtyidae (juv)	2.2
	Ditrupa arietina	2.2
D2	*Echinocyamus pusillus*	33.45
	Lumbrineris cingulata	21.66
	OPHIUROIDEA (juv)	8.09
	Galathowenia oculata	7.31
	Spiophanes kroyeri	4.17
	NEMERTEA	4.06
	Glycera oxycephala	4.03
	Sthenelais limicola	3.99
	Amphiura filiformis	2.06
	Hyalinoecia tubicola	1.15
	Unciola planipes	1.15

Group / Cluster	% Contribution of characterising species	
	Taxa / species	**Contribution (%)**
D3	*Echinocyamus pusillus*	66.08
	NEMERTEA	7.79
	OPHIUROIDEA (juv)	7.46
	Amphiura filiformis	3.14
	Galathowenia oculata	2.97
	Pista cristata	2.36
	Polycirrus	1.58
E1	OPHIUROIDEA (juv)	10.55
	Euclymene (Type A)	9.98
	Urothoe elegans	9.84
	Amphiura filiformis	9.83
	NEMERTEA	6.57
	Diplocirrus glaucus	5.98
	Terebellides stroemi	4.61
	Astrorhiza	3.84
	Thyasira flexuosa	3.62
	Galathowenia oculata	3.2
	Spiophanes kroyeri	3.12
	Ampharete falcata	2.9
	Amphictene auricoma	2.84
	Magelona minuta	2.72
	Clymenura	2.19
	Praxillella affinis	2.14
	Echinocyamus pusillus	2.12
	Abra (juv)	1.42
	Lumbrineris cingulata	0.89
	Streblosoma intestinalis	0.86
	Westwoodilla caecula	0.85
E2	*Magelona minuta*	15.14
	Lumbrineris cingulata	13.61
	Owenia fusiformis	10.16
	Spiophanes kroyeri	7.06
	Aspidosiphon muelleri	7
	NEMERTEA	5.99
	Notomastus latericeus	4.62
	TURBELLARIA	4.01
	Cirrophorus branchiatus	3.81
	Peresiella clymenoides	3.81
	Phoronis	3.03
	Ampharete falcata	3
	Amphictene auricoma	2.02
	Goniada maculata	1.62
	Minuspio cirrifera	1.62
	Euclymene (Type A)	1.62
	Abyssoninoe hibernica	1.18
	Galathowenia oculata	1.18

3.2.4 Spatial distribution of samples

Figure 3.9 shows the spatial distribution of the sample sites within the East of Haig Fras survey area, colour coded according to their cluster groups. The geographical distribution did not show any particular pattern to the spatial spread of the cluster groups, suggesting patchiness in the survey area rather than distinct boundaries between habitat types.

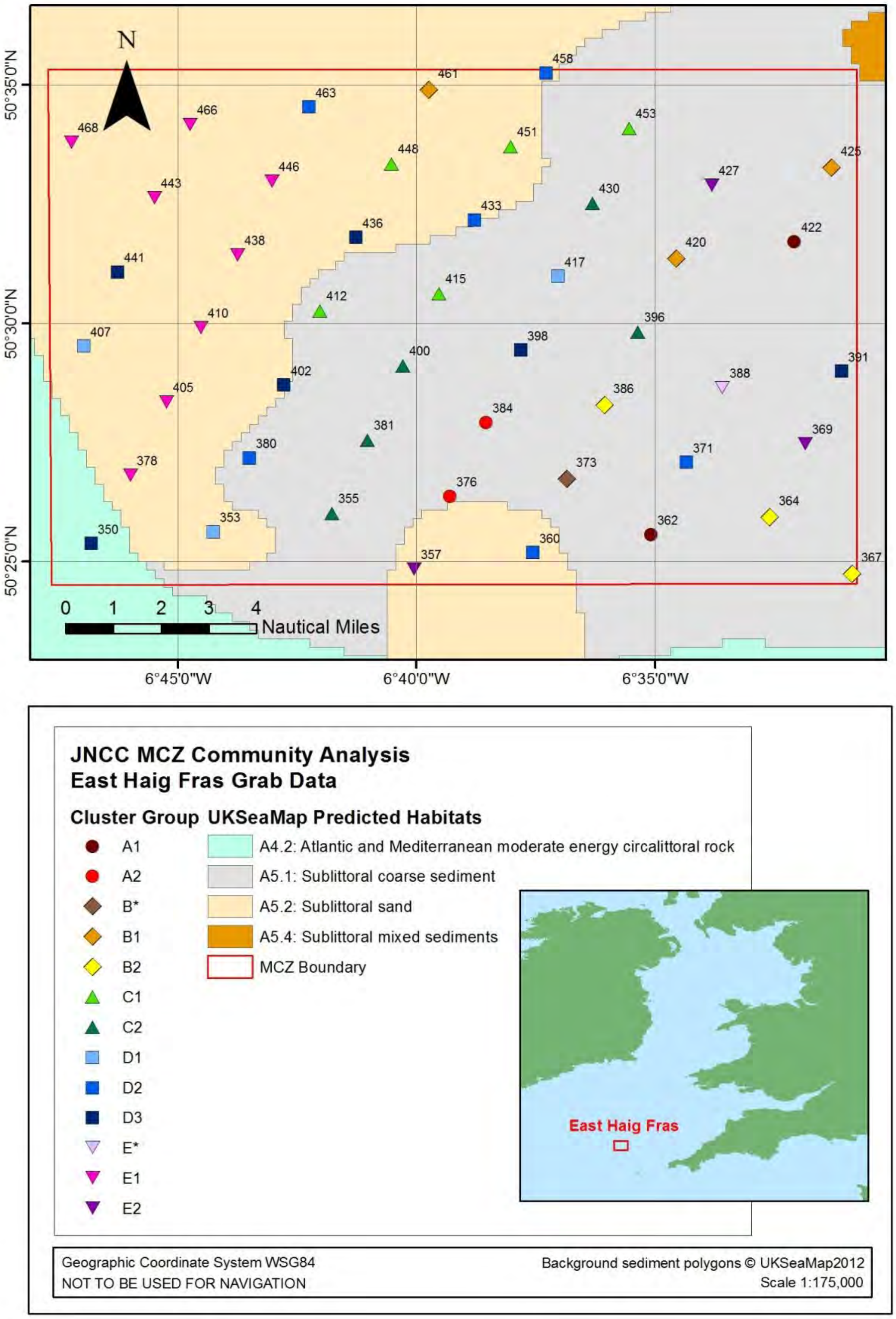


Figure 3.9. Geographical distribution of samples, East of Haig Fras grab data.

3.2.5 Biotope designation

A summary of the biotopes assigned to the East of Haig Fras grab data can be found in Table 3.6. The assignment of each biotope is described in more detail below.

The fauna present within sub-groups A1 and A2 were suggestive of coarse sand habitats, which were supported by the EUNIS sediments classification for these stations. Sub-group A2 appeared to be a slightly more impoverished version of sub-group A1. The fauna from these stations such as *Laonice bahusiensis*, *Lumbrineris cingulata,* and *Echinocyamus pusillus* are commonly found together within **SS.SCS.CCS** biotopes. The relatively sparse fauna identified from these stations, plus the depth of samples, meant that the most appropriate biotope was **SS.SCS.OCS**.

Sub-group B1 contained characteristic species such as *Echinocyamus pusillus, Ophelia borealis* and glycerid polychaetes typical of the biotope **SS.SSa.CFiSa.EpusOborApri**. Although not designated as a characteristic species via the SIMPER analysis, *Abra prismatica* was also identified in the samples from these stations. However, the presence of *Galathowenia oculata* and terebellid polychaetes was more indicative of a higher mud fraction within the sediment than suggested by the biotope description. Therefore sub-group B1 was classified as **SS.SSa.CFiSa.EpusOborApri** / **SS.SMx.OMx** to reflect the mix of fauna and the depth (~100m) of the samples.

The characteristic species for sub-group B2 included a large variety of polychaetes, such as *Spiophanes kroyeri, Galathowenia oculata, Lumbrineris cingulata, Mediomastus fragilis, Notomastus latericeus,* juvenile Goniadidae and *Chaetozone setosa*. These species occur together in lists of fauna characteristic of most mixed sediment biotopes. *Aspidosiphon muelleri* lives on discarded gastropod shells, indicating shell fragments must have been present within the habitat. Considering the depth of the stations (~100m) and some of the component polychaete species, the closest matching biotope would be **SS.SMx.OMx.PoVen**. However, the bivalve element of the biotope was not evident within the data, so the biotope **SS.SMx.OMx.(PoVen)** was assigned instead.

Sub-group C1 was characterised by the species *Galathowenia oculata, Amphiura filiformis, Lumbrineris cingulata,* and juvenile Ophiuroidea, which suggested either sandy mud or mixed sediment biotope. *Urothoe elegans* and *Echinocyamus pusillus* suggested an importance of sand, whilst *Terebellides stroemi* and *Astrorhiza* foraminifera were more indicative of mud. The list of characteristic species bore some resemblance to that of the **SS.SMu.CSaMu.ThyNten** biotope, although lacking many of the diagnostic species for this habitat. The numbers of most identified fauna aside from Ophiuroidea were relatively low, so it was deemed appropriate to assign a biotope at level 3. Due to the station depths (~100m) sub-group C1 was assigned the biotope **SS.SMu.OMu**, although the habitat also contained some shell material over the soft sediment indicated by the presence of *Aspidosiphon muelleri.*

The characteristic fauna from sub-group C2 was largely similar to C1, although lacking *Amphiura filiformis* and *Urothoe elegans.* Characteristic species such as *Lucinoma borealis* and *Owenia fusiformis* present in C2 are also found within sandy mud habitats. *Kurtiella bidentata* and *Thyasira* spp. were identified from some of the stations within this sub-group. Again, the presence of a degree of shell material was indicated by *Aspidosiphon muelleri.* The community within sub-group C2 was largely similar to C1, suggesting that the slight variations in the fauna identified between the sub-groups probably represented some patchiness within the same broadscale habitat. Therefore sub-group C2 was also assigned the biotope **SS.SMu.OMu.**

The most important species contributing to sub-group D1 was *Echinocyamus pusillus*, followed by *Galathowenia oculata*. The other species identified only occurred in low numbers. *Echinocyamus pusillus* generally indicates sandy sediments, whilst *Galathowenia* suggests mixed or muddy sediments. The majority of stations within this sub-group were classified as sand and muddy sand according EUNIS broadscale sediment categories, which agreed with the two main characteristic fauna. The depth of the stations was again ~100m, so the biotope **SS.SSa.OSa** was assigned. The habitat is probably better defined as muddy sand.

Sub-groups D2 and D3 also had *Echinocyamus pusillus* as the dominant characterising taxa. The presence of species such as *Amphiura filiformis* and *Spiophanes kroyeri* suggested similarities with the biotope **SS.SSa.OSa.OfusAfil**, although some diagnostic fauna from this biotope were absent (e.g. *Owenia fusiformis*). Again some species such as *Galathowenia oculata* indicated an element of mud within the habitat. The best fit biotope for both these sub-groups was **SS.SSa.OSa**, with the habitat better described as muddy sand.

Sub-groups E1 and E2 were characterised by combinations of species that are commonly found together in mixed sediments biotopes (e.g. *Galathowenia oculata, Owenia fusiformis, Amphiura filiformis,* and *Terebellides stroemi*). However, some species such as *Ampharete, Magelona, Thyasira* and *Diplocirrus glaucus* are more common in sandy mud biotopes. None of the species present within sub-group E1 suggested a component of gravel within the sediment, so a sandy mud habitat is probably more likely for this cluster. This was slightly reflected in the EUNIS sediments classifications for this cluster being either sand and muddy sand or mud and muddy sand. The best fit biotope was **SS.SMu.OMu,** reflecting the depth (~100m), and probably represented sandy mud.

Higher abundances of *Lumbrineris*, *Minuspio cirrifera, Aspidosiphon* and *Notomastus* in sub-group E2 compared to E1 suggest that there may have been a more important gravel fraction to the sediment, supported by the EUNIS classification of mixed sediments. Like sub-group B2, many of the polychaete species within the community can be found within the biotope **SS.SMx.OMx.PoVen**, but as per B2, many of the diagnostic species were not present. High numbers of *Magelona* suggest an important sandy mud component to the habitat. The biotope **SS.SMu.OMu / SS.SMx.OMx** was assigned to sub-group E2 to reflect the presence of *Magelona* combined with the variety of other polychaetes and the sediment data.

The outlying station 388 (E*) possessed many similar fauna to sub-group E1, so was assigned the biotope **SS.SMu.OMu**. Station 373 (B*) was relatively faunally sparse, so the biotope **SS.SCS.OCS** was designated according the depth of the station (103m) and the EUNIS sediment classification (coarse sediment).

As mentioned in the section on SIMPER analysis, many of the characteristic species occurred across a range of biotopes. The similarities between many of the fauna suggested that the assigned biotopes may overstate the differences between the stations. The faunal community across the survey area was largely composed of some ubiquitous species, with patchiness or slight variations in the sediment composition indicated by certain species (e.g. *Ophelia borealis* and sand; *Aspidosiphon muelleri* and shell). The **SS.SMu.OMu** biotopes would probably be better described as sandy mud, whilst the **SS.SSa.OSa** biotopes would be muddy sand.

A geographical spread of the assigned biotopes is displayed in Figure 3.10. The spread of the biotopes showed that the survey area appeared to be relatively patchy, possibly with areas of coarse sediment and shell gravel overlying soft sediment, and areas where greater proportions of fine sediment have aggregated. No patterns could be discerned between the UKSeaMap predicted sediments (McBreen *et al* 2011) and the assigned biotopes.

Table 3.6. Summary of biotopes assigned to faunal abundance counts from East of Haig Fras MCZ grab data.

Biotope	Description	Cluster Groups	Station No.	Depth Range
A5.15 : Deep circalittoral coarse sediment **SS.SCS.OCS**	**Uncertain match**. Characteristic fauna included *Laonice bahusiensis*, *Lumbrineris cingulata,* and *Echinocyamus pusillus.* Biotope assignment also based on sample depth and sediment classification	A1, A2, B*	362, 422, 376, 384, 373	98 – 103m
A5.251 : *Echinocyamus pusillus, Ophelia borealis* and *Abra prismatica* in circalittoral fine sand / A5.45 : Deep circalittoral mixed sediments **SS.SSa.CFiSa.EpusOborApri / SS.SMx.OMx**	**Uncertain match.** Characteristic fauna included *Echinocyamus pusillus, Ophelia borealis,* glycerids and *Abra prismatica*. Also present were *Galathowenia oculata* and terebellid polychaetes. Substratum from stations included mixed sediments, coarse sediments and sand and muddy sand	B1	420, 425,461	99 – 102m
A5.272 : Deep circalittoral sand **SS.SSa.OSa**	**Uncertain match.** Muddy sand sediments, characterised by *Echinocyamus pusillus, Galathowenia oculata, Amphiura filiformis* and *Spiophanes kroyeri.* Substratum included mixed sediment, coarse sediment, and sand and muddy sand	D1, D2, D3	353, 407, 417, 360, 371, 380, 433, 458, 463, 350, 391, 398, 402, 436, 441	99 – 102m
A5.37 : Deep circalittoral mud **SS.SMu.OMu**	**Uncertain match.** Sandy mud with shell fragments as indicated by the presence of *Aspidosiphon muelleri.* Common fauna included *Galathowenia oculata, Owenia fusiformis, Amphiura filiformis, Thyasira,* juvenile ophiuroids and *Terebellides stroemi*, but some variation between stations to the exact fauna present. Substratum included mixed sediment, coarse sediment, sand and muddy sand, and mud and sandy mud	C1, C2, E1	415, 453, 448, 412, 451, 430, 400, 381, 355, 399, 410, 438, 378, 446, 468, 466, 405, 443	98 – 103m
A5.37 : Deep circalittoral mud / A5.45 Deep circalittoral mixed sediments **SS.SMu.OMu / SS.SMx.OMx**	**Uncertain match.** Characteristic fauna included *Lumbrineris cingulata*, *Minuspio cirrifera, Aspidosiphon muelleri* and *Notomastus latericeus*, with high abundances of *Magelona*. Substratum included mixed sediments	E2	357, 369, 427	101 – 102m
A5.451 : Polychaete-rich deep *Venus* community in offshore mixed sediments **SS.SMx.OMx.(PoVen)**	**Uncertain match**. Characteristic fauna included a large variety of polychaetes, such as *Spiophanes kroyeri, Galathowenia oculata, Lumbrineris cingulata, Mediomastus fragilis, Notomastus latericeus,* juvenile Goniadidae and *Chaetozone setosa*. Substratum included mixed sediment and mud and sandy mud	B2	364, 367, 386	99 – 102m

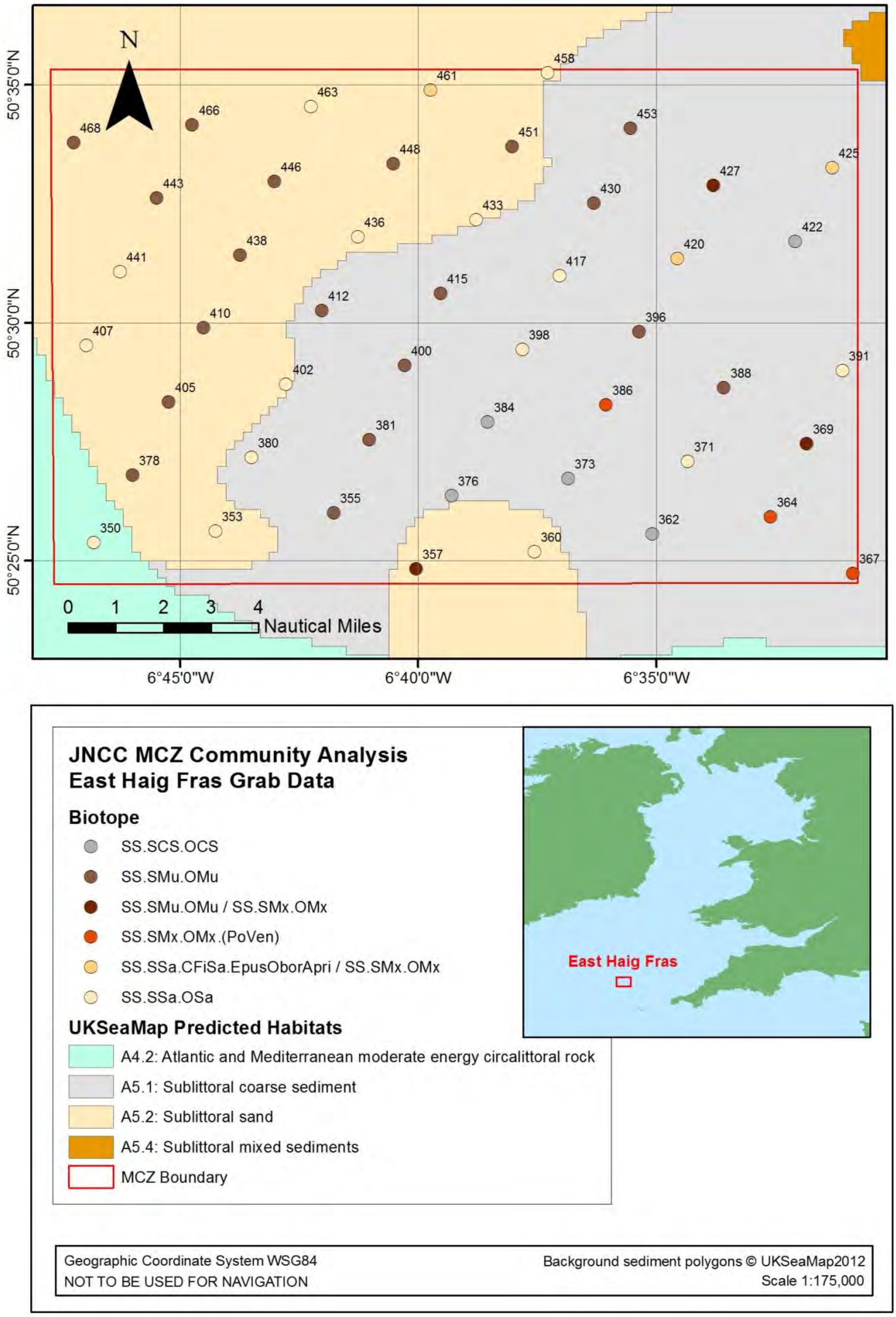


Figure 3.10. Geographical distribution of biotopes assigned to East of Haig Fras grab data following multivariate analysis.

3.3 South-West Deeps (West) MCZ – grab data

3.3.1 Data rationalisation

The raw faunal data matrix was rationalised according to the methodology. For this particular data set, faunal recorded as 'Present' were removed prior to analysis. These taxa mainly represented encrusting bryozoans, hydroids and fragments of individuals not sufficiently intact to count. Any taxa marked as 'dead' ('d' qualifier) within the matrix were excluded. Species recorded as juvenile were merged with adults where appropriate. Pelagic taxa (Copepoda and Chaetognatha) were removed, as were the meiofaunal Nematoda and parasitic copepods. The identification of *Mesacmaea mitchellii* was uncertain ('?' qualifier), so it was merged with Actiniaria at a higher taxonomic level. After rationalisation, station 41 had no taxa present, so was removed to avoid skewing any data analyses. The rationalised data were then imported into PRIMER for statistical analysis.

3.3.2 Univariate statistical analysis

Table 3.7 summarises the results of the species diversity analysis of the South-West Deeps (West) MCZ grab data. After rationalisation, station 41 had no fauna left (only one taxon recorded as present within the species matrix). Excluding station 41, the total numbers of individuals present within the 206 sediment grab samples ranged from 4 individuals to 201 individuals per sample. The total number of taxa ranged from 4 to 56 per sample, indicating that there were some differences between the various locations. Across all stations, the mean number of species/taxa per station was 19 ± 0.68 (±1 SE), and the mean number of individuals was 45 ± 2.24 (±1 SE). There was a large range in evenness across the samples, with J' values measured between 0.31 – 1.00. This suggested that some stations were dominated by an abundance of certain species, whilst at other stations the number of individuals was evenly spread across all taxa identified.

Table 3.7. Summary of infaunal community univariate statistics, South-West Deeps (West) MCZ grab data. Total number of individuals (N), number of species (S), Margalef's species richness (d), Pielou's equitability index (J'), Shannon-Wiener diversity index (H') and Simpson's Dominance Index.

Station	S	N	d	J'	H'($\log_e$)	Simpson's
1	7	7	3.08	1.00	1.95	1.00
2	12	15	4.06	0.96	2.40	0.96
3	4	4	2.16	1.00	1.39	1.00
5	6	10	2.17	0.95	1.70	0.89
7	12	17	3.88	0.92	2.28	0.92
8	12	15	4.06	0.98	2.43	0.97
9	13	16	4.33	0.95	2.43	0.95
10	10	16	3.25	0.90	2.08	0.90
12	18	26	5.22	0.95	2.74	0.96
13	29	37	7.75	0.98	3.30	0.99
16	23	36	6.14	0.95	2.99	0.97
17	20	54	4.76	0.82	2.44	0.86
20	26	42	6.69	0.96	3.12	0.97
22	13	24	3.78	0.95	2.44	0.94
23	23	93	4.85	0.53	1.67	0.57
24	16	29	4.46	0.89	2.47	0.91
26	5	7	2.06	0.92	1.48	0.86

Station	S	N	d	J'	H'(log_e)	Simpson's
27	8	11	2.92	0.95	1.97	0.93
29	18	25	5.28	0.94	2.73	0.96
30	11	17	3.53	0.92	2.20	0.91
32	15	29	4.16	0.87	2.36	0.90
33	12	22	3.56	0.91	2.26	0.91
35	10	15	3.32	0.95	2.18	0.93
36	13	17	4.24	0.95	2.45	0.96
38	12	15	4.06	0.96	2.40	0.96
39	11	17	3.53	0.93	2.23	0.93
41[4]	0	0	-	-	0.00	-
42	10	48	2.33	0.53	1.23	0.50
43	7	47	1.56	0.31	0.61	0.24
45	24	44	6.08	0.94	2.98	0.96
46	23	53	5.54	0.68	2.12	0.72
48	23	87	4.93	0.56	1.75	0.61
49	23	42	5.89	0.86	2.69	0.91
50	16	29	4.46	0.95	2.63	0.95
52	15	32	4.04	0.71	1.92	0.72
53	11	61	2.43	0.64	1.53	0.68
55	19	27	5.46	0.97	2.85	0.97
56	15	36	3.91	0.73	1.97	0.75
57	16	26	4.60	0.92	2.56	0.94
59	26	38	6.87	0.94	3.06	0.96
60	22	41	5.66	0.91	2.81	0.94
61	24	43	6.12	0.97	3.07	0.97
62	50	110	10.42	0.88	3.46	0.95
64	31	61	7.30	0.93	3.21	0.97
65	14	42	3.48	0.64	1.70	0.67
66	30	102	6.27	0.56	1.92	0.65
69	17	53	4.03	0.82	2.31	0.86
70	23	138	4.47	0.43	1.36	0.50
72	39	115	8.01	0.80	2.95	0.90
74	20	36	5.30	0.94	2.82	0.95
75	37	74	8.36	0.90	3.24	0.96
76	45	201	8.30	0.80	3.03	0.92
78	23	42	5.89	0.94	2.93	0.96
79	27	56	6.46	0.88	2.90	0.93
80	21	39	5.46	0.94	2.85	0.95
81	23	37	6.09	0.96	3.02	0.97
83	14	23	4.15	0.95	2.51	0.95
84	15	21	4.60	0.97	2.62	0.97
86	29	84	6.32	0.88	2.95	0.93
87	47	90	10.22	0.91	3.51	0.97
88	12	68	2.61	0.60	1.48	0.62

[4] Station 41 had no fauna remaining after rationalisation.

Station	S	N	d	J’	H'(log_e)	Simpson's
90	24	89	5.12	0.65	2.08	0.72
91	20	33	5.43	0.92	2.77	0.95
92	14	19	4.42	0.95	2.51	0.95
94	22	189	4.01	0.41	1.25	0.50
95	46	92	9.95	0.89	3.39	0.96
96	16	17	5.29	0.99	2.75	0.99
98	22	37	5.82	0.94	2.91	0.96
99	13	20	4.01	0.95	2.43	0.95
100	20	25	5.90	0.96	2.89	0.97
101	26	57	6.18	0.88	2.87	0.93
103	34	74	7.67	0.89	3.15	0.95
104	44	112	9.11	0.87	3.31	0.95
105	20	30	5.59	0.92	2.75	0.94
107	33	56	7.95	0.93	3.25	0.97
108	21	27	6.07	0.98	2.97	0.98
109	20	44	5.02	0.87	2.62	0.92
110	34	61	8.03	0.93	3.28	0.97
112	29	51	7.12	0.95	3.19	0.97
113	16	44	3.96	0.70	1.94	0.73
114	20	26	5.83	0.98	2.94	0.98
115	7	8	2.89	0.98	1.91	0.96
116	21	45	5.25	0.87	2.66	0.92
117	47	128	9.48	0.87	3.34	0.95
118	17	38	4.40	0.89	2.52	0.92
119	33	123	6.65	0.70	2.44	0.81
120	46	129	9.26	0.81	3.12	0.91
121	21	74	4.65	0.65	1.98	0.70
123	17	53	4.03	0.68	1.93	0.72
124	14	93	2.87	0.42	1.11	0.44
125	15	24	4.41	0.90	2.44	0.91
126	36	74	8.13	0.90	3.23	0.95
128	14	23	4.15	0.90	2.38	0.92
129	11	23	3.19	0.87	2.09	0.87
136	5	9	1.82	0.91	1.47	0.83
137	11	16	3.61	0.94	2.25	0.93
138	12	22	3.56	0.91	2.26	0.91
140	23	40	5.96	0.94	2.94	0.96
141	14	21	4.27	0.94	2.49	0.95
142	40	66	9.31	0.93	3.43	0.97
143	16	24	4.72	0.96	2.66	0.96
144	10	26	2.76	0.72	1.66	0.71
145	15	34	3.97	0.87	2.34	0.89
146	23	43	5.85	0.78	2.46	0.83
147	22	33	6.01	0.94	2.90	0.96
148	17	44	4.23	0.73	2.08	0.77
150	7	15	2.22	0.83	1.62	0.78

Station	S	N	d	J’	H'(log$_e$)	Simpson's
151	19	38	4.95	0.77	2.26	0.80
153	10	33	2.57	0.59	1.35	0.56
154	18	36	4.74	0.86	2.49	0.89
155	6	12	2.01	0.75	1.35	0.68
156	17	48	4.13	0.69	1.95	0.72
157	14	65	3.11	0.57	1.50	0.62
158	21	34	5.67	0.95	2.88	0.96
160	11	18	3.46	0.86	2.06	0.86
161	4	11	1.25	0.64	0.89	0.49
162	18	33	4.86	0.86	2.47	0.88
163	9	38	2.20	0.69	1.52	0.70
164	13	35	3.38	0.67	1.73	0.68
166	22	39	5.73	0.87	2.69	0.91
167	9	13	3.12	0.92	2.03	0.91
168	15	16	5.05	0.99	2.69	0.99
169	6	18	1.73	0.75	1.35	0.70
170	15	21	4.60	0.98	2.65	0.97
171	8	14	2.65	0.88	1.83	0.86
172	12	18	3.81	0.95	2.37	0.95
173	17	32	4.62	0.91	2.57	0.93
174	22	38	5.77	0.91	2.82	0.95
176	18	35	4.78	0.88	2.54	0.91
177	21	33	5.72	0.84	2.55	0.87
179	18	38	4.67	0.87	2.52	0.90
180	12	48	2.84	0.68	1.68	0.73
181	19	52	4.56	0.71	2.09	0.78
182	17	43	4.25	0.71	2.01	0.74
183	11	15	3.69	0.96	2.30	0.95
185	11	21	3.29	0.92	2.22	0.91
186	15	26	4.30	0.92	2.48	0.93
187	31	69	7.09	0.86	2.97	0.93
188	21	60	4.89	0.64	1.94	0.68
190	15	26	4.30	0.88	2.38	0.90
191	13	62	2.91	0.60	1.55	0.62
192	11	58	2.46	0.45	1.07	0.42
193	11	31	2.91	0.71	1.70	0.70
195	11	23	3.19	0.78	1.87	0.77
196	26	48	6.46	0.93	3.05	0.96
197	29	45	7.36	0.95	3.19	0.97
199	12	24	3.46	0.85	2.12	0.87
200	10	15	3.32	0.90	2.08	0.90
201	15	21	4.60	0.98	2.65	0.97
203	12	18	3.81	0.95	2.35	0.94
205	16	30	4.41	0.88	2.44	0.91
206	11	22	3.24	0.80	1.92	0.80
208	6	7	2.57	0.98	1.75	0.95

Station	S	N	d	J’	H'(log_e)	Simpson's
209	9	20	2.67	0.83	1.82	0.82
210	21	88	4.47	0.58	1.78	0.66
212	22	75	4.86	0.58	1.81	0.62
213	7	37	1.66	0.45	0.88	0.39
214	8	28	2.10	0.55	1.14	0.49
215	19	45	4.73	0.76	2.24	0.80
216	9	28	2.40	0.62	1.36	0.59
217	43	107	8.99	0.89	3.34	0.96
218	5	14	1.52	0.86	1.38	0.76
220	10	26	2.76	0.69	1.59	0.67
221	20	52	4.81	0.77	2.30	0.82
222	22	54	5.26	0.84	2.59	0.91
224	12	54	2.76	0.50	1.26	0.50
225	27	100	5.65	0.60	1.97	0.67
227	19	59	4.41	0.74	2.18	0.81
228	10	14	3.41	0.97	2.24	0.96
229	15	33	4.00	0.89	2.40	0.90
230	11	20	3.34	0.91	2.18	0.91
232	17	55	3.99	0.58	1.64	0.60
233	11	111	2.12	0.36	0.85	0.33
235	13	39	3.28	0.78	2.00	0.82
236	20	35	5.34	0.90	2.71	0.93
237	22	48	5.43	0.92	2.85	0.95
238	19	42	4.82	0.90	2.64	0.92
239	33	74	7.44	0.91	3.18	0.96
241	38	81	8.42	0.91	3.32	0.96
242	28	60	6.59	0.91	3.03	0.94
243	36	96	7.67	0.84	3.02	0.93
245	18	61	4.14	0.74	2.14	0.81
246	56	121	11.47	0.89	3.58	0.96
247	20	33	5.43	0.91	2.72	0.93
248	30	123	6.03	0.63	2.16	0.73
250	20	98	4.14	0.58	1.74	0.69
251	9	22	2.59	0.86	1.89	0.85
253	19	30	5.29	0.92	2.71	0.94
254	18	34	4.82	0.84	2.42	0.88
255	16	25	4.66	0.96	2.66	0.96
256	21	58	4.93	0.84	2.57	0.89
258	21	27	6.07	0.98	2.97	0.98
259	44	106	9.22	0.88	3.34	0.95
261	21	45	5.25	0.74	2.25	0.78
262	27	53	6.55	0.92	3.03	0.96
264	24	40	6.24	0.85	2.70	0.89
265	39	82	8.62	0.87	3.20	0.94
266	37	64	8.66	0.95	3.42	0.97
269	11	17	3.53	0.94	2.26	0.93

Station	S	N	d	J'	H'(log_e)	Simpson's
270	9	23	2.55	0.82	1.80	0.82
362	18	35	4.78	0.92	2.66	0.94
364	24	40	6.24	0.91	2.91	0.95
366	20	31	5.53	0.94	2.83	0.96
368	17	27	4.86	0.94	2.67	0.95
370	17	87	3.58	0.58	1.65	0.62
374	33	88	7.15	0.89	3.11	0.95
376	21	49	5.14	0.83	2.52	0.87

3.3.3 Multivariate statistical analysis

Only three taxa were recorded in abundances greater than 40 individuals per sample, so it was not deemed appropriate to use any transformations on the data set. A resemblance matrix using non-standardised, untransformed data was created using Bray Curtis similarity. Cluster analysis was then performed, and the resulting dendrogram plotted. Assessment of SIMPER analysis of the clusters defined by this first plot showed that the high abundances of two taxa, juvenile Spatangoida and Ophiuridae, masked the majority of the patterns underlying the faunal communities. Since these two taxa have a seasonal component, it was deemed appropriate to remove them from the data set, and re-run the cluster analysis. Details of the original dendrogram and SIMPER analysis can be found in Appendix 9. Due to the number of stations, the data was split into three sections. Each section was examined in turn to examine the structure of the clusters in more detail (Figure 3.11).

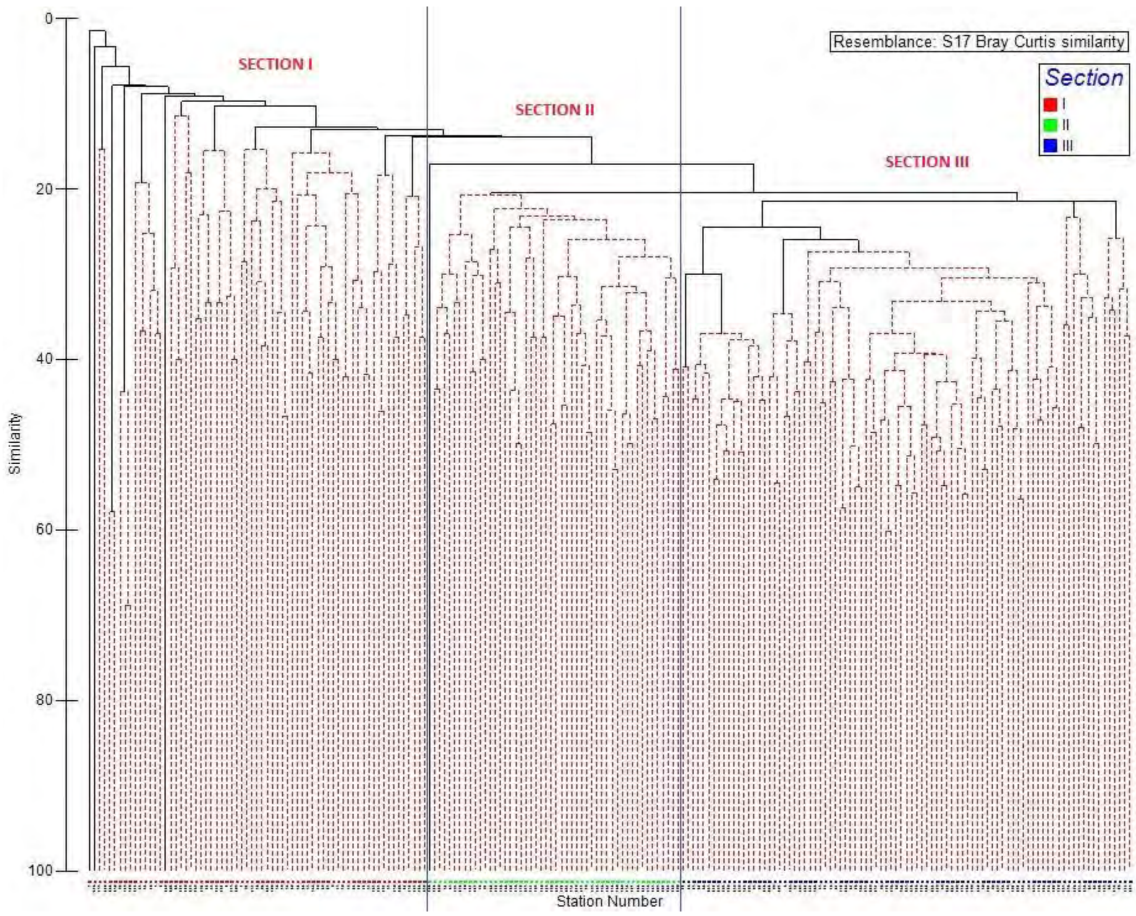


Figure 3.11. Dendrogram plot following cluster analysis of macrofaunal abundance counts, South-West Deeps (West) MCZ grab data. Plot shows the division of clusters into different sections – see Figures 3.12 – 3.14 for more detail of each section.

The samples split into Section I can be seen in Figure 3.12. Section I included 67 stations that were ~13% similar or less to the stations within Section II. There were four main clusters within Section I that were then split into smaller sub-groups. These 67 stations included two outliers from the whole data set, stations 218 and 3 (O*). Sub-groups A1 and A2 separated at ~4% similarity, with sub-group A1 splitting from A2 at ~5% similarity. At ~6% similarity sub-groups B1 and B2 branched off, with B1 separating at ~8% similarity from B2. Station 269 was an outlier (C*) of group C. Sub-group C1 split away at ~8% similarity, whilst sub-groups C2 and C3 both branched off at ~10% similarity into two distinctly separate clusters. Group D was divided into two sub-groups (D1 and D2) that branched away at ~14% similarity.

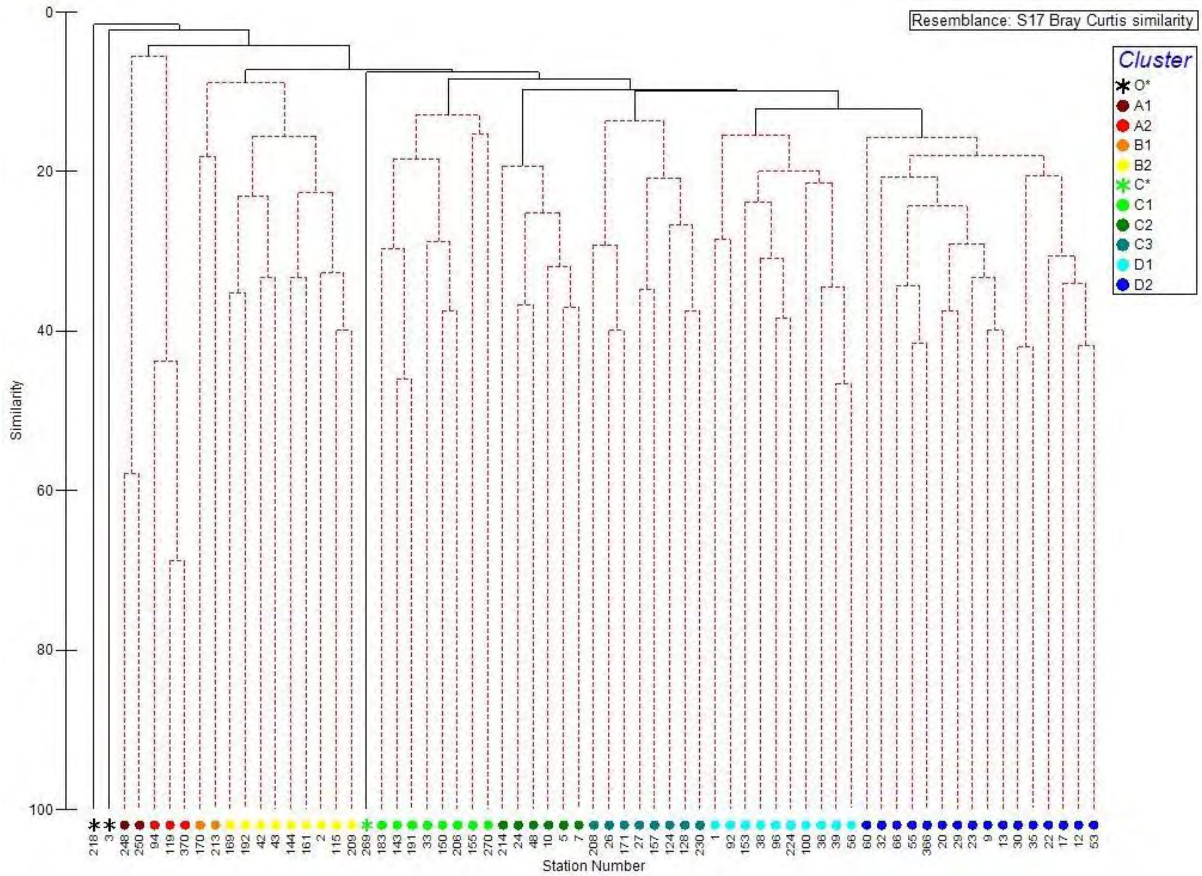


Figure 3.12. Dendrogram plot of Section I of South-West Deeps (West) MCZ grab data. Samples coloured according to assigned cluster group.

Figure 3.13 shows the dendrogram plot from Section II. Sections II and Section III split away from each other at ~20% similarity. Section II contained 50 stations, which were all broadly within one large cluster that was split into seven sub-groups (E1 – E7). There was one outlying station, station 166 (E*). The first sub-group, E1, split at ~21% similarity. Sub-group E2 was small, comprised of three stations, and split off at ~22% similarity. At ~23% similarity sub-group E3 branched off, followed by sub-group E4 at ~24% similarity. Sub-group E5 branched off at ~26% similarity. The last two sub-groups, E6 and E7 were ~28% similar to each other.

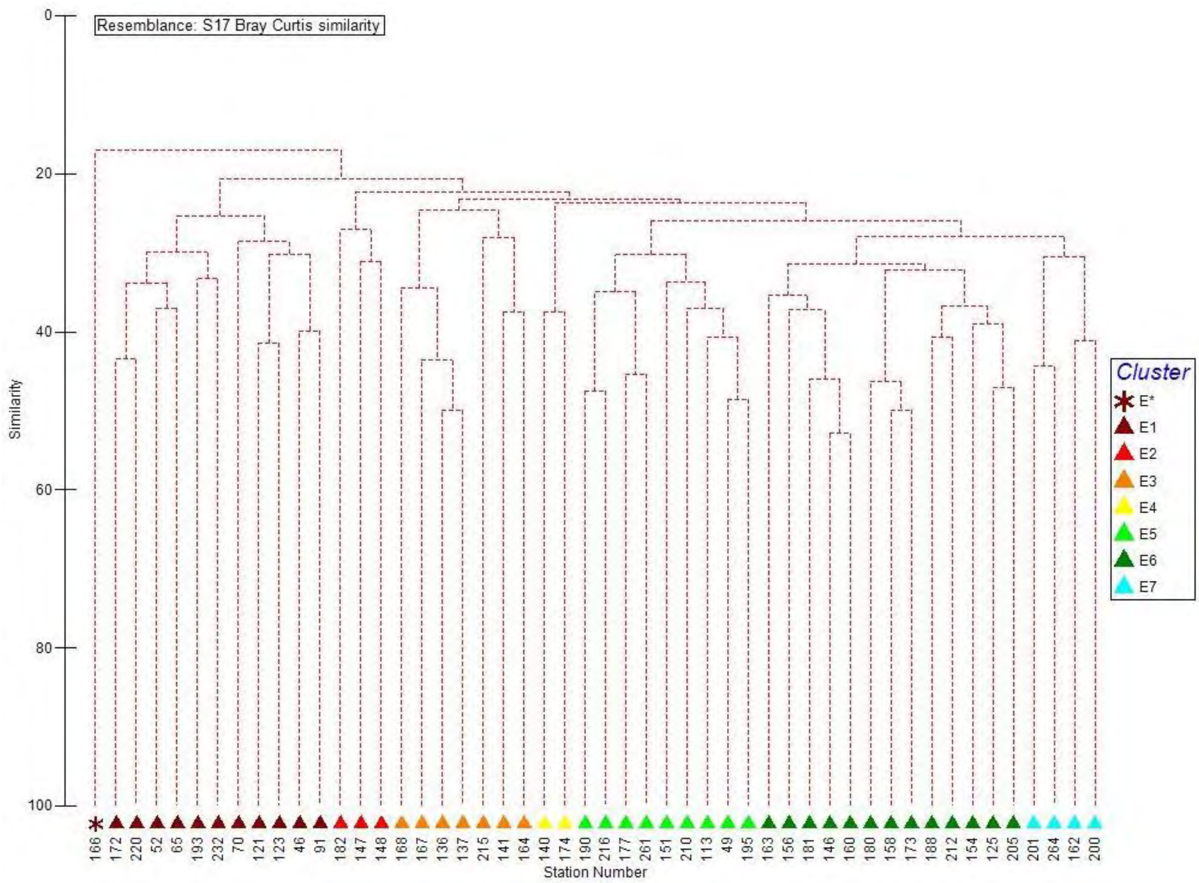


Figure 3.13. Dendrogram plot of Section II of South-West Deeps (West) MCZ grab data. Samples coloured according to assigned cluster group.

Section III contained the most stations (89), which were split into ten sub-groups across three main clusters (Figure 3.14). Sub-groups H1 and H2 both branched off at ~22% similarity level into two distinct groups. The cluster containing sub-groups F1 and F2 split off at ~25% similarity, with F1 branching away at ~30% similarity from F2. In the main cluster of stations, sub-group G1 branched off at ~27% similarity, followed by sub-group G2 at ~28% similarity. Sub-group G3 branched off at ~30%. At ~31% similarity sub-group G6 separated from a cluster containing sub-groups G4 and G5, which in turn split away from each other at ~32% similarity.

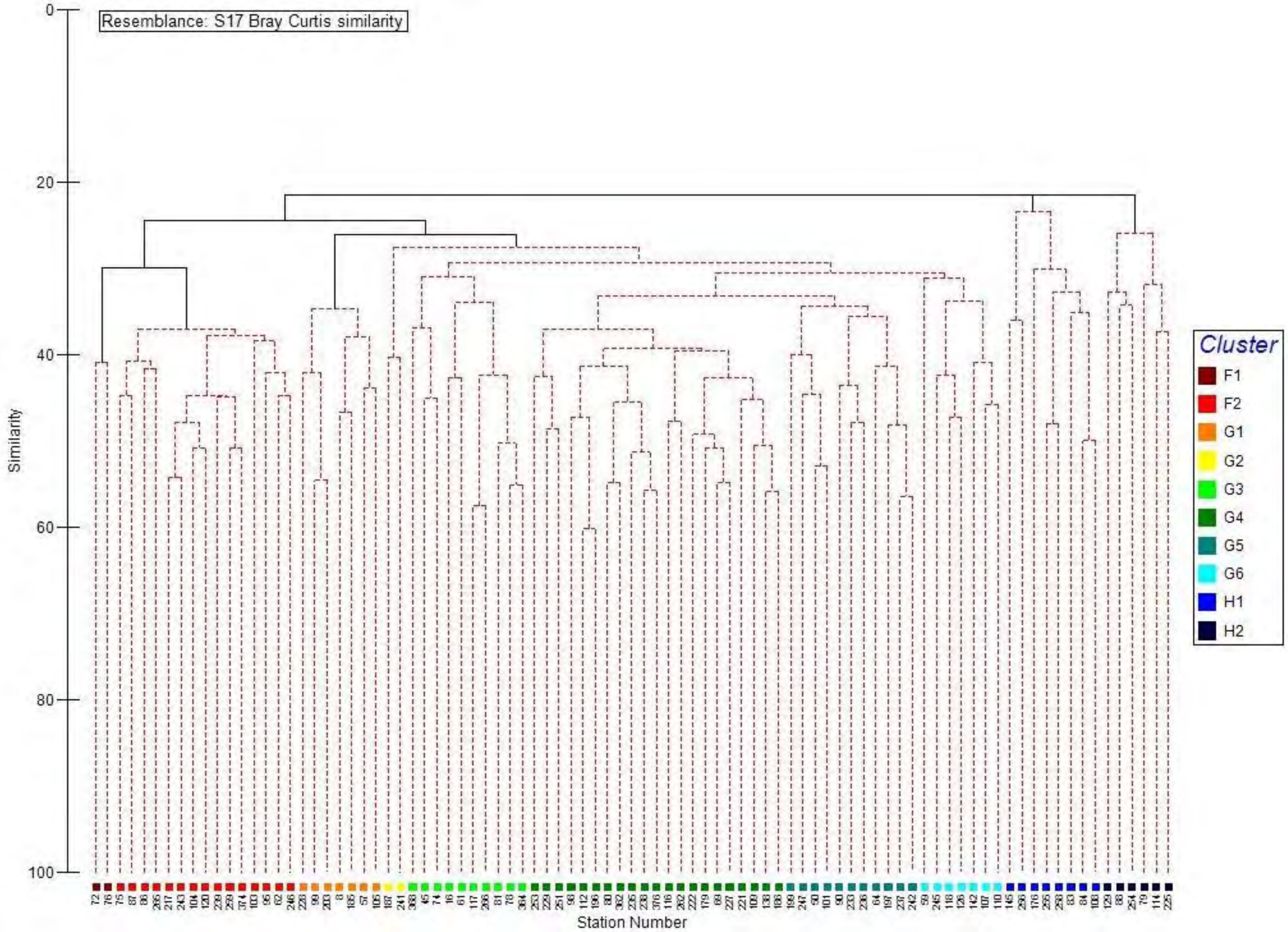


Figure 3.14. Dendrogram plot of Section II of South-West Deeps (West) MCZ grab data. Samples coloured according to assigned cluster group.

MDS ordination plots were constructed for Sections I – III (Figures 3.15 – 3.17). The 2D MDS ordination plots showed some support for the clustering of the stations seen in the dendrogram plots. In general, the stations within each sub-group plotted relatively close together. However, there was some merging between stations of certain sub-groups (e.g. E5, E6 and E7 in Figure 3.16). The stress values levels for all the 2D plots were 0.25 or higher, indicating that too much reliance should not be placed on these plots.

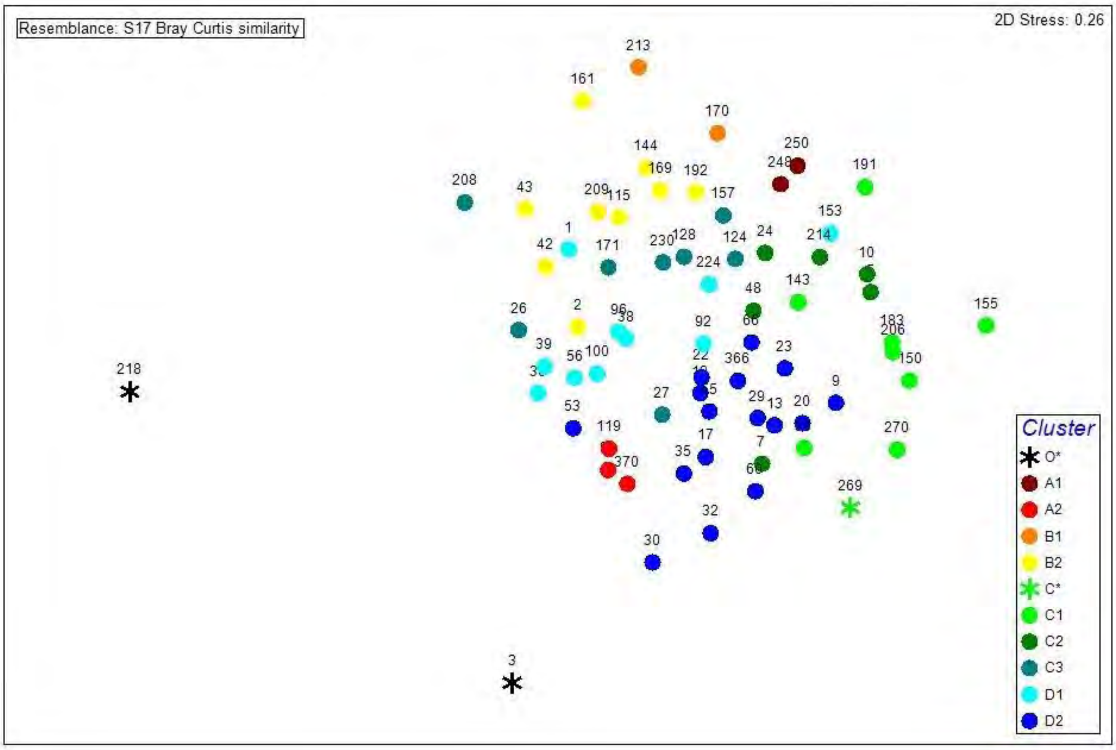


Figure 3.15. MDS ordination plot of Section I of South-West Deeps (West) MCZ grab data.

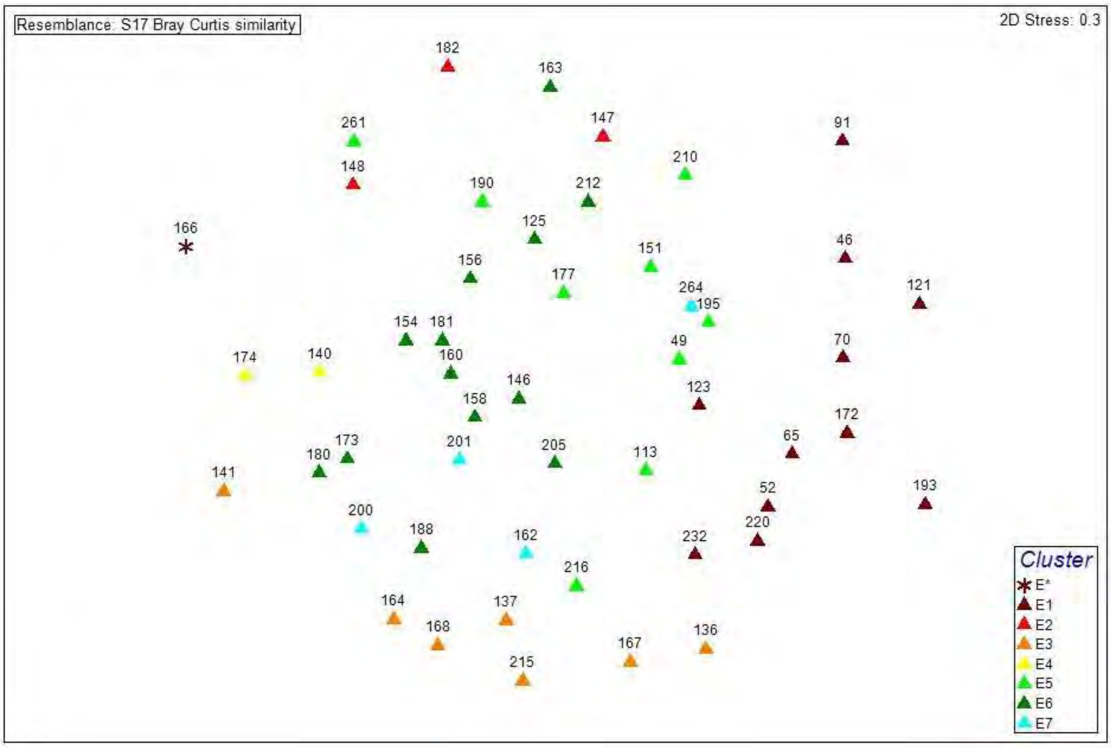


Figure 3.16. MDS ordination plot of Section II of South-West Deeps (West) MCZ grab data.

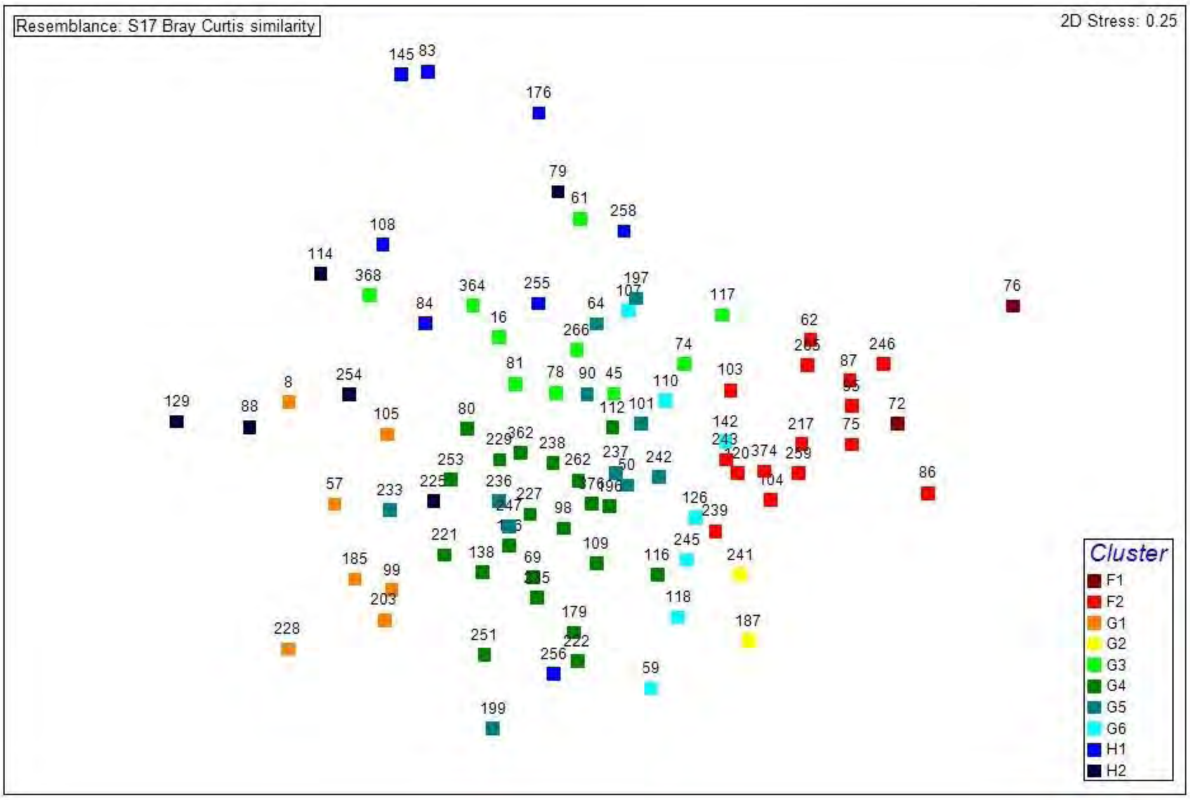


Figure 3.17. MDS ordination plot of Section III of South-West Deeps (West) MCZ grab data.

Figures 3.18 – 3.20 illustrate dendrograms for each section with the EUNIS sediment classification derived from the PSA results displayed. The majority of stations (160) were classified as sand and muddy sand, with nine stations classified as mud and sandy mud, 16 stations as mixed sediments, and 22 stations as coarse sediments. Despite the dominance of the sand and muddy sand stations, there appeared to be some pattern to the clustering of stations and their sediment classification. For example, sub-group D2 contained mud and sandy mud with sand and muddy sand stations, whilst sub-groups F1 and F2 were dominated by mixed and coarse sediments.

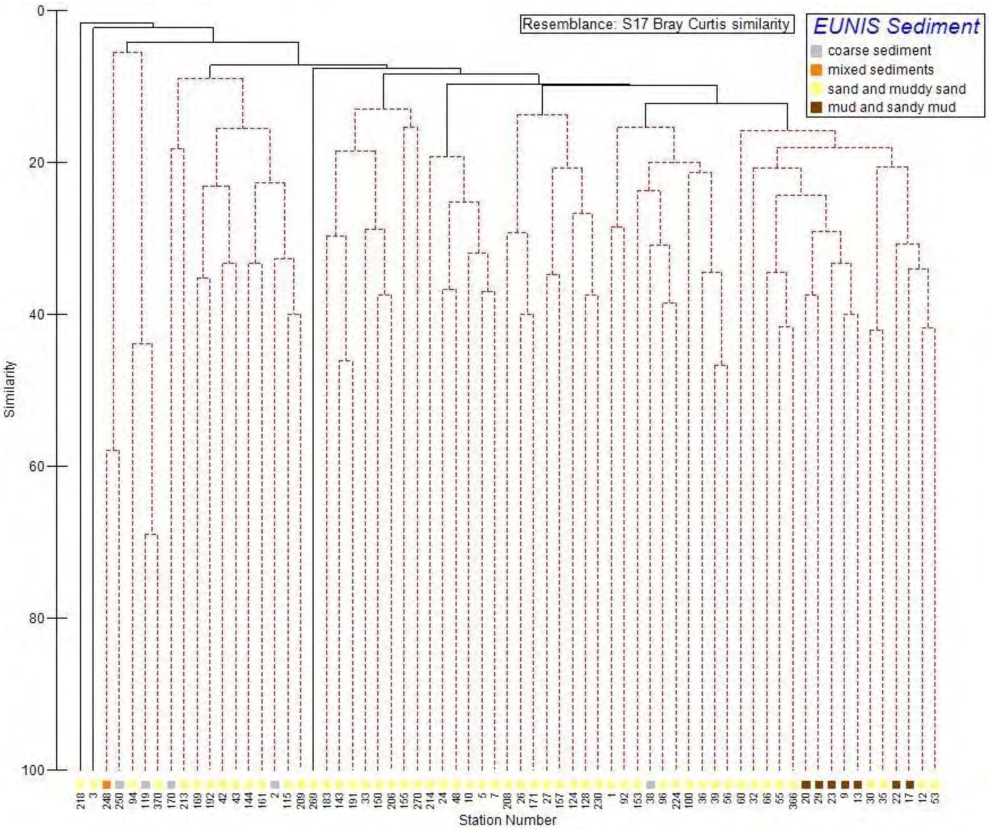


Figure 3.18. Dendrogram plot of Section I, South-West Deeps (West) MCZ grab data. Samples coloured according to EUNIS sediment classification based on PSA data.

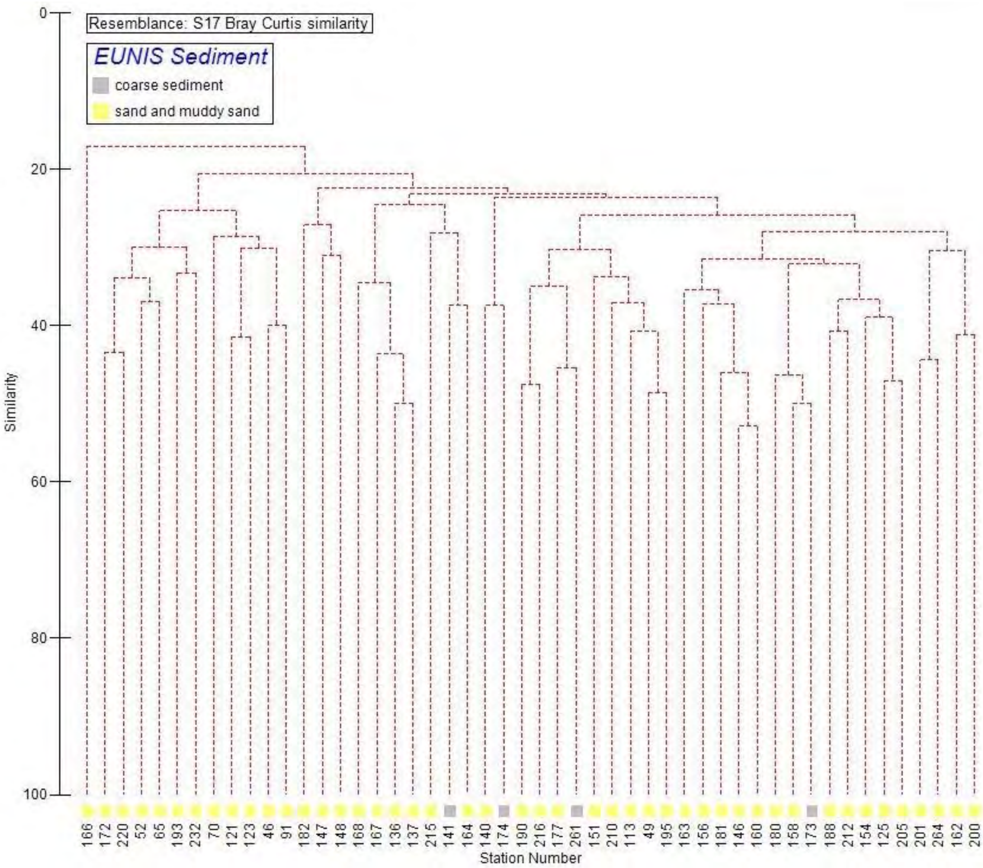


Figure 3.19. Dendrogram plot of Section II, South-West Deeps (West) MCZ grab data. Samples coloured according to EUNIS sediment classification based on PSA data.

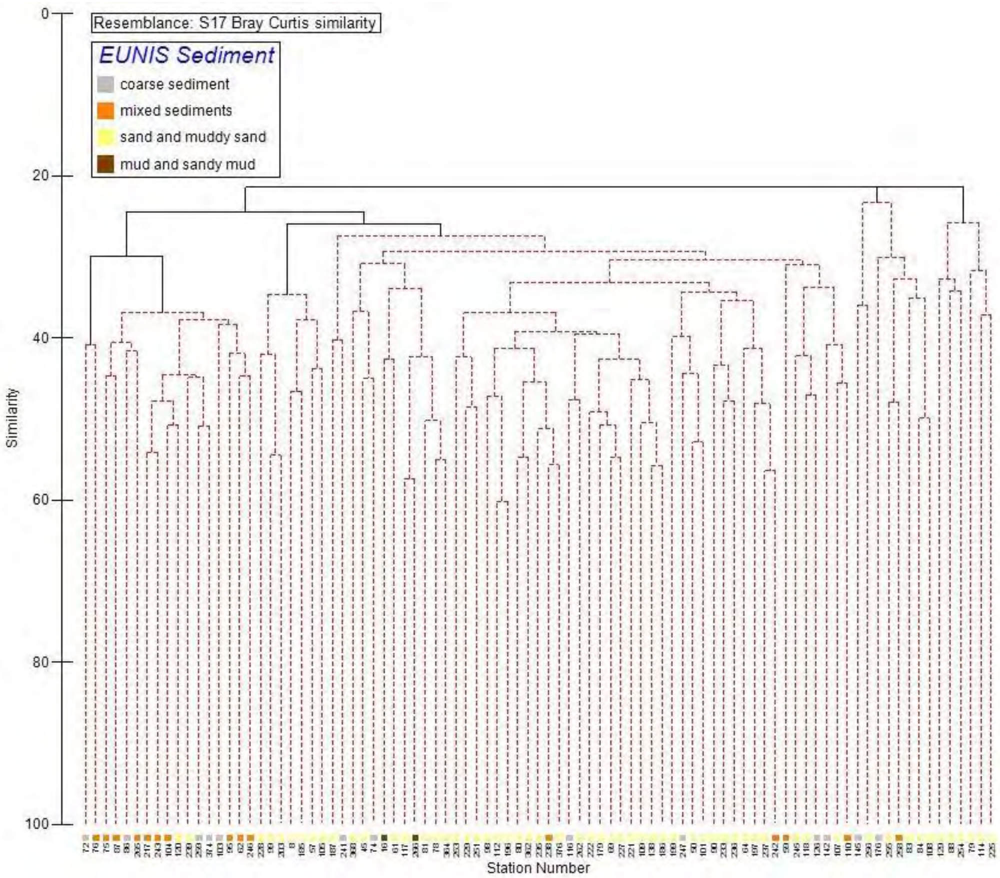


Figure 3.20. Dendrogram plot of Section III, South-West Deeps (West) MCZ grab data. Samples coloured according to EUNIS sediment classification based on PSA data.

SIMPER analysis was undertaken to assess which species were characteristic for each of the sub-groups identified from the cluster analysis. Table 3.8 outlines the characteristic taxa for each sub-group, listing those taxa that contributed at least 90% similarity for each sub-group. Full SIMPER results showing all contributing species for each sub-group can be found in Appendix 9.

Sub-group A1 was grouped together due to a high abundance of *Caryophyllia smithii* within both samples. The taxon that contributed the most to the similarity of samples within sub-group A2 was the veneroid bivalve *Montacuta substriata*, with 50 or more individuals of this species found at each station. The polychaetes *Notomastus* and *Loimia medusa* were also characteristic of this sub-group. Two polychaete species, *Chone* sp. and *Ampharete octocirrata* were characteristic of sub-group B1, whilst sub-group B2 was characterised a range of different taxa. These included polychaetes (*Polycirrus* and *Pista cristata*), the echinoid *Echinocyamus pusillus,* Nermetea, the ribbon worm *Cerebratulus*, and Actiniaria.

A range of polychaete species characterised the faunal communities within sub-group C1, but *Phoronis* contributed the most to the similarity between the stations within this sub-group. The anemone *Paraphellia expansa* was the most important contributing species in sub-group C2. Sub-group C2 was also characterised by other Actiniaria, Nemertea, *Scolelepis bonnieri, Harpinia antennaria* and *Galathowenia oculata*. Sub-group C3 showed some similarities to C2, with Actiniaria, Nemertea and *Galathowenia oculata* also appearing on the list of characterising species. However, *P. expansa* did not characterise sub-group C3, with terebellid polychaetes featuring instead.

Approximately half of the characterising taxa for sub-group D1 were also characteristic of sub-group D2, although they contributed different percentages to the similarity of stations within each sub-group. These fauna included the sipunculid *Aspidosiphon muelleri*, polychaetes such as *Pista cristata, Loimia medusa* and *Chaetozone* sp. D and the bivalve *Abra prismatica*. The average abundances of many of these taxa were low across both sub-groups. Sub-group D2 was characterised by a more diverse range of polychaetes than sub-group D1. The polychaetes that characterised sub-group D1 that were absent from D2 included *Aonides paucibranchiata, Aponuphis bilineata* and *Spiophanes bombyx*, which are more typical of finer sediment. The presence of characteristic polychaete species within sub-group D2 such as *Lumbrineris, Peresiella clymenoides, Spiophanes kroyeri* together with *Magelona* are more indicative of slightly more mixed sediments.

No taxa consistently appeared on the lists of characterising taxa for sub-groups E1 – E7. However, some characteristic taxa occurred within the majority of the sub-groups. For example *Galathowenia oculata* and *Pista cristata* characterised sub-groups E1, and E3 – E7, *Aonides paucibranchiata* sub-groups E1, E3, and E5 – E7, and *Paradialychone filicauda* sub-groups E2, E5 and E6. Each sub-group was generally characterised by taxa that were present in at least two of the other sub-groups from E1 – E7. This suggested that these stations probably represented slight variations of the same habitat, with patchiness and local environmental conditions influencing the composition of the faunal communities, rather than distinctly different habitats.

Sub-group F1 was characterised mainly by polychaete species. The top three contributing species (*Notomastus, Polycirrus* and *Aponuphis bilineata*) were also the top three contributing species for sub-group F2. Sub-group F2 was characterised by a large range of taxa that was also dominated by polychaetes, but included some amphipods (e.g. *Ampelisca, Nototropis* and *Othomarea*), gnathid isopods, and echinoderms (*Echinocyamus pusillus* and *Amphipholis squamata*).

Across sub-groups G1 – G6 several taxa were consistently listed as characterising species, although their percentage contribution varied between sub-groups. These taxa were *Galathowenia oculata, Aponuphis bilineata,* and Nemertea species. *Pista cristata* characterised sub-groups G1, G3 – G6, but *Pista malmgreni* characterised sub-group G2. Other species were consistently identified as characteristic across several of the sub-groups. For example *Chone* and *Aonides paucibranchiata* were characteristic of sub-groups G3 – G6, whilst *Peresiella clymenoides* and *Polycirrus* were characteristic from G2 – G6. The similarities between many of the characteristic fauna between these sub-groups suggested that they probably represented the same habitat, with slight differences in faunal community composition indicating patchiness in the distribution of certain taxa or sediment composition.

Sub-groups H1 and H2 both had many of the same characteristic species, including *Glycera oxycephala, Aonides paucibranchiata, Aponuphis bilineata, Pista cristata, Galathowenia oculata, Spiophanes kroyeri* and *Echinocyamus pusillus*, albeit all contributing different percentage to the similarity of the faunal communities within each sub-group. Each sub-group was also characterised by some species absent from the list of the other sub-group. For instance *Chone* and *Polycirrus* characterised sub-group H1 but not H2, whilst *Abra prismatica* and *Tubulanus polymorphus* characterised sub-group H2 but not H1.

Table 3.8. Results of SIMPER analysis of the sub-groups identified from cluster analysis of macrofaunal abundance counts, South-West Deeps (West) MCZ grab data.

Group / Cluster	% Contribution of characterising species	
	Taxa / species	**Contribution (%)**
A1	*Caryophyllia smithii*	94.34
A2	*Montacuta substriata*	85.14
	Loimia medusa	3.14
	Notomastus sp.	2.2
B1	*Ampharete octocirrata*	50
	Chone sp.	50
B2	*Pista cristata* sensu Jirkov	43.69
	Echinocyamus pusillus	28.33
	NEMERTEA	5.23
	Cerebratulus sp.	4.96
	ACTINIARIA	4.84
	Polycirrus sp.	4.73
C1	*Phoronis* sp.	37.9
	Galathowenia oculata	25.13
	Paradialychone filicaudata	6.33
	Nephtys cirrosa	4.9
	Aonides paucibranchiata	4.52
	Caulleriella species B	4.51
	Owenia fusiformis	4.39
	Lanice conchilega	2.65
C2	*Paraphellia expansa*	74.1
	ACTINIARIA	5.25
	NEMERTEA	4.38
	Scolelepis bonnieri	3.62
	Harpinia antennaria	2.36
	Galathowenia oculata	1.92
C3	NEMERTEA	53.51
	Loimia medusa	23.53
	Galathowenia oculata	5.45
	ACTINIARIA	3.45
	Laonice bahusiensis	3.27
	Chone	1.8
D1	*Aspidosiphon muelleri*	16.46
	Echinocyamus pusillus	14.22
	Aonides paucibranchiata	13.83
	Aponuphis bilineata	12.65
	Glycera oxycephala	6.78
	Loimia medusa	4.88
	Amphiuridae juv.	4.32
	Spiophanes bombyx	4.15
	Abra prismatica	3.88
	Phoronis	2.73
	Chaetozone species D	2.38
	Astrorhiza	2.33
	Pista cristata sensu Jirkov	2.24

Group / Cluster	% Contribution of characterising species	
	Taxa / species	**Contribution (%)**
D2	*Astrorhiza*	12.45
	Aspidosiphon muelleri	11.89
	Galathowenia oculata	10.05
	Peresiella clymenoides	9.73
	Lumbrineris aniara/cingulata	6.52
	Magelona minuta	6.12
	Phoronis	5.76
	Spiophanes kroyeri	4.55
	NEMERTEA	3.11
	Pista cristata sensu Jirkov	2.85
	Chaetozone species D	2.65
	Poecilochaetus serpens	2.37
	Falcidens crossotus	1.91
	Thyasira flexuosa	1.9
	Syllis parapari	1.82
	Loimia medusa	1.58
	Streblosoma	1.26
	Abra prismatica	1.08
	Glycera alba	0.97
	Nephtys kersivalensis	0.97
	Polycirrus	0.88
E1	*Pista cristata* sensu Jirkov	31.72
	Loimia medusa	30.21
	Aponuphis bilineata	4.83
	Echinocyamus pusillus	4.29
	Peresiella clymenoides	3.56
	Galathowenia oculata	2.49
	NEMERTEA	2.17
	Aonides paucibranchiata	1.92
	Poecilochaetus serpens	1.73
	Polycirrus	1.47
	Nephtys cirrosa	1.31
	Chaetozone species D	1.3
	Tubulanus polymorphus	1.2
	ACTINIARIA	1.19
	Glycera oxycephala	1.14
E2	*Aponuphis bilineata*	23.18
	Chone	16.85
	Othomaera othonis	10.41
	ACTINIARIA	6.33
	Spiophanes kroyeri	6.33
	Paradialychone filicaudata	5.32
	Serpulidae	5.32
	Eurydice truncata	5.32
	Cochlodesma praetenue	5.32
	Peresiella clymenoides	5.2
	Owenia fusiformis	5.2

Group / Cluster	% Contribution of characterising species	
	Taxa / species	**Contribution (%)**
E3	*Galathowenia oculata*	23.52
	Pista cristata sensu Jirkov	20.93
	Eurydice truncata	20.93
	Aonides paucibranchiata	9.1
	Chone	8.52
	ACTINIARIA	5.71
	Poecilochaetus serpens	1.98
E4	*Galathowenia oculata*	33.33
	Chone	25
	Loimia medusa	8.33
	Pista cristata sensu Jirkov	8.33
	Leptocheirus hirsutimanus	8.33
	Unciola planipes	8.33
E5	*Polycirrus*	22.86
	Notomastus	16.85
	Loimia medusa	10.72
	Aponuphis bilineata	6.94
	Pista cristata sensu Jirkov	6.64
	Phoronis	6.24
	Chone	5.92
	Galathowenia oculata	4.8
	NEMERTEA	3.22
	Paradialychone filicaudata	2.9
	Aonides paucibranchiata	2.33
	Eurydice truncata	1.83
E6	*Chone*	32.98
	NEMERTEA	14.92
	Pista cristata sensu Jirkov	7.88
	Aonides paucibranchiata	6.4
	Notomastus	5.31
	Loimia medusa	5.12
	Galathowenia oculata	4.6
	Eurydice truncata	3.65
	Poecilochaetus serpens	3.38
	Cochlodesma praetenue	2.51
	Polycirrus	2.49
	Paradialychone filicaudata	2.11
F1	*Notomastus*	52.38
	Polycirrus	14.29
	Aponuphis bilineata	6.35
	Lumbrineris aniara/cingulata	6.35
	Cerebratulus	3.17
	Glycera lapidum agg.	3.17
	Goniadella gracilis	3.17
	Lanice conchilega	3.17

Group / Cluster	% Contribution of characterising species	
	Taxa / species	Contribution (%)
F2	*Notomastus*	18.75
	Aponuphis bilineata	10.65
	Polycirrus	9.62
	Galathowenia oculata	6.9
	NEMERTEA	6.02
	Peresiella clymenoides	3.77
	Loimia medusa	3.76
	Pista cristata sensu Jirkov	3.3
	Aonides paucibranchiata	3.11
	Poecilochaetus serpens	2.61
	Goniadella gracilis	2.52
	Caryophyllia smithii	2.34
	Amphipholis squamata	2.3
	Golfingia elongata	1.88
	Ampelisca spinipes	1.55
	Pseudonotomastus southerni	1.51
	Spiophanes kroyeri	1.41
	Eunereis longissima	1.4
	Gnathia species A	1.04
	Chone	0.97
	Hydroides norvegicus	0.81
	Serpulidae	0.7
	Othomaera othonis	0.66
	Nototropis vedlomensis	0.66
	Chaetozone species E	0.65
	Echinocyamus pusillus	0.65
	Amaeana trilobata	0.6
G1	*Galathowenia oculata*	26.95
	Phoronis	19.61
	Pista cristata sensu Jirkov	18.72
	Aponuphis bilineata	18.34
	Loimia medusa	2.52
	NEMERTEA	2.16
	Astrorhiza	25
G2	*Poecilochaetus serpens*	16.67
	Galathowenia oculata	8.33
	Goniadella gracilis	8.33
	Aponuphis bilineata	8.33
	Parathelepus collaris	4.17
	NEMERTEA	4.17
	Glycera lapidum agg.	4.17
	Peresiella clymenoides	4.17
	Polygordius	4.17
	Pista malmgreni sensu Jirkov	4.17

Group / Cluster	% Contribution of characterising species	
	Taxa / species	Contribution (%)
G3	*Pista cristata* sensu Jirkov	16.82
	NEMERTEA	16.18
	Polycirrus	12.83
	Aponuphis bilineata	10.52
	Peresiella clymenoides	6.72
	Galathowenia oculata	4.81
	Aonides paucibranchiata	3.66
	Phoronis	3.54
	Lumbrineris aniara/cingulata	2.01
	Chone	2.01
	Notomastus	1.99
	Eurydice truncata	1.66
	Echinocyamus pusillus	1.59
	Astrorhiza	1.49
	Ampelisca spinipes	1.38
	Lanice conchilega	1.35
	Myriochele	0.94
	Loimia medusa	0.89
G4	*Galathowenia oculata*	30.29
	Aponuphis bilineata	26.67
	Pista cristata sensu Jirkov	13.08
	NEMERTEA	4.2
	Aonides paucibranchiata	3.96
	Chone	3.26
	Loimia medusa	3.19
	Peresiella clymenoides	2.39
	Notomastus	2.22
	Polycirrus	1.68
G5	*Loimia medusa*	19.52
	Notomastus	15.77
	Aponuphis bilineata	15.75
	Galathowenia oculata	10.06
	Pista cristata sensu Jirkov	9.24
	Peresiella clymenoides	4.92
	NEMERTEA	4.24
	Polycirrus	3.05
	Chone	2.98
	Aonides paucibranchiata	1.62
	Paradialychone filicaudata	1.47
	Goniadella gracilis	1.42

Group / Cluster	% Contribution of characterising species	
	Taxa / species	Contribution (%)
G6	*Aponuphis bilineata*	35.03
	Aonides paucibranchiata	10.56
	Pista cristata sensu Jirkov	7.55
	Notomastus	6.09
	NEMERTEA	4.77
	Peresiella clymenoides	3.61
	Polycirrus	3.27
	Chone	3.07
	Goniadella gracilis	2.95
	Ampelisca spinipes	2.78
	Galathowenia oculata	2.68
	Aricidea wassi	1.69
	Glycera lapidum agg.	1.68
	Echinocyamus pusillus	1.59
	Lumbrineris aniara/cingulata	1
	Aglaophamus agilis	0.92
	Laonice bahusiensis	0.84
H1	*Glycera oxycephala*	20.76
	Chone	13.95
	Peresiella clymenoides	12.66
	Aonides paucibranchiata	8.25
	Galathowenia oculata	8.13
	Aponuphis bilineata	6.13
	Pista cristata sensu Jirkov	5.12
	Spiophanes kroyeri	3.23
	Polycirrus	3.05
	Paradialychone filicaudata	2.91
	Caryophyllia smithii	2.36
	Echinocyamus pusillus	1.67
	ACTINIARIA	1.45
	Clymenura	1.45
H2	*Aponuphis bilineata*	29.53
	Galathowenia oculata	12.09
	Abra prismatica	9.24
	Tubulanus polymorphus	8.51
	Aonides paucibranchiata	6.95
	Glycinde nordmanni	5.45
	Phoronis	5.19
	Echinocyamus pusillus	3.81
	Glycera oxycephala	2.54
	Lumbrineris aniara/cingulata	2.35
	Spiophanes kroyeri	2.04
	Pista cristata sensu Jirkov	2.04
	NEMERTEA	1.77

3.3.4 Spatial distribution of samples

The geographical distribution of the assigned cluster groups for the South-West Deeps (West) grab data can be seen in Figure 3.21. Points have been assigned shapes/colours coded according to their cluster groups. The geographical distribution did not show any particular pattern to the spatial spread of the cluster groups. This suggests an element of patchiness in the survey area, and that the cluster analysis had potentially overstated small differences between faunal communities rather than identifying distinct boundaries between habitat types.

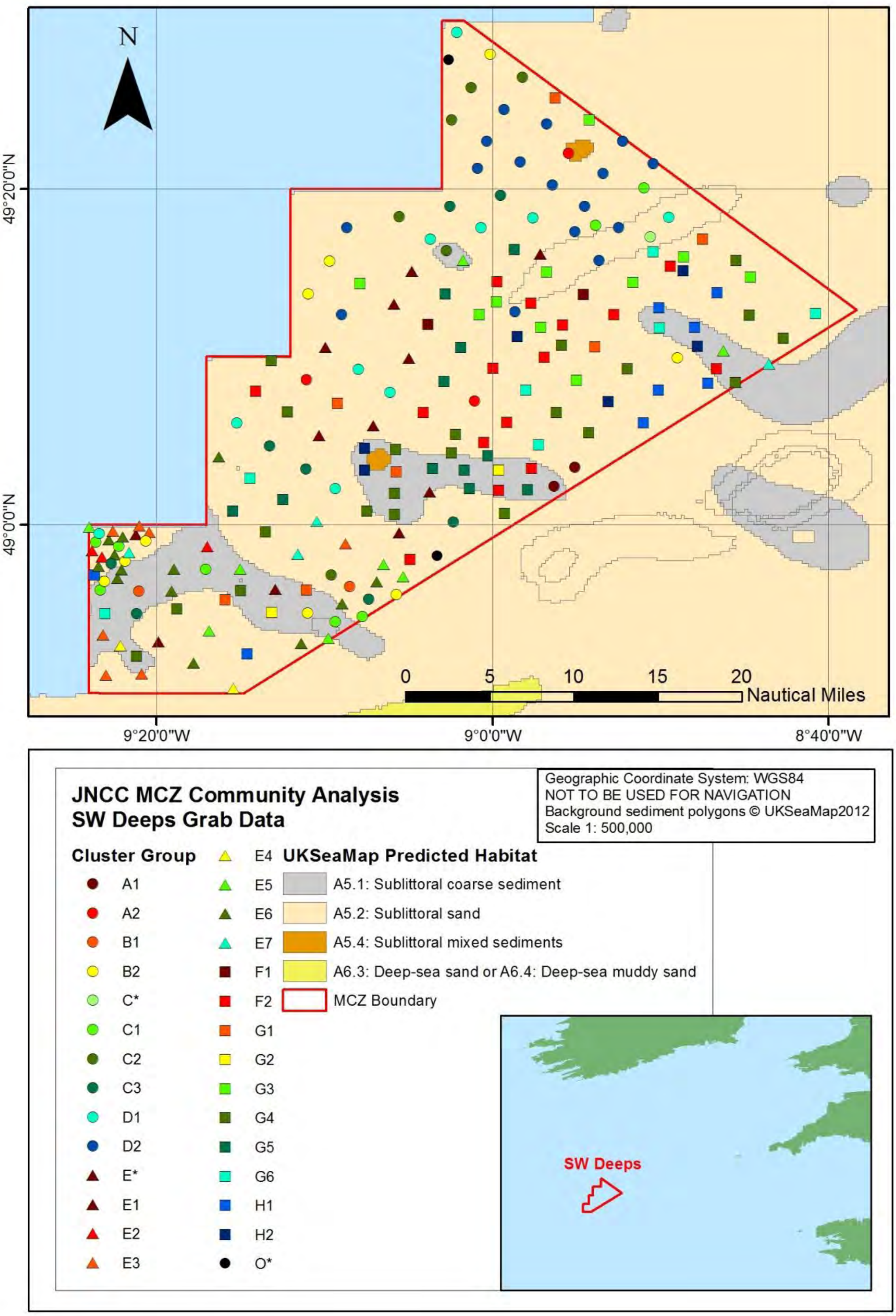


Figure 3.21. Geographical distribution of samples, South-West Deeps (West) grab data.

3.3.5 Biotope designation

Table 3.9 summarises the biotopes assigned to the South-West Deep grab data. The reasons behind the designations of the biotopes are described in more detail below. As previously mentioned, juvenile Ophiuridae and Spatangoida were present in the majority of the samples, often at very high abundances, which masked the underlying similarities between the faunal communities at different stations. These two taxa have a seasonal aspect, so have also been excluded from the following biotope considerations.

The very high abundances of *Caryophyllia smithii* caused sub-group A1 to cluster away from the other stations. No soft sediment biotopes have *C. smithii* as a characteristic species, suggesting that a **CR** biotope should be considered for this sub-group. However, examination of the full raw species matrix to examine epifauna removed by rationalisation did not reveal many epifaunal taxa, aside from some bryozoans such as *Alderina imbeliis.* The volumes of sediment collected by the grab (~4.5 litres for both stations) suggested that soft sediment dominated the substratum. Images of the grab samples did not show any large cobbles or pebbles that the *C. smithii* could have been attached to. The high abundance of *C. smithii* masked the other fauna present within the stations in the SIMPER analysis. The stations had a mixture of polychaetes, bivalves and amphipods including taxa like terebellids and veneroids that were typical of **CMx** biotopes. This was supported by the EUNIS sediment classification for these stations (coarse and mixed sediments). Based on depth, the most appropriate biotope would be **SS.SMx.OMx**. However, to reflect the presence of *C. smithii* a tentative new biotope has been assigned (**SS.SMx.OMx.Csmi**). Analysis of video data may clarify the biotope analysis for these stations.

Like sub-group A1, A2 separated out due to very high abundances of a single taxon. For sub-group A2 it was the bivalve *Montacuta substriata*. This is a commensal species that lives attached to the spines of the heart urchins *Spatangus* and *Echinocardium*. Another bivalve species commensal with *Echinocardium cordatum*, *Tellimya ferruginosa,* was also present within samples from sub-group A2. However, there was only one record of *Echinocardium cordatum* and one of *Spatangus purpureus* in the grab samples. High abundances of both commensal species suggested that these large urchins may have been under-sampled by the benthic grabbing operations. Other fauna present included terebellid polychaetes *Notomastus*, *Spiophanes kroyeri, Malmgrenia arenicolae* and *Poecilochaetus serpens.* The fauna suggested that the substratum was muddy sand, and therefore fitting within the biotope **SS.SSa.OSa**. Although the data showed that heart urchins were present within the samples, species such as *Echinocardium* have a wide range and can be quite mobile, making them unsuitable as diagnostic species to define biotopes. The biotope **SS.SSa.OSa.(Ech)** was assigned to flag the echinoid components of the community, but the biotope may ultimately have to be pushed up to biotope complex level.

The stations within sub-group B1 were characterised by *Ampharete octocirrata* and *Chone*, which suggested an element of finer sediment. Bivalves including *Kurtiella bidentata,* and *Gari tellinella* were also present, supporting the idea of a muddy sand habitat. However, the stations within this sub-group were generally faunally sparse, so it was deemed appropriate to classify them based on depth and sediment only. Therefore station 170 was classified as **SS.SCS.OCS**, whilst station 213 was classified as **SS.SSa.OSa**. The two stations within this sub-group only clustered together at a low similarity (~20%), supporting the use of two different biotopes for the sub-group.

Sub-group B2 was mainly characterised by *Pista cristata* and *Echinocyamus pusillus*. These two species can occur together in medium to coarse sand sediments. The ribbon worm *Cerebratulus* was also a characterising species, typically found in mud or sandy sediments. Some stations within the sub-group had *Glycera* and *Lumbrineris* present, again suggesting a medium to coarse sand habitat. The stations within sub-group B2 were again faunally sparse, so were classified according to depth and sediment classification as **SS.SSa.OSa**, but probably represent the coarser end of the sediment spectrum covered by this biotope complex.

Low faunal abundances were also evident in sub-group C1. The characterising polychaetes *Owenia fusiformis, Lanice conchilega* and *Nephtys cirrosa* all suggested sandy sediments. Several amphipod species typical of sandy sediments such as *Ampelisca spinipes* and *Urothoe elegans* were also present in some of the samples from this sub-group. The faunal community composition supported the EUNIS sediment classification of sand and muddy sand for this sub-group, which was assigned the biotope **SS.SSa.OSa**. The low average abundance of fauna prevented assignment of a biotope below complex level.

Anemones were characteristic of sub-group C2, particularly *Paraphellia expansa*, which is usually found in coarse sand and gravel. Stations within this sub-group were relatively faunally sparse. Several species of crustacean including *Corystes cassivelaunus* and the amphipods *Harpinia antennaria, Urothoe elegans* and *Bathyporeia gracilis* were infrequently found within the sub-group, all indicative of sandy sediments. However, some of the polychaete species found were more suggestive of finer or mixed sediments, such as *Galathowenia oculata* and *Paradoneis lyra.* Overall, the composition of the faunal community indicated a potentially muddy sand habitat. The PSA results indicated that the sub-group should fit within the **SS.SSa.OSa** biotope complex, and has been assigned the biotope **SS.SSa.OSa.(Pex)** to reflect the characterising presence of *P. expansa*.

The fauna characteristic of sub-group C3 included terebellid polychaetes, *Galathowenia oculata*, Actiniaria and nermeteans, which usually occur together in mixed sediment biotopes. However, the general scarcity of the fauna meant that no reliable determination of a biotope could be made on the faunal data, so the biotope **SS.SSa.OSa** was assigned to the sub-group on the basis of sample depths and EUNIS sediment classifications.

Sub-groups D1 and D2 were characterised by many of the same species, and the overall community within both sub-groups were relatively similar, albeit with sub-group D2 being slightly more diverse. The sipunculid *Aspidosiphon muelleri* characterised both sub-groups, indicating the presence of shell fragments within the sediment. The variety of polychaete species suggested that sub-group D1 probably represented muddy sand. The low abundance of individuals in each taxon again prevented classification beyond biotope complex level. Sub-group D1 was assigned the biotope **SS.SSa.OSa**, with the habitat being composed of muddy sand and shell fragments. The greater importance of fauna such as *Galathowenia oculata, Magelona minuta* and *Astrorhiza* foraminifera within sub-group D2 indicated a higher component of muddier sediment than was found in sub-group D1. These differences could also be seen in the EUNIS sediment classification, with half of the stations within D2 classified as mud and sandy mud. Sub-group D2 was classified as **SS.SSa.OSa** / **SS.SMu.OMu** to reflect the underlying similarities to sub-group D1, but to also highlight the presence of sandy mud within the stations indicated by some of the fauna and the PSA data.

As discussed during the section on the SIMPER analysis, sub-groups E1 – E7 had faunal communities that were broadly similar, with each characteristic taxon represented in at least three of the seven sub-groups. Aside from the four stations that were classified as coarse sediment, the remaining 45 stations were all classified as sand and muddy sand. Therefore sub-groups E1 – E7 were all classified within the **SS.SSa.OSa** biotope complex. Taxa such as *Cochlodesma praetenue, Eurydice truncata, Notomastus* and *Spiophanes kroyeri* suggested medium to coarse sand and/or the presence of some gravel. Although samples within sub-groups E1 – E7 were typically more taxa rich than many other samples, each taxon was again rarely recorded above one or two individuals. This lack of abundant characteristic fauna prevented a sub-biotope from being defined for these sub-groups.

The stations within sub-groups F1 and F2 contained some of highest faunal abundances and taxa richness recorded across the survey area. The EUNIS sediment classification for many of these stations was mixed sediments, which tend to have high species diversity. Sub-group F2 was characterised a range of taxa including polychaete species such as *Notomastus, Aponuphis bilineata, Polycirrus, Galathowenia oculata, Aonides paucibranchiata* and *Hydroides norvegicus*, all of which are described within the **SS.SMx.OMx.PoVen** biotope. Other fauna including *Amphipholis squamata* and *Ampelisca spinipes* that are described on the list of the biotope fauna also characterised sub-group F2. Although not drawn out in the SIMPER analysis, bivalves including *Kurtiella bidentata, Timoclea ovata* and other veneroids were present at some stations, suggesting a good match between **SS.SMx.OMx.PoVen** and sub-group F2. Sub-group F1 appeared to be a slightly impoverished version of sub-group F2, lacking the same range of taxa, particularly bivalves. Therefore F1 was assigned the biotope **SS.SMx.OMx.(PoVen).**

Sub-groups G1 – G6 were consistently characterised by four taxa: *Galathowenia oculata, Aponuphis bilinetata*, *Pista* spp. and Nemertea. Other species such as *Polycirrus, Peresiella clymenoides, Chone, Notomastus* and *Loimia medusa* were also regularly found within stations across these sub-groups. The EUNIS sediment classification showed the sediments to be mainly sand and muddy sand, with the occasional mud and sandy mud, mixed and coarse sediments. The different clustering of the stations probably resulted from some localised patchiness in habitat composition and species distribution. For example, sub-group G2 contained *Polygordius* and *Glycera lapidum,* which are usually found in coarse sand biotopes, which matches the coarse sediment classification from one of the stations within this sub-group. Many of the most common species within sub-groups G1 – G6 also characterised sub-groups F1 and F2, with the main differences being the relatively high abundances of *Galathowenia oculata* and Nemertea in G1 – G6, and the higher diversity of taxa in F1 and F2. This suggested that sub-groups G1 – G6 may be a transition from the mixed sediment habitats of F1 –and F2 to more sandy sediments, supported by the EUNIS sediment classification. Sub-group G1 probably represented the most extreme divergence from the mixed sediment communities seen in F2, and was assigned the biotope **SS.SSa.OSa**. Sub-group G2 was assigned the biotope **SS.SSa.OSa** / **SS.SCS.OCS** to reflect the presence of fauna characteristic of coarser sediments. The remaining sub-groups (G3 – G6) were assigned the biotope **SS.SSa.OSa** / **SS.SMx.OMx** to show their relationship to the communities identified in sub-group F2, but to highlight the EUNIS sediment classification of sand and muddy sand. Comparing sub-groups G1 – G6 to E1 – E7, many of the most common species were similar. However, sub-groups E1 – E7 had more taxa typical of medium to coarse sand, whilst G1 – G6 had higher abundances and more taxa typical of muddy sand habitats.

The faunal communities characterising sub-groups H1 and H2 were largely similar, with the differences between the fauna suggesting H2 had slightly coarser sediment than H1. The species *Aonides paucibranchiata, Aponuphis bilineata, Galathowenia oculata, Pista cristata* and *Spiophanes kroyeri* were characteristic, again showing similarities to sub-groups E1 – E7, F1 – F2, and G1 – G6. Sub-groups H1 and H2 were probably part of the same overall fauna community, with the species suggesting they represented a transition between sub-groups G1 – G6 and E1 – E7. Of interest was the presence of *Caryophyllia smithii* in two stations of sub-group H1, suggesting some link with sub-group A1. It may be that these two stations in sub-group H1 are a transition between the species poor, *C. smithii* dominated mixed sediment community seen in sub-group A1 and a more diverse polychaete dominated sandy sediment. Both sub-groups H1 and H2 were assigned the biotope **SS.SSa.OSa**.

Of the outlying stations, 218 and 3 (O*) were assigned the biotope **SS.SSa.OSa** based solely on EUNIS sediment classification and depth due to lack of fauna in the samples. Station 41, which had no fauna present after rationalisation, was also assigned the biotope **SS.SSa.OSa**. The fauna was relatively sparse in station 269 (C*), but tended to suggest coarse sand (e.g. *Tubulanus polymorphus, Glycera* and sipunculids). Station 166 (E*) had many fauna typical of the medium to coarse sands outlined for sub-groups E1 – E7. Both station 166 and 269 were assigned the biotope **SS.SSa.OSa.**

The data collected from the South-West Deeps (West) grab survey generally had taxa that were found only in very low numbers in each sample, typically only one or two individuals per taxon. There were some notable exceptions (e.g. sub-groups A1 and A2, the juvenile echinoderms removed before undertaking multivariate analysis *etc.*). The lack of high faunal abundances made it hard to define biotopes below the biotope complex level. Although the data clustered out after multivariate analysis into several different groups, the low incidences of high faunal abundances meant that clusters were defined on small differences between the faunal communities within each sub-group. The survey data suggested that the majority of stations were sandy sediment, with a range of fairly ubiquitous taxa whose relative abundances changed according to patchiness and the relative fractions of coarse, medium and fine sand. In general terms there appeared to be a transition from polychaete-rich mixed sediments (sub-groups F2, and to a lesser extent F1), through more muddy sand to medium and coarse sands (sub-groups G1 – G6, then H1 – H2, before reaching E1 – E7). Conversely, those stations with rarely encountered fauna at relatively high abundances like *Paraphelia expansa* and *Caryophyllia smithii* may have artificially clustered out. The new biotopes proposed for such stations are very tentative at best based on the available data, and may be better integrated at the biotope complex level.

The geographical distribution of the assigned biotopes can be seen in Figure 3.22. There appeared to be some evidence of a transition from more muddy habitats in the north-east to sandy sediments in the south-west of the survey site, via an area with slightly more species diversity and more mixed sediments in the centre of the survey area. The two new biotopes, **OSa.(Pex)** and **OSa.(Ech)**, did not show any distinct patterns, suggesting that they reflect patchiness in the distribution of particular species. The spread of **OSa** biotopes showed a fairly good agreement with the UKSeaMap predicted habitat (McBreen *et al* 2011), whilst predicted areas of coarse sediment appeared to be more closely aligned with sand and mixed sediment biotopes.

Table 3.9. Summary of biotopes assigned to faunal abundance counts from South-West Deeps (West) MCZ grab data.

Biotope	Description	Cluster Groups	Station No.	Depth Range
A5.15 : Deep circalittoral coarse sediment **SS.SCS.OCS**	**Uncertain match**. Biotope assignment principally based on sample depth and sediment classification	B1	170	170m
A5.451 : Polychaete-rich deep *Venus* community in offshore mixed sediments **SS.SMx.OMx.PoVen**	Characteristic fauna included a large variety of polychaetes, such as *Notomastus, Aponuphis bilineata, Polycirrus, Galathowenia oculata, Aonides paucibranchiata* and *Hydroides norvegicus*. Other fauna included A*mphipholis squamata* and veneroid bivalves. Impoverished version of biotope seen in sub-group F1. Substratum included mixed sediment , coarse sediment and sand and muddy sand	F2, (F1)	62, 75, 86, 87, 95, 103, 104, 120, 217, 239, 243, 246, 259, 265, 374, (72, 76)	141 – 172m
A5.45x : Deep circalittoral mixed sediment with *Caryophyllia smithii* **SS.SMx.OMx.Csmi**	**New biotope.** Faunally sparse mixed and coarse sediments dominated by high abundances of *Caryophyllia smithii*. Substratum from stations included mixed and coarse sediments	A1	248, 250	153 – 154m
A5.27 : Deep circalittoral sand **SS.SSa.OSa**	**Uncertain match.** Assigned to some stations based on depth and sediment classification. Range of polychaetes and bivalves, present in low abundances, with relative contributions of species shifting dependant on coarseness of sediment. Substratum included mixed sediment, coarse sediment, and sand and muddy sand	B1, C*, C1, C3, D1, E*, E1 – E7, H1, H2, O*	1, 2, 3, 8, 26, 27, 33, 36, 38, 39, 41, 42, 43, 46, 49, 52, 56, 57, 65, 70, 79, 83, 84, 88, 91, 92, 96, 99, 100, 105, 108, 113, 114, 115, 121, 123, 124, 125, 128, 129, 136, 137, 140, 141, 143, 144, 145, 146, 147, 148, 150, 151, 153, 154, 155, 156, 157, 158, 160, 161, 162, 163, 164, 166, 167, 168, 169, 171, 172, 173, 174, 176, 177, 180, 181, 182, 183, 185, 188, 190, 191, 192, 193, 195, 200, 201, 203, 205, 206, 208, 209, 210, 212, 213, 215, 216, 218, 220, 224, 225, 228, 230, 254, 255, 256, 258, 261, 264, 269, 270	127 – 167m

Biotope	Description	Cluster Groups	Station No.	Depth Range
A5.27x : Deep circalittoral sand with heart urchins **SS.SSa.OSa.(Ech)**	**Uncertain match, possible new biotope.** Characteristic fauna included high abundances of species commensal with heart urchins, including *Tellimya ferruginosa* and *Montacuta substriata,* although urchins may have been under-sampled. Substratum included sand and muddy sand and coarse sediments	A2	94, 119, 370	136 – 157m
A5.27x : Deep circalittoral sand with *Paraphellia expansa* **SS.SSa.OSa.(Pex)**	**Uncertain match, possible new biotope.** Actiniaria in deep circalittoral sands, including *Paraphellia expansa*, with sparse amphipods and polychaetes. Substratum included sand and muddy sand	C2	5, 7, 10, 24, 48, 214	129 – 156m
A5.27 : Deep circalittoral sand / A5.15 : Deep circalittoral coarse sediments **SS.SSa.OSa** / **SS.SCS.OCS**	**Uncertain match.** Characteristic fauna included taxa diagnostic of coarse sediments such as *Polygordius* and *Glycera lapdium,* in addition to those found more typically in finer sediments such as *Galathowenia oculata* and *Aponuphis bilineata.* Substratum included sand and muddy sand and coarse sediments	G2	187, 241	150 – 165m
A5.27 : Deep circalittoral sand / A5.37 : Deep circalittoral mud **SS.SSa.OSa** / **SS.SMu.OMu**	**Uncertain match.** Characteristic fauna included *Galathowenia oculata, Magelona minuta* and *Astrorhiza* foraminifera and *Aspidosiphon muelleri*. Transition from muddy sand to sandy mud sediments. Substratum included sand and muddy sand and mud and sandy mud sediments	D2	9, 12, 13, 17, 20, 22, 23, 29, 30, 32, 35, 53, 55, 60, 66, 366	145 – 160m
A5.27 : Deep circalittoral sand / A5.37 : Deep circalittoral mixed sediment **SS.SSa.OSa** / **SS.SMx.OMx**	**Uncertain match.** Transition between polychaete rich **OMx.PoVen** biotope to less diverse sandy sediments. Characteristic species included *Galathowenia oculata, Aponuphis bilinetata*, *Pista* spp. and Nemertea. Other species such as *Polycirrus, Peresiella clymenoides, Chone, Notomastus* and *Loimia medusa* were also regularly found. Substratum included mainly sand and muddy sand, but also mud and sandy mud, mixed and coarse sediments	G3 – G6	16, 45, 50, 59, 61, 64, 69, 74, 78, 80, 81, 90, 98, 101, 107, 109, 110, 112, 116, 117, 118, 126, 138, 142, 179, 186, 196, 197, 199,221, 222, 227, 229, 233, 235, 236, 237, 242, 245, 247, 251, 253, 262, 266, 362, 364, 368, 376	139 – 169m

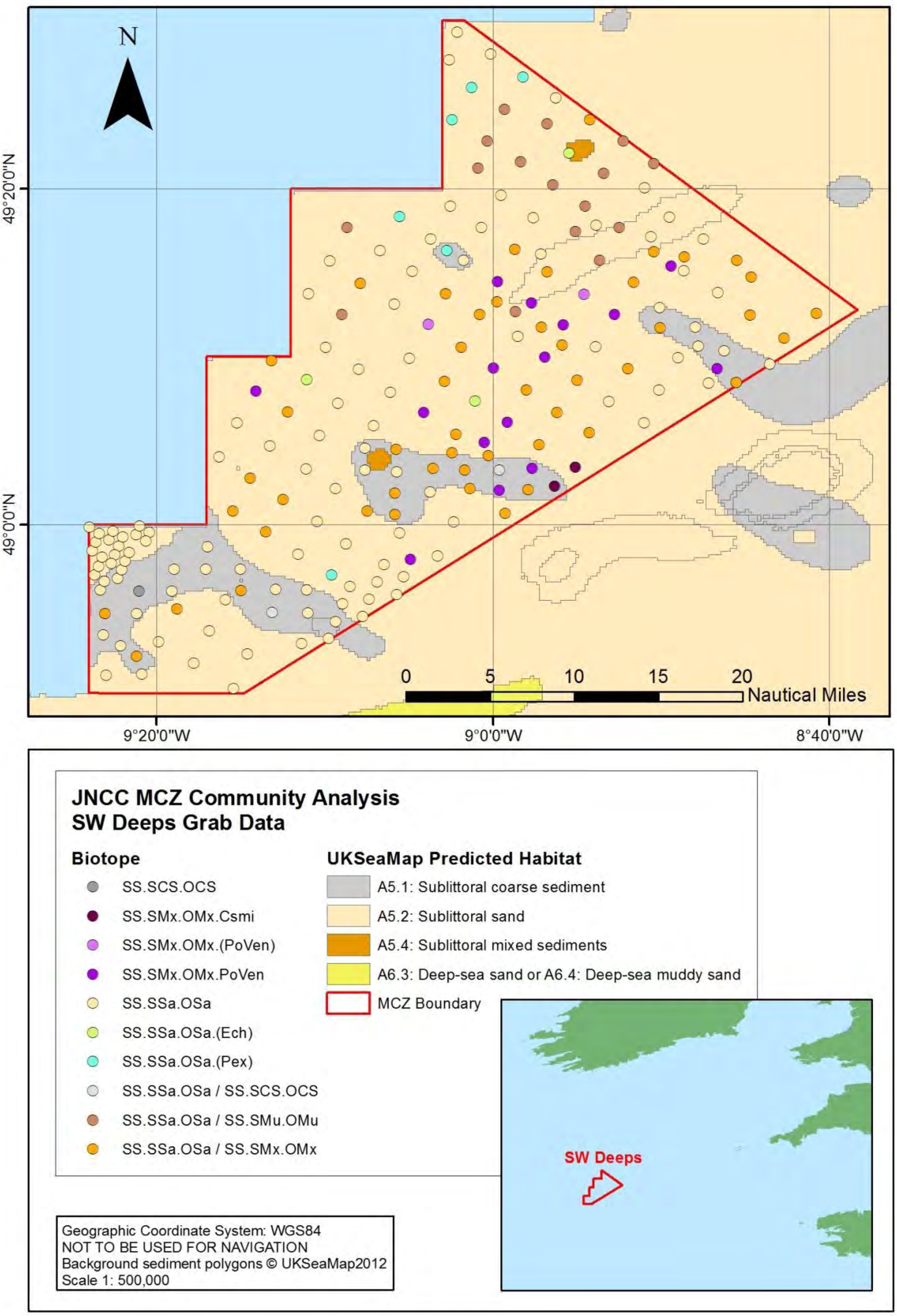


Figure 3.22. Geographical distribution of biotopes assigned to South-West Deeps (West) grab data following multivariate analysis.

3.4 Swallow Sand MCZ – grab data

3.4.1 Data rationalisation

The raw faunal data matrix was rationalised according to the methodology. For this particular data set, faunal recorded as 'Present' were removed prior to analysis. These taxa included some hydroids, bryozoans and fragments of individuals not sufficiently intact to count. Species recorded as juvenile were merged with adults where appropriate. Pelagic taxa (e.g. Copepoda and Chaetognatha) were removed, as were the meiofaunal Nematoda. Two insect taxa were removed as these were assumed to be a post sampling artefact, as such taxa would not be found in seabed habitats. As per the South-West Deeps (West) grab data, juvenile Echinoidea and Spatangoida were removed, as high numbers of these seasonal taxa potentially masked the actual trends in the faunal communities sampled. The rationalised data were then imported into PRIMER for statistical analysis.

3.4.2 Univariate statistical analysis

Table 3.10 summarises the results from the species diversity analysis of the Swallow Sand MCZ grab data. The total numbers of individuals present within the 103 sediment grab samples ranged from 19 individuals to 175 individuals per sample. The total number of taxa ranged from 10 to 56 per sample, indicating that there were some differences between the sample locations. Across all stations, the mean number of species/taxa per station was 30 ± 0.85 (±1 SE), and the mean number of individuals was 62 ± 2.96 (±1 SE). The samples showed a relatively high degree of evenness, with all samples having a J' value of 0.82 or higher, except station 388 (J' = 0.55) and station 509 (J' = 0.78). This suggested that the samples were not dominated by any particular taxa, with individuals spread evenly across the taxa present in each sample.

Table 3.10. Summary of infaunal community univariate statistics, Swallow Sand MCZ grab data. Total number of individuals (N), number of species (S), Margalef's species richness (d), Pielou's equitability index (J'), Shannon-Wiener diversity index (H') and Simpson's Dominance Index.

Station	S	N	d	J'	H'(log_e)	Simpson's
356	18	30	5.00	0.93	2.68	0.94
359	27	43	6.91	0.91	3.01	0.95
361	36	67	8.32	0.89	3.18	0.95
363	16	31	4.37	0.90	2.51	0.92
366	28	49	6.94	0.94	3.14	0.97
368	33	64	7.69	0.94	3.29	0.97
370	27	33	7.44	0.98	3.23	0.99
373	40	70	9.18	0.94	3.45	0.97
375	17	19	5.43	0.99	2.80	0.99
377	10	19	3.06	0.87	2.01	0.87
379	27	58	6.40	0.90	2.97	0.95
382	22	32	6.06	0.93	2.88	0.96
384	42	107	8.77	0.88	3.27	0.95
386	16	29	4.46	0.92	2.56	0.94
388	28	142	5.45	0.55	1.84	0.63
391	38	126	7.65	0.86	3.14	0.95
394	17	27	4.86	0.94	2.67	0.95
396	27	49	6.68	0.95	3.14	0.97

Station	S	N	d	J'	H'(log_e)	Simpson's
398	28	57	6.68	0.93	3.10	0.96
400	21	36	5.58	0.95	2.90	0.96
403	37	68	8.53	0.94	3.41	0.97
405	26	90	5.56	0.88	2.86	0.93
408	31	69	7.09	0.94	3.21	0.97
410	29	54	7.02	0.91	3.08	0.95
412	28	55	6.74	0.93	3.10	0.96
415	24	41	6.19	0.92	2.94	0.95
417	50	147	9.82	0.87	3.39	0.96
419	21	32	5.77	0.95	2.90	0.97
422	20	36	5.30	0.93	2.80	0.95
424	26	47	6.49	0.94	3.06	0.96
426	29	67	6.66	0.94	3.17	0.96
429	30	72	6.78	0.88	3.01	0.94
431	30	70	6.83	0.92	3.13	0.96
434	32	59	7.60	0.95	3.29	0.97
436	26	57	6.18	0.93	3.03	0.96
439	21	34	5.67	0.94	2.87	0.96
441	34	78	7.58	0.93	3.27	0.97
444	53	134	10.62	0.89	3.55	0.96
446	39	83	8.60	0.91	3.34	0.96
448	24	50	5.88	0.90	2.86	0.94
450	24	45	6.04	0.94	3.00	0.96
453	23	34	6.24	0.94	2.95	0.96
455	33	54	8.02	0.94	3.29	0.97
458	54	119	11.09	0.93	3.72	0.97
460	30	47	7.53	0.93	3.17	0.97
463	20	35	5.34	0.92	2.75	0.94
465	15	29	4.16	0.88	2.38	0.89
467	27	45	6.83	0.96	3.17	0.97
469	41	86	8.98	0.89	3.32	0.95
471	26	47	6.49	0.92	3.00	0.95
473	22	40	5.69	0.93	2.88	0.96
475	28	53	6.80	0.93	3.11	0.96
476	26	46	6.53	0.92	2.99	0.95
478	32	71	7.27	0.91	3.16	0.96
480	41	118	8.39	0.85	3.15	0.94
483	29	50	7.16	0.95	3.18	0.97
486	50	123	10.18	0.91	3.55	0.97
488	22	43	5.58	0.92	2.84	0.94
491	35	75	7.88	0.86	3.05	0.92
493	29	70	6.59	0.90	3.02	0.95
496	34	55	8.24	0.92	3.24	0.96
498	38	93	8.16	0.91	3.32	0.96
500	27	34	7.37	0.98	3.24	0.99
502	38	80	8.44	0.89	3.23	0.95

Station	S	N	d	J'	H'(log_e)	Simpson's
504	31	60	7.33	0.90	3.10	0.95
507	32	72	7.25	0.89	3.09	0.95
509	33	95	7.03	0.78	2.72	0.85
512	22	37	5.82	0.94	2.92	0.96
515	25	53	6.05	0.93	2.99	0.96
517	30	71	6.80	0.89	3.04	0.95
519	30	63	7.00	0.94	3.20	0.97
521	28	47	7.01	0.93	3.10	0.96
524	34	50	8.44	0.95	3.35	0.98
527	18	38	4.67	0.89	2.58	0.92
529	26	56	6.21	0.93	3.02	0.96
532	29	75	6.49	0.90	3.03	0.95
534	18	33	4.86	0.92	2.66	0.94
537	28	48	6.98	0.93	3.09	0.96
539	43	110	8.94	0.90	3.38	0.96
543	31	65	7.19	0.90	3.08	0.95
545	31	47	7.79	0.97	3.34	0.98
548	16	38	4.12	0.90	2.50	0.92
550	37	98	7.85	0.86	3.11	0.93
553	19	36	5.02	0.93	2.72	0.94
555	31	70	7.06	0.83	2.85	0.89
558	19	49	4.63	0.86	2.54	0.91
560	27	61	6.33	0.86	2.83	0.92
563	26	55	6.24	0.94	3.07	0.96
566	25	57	5.94	0.90	2.91	0.94
568	28	43	7.18	0.96	3.19	0.97
570	29	56	6.96	0.94	3.16	0.97
573	22	29	6.24	0.97	2.99	0.98
575	35	67	8.09	0.88	3.12	0.93
578	56	175	10.65	0.85	3.43	0.94
580	28	44	7.14	0.89	2.95	0.92
582	40	100	8.47	0.86	3.18	0.93
585	28	57	6.68	0.89	2.98	0.94
588	45	123	9.14	0.82	3.13	0.91
590	27	49	6.68	0.92	3.02	0.95
593	32	67	7.37	0.92	3.18	0.96
595	29	47	7.27	0.93	3.13	0.96
597	21	31	5.82	0.96	2.94	0.97
600	36	112	7.42	0.84	3.02	0.93

3.4.3 Multivariate statistical analysis

After rationalisation, only two taxa were recorded in abundances greater than 35 individuals per sample, so it was not deemed appropriate to use any transformations on the data set. A resemblance matrix using non-standardised, untransformed data was created using Bray Curtis similarity. Cluster analysis was then performed, and the resulting dendrogram plotted (Figure 3.23).

The dendrogram for the Swallow Sand MCZ grab data showed one outlier (station 388; O*), which diverged at ~10% similarity. Group A was a small cluster of four stations that branched off at ~20%. Sub-group B1 and an outlier (station 439; B*) split away at ~22% similarity, followed by sub-group B2 at ~24% similarity. Three small clusters of stations separated off at between ~25 – 27%, and were placed together in sub-group B3. Two large clusters of stations then diverged at ~28% similarity. The first group included 56 stations, divided into sub-groups C1 and C2, with two outlying stations (C*). The outlying stations, 370 and 460, branched away at ~29% and ~31% similarity respectively. Sub-group C1 contained 23 stations, and diverged from sub-group C2, which contained 31 stations, at ~32% similarity. All stations within C1 were at least ~35% similar, and those within C2 were at least ~33% similar. The last large cluster was split into three sub-groups, D1 – D3. Sub-group D1 contained two stations, and branched away at ~29% similarity. Sub-group D2 was also small, containing three stations, and separated away from sub-group D3 at ~35% similarity. The 15 stations within sub-group D3 were all at least ~38% similar. Apart from the outlying station 388, all stations within the Swallow Sand grab survey were at least 20% similar.

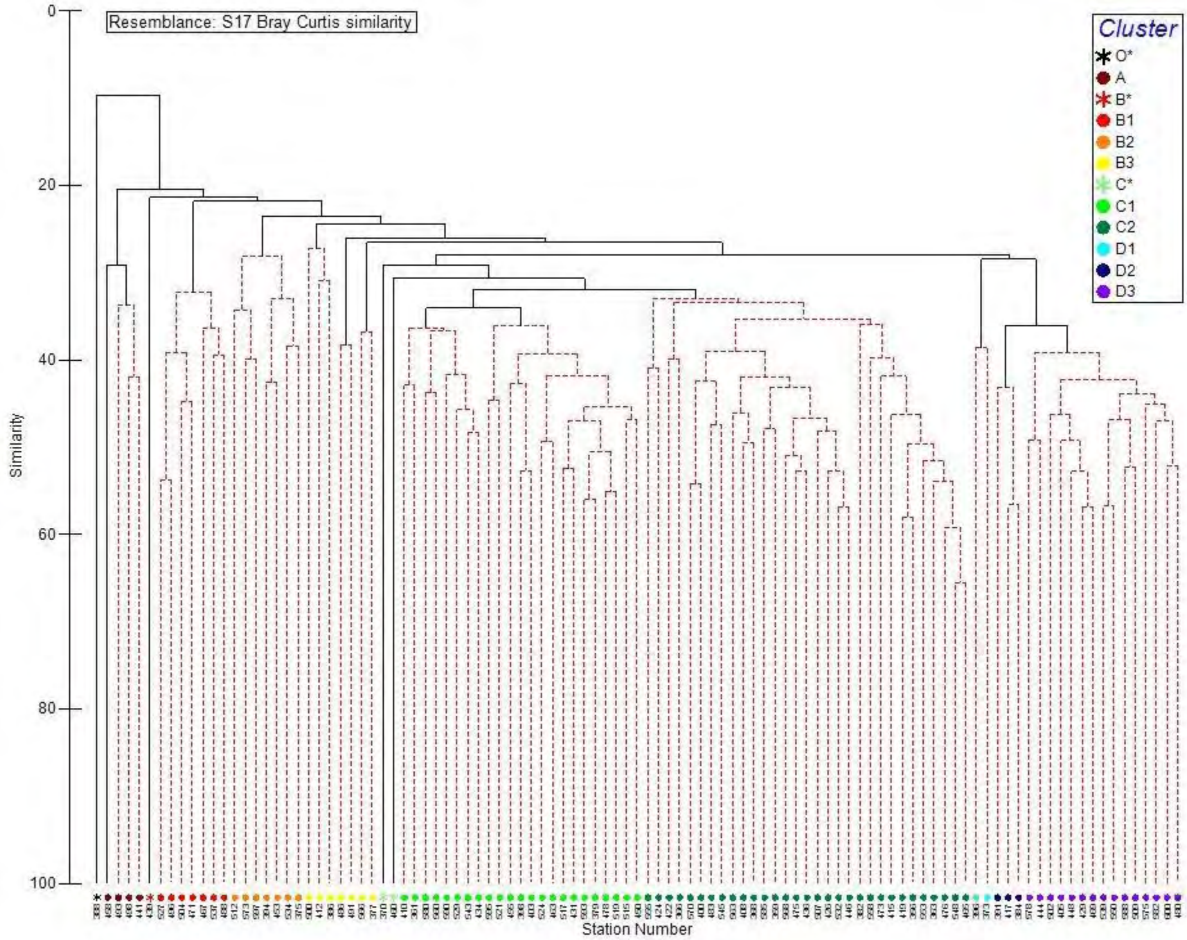


Figure 3.23. Dendrogram plot following cluster analysis of macrofaunal abundance counts, Swallow Sand MCZ grab data. Samples coloured according to assigned cluster groups.

Figure 3.24 displays a 2D MDS ordination plot of the cluster analysis. The large cluster of stations in the middle of the plot reflected the relatively high similarity seen between all the stations in the dendrogram. The MDS plot showed some support for the dendrogram, with stations tending to be grouped together according to their assigned sub-groups. Sub-group B3 did not appear to be well supported. The stress value of 0.24 was relatively high, so too much reliance should not be placed on the exact details within the 2D MDS plot.

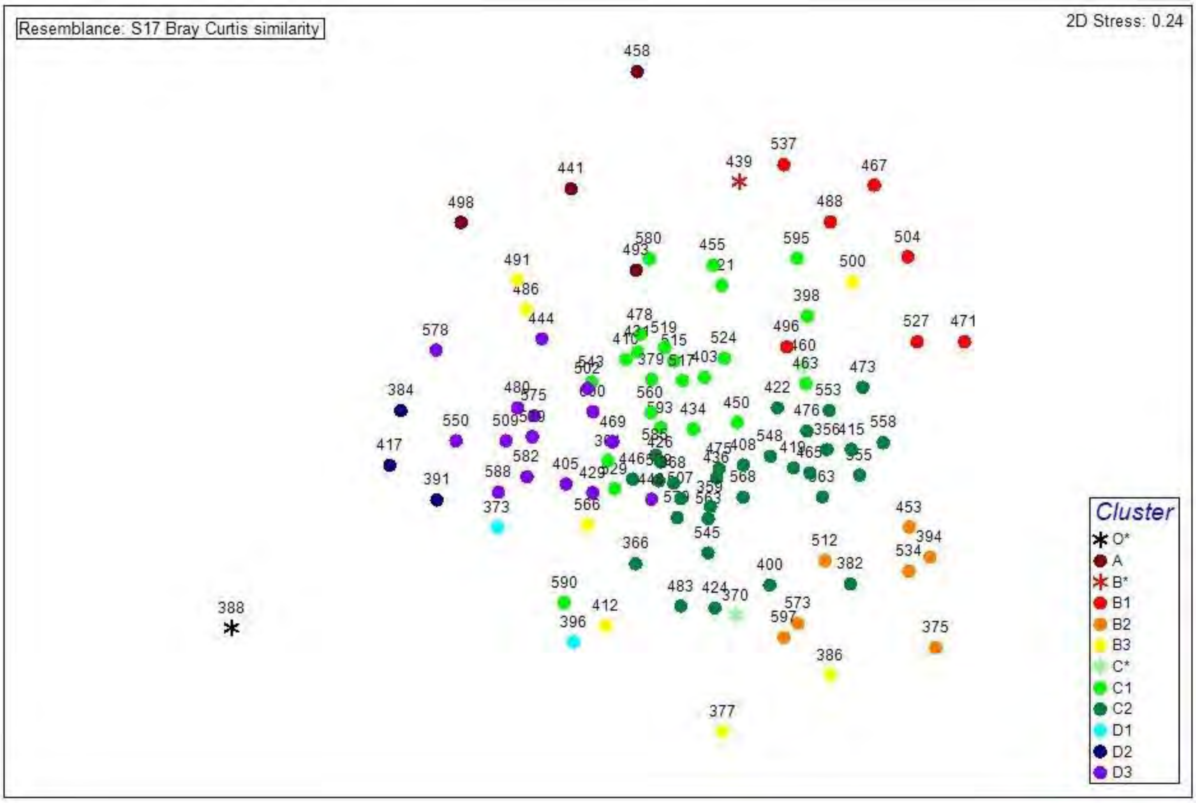


Figure 3.24. MDS ordination plot of Swallow Sand MCZ grab data.

Figure 3.25 shows the dendrogram with the EUNIS sediment classification derived from the PSA results for each sample displayed. The patterns of clustering derived from the faunal abundance data did not appear to relate to the EUNIS sediment classifications of the samples, with a spread of mud and sandy mud, mixed sediments and sand and muddy sand found across most of the clusters.

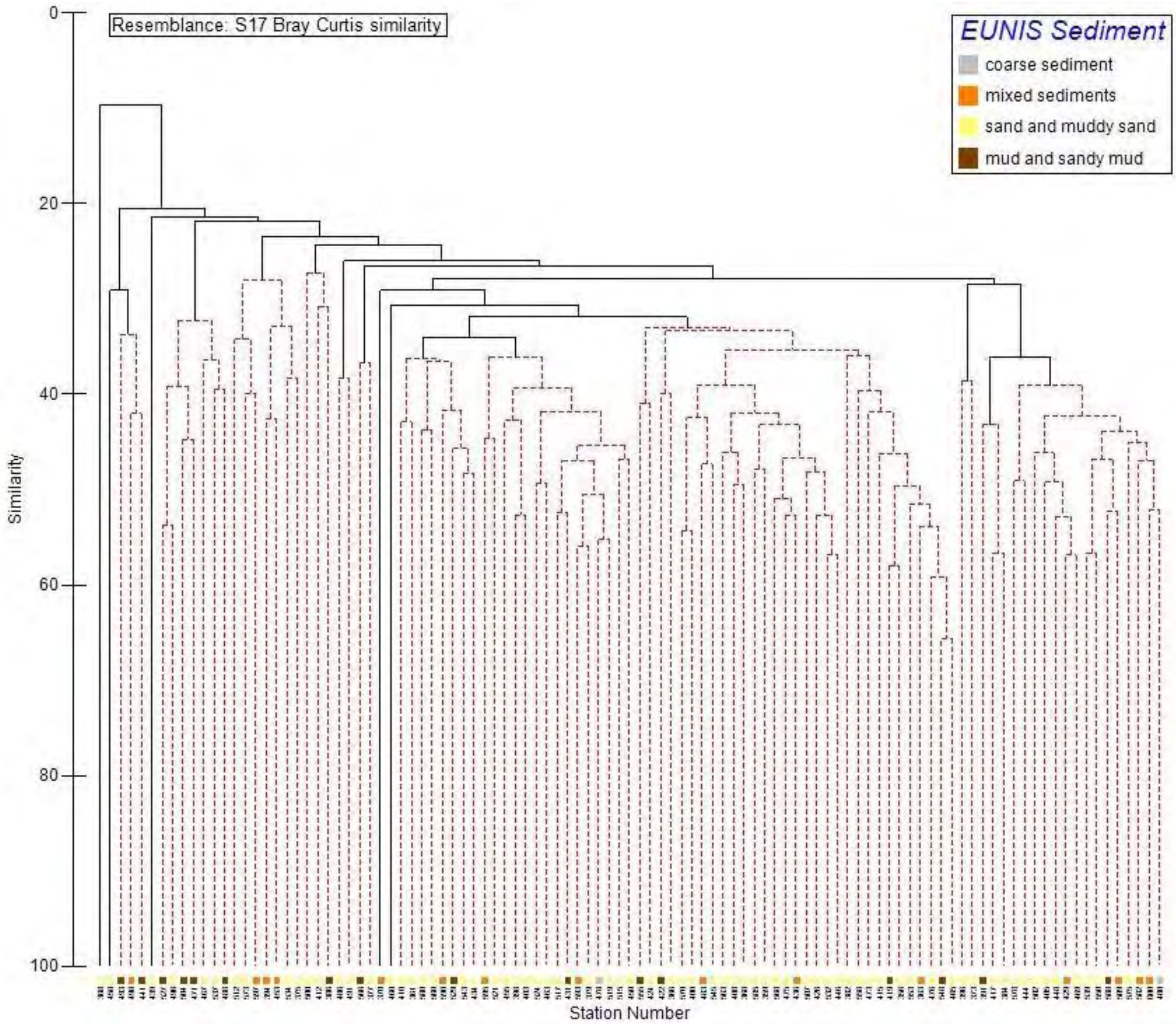


Figure 3.25. Dendrogram plot following cluster analysis of macrofaunal abundance counts, Swallow Sand grab data. Samples coloured according to EUNIS sediment classification based on PSA data.

SIMPER analysis was undertaken to assess which species were characteristic for each of the sub-groups identified from the cluster analysis. Table 3.11 outlines the characteristic taxa for each sub-group, listing those taxa that contributed at least 90% similarity for each sub-group. Full SIMPER results showing all contributing species for each sub-group can be found in Appendix 10.

Group A was characterised by a variety of different polychaete species, including *Paramphinome jeffreysii, Glycera lapidum, Owenia fusiformis, Laonice bahusiensis* and *Notomastus.* Aside from polychaetes, other characterising fauna included Nemertea, *Phoronis*, the amphipod *Atylus vedlomensis* and the echinoderms *Echinocyamus pusillus* and juvenile Ophiuridae.

The relative abundance of *Echinocyamus pusillus* contributed ~35% to the similarity of the stations within sub-group B1, followed by juvenile Amphiuridae at ~14%, then *Galathowenia oculata* and *Aricidea cerrutii* at ~5% and ~4% respectively. Some of the characterising species were similar to those from group A, including *Paramphinome jeffreysii, Aricidea cerrutii, Notomastus,* and *Spiophanes bombyx.* These species contributed different percentages to similarity of the stations within group A and sub-group B1. Stations within group A tended to have slightly more taxa present compared to B1.

Juvenile Amphiuridae also had a high relative contribution to sub-group B2 (~19%). Other species that characterised both sub-group B1 and B2 included *Galathowenia oculata, Nephtys longosetosa, Phoronis, Antalis entalis,* and *Owenia fusiformis.* Sub-group B2 was characterised by more species of bivalves than sub-group B2, including *Chamelea striatula, Arctica islandica* and *Thyasira flexuosa*.

The list of taxa that characterised sub-group B3 contained some that were present in both sub-groups B1 and B2 (e.g. *Phoronis,* juvenile Amphiuridae, *Antalis entails, Galathowenia oculata* and *Nephtys longosetosa*). Other species were only present in B2 (e.g. *Goniada maculate, Amphiura filiformis* and *Arctica islandica*). The top two contributing species for sub-group B3 were *Scoloplos armiger* and *Trichobranchus roseus* (~25% and 11% respectively) did not characterise either sub-groups B1 and B2.

Five of the six top contributing taxa in sub-groups C1 and C2 were the same. These taxa were *Paramphinome jeffreysii, Galathowenia oculata,* Nemertea, *Scoloplos armiger* and juvenile Amphiuridae, which together contributed a total of ~48% and ~56% similarity between the stations in sub-groups C1 and C2 respectively. Other taxa that characterised both sub-groups included *Phoronis, Notomastus, Spiophanes bombyx, Amphiura filiformis, Chaetozone setosa, Owenia fusiformis, Antalis entalis, Echinocyamus pusillus* and *Goniada maculata.* Sub-group C1 was also characterised by *Paradoneis lyra, Urothoe elegans, Myriochele* and *Labidoplax buskii.* Species that characterised only sub-group C2 included *Thyasira flexuosa, Eudorellopsis deformis, Trichobranchus roseus* and *Echinocardium flavescens*. The outlying group C* was characterised by many of the same taxa as sub-groups C1 and C2 (*Spiophanes bombyx, Antalis entalis, Nephtys longosetosa, Paramphinome jeffreysii, Scoloplos armiger, Galathowenia oculata* and juvenile Amphiuridae). C* was characterised by two species not seen on the list of characteristic species for C1 and C2, which were *Aonides paucibranchiata* and *Samytha sexcirrata*.

Sub-groups D1 – D3 had some taxa that characterised all three clusters, such as Nemertea, *Chaetozone setosa,* juvenile Amphiuridae, *Notomastus* and *Thyasira flexuosa*. However, there were more differences between sub-groups D1 – D3 compared to C1 and C2. Sub-group D1 was characterised by some taxa that were absent from D2, but present in D3, including *Streblosoma bairdi, Labidoplax buskii, Trichobranchus roseus,* and *Antalis entalis*. Sub-group D2 was characterised by some taxa that did not characterise D1 or D3, including *Diplocirrus glaucus, Praxillella affinis, Laonice sarsi, Minuspio cirrifera, Levinsenia gracilis* and *Lucinoma borealis.* Many of the taxa that characterised sub-group D3 also characterised sub-group C1, albeit with different percentage contributions to the similarities between the stations.

The SIMPER results demonstrated that some taxa appeared to be relatively ubiquitous across the different sub-groups. These included *Paramphinome jeffreysii, Galathowenia oculata* and juvenile Amphiuridae for example. Overall there were many similarities between the taxa present within the lists of fauna that characterised each station. This suggested that there may have been a transition between broadly similar habitats across the survey site rather than distinctly different habitats.

3.4.4 Spatial distribution of samples

Figure 3.26 shows the spatial distribution of the sample sites within the survey area. No pattern was discernible in the distribution of the assigned sub-groups, suggesting some patchiness in habitats over the survey area.

Table 3.11. Results of SIMPER analysis of the sub-groups identified from cluster analysis of macrofaunal abundance counts, Swallow Sand MCZ grab data.

Group / Cluster	% Contribution of characterising species	
	Taxa / species	**Contribution (%)**
A	*Paramphinome jeffreysii*	12.56
	Glycera lapidum (agg.)	12.03
	NEMERTEA	10.81
	Owenia fusiformis	7.48
	Laonice bahusiensis	6.54
	Notomastus	6.52
	Echinocyamus pusillus	4.5
	Galathowenia oculata	3.79
	Phoronis	3.43
	Atylus vedlomensis	3.17
	Aricidea cerrutii	3.11
	Spiophanes bombyx	2.81
	Pseudonotomastus southerni	2.57
	Similipecten similis	2.54
	Aonides paucibranchiata	2.25
	Spiophanes kroyeri	2.18
	Dipolydora caulleryi	1.74
	Glycinde nordmanni	1.64
	Ophiuridae (juv.)	1.59
B1	*Echinocyamus pusillus*	35.25
	Amphiuridae (juv.)	14.35
	Galathowenia oculata	4.95
	Aricidea cerrutii	4.35
	Paramphinome jeffreysii	3.51
	Polycirrus	3.44
	Spiophanes bombyx	3.07
	Nephtys longosetosa	3.02
	Notomastus	2.8
	Phoronis	1.89
	Crenella decussata	1.84
	Antalis entalis	1.74
	Goniada maculata	1.56
	NEMERTEA	1.53
	Ophelia borealis	1.53
	Spatangus purpureus	1.16
	Edwardsia claparedii	0.87
	Cerianthus lloydii	0.84
	Harmothoe glabra	0.81
	Owenia fusiformis	0.78
	Aricidea simonae	0.78

Group / Cluster	% Contribution of characterising species	
	Taxa / species	Contribution (%)
B2	Amphiuridae (juv.)	18.95
	Antalis entalis	11.9
	Goniada maculata	9.18
	Galathowenia oculata	8.28
	Amphiura filiformis	5.63
	Owenia fusiformis	5.34
	Nephtys longosetosa	5
	NEMERTEA	4.76
	Sthenelais limicola	4.76
	Chamelea striatula	3.27
	Arctica islandica	3.15
	Thyasira flexuosa	1.8
	Echinocardium cordatum	1.75
	Phoronis	1.61
	Labidoplax buskii	1.57
	Glycera alba	1.45
	Nephtys (juv.)	1.45
	Spiophanes kroyeri	1.45
B3	*Scoloplos armiger*	25.21
	Trichobranchus roseus	11.08
	Phoronis	9.3
	Galathowenia oculata	8.03
	Paramphinome jeffreysii	6.69
	Goniada maculata	4.51
	Notomastus	4.08
	Amphiura filiformis	3.39
	Amphiuridae (juv.)	3.08
	Chaetozone setosa	2.93
	Paradoneis lyra	2.78
	Antalis entalis	2.13
	Thyasira equalis	1.78
	Nephtys longosetosa	1.65
	Aricidea simonae	1.64
	Arctica islandica	1.37
	Labidoplax buskii	1.31
C*	*Spiophanes bombyx*	16.67
	Antalis entalis	16.67
	Nephtys longosetosa	8.33
	Paramphinome jeffreysii	8.33
	Scoloplos armiger	8.33
	Aonides paucibranchiata	8.33
	Galathowenia oculata	8.33
	Samytha sexcirrata	8.33
	Amphiuridae (juv.)	8.33

Group / Cluster	% Contribution of characterising species	
	Taxa / species	Contribution (%)
C1	*Paramphinome jeffreysii*	12.58
	Galathowenia oculata	12.51
	Phoronis	10.02
	NEMERTEA	8.2
	Scoloplos armiger	7.99
	Amphiuridae (juv.)	6.57
	Notomastus	5.65
	Labidoplax buskii	5.16
	Amphiura filiformis	4.67
	Spiophanes bombyx	2.42
	Antalis entalis	1.78
	Chaetozone setosa	1.51
	Paradoneis lyra	1.28
	Echinocyamus pusillus	1.28
	Goniada maculata	1.27
	Aricidea catherinae	1.25
	Myriochele	1.01
	Owenia fusiformis	0.96
	Nephtys longosetosa	0.92
	Urothoe elegans	0.87
	Anaitides groenlandica	0.84
	Aonides paucibranchiata	0.84
	Spiophanes kroyeri	0.69
C2	Amphiuridae (juv.)	18.39
	Scoloplos armiger	13.86
	NEMERTEA	10.14
	Paramphinome jeffreysii	7.15
	Galathowenia oculata	6.31
	Spiophanes bombyx	6.1
	Trichobranchus roseus	4.32
	Owenia fusiformis	3.44
	Phoronis	2.97
	Goniada maculata	2.93
	Chaetozone setosa	2.71
	Antalis entalis	2.36
	Nephtys longosetosa	2.09
	Phaxas pellucidus	1.35
	Echinocyamus pusillus	1.24
	Amphiura filiformis	1.14
	Echinocardium flavescens	1.07
	Thyasira flexuosa	0.99
	Notomastus	0.8
	Eudorellopsis deformis	0.78

Group / Cluster	% Contribution of characterising species	
	Taxa / species	**Contribution (%)**
D1	NEMERTEA	13.04
	Chaetozone setosa	8.7
	Notomastus	8.7
	Ampharete lindstroemi	8.7
	Thyasira flexuosa	8.7
	Amphiuridae (juv.)	8.7
	Labidoplax buskii	8.7
	Nephtys (juv.)	4.35
	Heteromastus filiformis	4.35
	Galathowenia oculata	4.35
	Trichobranchus roseus	4.35
	Streblosoma bairdi	4.35
	Antalis entalis	4.35
D2	*Paramphinome jeffreysii*	19.92
	Chaetozone setosa	13.29
	NEMERTEA	12.01
	Praxillella affinis (Type A)	10.49
	Thyasira flexuosa	6.64
	Notomastus	4.95
	Diplocirrus glaucus	3.2
	Amphiuridae (juv.)	3.2
	Laonice sarsi	2.86
	Goniada maculata	1.66
	Minuspio cirrifera	1.66
	Lucinoma borealis	1.66
	Parvicardium minimum	1.66
	Ampharete falcata	1.53
	Levinsenia gracilis	1.2
	Nephasoma (?)	1.1
	Abyssoninoe hibernica	1.1
	Amphictene auricoma	1.02
	Phaxas pellucidus	1.02
D3	*Paramphinome jeffreysii*	37.61
	NEMERTEA	8.06
	Galathowenia oculata	6.91
	Amphiuridae (juv.)	5.3
	Scoloplos armiger	5.23
	Chaetozone setosa	4.12
	Amphiura filiformis	2.73
	Goniada maculata	2.65
	Notomastus	2.48
	Phoronis	2.3
	Antalis entalis	2.12
	Trichobranchus roseus	1.83
	Owenia fusiformis	1.68
	Labidoplax buskii	1.47
	Thyasira flexuosa	1.21
	Spiophanes kroyeri	1.11
	Thyasira equalis	0.86
	Paradoneis lyra	0.74
	Spiophanes bombyx	0.7
	Streblosoma bairdi	0.65

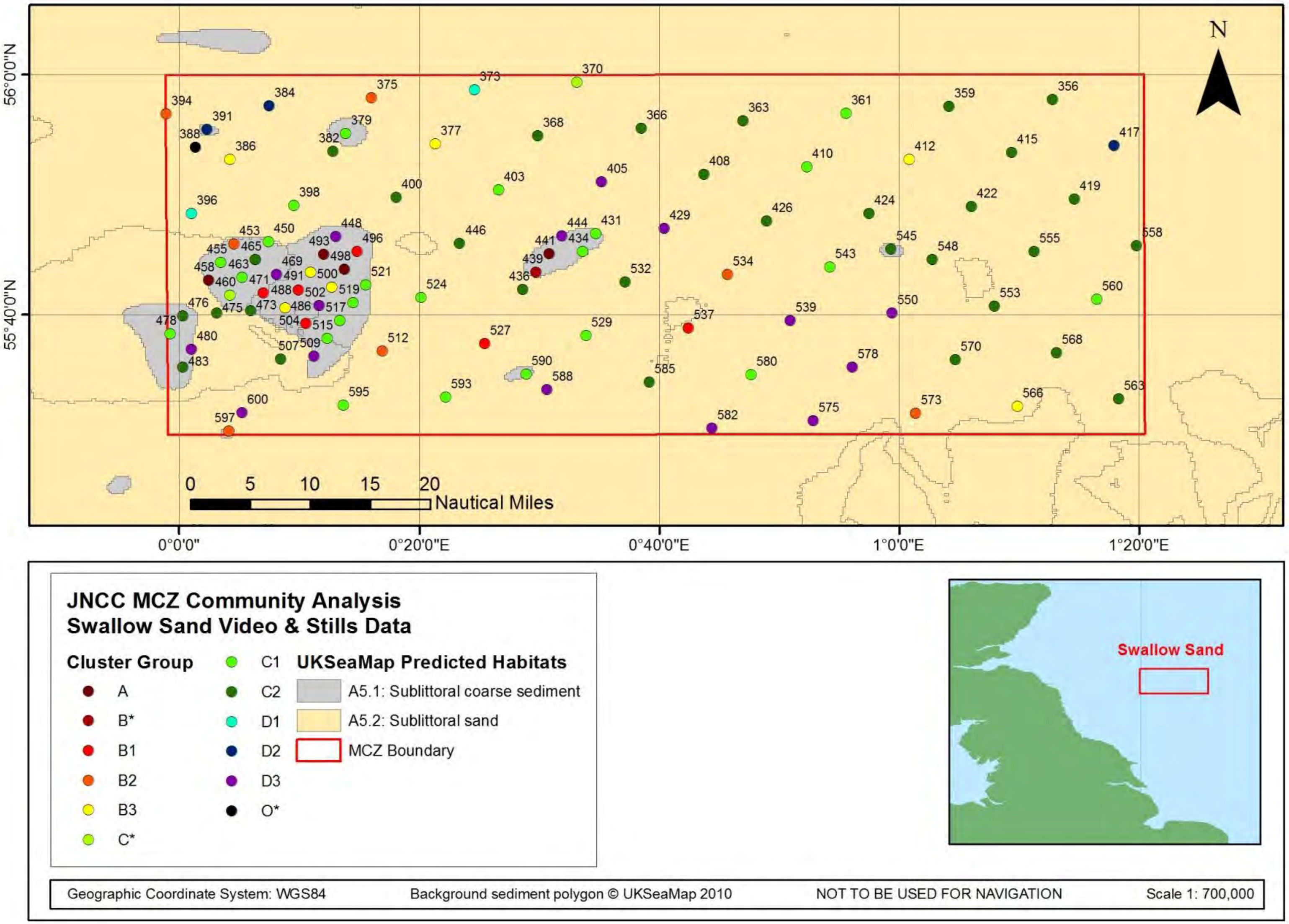


Figure 3.26. Geographical distribution of samples, Swallow Sand MCZ grab data.

3.4.5 Biotope designation

Table 3.12 summarises the biotopes designated to the Swallow Sand MCZ grab data. The assignment of each biotope is described in more detail below. As discussed within the SIMPER analysis, the commonality of many of the characteristic species across the sub-groups suggested that the samples probably represented slight variations on the same habitat, or a gradual transition between two habitats.

The combination of species that characterised sub-group D3 bore very close resemblance to that described by the biotope **SS.SMu.OMu.PjefThyAfil.** *Paramphinome jeffreysii*, *Amphiura filiformis,* and two species of *Thyasira* were present within this sub-group, in addition to *Goniada maculata, Labidoplax buskii, Spiophanes kroyeri* and juvenile Amphiuridae. Looking at the faunal matrix in more detail, stations within sub-group D2 had many of same species present as those characteristic of **PjefThyAfil**, although they were not drawn out in the SIMPER analysis. Sub-group D2 had some species such as *Diplocirrus glaucus* present in relatively high abundances, which suggested a slightly higher sand fraction within the sediment compared to sub-group D3. The presence of some species within sub-groups D1 – D2 such as *Chaetozone setosa, Scoloplos armiger* and *Parvicardium minimum* also suggested some affinity with the biotope complex **SS.SSa.OSa.** The EUNIS sediment classification also showed a predominance of sandy and muddy sediments within sub-groups D1 – D3. However, the taxa that characterised **PjefThyAfil** were present in higher abundances, making this biotope a better fit for the faunal communities sampled. Sub-group D1 had a noticeable lack of *Paramphinome jeffreysii*, and slightly lower abundances of amphiurid brittlestars*.* However, the other fauna were generally very similar to those within sub-groups D2 and D3. It was deemed that the biotope **SS.SMu.OMu.(PjefThyAfil)** was the best biotope to assign to sub-group D1.

The presence of the cumacean *Eudorellopsis deformis* within sub-group C2 suggested some similarities with the biotope **SS.SSa.OSa.MalEdef.** Other species within the biotope description such as *Amphiura filiformis, Harpinia antennaria, Scoloplos armiger* and *Chaetozone setosa* were also found within the samples from sub-group C2. However, there was a general lack of maldanid polychaetes within the samples in this sub-group. The presence of fauna such as *Paramphinome jeffreysii* and *Galathowenia oculata* suggested that the habitat probably represented muddy sand, and showed some similarities to the fauna present within sub-groups D2 – D3. Sub-group C2 was therefore assigned the biotope **SS.SSa.OSa.(MalEdef)** / **SS.SMu.OMu.** Sub-group C1 also showed a combination of species that were characteristic of both sand and mud habitats. *Scoloplos armiger, Owenia fusiformis* and *Nephtys longosetosa* suggested sandy habitats, whilst the presence of *Paramphinome jeffreysii* together with amphiurid brittlestars, *Labidoplax buskii, Aricidea catherinae* and *Spiophanes bombyx* were more reminiscent of the **OMu.PjefThyAfil** biotope. Abundances of many of these characteristic species were low, so sub-group C1 was assigned the biotope **SS.SSa.OSa** / **SS.SMu.OMu.(PjefThyAfil)** to highlight the similarities between the identified fauna and these two biotopes. The presence of taxa like *Pennatula phosphorea, Edwardsia claparedii* and *Cerianthus lloydii* also suggested some affinity with circalittoral sandy mud biotopes. The outlying group C* again contained fauna from both muddy and sandy habitats, although lacked enough characteristic species to suggest an appropriate sub-biotope. These stations were therefore assigned the biotope **SS.SSa.OSa** / **SS.SMu.OMu**.

The fauna that characterised sub-groups B1 – B3 were also typical of both mud and sand environments, containing many of the species seen in the other sub-groups. Sub-groups B1 – B3 contained lower abundances of *Paramphinome jeffreysii* compared to stations within sub-groups C1, C2, D2 and D3. Sub-groups B1 – B3 had faunal communities that included a range of polychaetes such as *Owenia fusiformis, Galathowenia oculata, Goniada maculata, Aricidea* spp., and *Nephtys* spp. that were characteristic of both sand and mud habitats, along with Amphiuridae brittlestars, veneroid bivalves, *Labidoplax buskii, Thyasira* and *Antalis entalis.* No combinations of fauna matched any particular sub-biotopes. The biotope **SS.SSa.OSa** / **SS.SMu.OMu** was assigned as a best fit in order to reflect the community components that were typical of both biotope complexes.

Group A was similar to sub-groups B1 – B3 in that the fauna was characteristic of both sand and mud, without any combinations of fauna that suggested a particular sub-biotope. The stations within group A were also assigned the biotope **SS.SSa.OSa** / **SS.SMu.OMu**.

Of the remaining outlying groups, station 439 (B*) had a faunally community very similar to sub-groups A, B1 – B3, although lacking certain fauna such as Amphiuridae brittlestars that were typical of stations within these clusters. The biotope **SS.SSa.OSa** / **SS.SMu.OMu** was also assigned to this station. Station 388 (O*) was dominated by high abundances of *Ditrupa arietina*, with 86 individuals recorded. This was very distinct from the other stations sampled within the survey area, although the rest of the faunal community was relatively similar to that seen in the other samples. Station 388 was also the deepest station sampled, ~50m deeper than any other sample, which may also explain the high abundances of *D. arietina* that were not seen in any other sample. The biotope **SS.SSa.OSa.Dari** was assigned to reflect the high abundance of *D. arietina* on muddy sand sediment.

From the biotopes assigned, it can be seen that the stations within the survey area were principally characterised by faunal communities that indicative of both sand and mud habitats. Examining the percentage mud content of the sediments, 65 of the 103 stations had mud fractions greater than 10% by weight of the sample, and 99 samples had mud contents in excess of 2%. The PSA results also showed that 61 stations had a mean sediment classification of fine sand or smaller particle size. The faunal communities correlate well with the large amount of fine material seen from the PSA results. There were broad agreements with the assigned biotopes and the sand and muddy sand EUNIS sediment classification for the majority of the samples. The faunal communities represented a transition from a sandy mud biotope to a muddy sand biotope, retaining species characteristic of both broad habitat types. The muddier biotope appeared to be very similar to **SS.SMu.OMu.PjefThyAfil**, whilst the sandier biotope showed some affinity to **SS.SSa.OSa.MalEdef** or some of the circalittoral sandy mud biotopes (e.g. **SS.SMu.CSaMu.ThyNten**).

It is worth noting that the bivalve *Arctica islandica* was present in 31 out of the 103 samples taken from the survey area. The bivalve was present both as adults and juveniles, typically numbering one or two individuals in a sample. *Arctica islandica* is on the OSPAR List of Threatened and /or Declining Species and Habitats.

A geographical spread of the assigned biotopes is displayed in Figure 3.27. There appeared to be some patches where **OMu.PjefThyAfil** was more dominant, with some transitional habitats characterised by sandier sediments between them. The distribution of the biotopes was probably closely related to patchiness in the underlying sediment composition.

Table 3.12. Summary of biotopes assigned to faunal abundance counts from Swallow Sand MCZ grab data

Biotope	Description	Cluster Groups	Samples	Depth Range
A5.27x : Deep circalittoral muddy sand with *Ditrupa arietina* **SS.SSa.OSa.Dari**	**New biotope.** Muddy sand sediment characterised by high numbers of *Ditrupa arietina.* Uncertain biotope, only based on data from one station.	O*	388	140m
A5.27 : Deep circalittoral sand / A5.37 : Deep circalittoral mud **SS.SSa.OSa / SS.SMu.OMu**	**Uncertain match**. Fauna present characteristic of both sand and mud habitats, including *Paramphinome jeffreysii*, *Amphiura filiformis, Thyasira, Labidoplax buskii, Owenia fusiformis, Scoloplos armiger* and *Chaetozone setosa*. Substratum for stations included sand and muddy sand, mixed sediments and mud and muddy sand	A, B*, B1 – B3, C*	441, 458, 493, 498, 439, 467, 471, 488, 496, 504, 527, 537, 375, 394, 453, 512, 534, 573, 597, 377, 386, 412, 486, 491, 500, 566, 370, 460	61 – 90m
A5.27 : Deep circalittoral sand / A5.376 : *Paramphinome jeffreysii*, *Thyasira* spp. and *Amphiura filiformis* in offshore circalittoral sandy mud **SS.SSa.OSa / SS.SMu.OMu.(PjefThyAfil)**	**Uncertain match**. Fauna present included *Paramphinome jeffreysii* together with amphiurid brittlestars, *Labidoplax buskii, Aricidea catherinae* and *Spiophanes bombyx,* together with *Scoloplos armiger, Owenia fusiformis* and *Nephtys longosetosa.* Substratum for stations included coarse sediment, sand and muddy sand, mixed sediments and mud and muddy sand	C1	361, 379, 398, 403, 410, 431, 434, 450, 463, 478, 515, 517, 519, 521, 524, 529, 543, 560, 580, 590, 593, 595	63 – 86m
A5.271 : Maldanid polychaetes and *Eudorellopsis deformis* in deep circalittoral sand or muddy sand / A5.37 : Deep circalittoral mud **SS.SSa.OSa.(MalEdef) / SS.SMu.OMu**	**Uncertain match.** Characteristic fauna included *Eudorellopsis deformis, Amphiura filiformis, Harpinia antennaria, Scoloplos armiger* and *Chaetozone setosa* alongside *Paramphinome jeffreysii* and *Galathowenia oculata.* Substratum for stations included sand and muddy sand, mixed sediments and mud and muddy sand	C2	356, 363, 366, 382, 400, 408, 415, 419, 422, 424, 426, 436, 446, 465, 473, 475, 476, 483, 507, 532, 545, 548, 553, 555, 558, 563, 568, 570, 585	66 – 94m
A5.376 : *Paramphinome jeffreysii*, *Thyasira* spp. and *Amphiura filiformis* in offshore circalittoral sandy mud **SS.SMu.OMu.PjefThyAfil**	Characteristic fauna included *Paramphinome jeffreysii*, *Amphiura filiformis,* and *Thyasira* spp., in addition to *Goniada maculata, Labidoplax bushii, Spiophanes kroyeri* and juvenile Amphiuridae. Some fauna such as *Chaetozone setosa, Scoloplos armiger* and *Parvicardium minimum* characteristic of sandier sediments also present. Sub-group D1 assigned to **(PjefThyAfil)** as lacking *P. jeffreysii*, and only low abundances of Amphiuridae brittlestars.	D2, D3, (D1)	384, 391, 417, 405, 429, 444, 448, 469, 480, 502, 509, 539, 550, 575, 578, 582, 588, 600, (373, 396)	62 – 85m

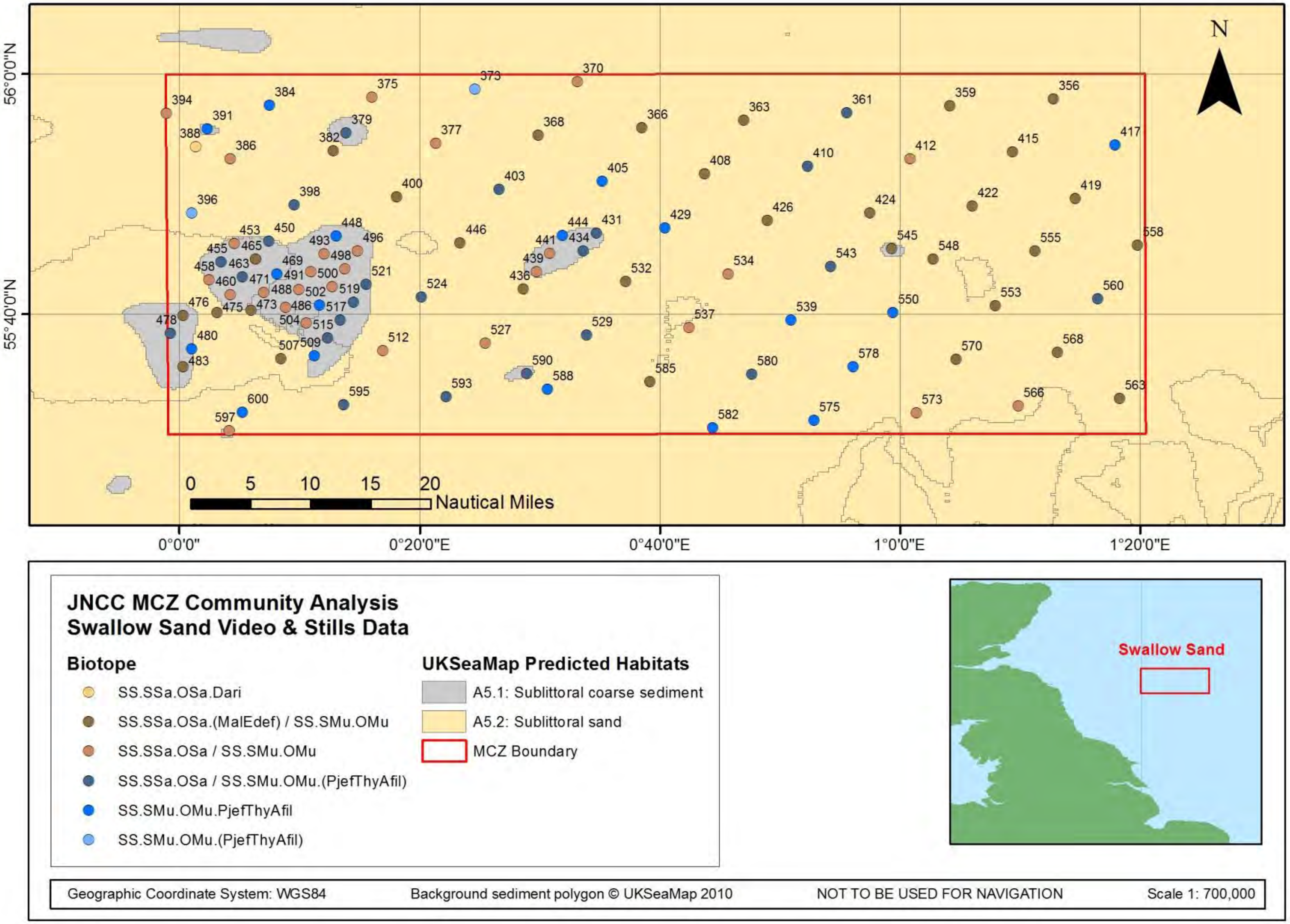


Figure 3.27. Geographical distribution of biotopes assigned to Swallow Sand MCZ grab data following multivariate analysis.

3.5 North East of Farnes Deep MCZ – video and stills data

3.5.1 Video data

3.5.1.1 Data rationalisation

The raw faunal data matrix was rationalised according to the methodology. For the North East of Farnes Deep video data set, all pelagic and highly mobile fauna were removed from the data set. These taxa included Osterichthyes, *Callionymus*, Pleuronectidae and *Myxine glutinosa*. After rationalisation, two video segments had no visible fauna recorded (171_S2 and 182_S2), so were excluded from the multivariate analysis to prevent any skewing of the data. The rationalised data were then imported into PRIMER for statistical analysis.

3.5.1.2 Multivariate statistical analysis

Due to the data being based on SACFOR abundances, no data transformation was undertaken. A resemblance matrix using non-standardised, untransformed data was created using Bray Curtis similarity. Cluster analysis was then performed, and the resulting dendrogram plotted (Figure 3.28).

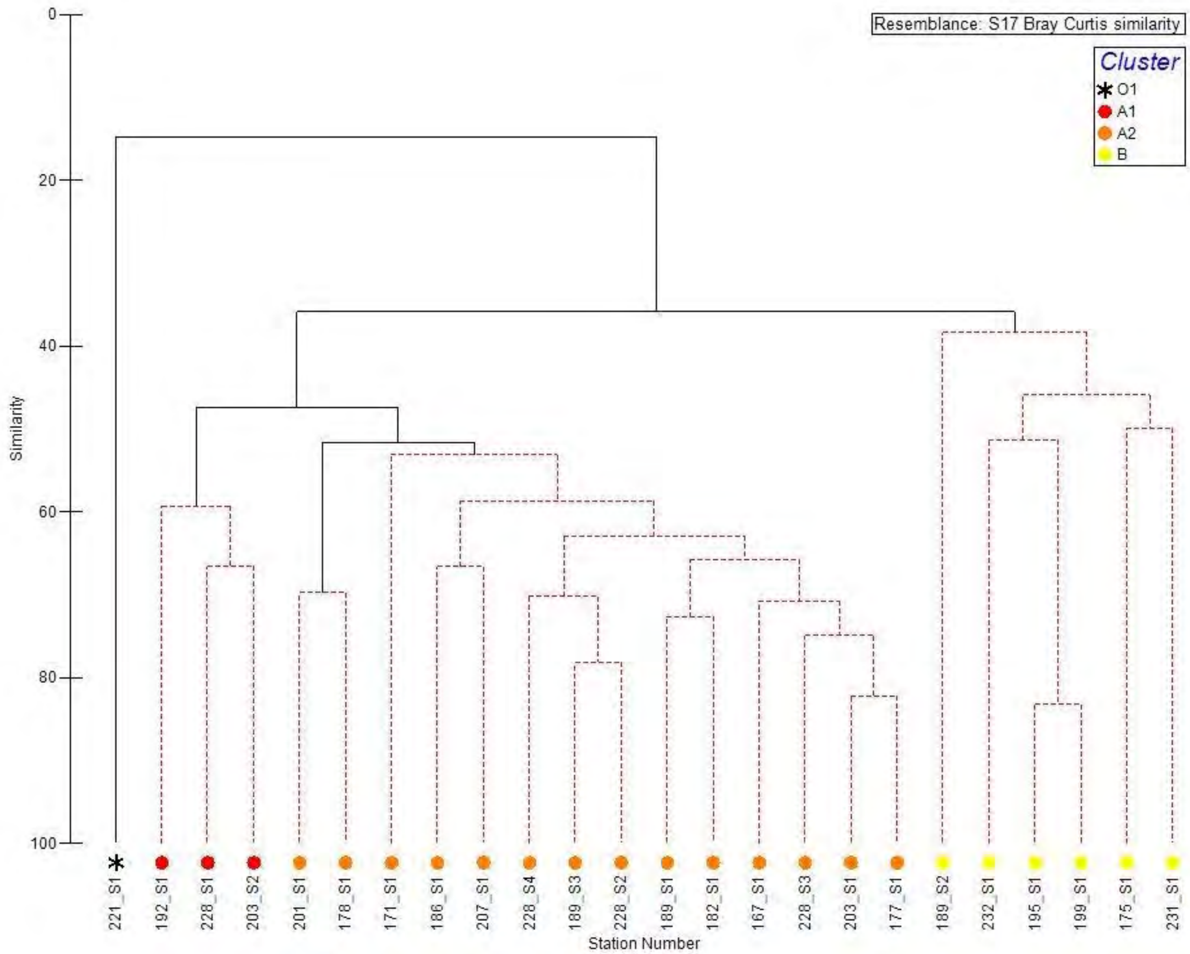


Figure 3.28. Dendrogram plot following cluster analysis of adjusted macrofaunal SACFOR data North East Farnes Deep video data. Samples coloured according to assigned cluster groups.

There was one outlying station (221_S1) that split away at ~16% similarity. The rest of the video segments were all at least ~37% similar. At ~37% similarity, six stations branched away and were classified together as group B. The remaining 17 video segments separated at ~48% similarity, with three stations forming sub-group A1, and 14 stations forming sub-group A2.

Figure 3.29 shows a 2D MDS ordination plot of the cluster analysis. The stress value of 0.14 was fairly moderate, so the visual grouping of the video segments in the MDS plot could be regarded with some confidence. There was some agreement between the MDS plot and dendrogram, with the groups of stations defined from the dendrograms roughly clustering together.

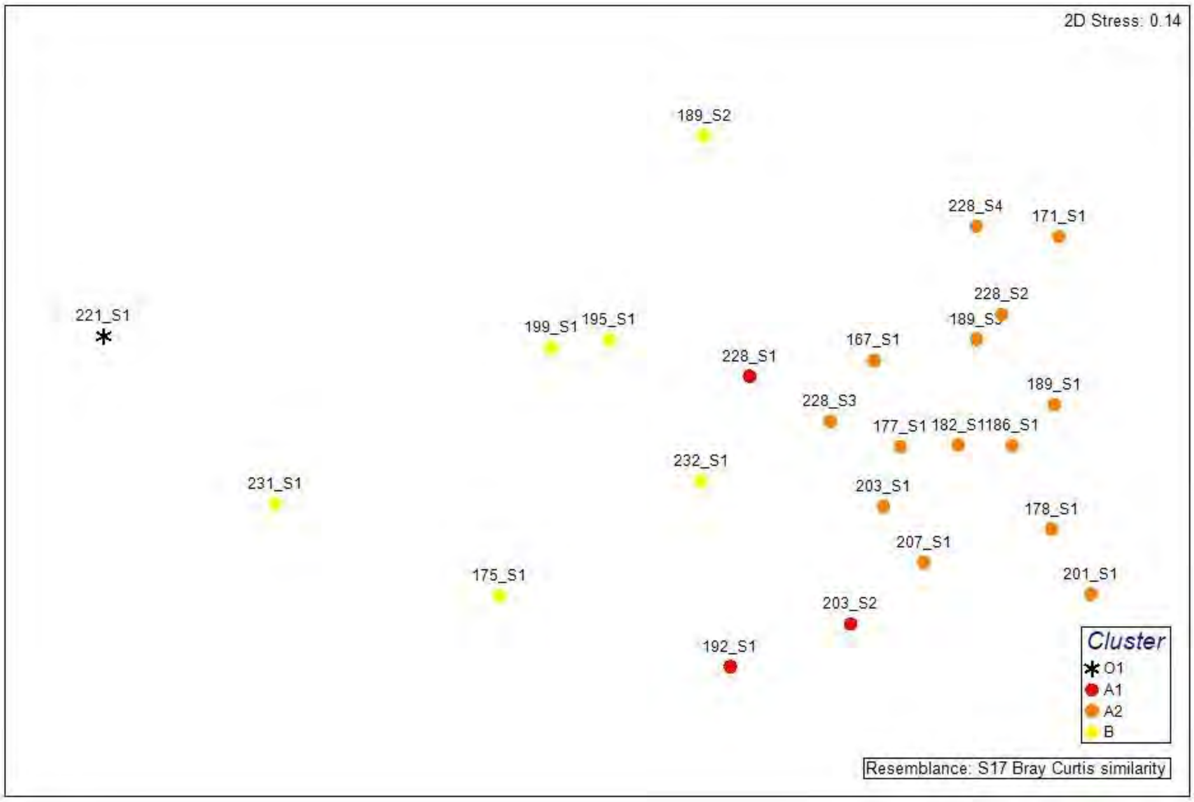


Figure 3.29. MDS ordination plot of North East Farnes Deep MCZ video data.

Figure 3.30 shows the cluster analysis with the biotopes assigned to each station following the original visual video analysis. On first inspection, the original visual assessment of biotopes does not appear to show very close agreement with the clustering of stations. However, sub-groups A1 and A2 were dominated by the biotopes **SS.SCS.OCS.SerHydBry**, **SS.SSx.OMx.SerHydBry** and **SS.SSa.OSa.BurrSerHydBry**. These three biotopes were newly proposed by the original analysts. As reflected in the biotope code, they largely contained the same faunal community, which was present over a range of substrata. The similarities in the faunal communities can be recognised in the clustering of the stations during the multivariate analysis. Group B contained stations that were all designated as various **SS.SSa.OSa** biotopes by the original analysis.

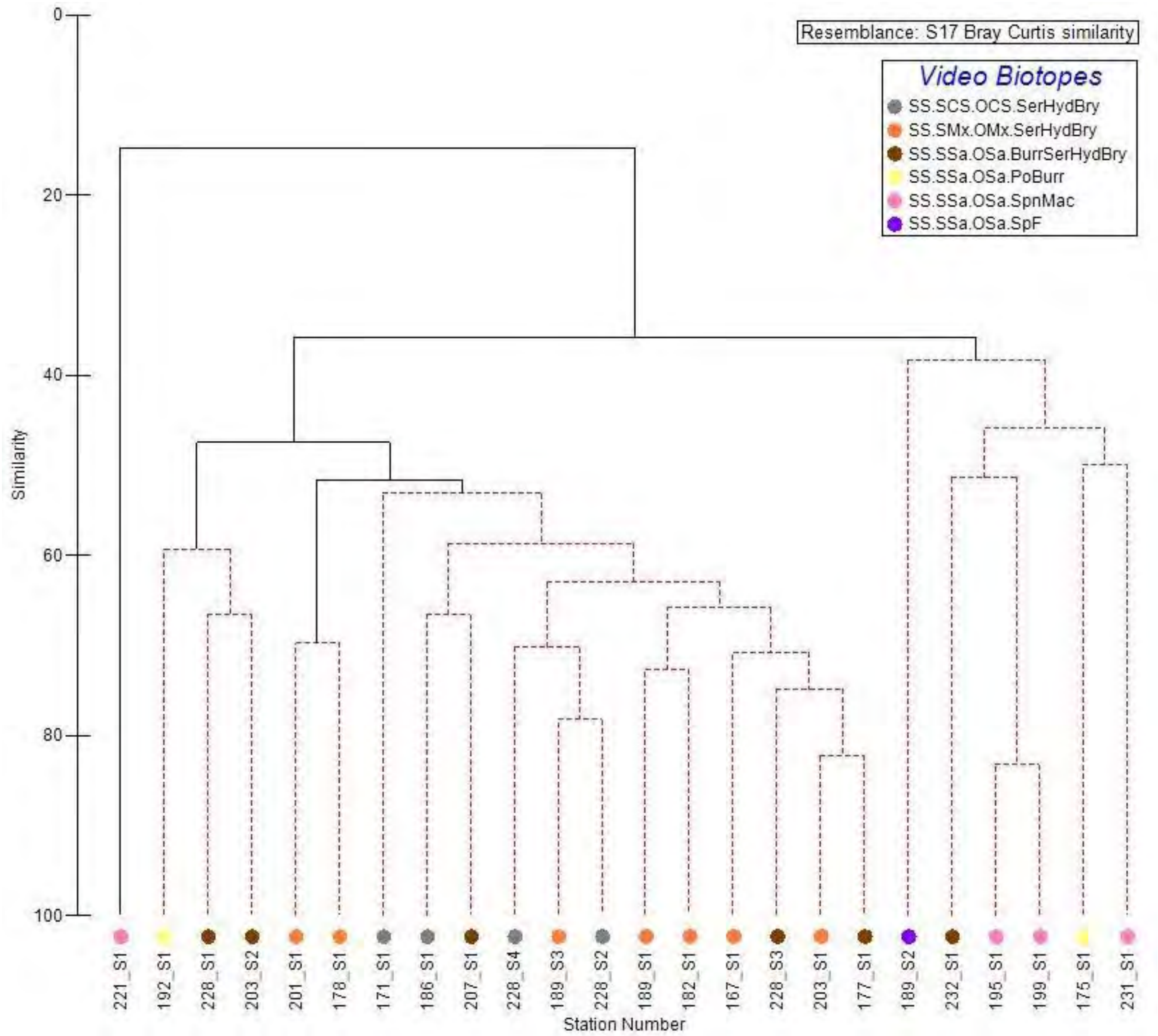


Figure 3.30. Dendrogram plot following cluster analysis of adjusted macrofaunal SACFOR data North East of Farnes Deep video data. Samples coloured according biotopes assigned from original analysis of data.

Two different SIMPER analyses were undertaken. The first was to examine which components of the faunal communities were responsible for the clustering of the stations into the assigned sub-groups. The second was to identify the characteristic fauna from each of the biotopes assigned from the original visual analysis of the video data, thus allowing for a degree of assessment on the level of differentiation in the faunal communities assigned to different biotopes.

Table 3.13 shows the characteristic taxa for each sub-group defined from the cluster analysis, listing those taxa that contributed at least 90% similarity for each sub-group. Full SIMPER results showing all contributing species for each sub-group can be found in Appendix 11.

The taxa Hydrozoa, Paguridae, and *Flustra foliacea* were characteristic of all three groups (A1, A2 and B), albeit with different percentage contributions. Sub-group A2 was characterised by the same taxa as A1, but with Asteroidea and *Echinus* as additional characterising taxa. In addition to *F. foliacea*, Hydrozoa and Paguridae, group B was characterised by *Pennatula phosphorea,* Sabellidae and Asteroidea.

Table 3.13. Results of SIMPER analysis of the sub-groups identified from cluster analysis of video faunal data, North East of Farnes Deep MCZ video data.

Group / Cluster	% Contribution of characterising species	
	Taxa / species	**Contribution (%)**
A1	Hydrozoa	28.85
	Paguridae	28.85
	Serpulidae	19.57
	Flustra foliacea	14.43
A2	Serpulidae	30.97
	Flustra foliacea	21.75
	Hydrozoa	16.8
	Paguridae	7.69
	Asteroidea	7.65
	Echinus	5.16
B	Paguridae	22.45
	Hydrozoa	22.1
	Pennatula phosphorea	22.01
	Flustra foliacea	12.4
	Sabellidae	6.61
	Asteroidea	5.39

The results on the SIMPER analysis of the original visual biotope analysis can be seen in Table 3.14. The taxa Hydrozoa and *Flustra foliacea* characterised five of the six originally designated biotopes, with Serpulidae and Paguridae also seen within many of the biotopes. These similarities suggest some uncertainties to the distinctness of the original biotopes. *Pennatula phosphorea* was a characteristic taxon of only **SS.SSa.OSa.SpnMac**, offering support to splitting these stations into a separate biotope.

SS.SSa.OSa.SpF had no characteristic fauna different from **SS.SSa.OSa.PoBurr**, **SS.SSa.OSa.BurrSepHydBry** and **SS.SMx.OMx.SerHydBry**, suggesting that the faunal community used to identify these biotopes were not characteristic of a particular habitat type.

The presence of *Munida rugosa* as a characteristic taxon from **OMx.SepHydBry** suggested that some element of larger substrata was present within this particular habitat compared to the other originally designated biotopes. However, the similarities in the other fauna suggested that this might have reflected local patchiness in sediment composition.

Table 3.14. Results of SIMPER analysis of the biotopes assigned after visual analysis of video data, North East of Farnes Deep MCZ video data.

Biotope	% Contribution of characterising species	
	Taxa / species	Contribution (%)
SS.SSa.OSa.PoBurr	Hydrozoa	25
	Paguridae	25
	Nephtyidae	12.5
	Sabellidae	12.5
	Serpulidae	12.5
	Flustra foliacea	12.5
SS.SCS.OCS.SerHydBry	Serpulidae	32.23
	Flustra foliacea	28.06
	Hydrozoa	19.78
	Asteroidea	14.66
SS.SMx.OMx.SerHydBry	Hydrozoa	23.77
	Flustra foliacea	22.08
	Serpulidae	21.04
	Paguridae	9.22
	Asteroidea	7.22
	Munida rugosa	4.05
	Echinus	2.89
SS.SSa.OSa.BurrSerHydBry	Serpulidae	25.78
	Paguridae	24.18
	Hydrozoa	20.02
	Flustra foliacea	15
	Echinus	6.33
SS.SSa.OSa.SpF	Hydrozoa	33.33
	Paguridae	33.33
	Flustra foliacea	33.33
SS.SSa.OSa.SpnMac	*Pennatula phosphorea*	58.15
	Paguridae	35.46

3.5.2 Stills data

3.5.2.1 Data rationalisation

The raw faunal data matrix was rationalised according to the methodology. Pelagic and highly mobile fauna were removed from the data set (Osterichthyes, *Callionymus* and *Myxine glutinosa*). Still image data were combined for each parent video segment. Abundance of taxa were expressed as a percentage of the total images within each segment that they were present. Two video segments (228_S2 and 228_S4) had no still images, so were excluded from the analysis. After rationalisation, two video segments had no visible fauna recorded from their constituent still images (171_S2), so were excluded from the multivariate analysis to prevent any skewing of the data. The rationalised data were then imported into PRIMER for statistical analysis.

3.5.2.2 Multivariate statistical analysis

Due to the prior manipulation of data, no further transformations were undertaken. A resemblance matrix using non-standardised, untransformed data was created using Bray Curtis similarity. Cluster analysis was then performed, and the resulting dendrogram plotted (Figure 3.31).

There were two outlying stations, 195_S1 and 231_S1, that separated away at 0% and ~4% similarity respectively. Group A contained two stations, and branched away at ~13% similarity. The remaining 19 stations were split into two sub-groups. The smaller of the two sub-groups was B2, which contained three stations, and split away at ~25% similarity. Sub-group B1 was the largest cluster, containing 16 stations, all ~45% similar to one another

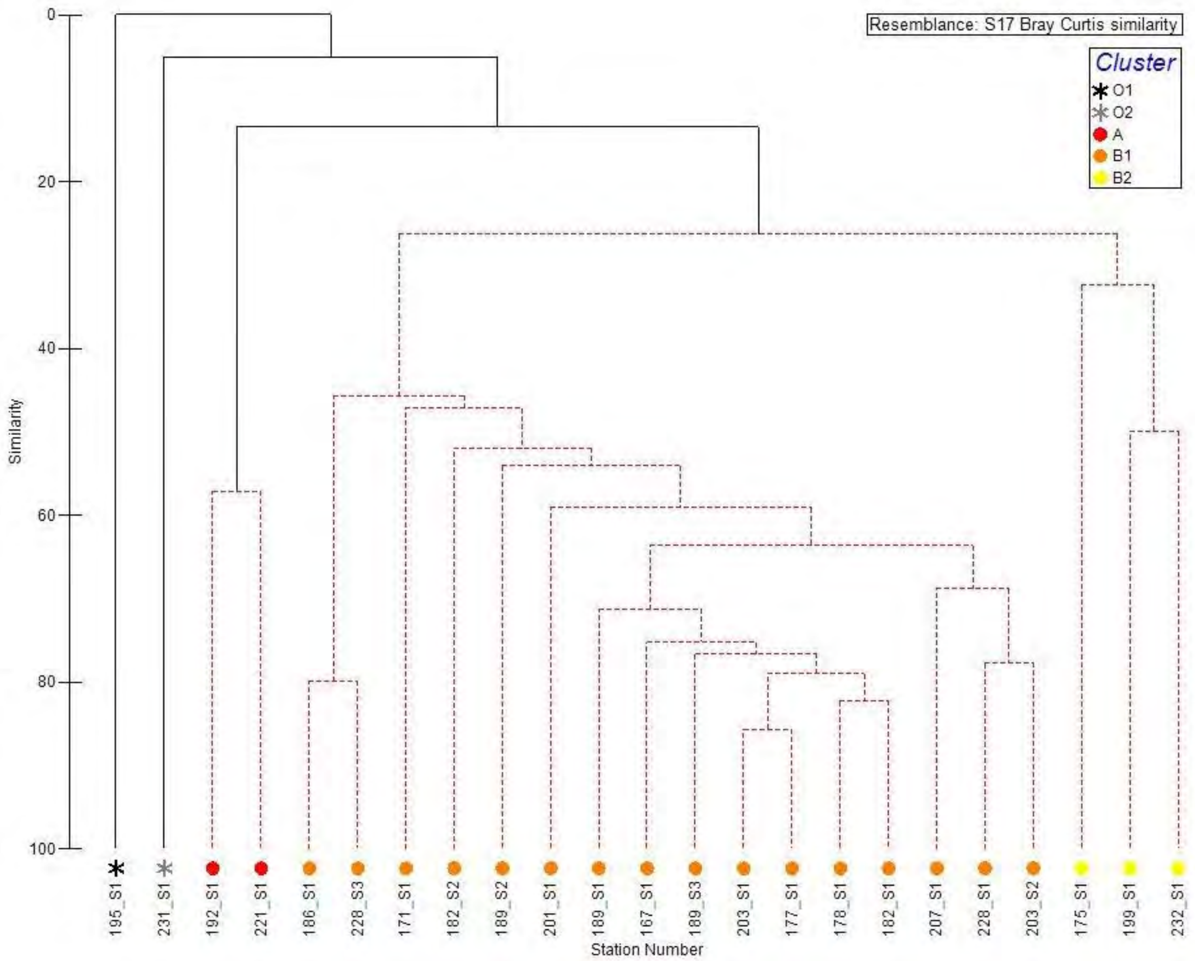


Figure 3.31. Dendrogram plot following cluster analysis of North East of Farnes Deep MCZ still data. Samples coloured according to assigned cluster groups.

A 2D MDS ordination plot of the cluster analysis can be seen in Figure 3.32. Station 195_S1 was removed as the station skewed the plot too much. The stress value was relatively low (0.12), suggesting that the visual representation of the station clustering within the 2D plot was relatively accurate. The MDS plot showed good agreement with the dendrogram plot, with stations clustering together according to the sub-groups assigned from the dendrogram.

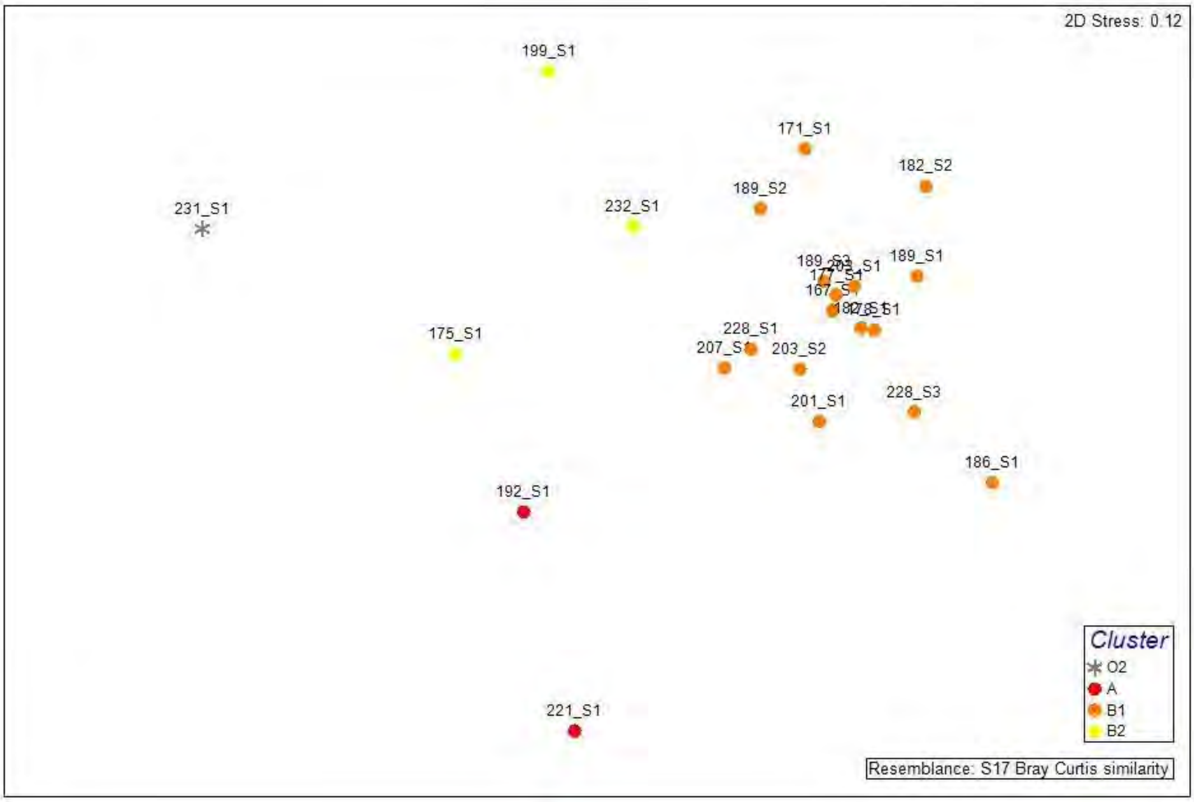


Figure 3.32. MDS ordination plot of North East of Farnes Deep MCZ still data.

Figure 3.33 shows the dendrogram created from the cluster analysis of the still data overlain with the biotopes assigned from the original visual video analysis. As seen in the video data analysis, stations assigned to the biotopes **SS.SSa.OSa.BurrSerHydBry**, **SS.SCS.OCS.SerHydBry,** and **SS.SMx.OMx.SerHydBry** tended to group together within sub-group B1, whilst **SS.SSa.OSa.PoBurr** and **SS.SSa.OSa.SpnMac** tended to be found within groups A and B2. Within sub-group B1 the stations that had been assigned to the **SS.SMx.OMx.SerHydBry** biotope following the original analysis were all at least ~60% similar to one another.

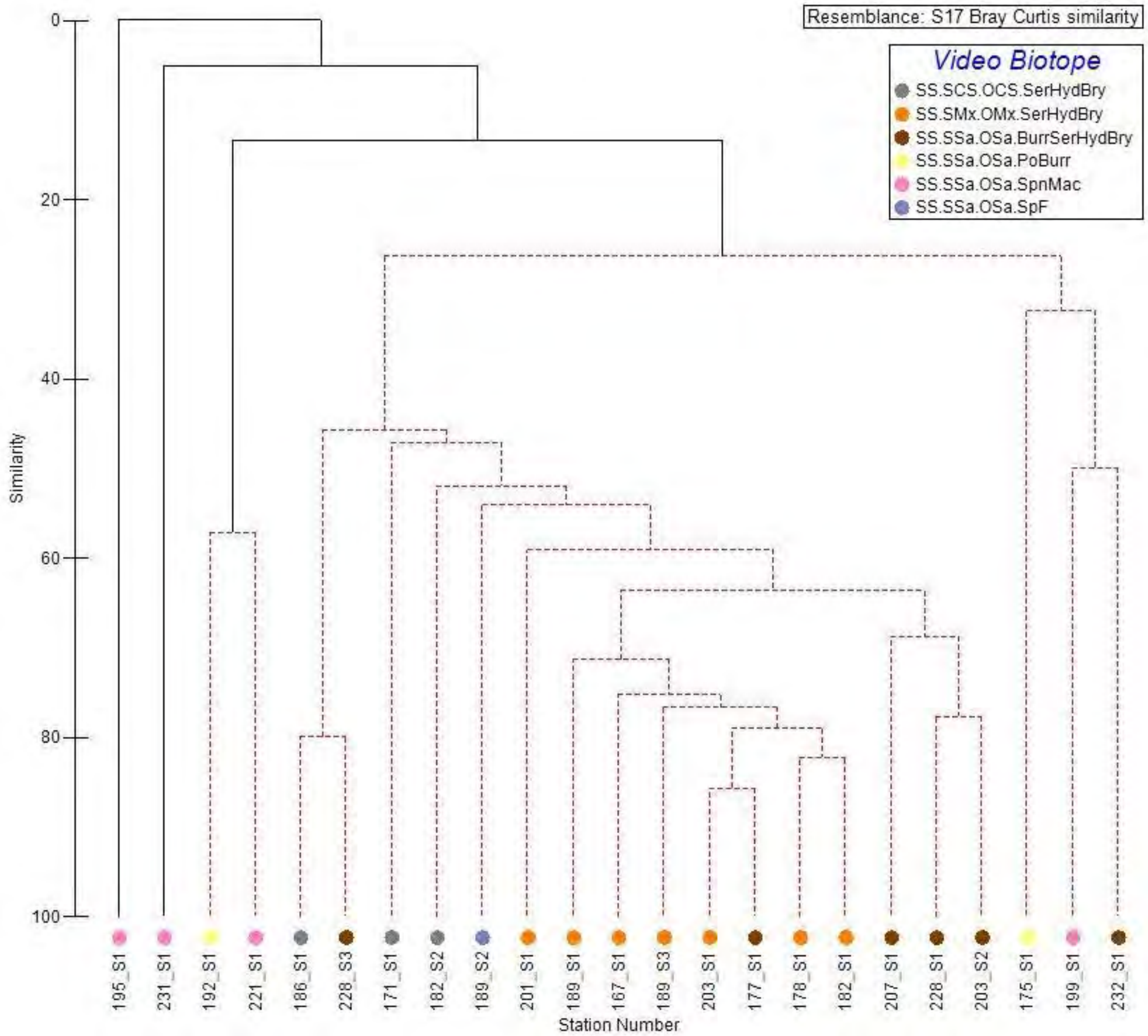


Figure 3.33. Dendrogram plot following cluster analysis of North East of Farnes Deep MCZ still data. Samples coloured according to biotopes assigned from original visual analysis of data.

Two SIMPER analyses were undertaken, examining both the groups assigned from the cluster analysis, and the biotopes assigned from the original visual data analysis of the still images. Table 3.15 outlines the characteristic taxa for each sub-group, listing those taxa that contributed at least 90% similarity for each sub-group. Full SIMPER results showing all contributing species for each sub-group can be found in Appendix 11.

Groups A, B1 and B2 were characterised by very few taxa. Groups A was only characterised by faunal burrows. Sub-groups B1 and B2 were both characterised by Hydrozoa. However B1 was also characterised by Serpulidae and *Flustra foliacea*, whilst B2 was characterised by Paguridae, Sabellidae and *Pennatula phosphorea.*

Table 3.15. Results of SIMPER analysis of the sub-groups identified from cluster analysis of still faunal data, North East of Farnes Deep MCZ.

Group / Cluster	% Contribution of characterising species	
	Taxa / species	Contribution (%)
A	Burrows	100
B1	Serpulidae	49.5
	Hydrozoa	31.83
	Flustra foliacea	12.16
B2	Hydrozoa	55.18
	Paguridae	15.82
	Pennatula phosphorea	14.5
	Sabellidae	14.5

Table 3.16 shows the results of the SIMPER analysis of the biotopes assigned after the original visual analysis of the data. The lists of characteristic species were again very short. Hydrozoa characterised the biotopes **OSa.PoBurr**, **OCS.SerHydBry**, **OMx.SerBryHyd** and **OSa.BurrSerHydBry**. Serpulidae characterised **OCS.SerHydBry**, **OMx.SerHydBry** and **OSa.BurrSerHydBry**. The seapen *Pennatula phosphorea* was the only species that characterised the biotope **OSa.SpnMac.**

Table 3.16. Results of SIMPER analysis of the biotopes assigned after visual analysis of data, North East of Farnes Deep MCZ still data. NB. After rationalisation of still data, fauna were only present in one station assigned to **SS.SSa.OSa.SpF**, so no SIMPER analysis was performed for this biotope.

Biotope	% Contribution of characterising species	
	Taxa / species	Contribution (%)
SS.SSa.OSa.PoBurr	Hydrozoa	50
	Paguridae	50
SS.SCS.OCS.SerHydBry	Serpulidae	75.86
	Hydrozoa	8.05
	Bryozoa	8.05
SS.SMx.OMx.SerHydBry	Hydrozoa	41.5
	Serpulidae	41.5
	Flustra foliacea	9.28
SS.SSa.OSa.BurrSerHydBry	Serpulidae	41.72
	Hydrozoa	32.7
	Flustra foliacea	13.96
	Paguridae	4.07
SS.SSa.OSa.SpnMac	*Pennatula phosphorea*	100

One of the main limitations of the still image data set was the lack of analysed data. Only three photos were analysed from each parent video segment during the original data analysis. This resulted in a very limited set of data on which to perform multivariate analysis, and as such the analysis of this still data should be used with extreme caution. After combining data from still images for each parent video segment, only 24 taxa had been recorded. Only 26 video segments had fauna present from their constituent still images, with nine taxa the most seen in a single video segment. Of the 26 video segments, 20 had six or fewer taxa present, with 12 of these having only 2 or fewer taxa. The scarcity of fauna within the still image data set resulted in short, less informative lists of characteristic fauna from the SIMPER analysis. If all the still images had been analysed originally then the greater pool of data may have elucidated more patterns within the faunal communities after multivariate analysis.

3.5.3 Biotope designation

Biotope designation was principally based on the results of the video analysis, with little consideration of the still image results due to the scarcity of the associated faunal data.

The original visual assessment of the data found six different biotopes within the survey area. The first was **SS.SSa.OSa.SpF**, sparse fauna in offshore circalittoral sand. These stations did indeed have sparse epifauna, but the video and stills data cannot accurately inform on whether the infaunal component of the station was faunally sparse or rich. With a lack of visible epifauna, these stations have been assigned to the biotope **SS.SSa.OSa,** based on depth and the sediment observed during the original analysis.

The biotope **SS.SSa.OSa.SpnMac** was described as ‘Seapens and burrowing megafauna in offshore fine muddy sand’. The presence of *Pennatula phosphorea* separated these stations from the others. Other than the seapens, the fauna recorded was sparse, and the fauna seen were generally similar to that found in the other stations. Faunal records such as Paguridae, Sabellidae and Hydrozoa did not provide much additional information on the community. Bearing in mind the sparse faunal data, the biotope **SS.SMu.CFiMu.SpnMeg** was flagged as a potential match. However, examination of the still images revealed clear sand ripples across the sediment, suggesting a relatively high sand component. Samples were collected from 79 – 89m, at the bottom end of the circalittoral depth range. It was therefore deemed that the originally proposed new biotope (**SS.SSa.OSa.SpnMac**) was probably a suitable designator for these stations.

The fauna identified as being characteristic of the biotope **SS.SSa.OSa.PoBurr** included some Nephtyidae, in addition to Serpulidae, Paguridae and *Flustra foliacea.* Many of these fauna were the same as those identified as being characteristic of other biotopes. Due the similarities of the majority of the faunal community to other biotopes, the community present at these stations could not be considered as diagnostic of a separate discrete habitat. These stations were assigned the biotope **SS.SSa.OSa** to reflect the sediment and depth.

The three other originally assigned biotopes were **OCS.SerHydBry**, **OMx.SerHydBry** and **OSa.BurrSerHydBry**. As previously discussed, all three of these biotopes had Serpulidae, Hydrozoa and *Flustra foliacea* as characteristic species. The presence of the same taxa on a range of different substrata suggested that they were not appropriate to use as diagnostic species with which to define biotopes and habitats. Stations originally assigned to these three biotopes were raised to level 3 biotopes (i.e. **SS.SCS.OCS**, **SS.SMx.OMx** and **SS.SSa.OSa**) to reflect the differences in sediment composition and the station depths. The characteristic fauna from these stations bore some resemblance to the biotope **SS.SMx.CMx.FluHyd**. However, the video data records suggested that a greater range of sediment compositions could be recognised, so **CMx.FluHyd** was not assigned to any stations.

The video and still image data from this survey was generally faunally sparse, and mainly identified to higher taxonomic levels. The data appeared to suggest a very patchy habitat, with records of Serpulidae, Hydrozoa and *Flustra folicacea* being present at almost every station indicating a degree of mixed sediment composition throughout the site. Table 3.17 summarises the biotope designation following the multivariate analysis of the North East of Farnes Deep MCZ video and stills data.

Table 3.17. Summary of biotopes assigned to video and still data, North East of Farnes Deep MCZ.

Biotope	Description	Original Biotope/s	Video Segment No.	Depth Range
A5.15 : Deep circalittoral coarse sediment **SS.SCS.OCS**	Areas of coarse sediment according to original visual assessment. Sparse epifauna, some hydroids, serpulids and *Flustra folicacea*. Faunal community not very different from **SMx.OMx** stations. Some resemblance to **SS.SMx.CMx.FluHyd** biotope.	**SS.SCS.OCS. SerHydBry**	186_S1, 228_S2, 228_S4, 171_S2, 182_S2	64 – 72m
A5.27 : Deep circalittoral sand **SS.SSa.OSa**	Areas of sandy sediment according to original visual assessment. Sparse epifauna, including some hydroids, serpulids and *Flustra folicacea*. Some evidence of burrowing fauna. Some resemblance to **SS.SMx.CMx.FluHyd** biotope in places.	**SS.SSa.OSa. BurrSerHydBry;** **SS.SSa.OSa.SpF;** **SS.SSa.OSa.PoBurr**	207_S1, 228_S1, 228_S3, 203_S2, 177_S1, 232_S1, 192_S1, 175_S1, 189_S2, 171_S2	66 – 83m
A5.27x : Seapens and burrowing megafauna in offshore fine muddy sand **SS.SSa.OSa.SpnMac**	**New biotope.** Fine muddy sand sediments with ripples characterised by burrowing fauna and the presence of *Pennatula phosphorea.*	**SS.SSa.OSa.SpnMac**	221_S1, 195_S1, 199_S1, 231_S1	79 – 89m
A5.45 : Deep circalittoral mixed sediments **SS.SMx.OMx**	Areas of mixed sediment according to original visual assessment. Sparse epifauna, some hydroids, serpulids and *Flustra folicacea*. Faunal community not very different from **SCS.OCS** stations. Some resemblance to **SS.SMx.CMx.FluHyd** biotope.	**SS.SMx.OMx. SerHydBry**	189_S1, 189_S3, 201_S1, 178_S1, 167_S1, 203_S1, 182_S1	61 – 73m

Figure 3.34 displays the geographical distribution of the biotopes designated after the multivariate statistical analysis of the North East of Farnes Deep video and still data. The assigned biotopes did not show a good agreement with the predicative sediment mapping from the UKSeaMap 2010 project (McBreen *et al* 2011).

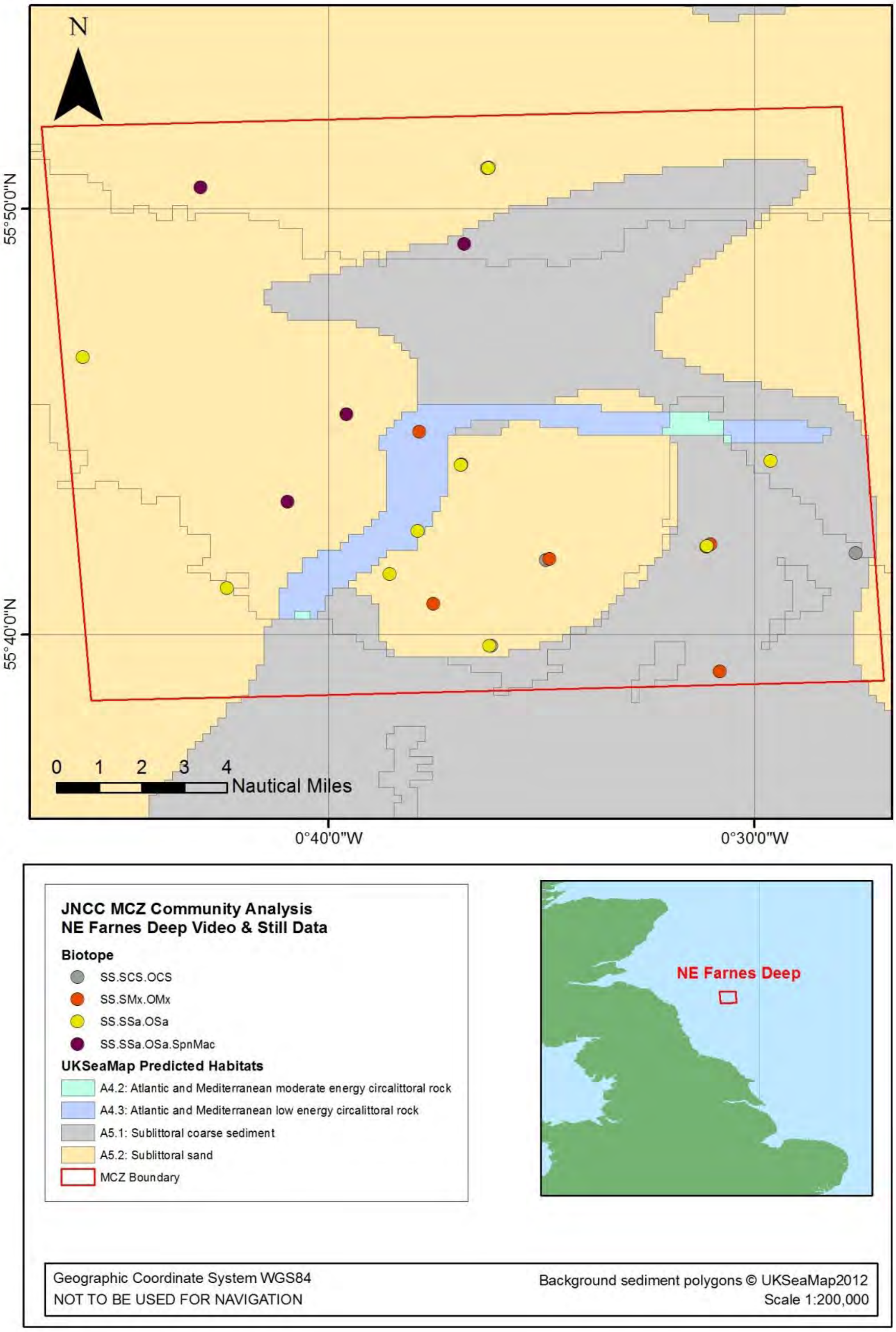


Figure 3.34. Geographical distribution of biotopes designated after multivariate analysis of video and still data, North East of Farnes Deep MCZ.

3.6 East of Haig Fras MCZ – video and stills data

Please note that video and still images from the East of Haig Fras were collected from two different survey cruises (CEND0312 and CEND0513), and originally analysed by two different contractors. Therefore, the data set from each cruise has been considered separately.

3.6.1 CEND0513 video data

3.6.1.1 Data rationalisation

The raw faunal data matrix was rationalised according to the methodology. For this particular data set, all pelagic and highly mobile fauna were removed from the data set. These taxa included Ammodytidae, *Chelidonichthys lucernus, Ctenolabrus rupestris,* Gadidae, Gobiidae, Pleuronectidae and *Solea solea.* After rationalisation, seven video segments had no visible fauna recorded (115_S2, S2, 124_S3, 107_S3, 113_S1, 113_S3 and 114_S3), so were excluded from the multivariate analysis to prevent any skewing of the data. The rationalised data were then imported into PRIMER for statistical analysis.

3.6.1.2 Multivariate statistical analysis

Due to the data being based on SACFOR abundances, no data transformation was undertaken. A resemblance matrix using non-standardised, untransformed data was created using Bray Curtis similarity. Cluster analysis was then performed, and the resulting dendrogram plotted (Figure 3.35).

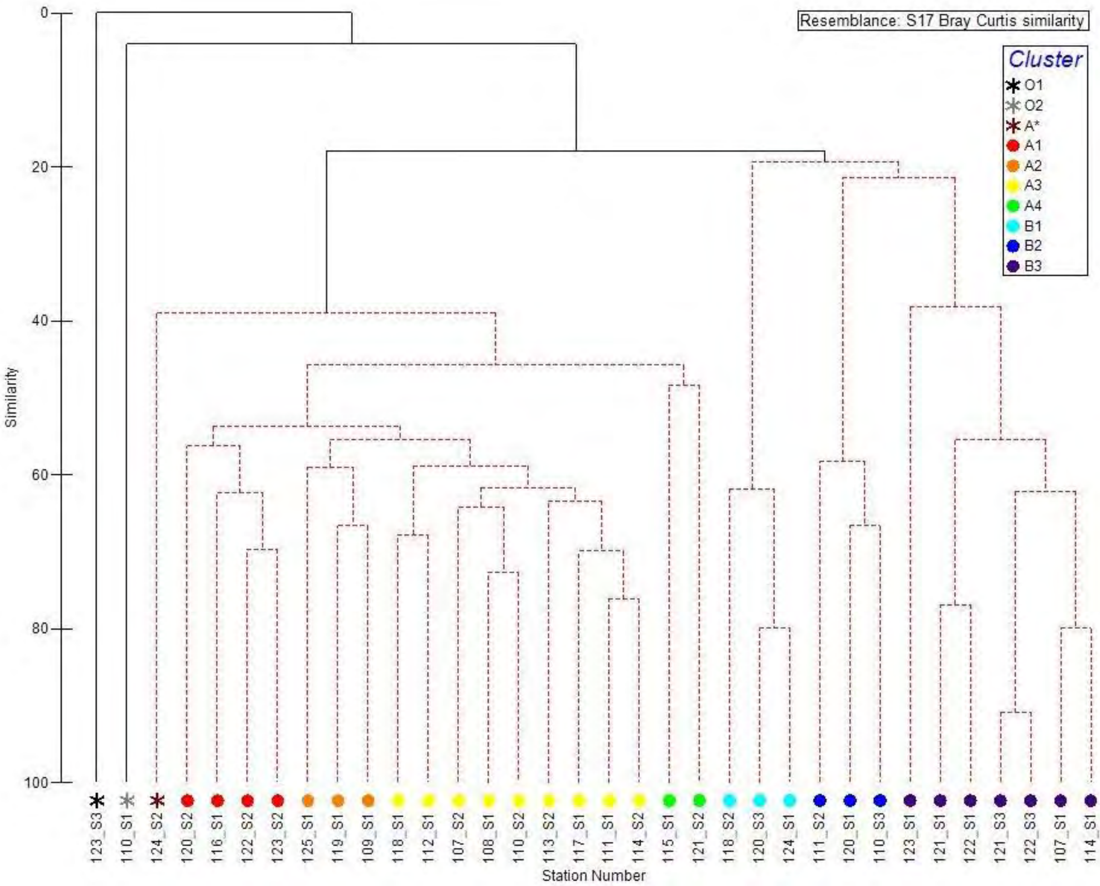


Figure 3.35. Dendrogram plot following cluster analysis of adjusted macrofaunal SACFOR data East of Haig Fras CEND0513 video data. Samples coloured according to assigned cluster groups.

Video segments 123_S3 and 110_S1 were outliers, separating at 0% and ~4% similarity from the other stations. The remaining stations split into two large clusters at ~18% similarity. The first cluster contained 19 video segments, and was split into four sub-groups (A1 – A4), with one outlier (A*; 124_S2) that branched away at ~39% similarity. Sub-group A4 split off at ~46% similarity, whilst sub-group A1 split off at 55% similarity. Sub-groups A2 and A3 branched from each other at ~57% similarity. The second cluster contained 13 stations, and was divided into three sub-groups, B1 – B3. Both sub-groups B1 and B2 contained three video segments, and split away at ~20% and ~23% similarity respectively.

Figure 3.36 shows a 2D MDS ordination plot of the cluster analysis. The outlier 123_S3 (O1) was removed prior to plotting, since the presence of the station within the data set skewed the MDS plot too much. The stress value of 0.13 was fairly moderate, so the visual grouping of the video segments in the MDS plot could be regarded with some confidence. There were good agreements between the MDS plot and dendrogram, with sub-groups A1 – A4 clustering together, and sub-groups B1 – B3 being more distinct.

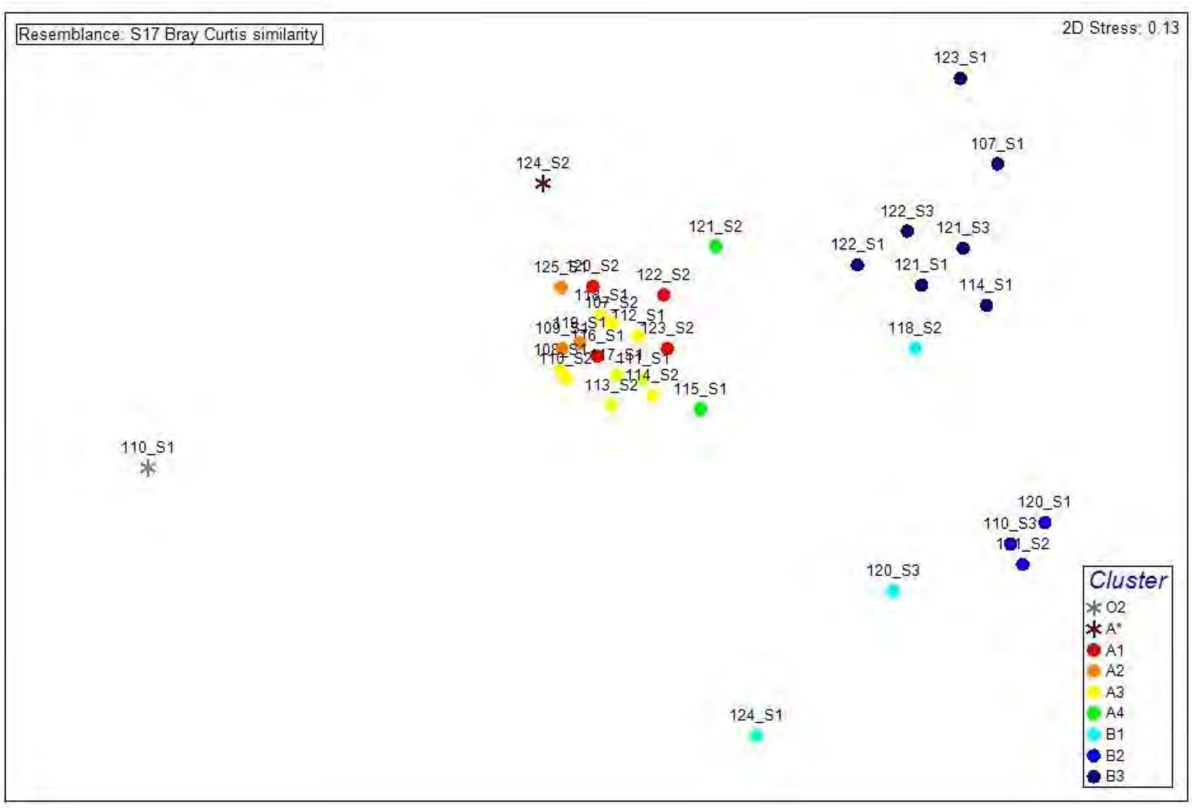


Figure 3.36. MDS ordination plot of CEND0513 East of Haig Fras MCZ video data.

Figure 3.37 shows the cluster analysis with the biotopes assigned to each station following the original visual video analysis. The two main clusters were generally defined by the habitats being either soft sediment (**SS.SCS** and **SS.SSa**) or hard substrata (**CR.HCR.XFa** and **CR.MCR.EcCr**), with the exception of video segment 112_S1. The clustering of **SS.SCS** and **SS.SSa** stations together is unsurprising, as these habitats are typically faunally sparse with regards to identifiable epifauna from video footage. The grouping of **CR.HCR.XFa** and **CR.MCR.EcCr** together suggested that similar faunal communities were present in both habitats.

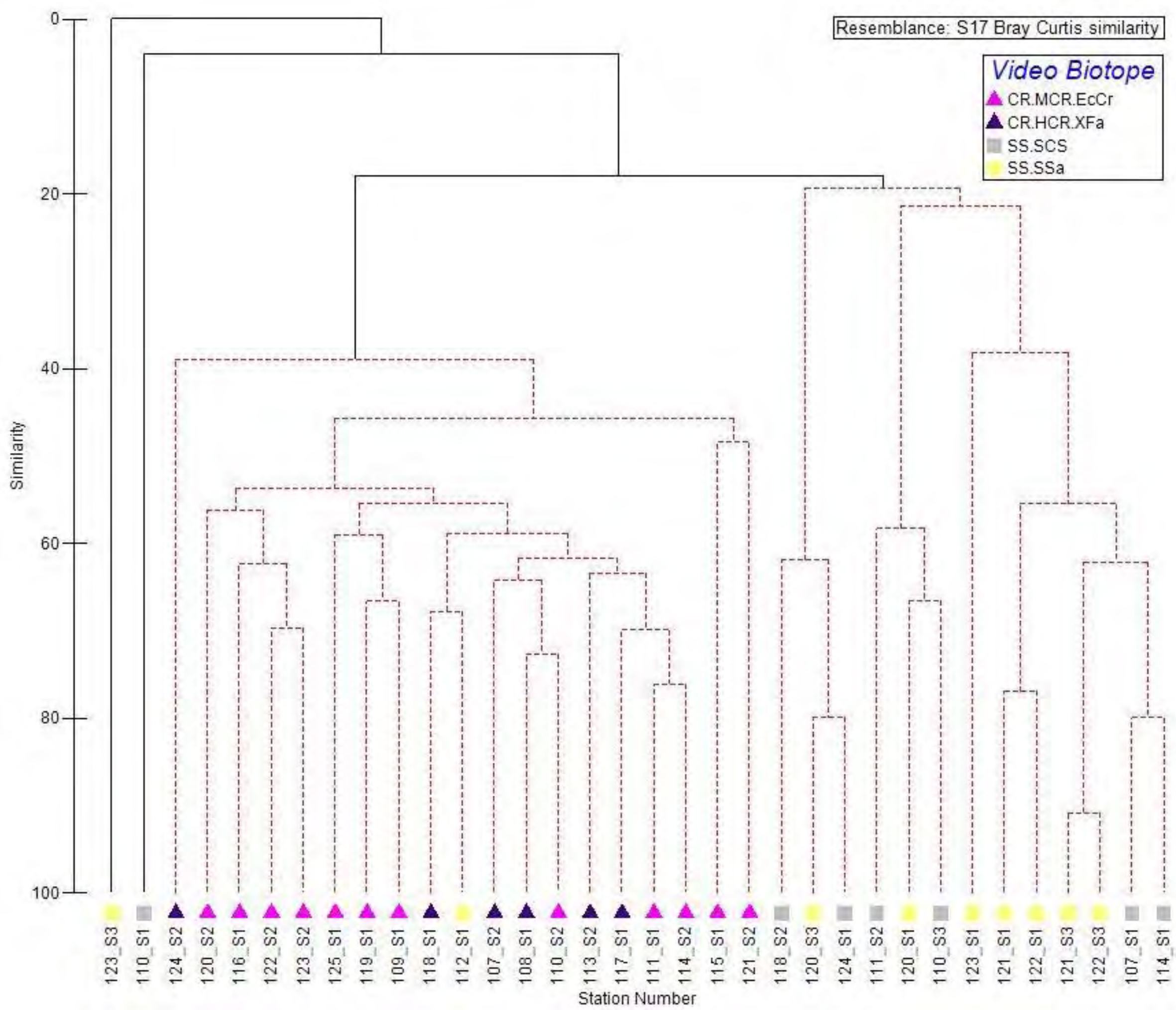


Figure 3.37. Dendrogram plot following cluster analysis of adjusted macrofaunal SACFOR data CEND0513 East of Haig Fras MCZ video data. Samples coloured according biotopes assigned from original analysis of data.

Two different SIMPER analyses were undertaken. The first was to examine which components of the faunal communities were responsible for the clustering of the stations into the assigned sub-groups. The second was to identify the characteristic fauna from each of the biotopes assigned from the visual analysis of the video data, and to assess whether differences between them. This second analysis was principally designed to identify whether the **XFa** and **EcCr** biotopes were composed of different faunal communities.

Table 3.18 shows the characteristic taxa for each sub-group defined from the cluster analysis, listing those taxa that contributed at least 90% similarity for each sub-group. Full SIMPER results showing all contributing species for each sub-group can be found in Appendix 12.

Sub-groups A1 – A4 were characterised by many of the same taxa. All four sub-groups were characterised by hydroid / bryozoan turf, *Henricia* sp., *Axinella* and Porifera. Sub-groups A1 – A3 also had *Echinus acutus* and *Porania pulvillus* in common. The similarities between the characterising faunal suggested that these sub-groups represented slight variations of the same faunal community.

Sub-groups B1 – B3 were only characterised by very restricted lists of fauna. These video segments were typically faunally sparse. The characteristic species such as *Porania* *pulvillus*, hydroid/bryozoan turf and *Henricia* sp. also occurred in sub-groups A1 – A4. In terms of hydroid/bryozoan turf, this fairly ubiquitous taxon is found from most habitats. The two asteroids suggested that these more mobile fauna may be common over the survey area, irrespective of habitat.

Table 3.18. Results of SIMPER analysis of the sub-groups identified from cluster analysis of video faunal data, CEND0513 East of Haig Fras MCZ video data.

Group / Cluster	% Contribution of characterising species	
	Taxa / species	**Contribution (%)**
A1	Hydroid/bryozoan turf	17.31
	Henricia sp.	14.16
	Axinella	12.27
	Astropecten irregularis	11.54
	Echinus acutus	11.54
	Porania pulvillus	11.54
	Porifera	6.79
	Munida rugosa	5.19
A2	Hydroid/bryozoan turf	13.63
	Axinella	12.34
	Caryophyllia smithii	12.34
	Echinus acutus	8.23
	Henricia sp.	8.23
	Porifera (peach; erect)	8.23
	Salmacina dysteri	8.23
	Porifera	5.4
	Porifera (orange; lumpy)	4.11
	Serpulidae	4.11
	Axinella infundibuliformis	3.01
	Porania pulvillus	3.01
A3	Hydroid/bryozoan turf	19.03
	Axinella	13.33
	Henricia sp.	11.17
	Porania pulvillus	11.17
	Bolocera tuediae	11.17
	Reteporella	6.45
	Echinus acutus	6.27
	Caryophyllia smithii	6.22
	Porifera	4.72
	Serpulidae	3.13
A4	Hydroid/bryozoan turf	37.5
	Axinella	25
	Henricia sp.	25
	Porifera	12.5
B1	*Porania pulvillus*	100
B2	Hydroid/bryozoan turf	100
B3	*Henricia* sp.	76.65
	Hydroid/bryozoan turf	16.39

The results on the SIMPER analysis of the visual biotope analysis can be seen in Table 3.19. The video segments assigned to **EcCr** and **XFa** both had the same top five characterising taxa – hydroid/bryozoan turf, *Axinella, Henricia* sp., *Porania pulvillus* and *Echinus acutus*, albeit with different percentage contributions. Other taxa that co-occurred between the two biotopes were Porifera and *Bolocera tuediae*. The similarities between the lists of characterising species suggested that the faunal communities were not sufficiently different to justify splitting into separate biotopes.

The taxa that characterised **SCS** and **SSa** were also very similar, both containing *Henricia* sp. and hydroid/bryozoan turf as the top two taxa. The differences between the two were the presence of *Porania pulvillus* within the **SCS**, and *Bolocera tuediae* in the **SSa**. Again, the similarities between the faunal communities suggest that splitting these into separate biotopes based solely on the faunal community data may not be justified. However, the difference in the sedimentary environment between sand and coarse sediment can be relatively easily discerned by visual inspection, and the epifaunal communities identified are often similar between both habitats.

Table 3.19. Results of SIMPER analysis of the biotopes assigned after visual analysis of video data, CEND0513 East of Haig Fras MCZ video data.

Biotope	% Contribution of characterising species	
	Taxa / species	Contribution (%)
CR.MCR.EcCr	Hydroid/bryozoan turf	22.73
	Axinella	16.24
	Henricia sp.	14.05
	Porania pulvillus	9.35
	Echinus acutus	8.75
	Porifera	5.63
	Caryophyllia smithii	5.02
	Bolocera tuediae	3.69
	Astropecten irregularis	2.66
	Porifera (orange; lumpy)	2.55
CR.HCR.XFa	*Axinella*	15.94
	Hydroid/bryozoan turf	12.81
	Henricia sp.	11.98
	Porania pulvillus	11.98
	Echinus acutus	7.91
	Bolocera tuediae	7.8
	Porifera	6.24
	Reteporella	4.67
	Ophiocomina nigra	2.33
	Munida rugosa	2.3
	Porifera (peach; erect)	2.3
	Serpulidae	2.3
	Abietinaria	1.65
SS.SCS	*Henricia* sp.	50.89
	Hydroid/bryozoan turf	32.46
	Porania pulvillus	16.65
SS.SSa	*Henricia* sp.	42.95
	Hydroid/bryozoan turf	42.65
	Bolocera tuediae	6.06

3.6.2 CEND0513 stills data

3.6.2.1 Data rationalisation

The raw faunal data matrix was rationalised according to the methodology. For this particular data set, all pelagic and highly mobile fauna were removed. These taxa included Ammodytidae, *Chelidonichthys lucernus, Ctenolabrus rupestris,* Gadidae, Gobiidae, Pleuronectidae and *Solea solea.* Still image data were combined for each parent video segment. Abundance of taxa were expressed as a percentage of the total images within each segment that they were present. After rationalisation, three video segments had no visible fauna recorded from their constituent still images (113_S1, 114_S1 and 114_S3), so were excluded from the multivariate analysis to prevent any skewing of the data. The rationalised data were then imported into PRIMER for statistical analysis.

3.6.2.2 Multivariate statistical analysis

Due to the prior manipulation of data, no further transformations were undertaken. A resemblance matrix using non-standardised, untransformed data was created using Bray Curtis similarity. Cluster analysis was then performed, and the resulting dendrogram plotted (Figure 3.38).

There were two outlying stations, 123_S3 and 110_S3. Group A contained two stations, and split away at ~7% similarity. Group B separated at ~10% similarity, followed by group C at ~17% similarity. A cluster of eight stations (Group D) branched off at ~29% similarity. Group E included three stations, one of which (118_S2) branched away at ~33% similarity, whilst the other two separated at ~44% similarity. The largest cluster was group F, which contained 18 stations. Group F separated at ~48% similarity. One station was an outlier within the group (122_S2), whilst the remaining stations were at least ~55% similar to one another.

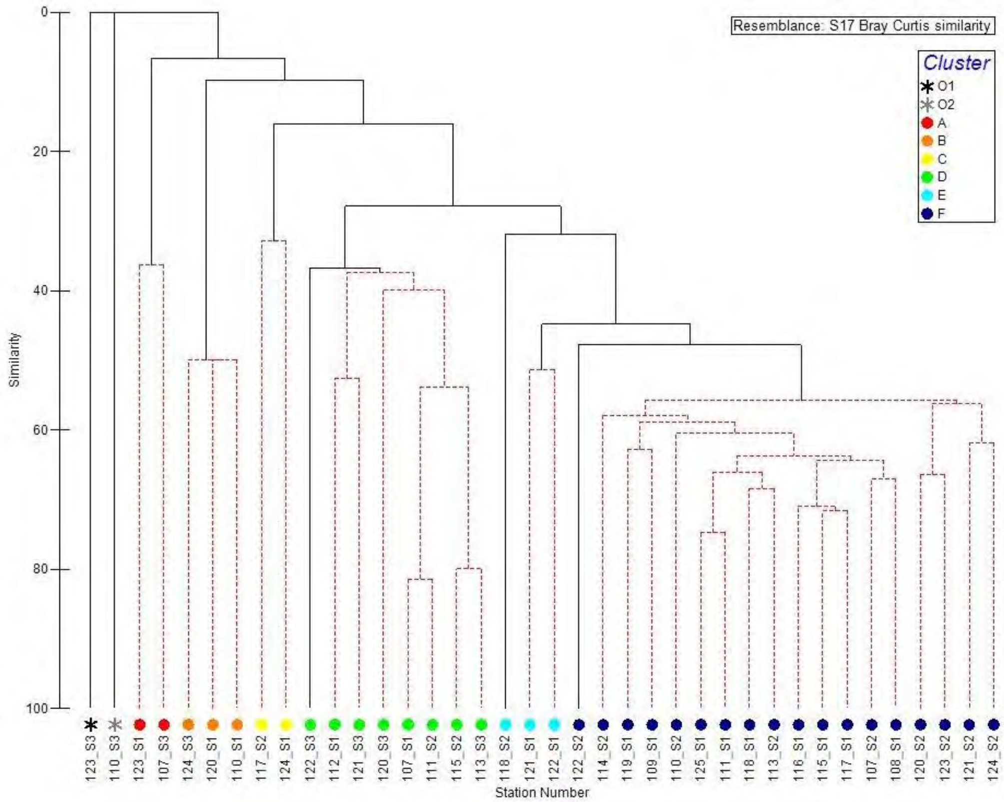


Figure 3.38. Dendrogram plot following cluster analysis of East of Haig Fras CEND0513 still data. Samples coloured according to assigned cluster groups.

A 2D MDS ordination plot of the cluster analysis can be seen in Figure 3.39. The stress value was low (<0.1), suggesting that the visual representation of the station clustering within the 2D plot was relatively accurate. The MDS plot showed good agreement with the dendrogram plot, with stations clustering together according to the sub-groups assigned from the dendrogram.

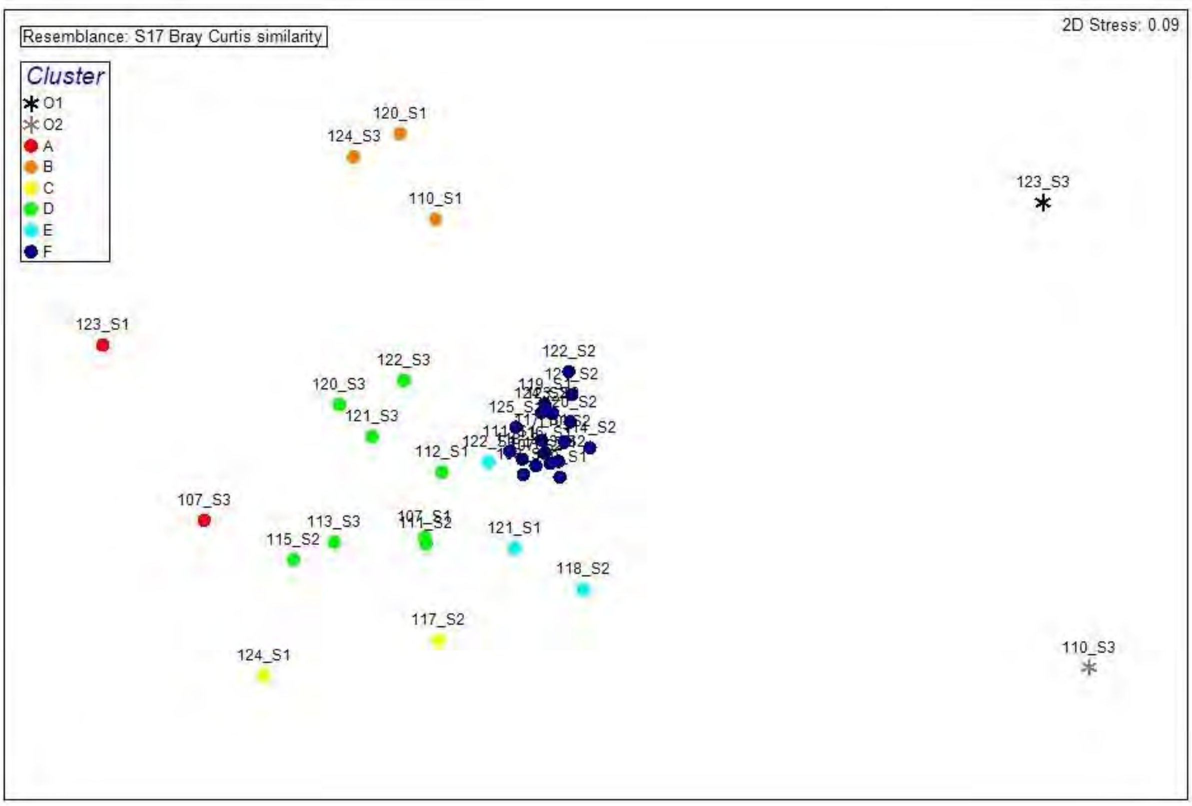


Figure 3.39. MDS ordination plot of CEND0513 East of Haig Fras MCZ still data.

Figure 3.40 shows the cluster analysis with the biotopes assigned to each station following the original visual video analysis. The stations designated as **CR.HCR.XFa** and **CR.MCR.EcCr** could be seen to all clustered together within group F. Station 112_S1 clustered with these stations when examining the video data, but had been separated when examining the still data.

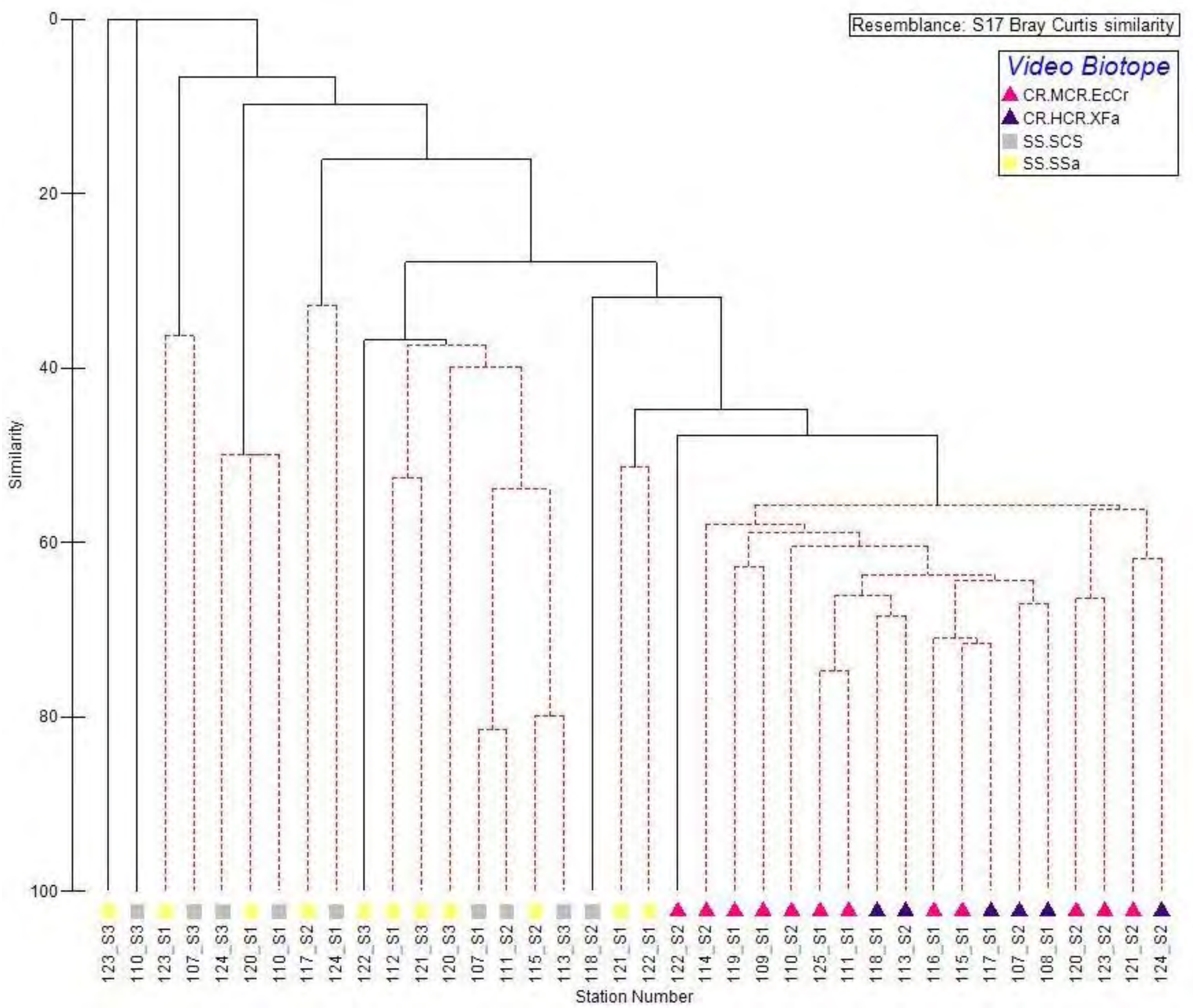


Figure 3.40. Dendrogram plot following cluster analysis of East of Haig Fras CEND0513 still data. Samples coloured according to biotopes assigned from original visual analysis of data.

As per the video data, two different SIMPER analyses were undertaken. The first was undertaken on the groups assigned from the cluster analysis, whilst the second was performed using the visually assessed biotopes from the original analysis of the data. Table 3.20 outlines the characteristic taxa for each sub-group, listing those taxa that contributed at least 90% similarity for each sub-group. Full SIMPER results showing all contributing species for each sub-group can be found in Appendix 12.

Groups A to E were characterised by few taxa. Groups A and B had only *Ophiura* and Paguridae as characteristic taxa, both typically found across a range of soft sediment habitats. Hydroid / bryozoan turf was characteristic of groups C, D and E, suggesting the presence of some larger sized sediment components. This was supported by the presence of other characteristic taxa such as Serpulidae and Porifera that require some larger substrata on which to live.

Group F was characterised by a range of taxa characteristic of habitats were cobbles and boulders are present. The cobbles provide a hard substratum for hydroid and bryozoan turf, Serpulidae, Porifera, *Caryophyllia smithii* and *Novocrania anomala*, whilst providing crevices for *Munida rugosa* to hide within.

Table 3.20. Results of SIMPER analysis of the sub-groups identified from cluster analysis of still faunal data, East of Haig Fras CEND0513.

Group / Cluster	% Contribution of characterising species	
	Taxa / species	Contribution (%)
A	*Ophiura* sp.	100
B	Paguridae	100
C	Hydroid/bryozoan turf	50
	Polychaete tube	50
D	Hydroid/bryozoan turf	85.93
	Porifera	6.72
E	Hydroid/bryozoan turf	53.54
	Porifera	25
	Henricia sp.	7.38
	Serpulidae	7.38
F	Hydroid/bryozoan turf	29.68
	Porifera	20.65
	Serpulidae	9.05
	Caryophyllia smithii	8.83
	Axinella	6.3
	Novocrania anomala	4.9
	Paguridae	4.83
	Henricia sp.	4.17
	Porifera (yellow; fluffy)	1.49
	Munida rugosa	1.28

Table 3.21 shows the results of the SIMPER analysis of the biotopes assigned after the original visual analysis of the data. As seen with the video data, the still data showed that the characteristic taxa for **CR.MCR.EcCr** and **CR.HCR.XFa** were largely similar. Both biotopes contained hydroid and bryozoan turf, Porifera, *Caryophyllia smithii*, Serpulidae, *Axinella* and *Henricia* sp., suggesting that the split between these two biotopes was not supported by the faunal communities observed. Both **SS.SSa** and **SS.SCS** were characterised by hydrozoan and bryozoan turf and Paguridae. The presence of Serpulidae, Porifera and *Caryophyllia smithii* suggested some patches of harder substrata within these soft sediment biotopes.

Table 3.21. Results of SIMPER analysis of the biotopes assigned after visual analysis of data, CEND0513 East of Haig Fras MCZ still data.

Biotope	% Contribution of characterising species	
	Taxa / species	Contribution (%)
CR.MCR.EcCr	Hydroid/bryozoan turf	28.26
	Porifera	19.07
	Caryophyllia smithii	13
	Serpulidae	8.29
	Paguridae	5.27
	Axinella	5.1
	Novocrania anomala	5.07
	Henricia sp.	3.91
	Porifera (yellow; fluffy)	1.76
	Porifera (orange; lumpy)	1.4
CR.HCR.XFa	Hydroid/bryozoan turf	31.69
	Porifera	23.08
	Serpulidae	10.16
	Axinella	9.22
	Henricia sp.	4.24
	Novocrania anomala	4.23
	Paguridae	4.23
	Caryophyllia smithii	3.77
SS.SCS	Hydroid/bryozoan turf	82.38
	Paguridae	9.27
SS.SSa	Hydroid/bryozoan turf	57.7
	Paguridae	14.41
	Porifera	8.78
	Serpulidae	5.22
	Caryophyllia smithii	5.15

3.6.3 CEND0513 biotope designation

The multivariate analysis of both the video and still data suggested that the original analysis of the data may have artificially split the **CR.MCR.EcCr** and **CR.HCR.XFa** habitats. SIMPER analysis of the faunal communities showed that the characteristic taxa from these two biotopes were largely identical, whilst clustering analysis also grouped stations from these two biotopes together. This suggested that a single biotope should be assigned to these stations.

The characteristic fauna included hydroid/bryozoan turf, Serpulidae, Porifera, *Caryophyllia smithii, Axinella* sponges, *Henricia* sp. and Paguridae. Whilst these taxa do bear some resemblance to those described under **CR.HCR.XFa**, there were also similarities with the **CR.HCR.DpSp** biotope. Looking into the faunal matrix in more detail, the sponges *Axinella, A. infundibuliformis* and *Phakellia ventilabrum* were all identified from the video and stills footage. These are characteristic of the sub-biotope **CR.HCR.DpSP.PhaAxi**. The biotope description states that *C. smithii* can be locally abundant, which could be seen in the faunal data. Large echinoderms such as *Henricia* and *Echinus esculentus* are also characteristic of **DpSp.PhaAxi**. *Henricia* was identified from the video and stills, although *Echinus acutus* rather than *E. esculentus* was observed. However, the presence of *Phakellia ventilabrum* was recorded only at one station (120_S2), and there was a lack of *Alcyonium.* The biotope description lists many different species of sponges, which were not recorded during the analysis. This may reflect the difficulty in accurately identifying sponges to species level from video and stills, but also could represent their absence. Due to these reasons, the biotope **CR.HCR.DpSp.(PhaAxi)** was assigned rather than the full biotope.

It should be acknowledged that the descriptions of the habitats within the original video and stills analysis showed that the habitats were patchy, with areas of cobbles/pebbles within sand and gravel. The assignment of the two **CR** biotopes was probably due to a slightly more impoverished or patchy nature of some areas, which therefore may visually have looked like a different habitat. However, assessment of the faunal communities did not support this separation. The faunal communities identified from the hard substrata biotopes suggested that these areas may be potential Annex I stony reef habitats, probably representing a mosaic of gravelly sand and cobbles. This was not highlighted in the original visual analysis of the data set, perhaps because the amount of cobble/boulder coverage within each habitat was insufficient to warrant such a designation.

The **SS.SCS** and **SS.SSa** stations were typically faunally sparse compared to the hard substrata stations. There appeared to be some patchiness within the soft sediment areas, reflected by the presence of hydrozoan and bryozoan turf as characteristic fauna of the **SS.SSa** and **SS.SCS** biotopes. The similarities between some of the soft sediment stations to some of the hard substrata stations probably reflected different levels of patchiness within the various habitats. This patchiness was noted in the original habitat descriptions from the visual data analysis. The division between coarse and sand habitats was not clear based on analysis of the faunal communities. The differences between these two habitats would be clearer from visual assessment of the sediment composition rather than the epifauna observed. Therefore, the biotopes for the soft sediment stations remained as those originally designated, although changed to either **SS.SSa.OSa** or **SS.SCS.OCS** to reflect the depth of the stations.

The biotope designation of the video segments from the CEND0513 East of Haig Fras data, based on both video and still multivariate analyses, is summarised in Table 3.22. Figure 3.41 displays the geographical distribution of the biotopes designated after the multivariate statistical analysis of the CEND0513 East of Haig Fras video and still data. The predicative mapping from UKSeaMap 2010 (McBreen *et al* 2011) project showed that the survey area covered by the CEND0513 cruise was predicted to be coarse sediments. The analysis showed that this area is relatively patchy, with areas of sand and coarse gravelly sediment that roughly agreed with the predicative habitat mapping, but also with areas of cobble, potentially Annex I stony reef.

Table 3.22. Summary of biotopes assigned to video data, CEND0513 East of Haig Fras MCZ.

Biotope	Description	Original Biotope/s	Video Segment No.	Depth Range
A4.121 : *Phakellia ventilabrum* and axinellid sponges on deep, wave-exposed circalittoral rock **CR.HCR.DpSp.(PhaAxi)**	**Uncertain match**. The characteristic fauna included hydroid / bryozoan turf, Serpulidae, Porifera, *Caryophyllia smithii, Axinella* sponges, *Henricia* sp. and Paguridae. Various other species of Porifera and echinoderms present. Substrata included cobbles / boulders with patches of gravelly sand. Possible Annex I stony reef?	**CR.HCR.XFa; CR.MCR.EcCr**	115_S1, 116_S1; 117_S1, 118_S1, 119_S1, 120_S2, 121_s2, 122_S2, 123_S2, 124_S2, 125_S1, 107_s2, 108_S1, 109_S1, 110_S2, 111_S1, 113_S2, 114_S2	99 – 105m
A5.15 : Deep circalittoral coarse sediment **SS.SCS.OCS**	Areas of coarse sediment according to original visual assessment, with patches of cobbles. Sparse epifauna, some hydroids / bryozoan turf, serpulids and Porifera on cobble patches, Paguridae and *Porania pulvillus* on soft sediment. Faunal community not very different from **SSa.OSa** stations	**SS.SCS**	118_S2, 124_S1, 124_S3, 107_S1, 107_S3, 110_S1, 111_S2, 113_S1, 113_S3, 114_S1, 114_S3	100 – 105m
A5.27 : Deep circalittoral sand **SS.SSa.OSa**	Areas of sandy sediment according to original visual assessment, with patches of cobbles. Sparse epifauna, some hydroids / bryozoan turf, serpulids and Porifera on cobble patches, Paguridae and *Porania pulvillus* on soft sediment. Faunal community not very different from **SCS.OCS** stations	**SS.SSa**	115_S2, 117_S2, 112_S1, 120_S1, 120_S3, 121_S1, 121_S3, 122_S1, 122_S3, 123_S1, 123_S3	99 – 104m

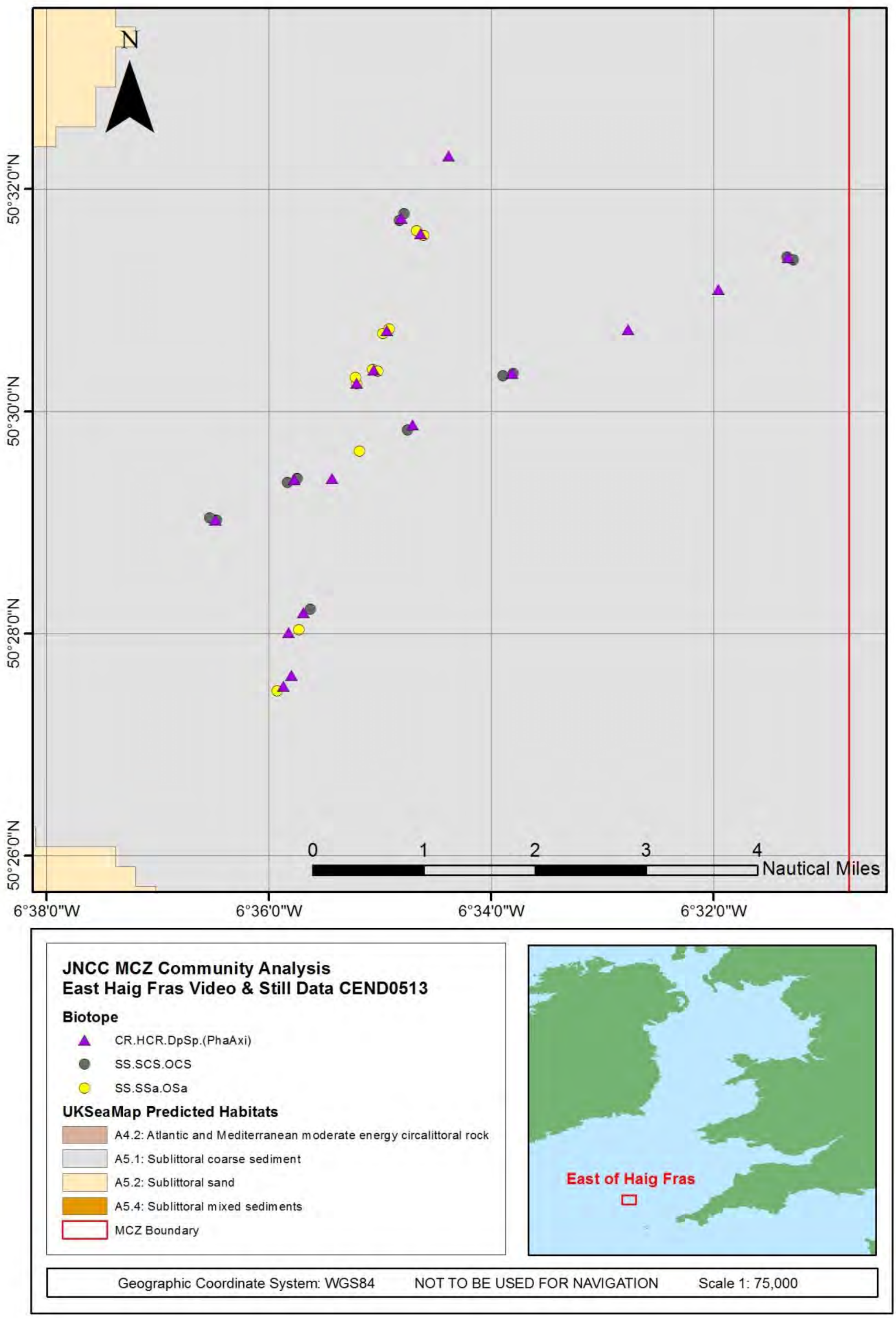


Figure 3.41. Geographical distribution of biotopes designated after multivariate analysis of CEND0513 video and still data, East of Haig Fras MCZ.

3.6.4 CEND0312 video data

3.6.4.1 Data rationalisation

The raw faunal data matrix was rationalised according to the methodology. All pelagic and highly mobile fauna were removed from the data set. These taxa included Octopodidae, Scyliorhinus, Osteichthyes, *Trisopterus luscus* and *Arnoglossus laterna.* As a result of the rationalisation procedure, four video segments had no visible fauna recorded (382_S1, 408_S3, 408_S9 and 469_S3), so were excluded from the multivariate analysis to prevent any skewing of the data. The rationalised data were then imported into PRIMER for statistical analysis.

3.6.4.2 Multivariate statistical analysis

Due to the data being based on SACFOR abundances, no data transformation was undertaken. A resemblance matrix using non-standardised, untransformed data was created using Bray Curtis similarity. Cluster analysis was then performed, and the resulting dendrogram plotted (Figure 3.42).

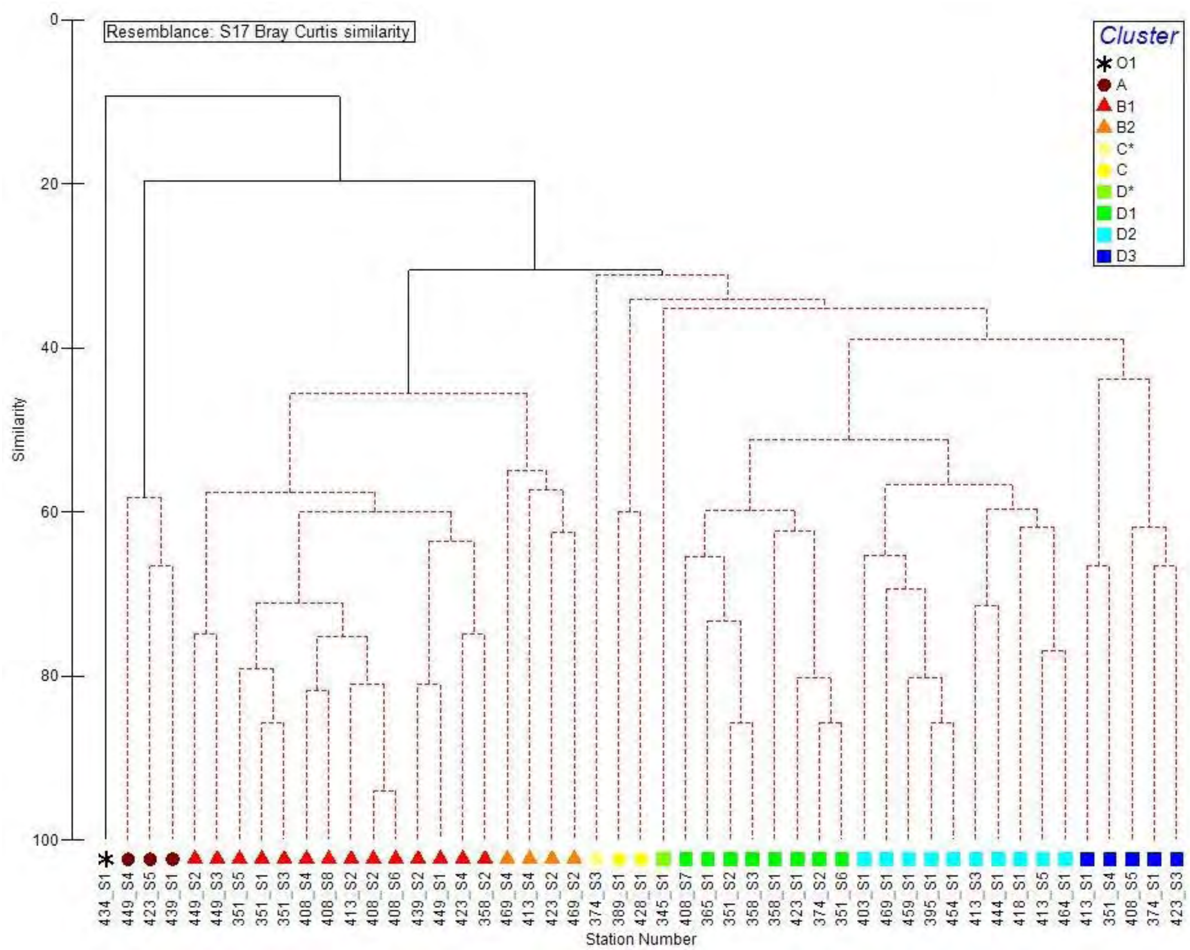


Figure 3.42. Dendrogram plot following cluster analysis of adjusted macrofaunal SACFOR data East of Haig Fras CEND0312 video data. Samples coloured according to assigned cluster groups.

There was one outlying station (434_S1) that split away at ~8% similarity. Group A contained three stations that separated at ~19% similarity. Group B was a large cluster that contained 18 stations that branched off at ~31% similarity. Group B was further divided into two sub-groups, B1 and B2, which separated at ~47% similarity. The remaining stations clustered together at ~32% similarity. Three stations split away between ~32% and ~35% similarity (groups C* and C), leaving 24 stations in group D. Group D had one outlying station (345_S1) that branched off at ~36% similarity. The remaining stations were divided into three sub-groups (D1 – D3). Sub-group D3 separated at ~39% similarity, whilst D1 and D2 branched from each other at ~53% similarity.

Figure 3.43 shows a 2D MDS ordination plot of the cluster analysis. The stress value of 0.18 was moderate, so the visual grouping of the video segments in the MDS plot can be regarded with some confidence. There were some agreements between the MDS plot and dendrogram, with the sub-groups defined from the dendrogram clustering relatively close together in the MDS plot.

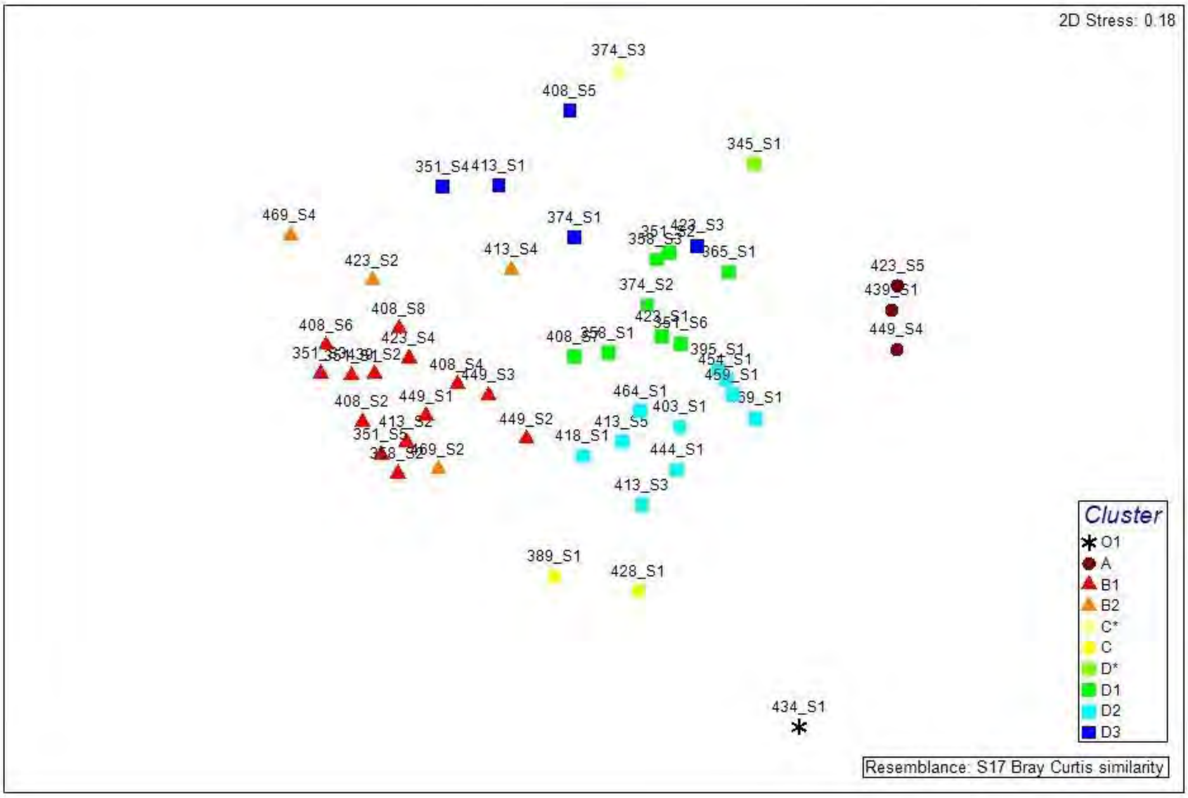


Figure 3.43. MDS ordination plot of CEND0312 East of Haig Fras MCZ video data.

Figure 3.44 shows the dendrogram plotted from the cluster analysis of the video data overlain with the biotopes assigned from the original visual video analysis. The pattern of station clustering within the dendrogram did not appear to show a very good correlation with the originally assigned biotopes. Sub-groups B1 and B2 were generally comprised of stations assigned the biotope **SS.SMx.OMx.HydBryBurr**, although there were some stations within these sub-groups assigned **SS.SSa.OSa.PoBurr**. The remaining groups identified from the cluster analysis were a combination of **SS.SSa.OSa.PoBurr** and **SS.SSa.OSa.SpF**.

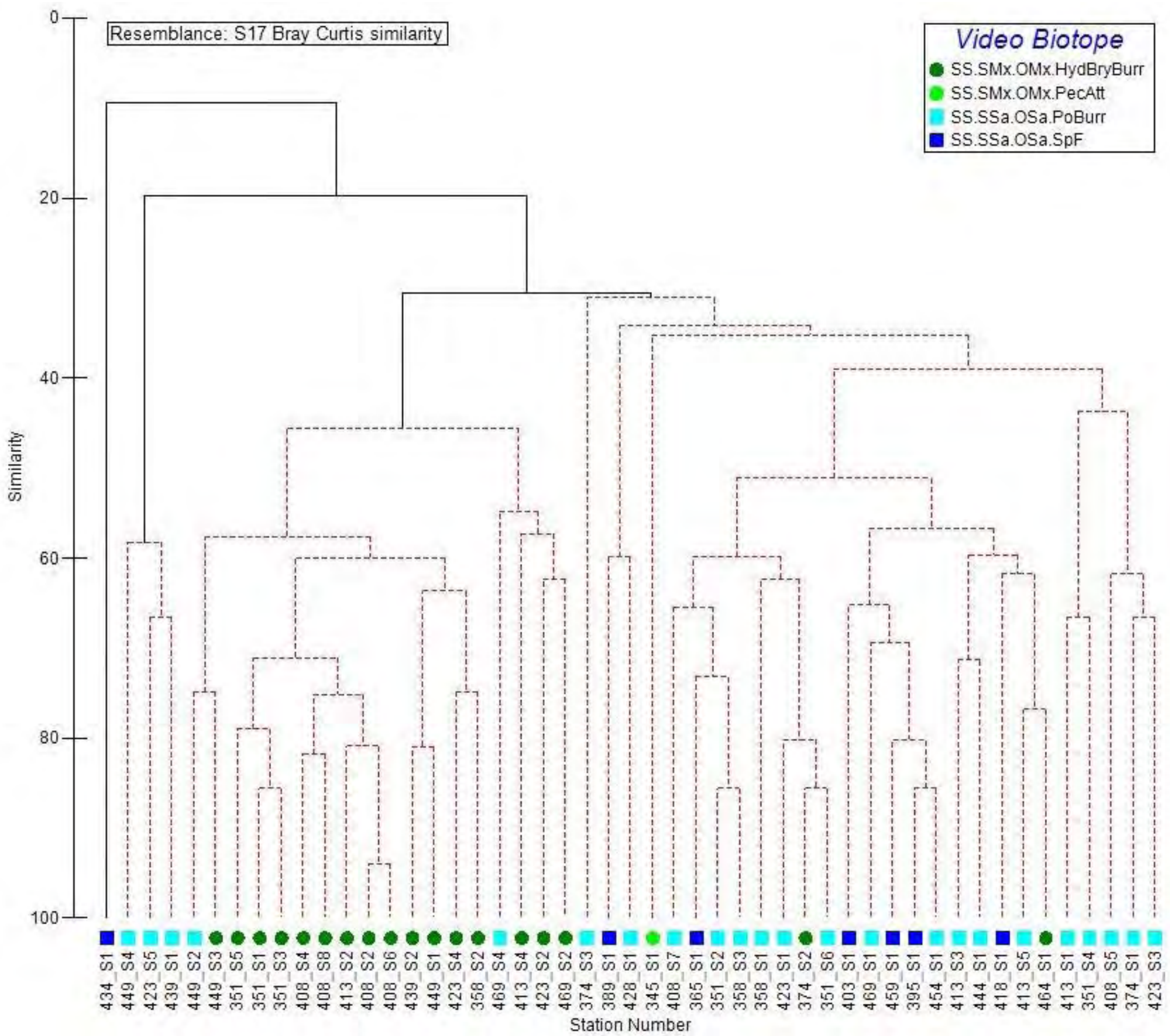


Figure 3.44. Dendrogram plot following cluster analysis of adjusted macrofaunal SACFOR data CEND0312 East of Haig Fras MCZ video data. Samples coloured according biotopes assigned from original analysis of data.

Two different SIMPER analyses were undertaken to assess both the faunal components that characterised stations based on the groups assigned after cluster analysis, and those that characterised stations assigned to biotopes designated from the original visual data analysis. Table 3.23 shows the characteristic taxa for each sub-group defined from the cluster analysis, listing those taxa that contributed at least 90% similarity for each sub-group. Full SIMPER results showing all contributing species for each sub-group can be found in Appendix 12.

All groups apart from group A were characterised by Hydrozoa. Group A had only Actiniaria as a characterising species. B1 was also characterised by Actiniaria, in addition to Bryozoa, Serpulidae, Asteroidea and Caryophylliidae. Both sub-group B2 and group C were characterised only by three taxa, one of which was Hydrozoa. B2 was also characterised by Porifera and *Munida rugosa*, whilst group C was characterised by Asteroidea and Sabellidae. In addition to Hydrozoa, sub-groups D1 and D2 both had Actiniaria and Asteroidea as characteristic species. Sub-group D2 was also characterised by Paguridae. Two other taxa characterised sub-group D3 (Porifera and Bryozoa).

In general, all the groups had relatively restricted lists of characteristic fauna. Characteristic taxa were typically only recognised at family or higher taxonomic levels. Many of the characteristic taxa could be found from a broad range of habitats with some element of gravel or shell material (e.g. Hydrozoa, Bryozoa and Serpulidae). Other taxa represented relatively large mobile fauna that also tend not to be characteristic of any particular habitat (e.g. Paguridae, Asteroidea).

Table 3.23. Results of SIMPER analysis of the sub-groups identified from cluster analysis of video faunal data, CEND0312 East of Haig Fras MCZ video data.

Group / Cluster	% Contribution of characterising species	
	Taxa / species	Contribution (%)
A	Actiniaria	100
B1	Hydrozoa	37.41
	Bryozoa	31.64
	Serpulidae	10.35
	Asteroidea	4.64
	Caryophylliidae	4.21
	Actiniaria	4.16
B2	Hydrozoa	75.91
	Porifera	12.04
	Munida rugosa	4.5
C	Hydrozoa	33.33
	Sabellidae	33.33
	Asteroidea	33.33
D1	Hydrozoa	39.61
	Actiniaria	39.61
	Asteroidea	11.87
D2	Actiniaria	30.38
	Hydrozoa	29.66
	Paguridae	29.66
	Asteroidea	5.19
D3	Hydrozoa	50.57
	Porifera	28.31
	Bryozoa	12.57

Table 3.24 summarises the SIMPER analysis results based on the biotopes assigned from the original video analysis. Of the four originally assigned biotopes, **SS.SMx.OMx.PecAtt** was only assigned to one video segment, and therefore could not be compared using SIMPER analysis.

The other three biotopes were all characterised by Hydrozoa and Actiniaria. Both **SS.SSa.OSa.SpF** and **SS.SMx.OMx.HydBryBurr** were also characterised by Porifera. Asteroidea and Serpulidae were both characteristic taxa of **OMx.HydBryBurr** and **SS.SSa.OSa.PoBurr**, whilst Bryozoa only characterised **OMx.HydBryBurr.**

As with the SIMPER analysis based on station grouping, the analysis based on biotopes had restricted lists of characteristic fauna, which also were typically only defined at higher taxonomic levels. The commonality in some of the characteristic taxa between the biotopes suggested that the faunal communities could potentially be quite similar. This suggested that assessment based on sediment composition rather than the identified epifauna may be more sensible for this particular set of survey data.

Table 3.24. Results of SIMPER analysis of the biotopes assigned after visual analysis of video data, CEND0312 East of Haig Fras MCZ video data.

Biotope	% Contribution of characterising species	
	Taxa / species	Contribution (%)
SS.SSa.OSa.SpF	Hydrozoa	38.2
	Paguridae	29.61
	Actiniaria	27.05
SS.SMx.OMx.HydBryBurr	Hydrozoa	44.18
	Bryozoa	20.5
	Serpulidae	8.67
	Asteroidea	7.3
	Porifera	5.54
	Actiniaria	5.42
SS.SSa.OSa.PoBurr	Hydrozoa	44.86
	Actiniaria	35.57
	Asteroidea	6.77
	Serpulidae	3.45

3.6.5 CEND0312 stills data

3.6.5.1 Data rationalisation

The raw faunal data matrix was rationalised according to the methodology. All pelagic and highly mobile fauna were removed from the data set. For this particular data set, this included *Arnoglossus laterna,* Osteichthyes and Scyliorhinus. Still image data were combined for each parent video segment. Abundance of taxa were expressed as a percentage of the total images within each segment that they were present. After rationalisation, 11 video segments had no visible fauna recorded from their constituent still images (365_S1, 382_S1, 403_S1, 395_S1, 428_S1, 408_S1, 408_S3, 408_S9, 439_S1, 469_S3 and 459_S1). These were excluded from the multivariate analysis to prevent any skewing of the data. The rationalised data were then imported into PRIMER for statistical analysis.

3.6.5.2 Multivariate statistical analysis

Due to the prior manipulation of data, no further transformations were undertaken. A resemblance matrix using non-standardised, untransformed data was created using Bray Curtis similarity. Cluster analysis was then performed, and the resulting dendrogram plotted (Figure 3.45).

There were three outlying stations that separated away at 0% similarity. The first video segment (345_S1; O1) was a complete outlier, whilst the next two were ~50% similar to each other (389_S1 and 423_S3; sub-group O2). Group A was also a relative outlier, and split away at ~2% similarity. The three stations within the group were at least ~66% similar to each other. The next cluster (group B) separated away at ~16% similarity, and was sub-divided into sub-groups B1 and B2 after they branched away from each other at ~19% similarity. The remaining 32 stations were all at least 25% similar to each other. At ~25% similarity, three stations split away and were assigned to group E. A further four station branched away at ~37% similarity (group C). The last 25 stations branched into two clusters at ~47% similarity. Sub-group D1 contained nine stations, whilst D2 contained 16 stations.

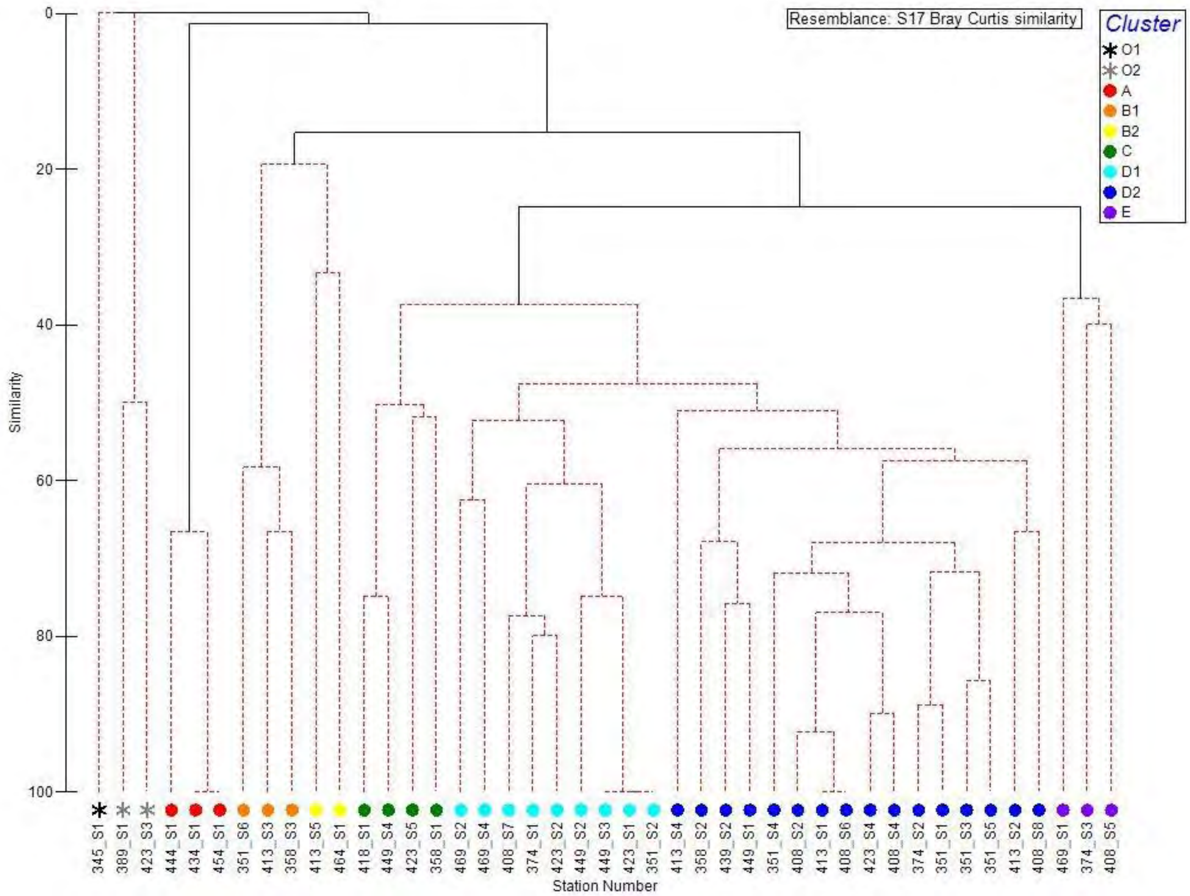


Figure 3.45. Dendrogram plot following cluster analysis of East of Haig Fras CEND0312 still data. Samples coloured according to assigned cluster groups.

A 2D MDS ordination plot of the cluster analysis can be seen in Figure 3.46. The three outlying stations (423_S3, 345_S1 and 389_S1) heavily skewed the MDS plot, so were removed from the plot. The stress value was relatively low (0.12), suggesting that the visual representation of the station clustering within the 2D plot was relatively accurate. The MDS plot showed good agreement with the dendrogram plot, with stations clustering together according to the sub-groups assigned from the dendrogram.

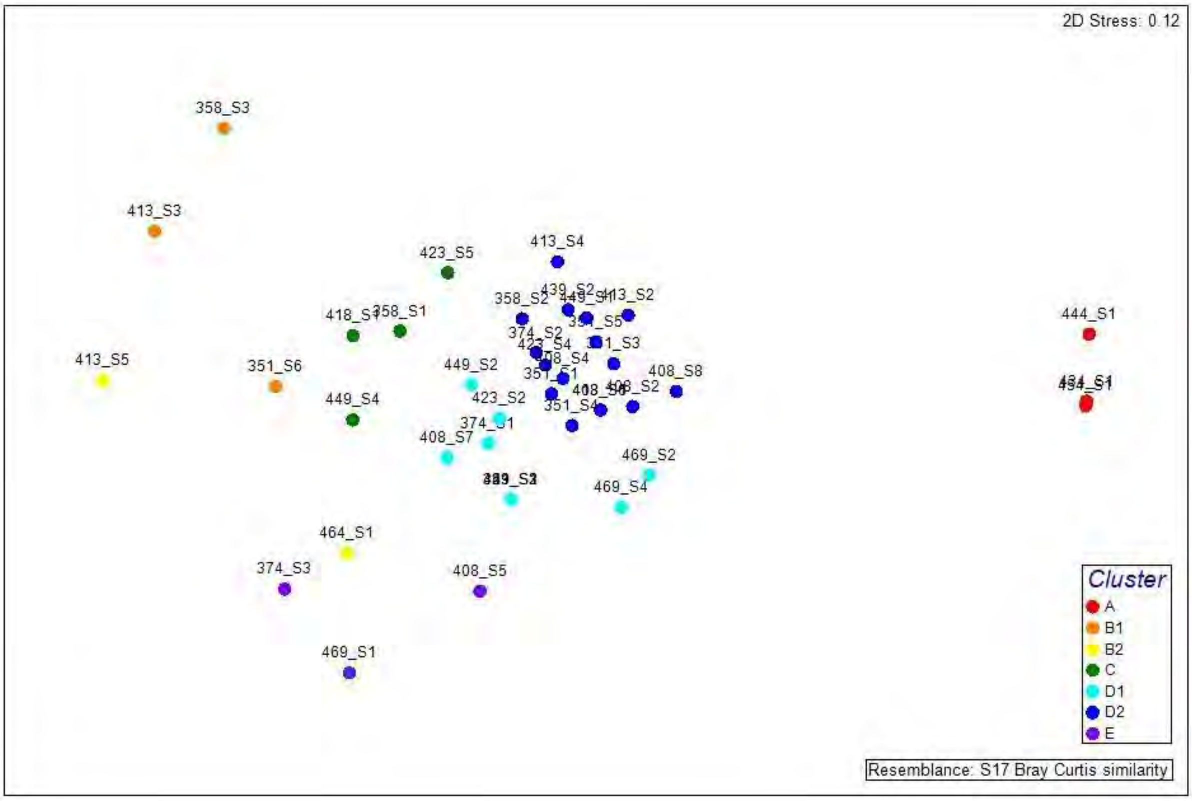


Figure 3.46. MDS ordination plot of CEND0312 East of Haig Fras MCZ still data.

Figure 3.47 shows the cluster analysis with the biotopes assigned to each station following the original visual video analysis. Sub-group D2 contained the majority of the stations assigned to the **SS.SMx.OMx.HydBryBurr** biotope, although some were present within other groups. Aside from this, there did not appear to be a particular pattern between the assigned biotopes and the structure of the clustering within the dendrogram.

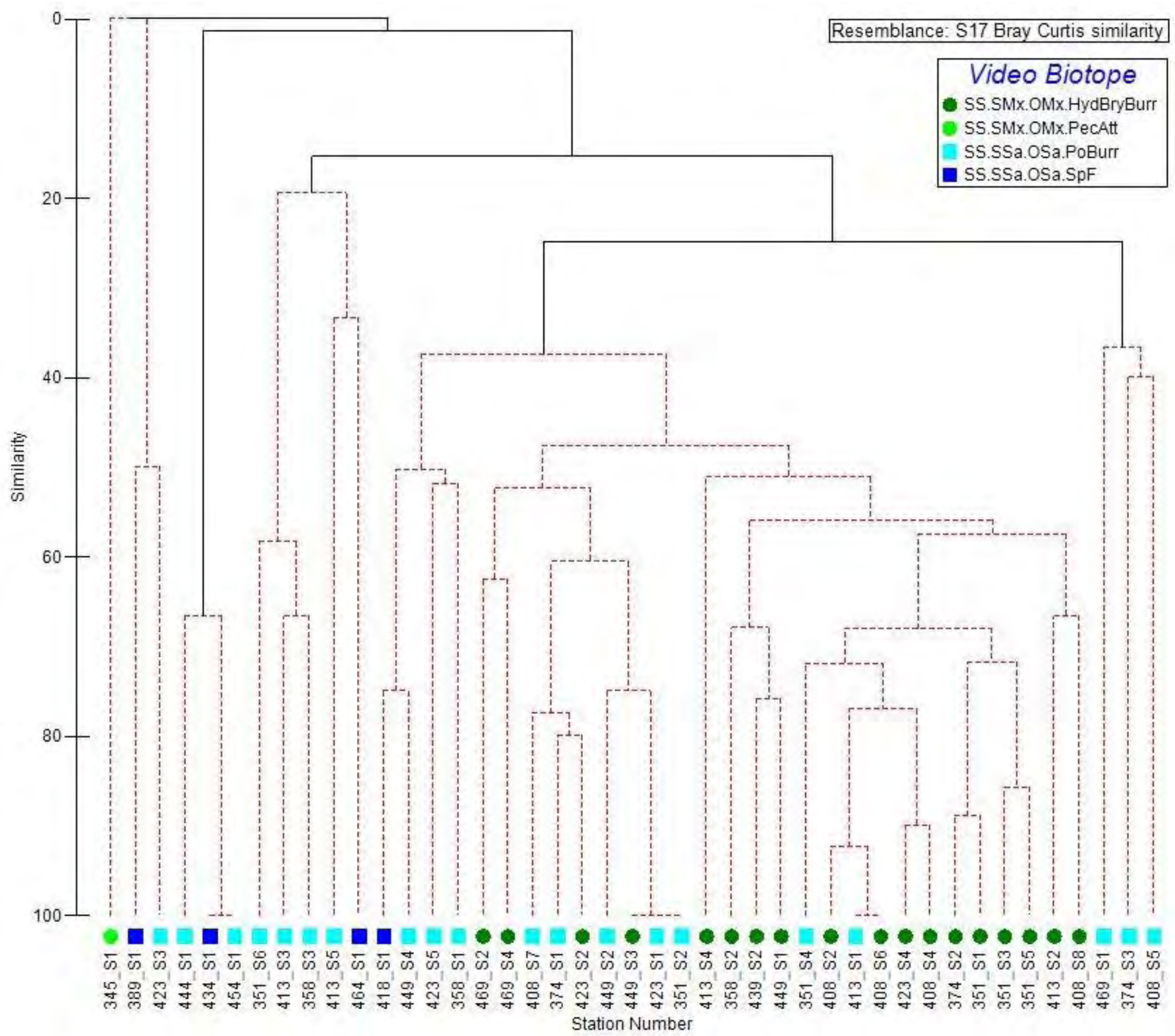


Figure 3.47. Dendrogram plot following cluster analysis of East of Haig Fras CEND0312 still data. Samples coloured according to biotopes assigned from original visual analysis of data.

As per the video data, two different SIMPER analyses were undertaken. The first was undertaken on the groups assigned from the cluster analysis, whilst the second was performed using the visually assessed biotopes from the original analysis of the data. Table 3.25 outlines the characteristic taxa for each sub-group, listing those taxa that contributed at least 90% similarity for each sub-group. Full SIMPER results showing all contributing species for each sub-group can be found in Appendix 12.

All the sub-groups had short lists of characterising taxa. Groups O2, A, B1, B2 and E were characterised only by a single taxa. The outlying group O2 was characterised by *Luidia ciliaris*, group A by Paguridae, B1 by Actiniaria, B2 by *Astropecten irregularis* and group E by Hydrozoa. Groups C, D1 and D2 were all characterised by Hydrozoa. D1 and D2 were both characterised by Serpulidae, whilst D2 and C both had Bryozoa in common.

Similar to the video data, characteristic taxa were typically identified only at family level or higher. Many of these taxa could be representative of a range of habitats (e.g. Hydrozoa, Bryozoa, and Actiniaria *etc.*).

Table 3.25. Results of SIMPER analysis of the sub-groups identified from cluster analysis of still faunal data, East of Haig Fras CEND0312.

Group / Cluster	% Contribution of characterising species	
	Taxa / species	Contribution (%)
O2	*Luidia ciliaris*	100
A	Paguridae	100
B1	Actiniaria	100
B2	*Astropecten irregularis*	100
C	Hydrozoa	37.41
	Asteroidea	19.94
	Bryozoa	18.31
	Actiniaria	14.94
D1	Hydrozoa	88.41
	Serpulidae	4.94
D2	Hydrozoa	42.73
	Bryozoa	30.09
	Serpulidae	16.22
	Caryophylliidae	5.71
E	Hydrozoa	100

Table 3.26 shows the results of the SIMPER analysis of the biotopes assigned after the original visual analysis of the data. The biotope **SS.SMx.OMx.PecAtt** was not included in the analysis since only one station was assigned this biotope. Hydrozoa were characteristic of the other three biotopes, and Bryozoa were characteristic of **OSa.PoBurr** and **OMx.HydBryBurr**. Actiniaria were only characteristic of **OSa.PoBurr**, whilst Serpulidae and Caryophyllidae were characteristic of **OMx.HydBryBurr**.

Table 3.26. Results of SIMPER analysis of the biotopes assigned after visual analysis of data, CEND0312 East of Haig Fras MCZ still data.

Biotope	% Contribution of characterising species	
	Taxa / species	Contribution (%)
SS.SMx.OMx.HydBryBurr	Hydrozoa	54.26
	Bryozoa	22.26
	Serpulidae	12.59
	Caryophylliidae	4.92
SS.SSa.OSa.PoBurr	Hydrozoa	73.07
	Actiniaria	10.67
	Bryozoa	6.7
SS.SSa.OSa.SpF	Hydrozoa	100

The original data analysis only examined three still images from each parent video segment, resulting in a restricted data set for the still image analysis. Only 23 different taxa were recorded across the 54 video segments. Approximately 92% of the video segments had only five or less taxa recorded. 15 of the recorded taxa were seen in only three or fewer video segments. The results of the multivariate analysis of the still images should therefore be taken under extreme caution, with the structure of the clustering within the dendrogram potentially based on small differences/similarities between data points.

3.6.6 CEND0312 biotope designation

The faunal data from the original visual analysis of the video and still images for CEND0312 was generally taxa poor. After rationalisation, only 30 taxa were present within the video data set, whilst the still data set contained only 23 taxa. Most of the taxa from both the video and still data sets were identified only at family or higher taxonomic levels, and typically represented fauna that could be found across a range of different habitats. Therefore the faunal community data relating to the video and still data from this particular contract was not particularly informative.

The original visual assessment of the survey data led to four biotopes being assigned to various video segments. The first was **SS.SSa.OSa.SpF**, sparse fauna in offshore circalittoral sand. Stations designated this biotope did have sparse epifauna, but the scarcity or richness of infauna cannot be assessed from video data alone. This biotope designation was therefore deemed misleading. The biotope **SS.SSa.OSa** was assigned instead based in station depths and sediment composition (as assessed during the original visual analysis), due to the lack of data concerning the faunal community present.

The second originally assigned biotope was **SS.SSa.OSa.PoBurr**, infaunal polychaetes with burrowing fauna in deep circalittoral sand. As mentioned above, as the amount of infaunal species cannot be assessed from video data only, raising concerns over the appropriateness of this biotope description. The multivariate analysis of the faunal community data showed that faunal characteristic of this assigned biotope was largely the same as **SS.SSa.OSa.SpF**. There was no evidence within the faunal community data to support a split between **OSa.SpF** and **OSa.PoBurr**. Therefore, the **OSa.PoBurr** stations were assigned to the biotope **SS.SSa.OSa**.

The biotope **SS.SMx.OMx.PecAtt** (Scallops (pectinidae) and some attached fauna on deep circalittoral mixed sediment) did cluster out separately from the other stations based on the presence of scallops. Only one record of this biotope was made. The other fauna present at the station were Hydrozoa, Actiniaria, Bryozoa and Buccinidae. This community was not felt to be significantly different to that expected for mixed sediments in general, so the biotope **SS.SMx.OMx** was assigned instead.

The stations assigned to the biotope **SS.SMx.OMx.SerBryBurr** (Epifauna, particularly hydroids and bryozoans with some evidence of infauna on deep circalittoral mixed sediment) tended to cluster away from those stations assigned to **SS.SSa.OSa** biotopes. The multivariate analysis listed these stations to be characterised by epifauna including hydroids, bryozoans, sponges and Serpulidae. This indicated that these stations had a different sediment composition to the sandy sediment stations. Aside from the presence of caryophyllids, it was felt that this community as not significantly different from that expected to be found within mixed sediment habitats in general. Also, many of the fauna were not deemed to be good ‘characteristic’ taxa for defining a biotope since they occur across a range of habitats, providing some suitable substratum is present. Indeed, hydrozoans were recorded at almost every station from the East of Haig Fras CEND0312 data set. Therefore these stations were assigned to the biotope **SS.SMx.OMx**.

The biotope designation of the video segments from the CEND0312 East of Haig Fras data is summarised in Table 3.27. Figure 3.48 displays the geographical distribution of the biotopes designated after the multivariate statistical analysis of the CEND0312 East of Haig Fras video and still data. The predicative mapping from UKSeaMap 2010 project (McBreen *et al* 2011) showed that the survey area covered by the CEND0312 cruise was predicted to be coarse and sandy sediments. The biotopes were sand with bands of mixed sediment.

Table 3.27. Summary of biotopes assigned to video data, CEND0312 East of Haig Fras MCZ.

Biotope	Description	Original Biotope/s	Video Segment No.	Depth Range
A5.27 : Deep circalittoral sand **SS.SSa.OSa**	Areas of rippled sandy sediment according to original visual assessment. Sparse epifauna, some hydroids on shell fragment / occasional gravel and evidence of burrowing fauna.	**SS.SSa.OSa.PoBurr;** **SS.SSa.OSa.SpF**	374_S1, 374_S3, 413_S1, 413_S3, 413_S5, 423_S1, 423_S3, 423_S5, 428_S1, 454_S1, 351_S2, 351_S4, 351_S6, 358_S1, 358_S3, 408_S1, 408_S3, 408_S5, 408_S7, 408_S9, 439_S1, 444_S1, 449_S2, 449_S4, 469_S1, 469_S3, 365_S1, 382_S1, 389_S1, 403_S1, 395_S1, 418_S1, 434_S1, 464_S1, 459_S1	98 – 103m
A5.45 : Deep circalittoral mixed sediments **SS.SMx.OMx**	Mixed sediments with epifauna such as hydroids, bryozoans and serpulids on patches of cobbles / pebbles. Some burrowing fauna within areas of finer sediment.	**SS.SMx.OMx.PecAtt;** **SS.SMx.OMx.HydBry Burr**	374_S2, 413_S2, 413_S4, 423_S2, 423_S4, 351_S1, 351_S3, 351_S5, 358_S2, 408_S2, 408_S4, 408_S6, 408_S8, 439_S2, 449_S1, 449_S3, 469_S2, 469_S4, 345_S1	99 – 106m

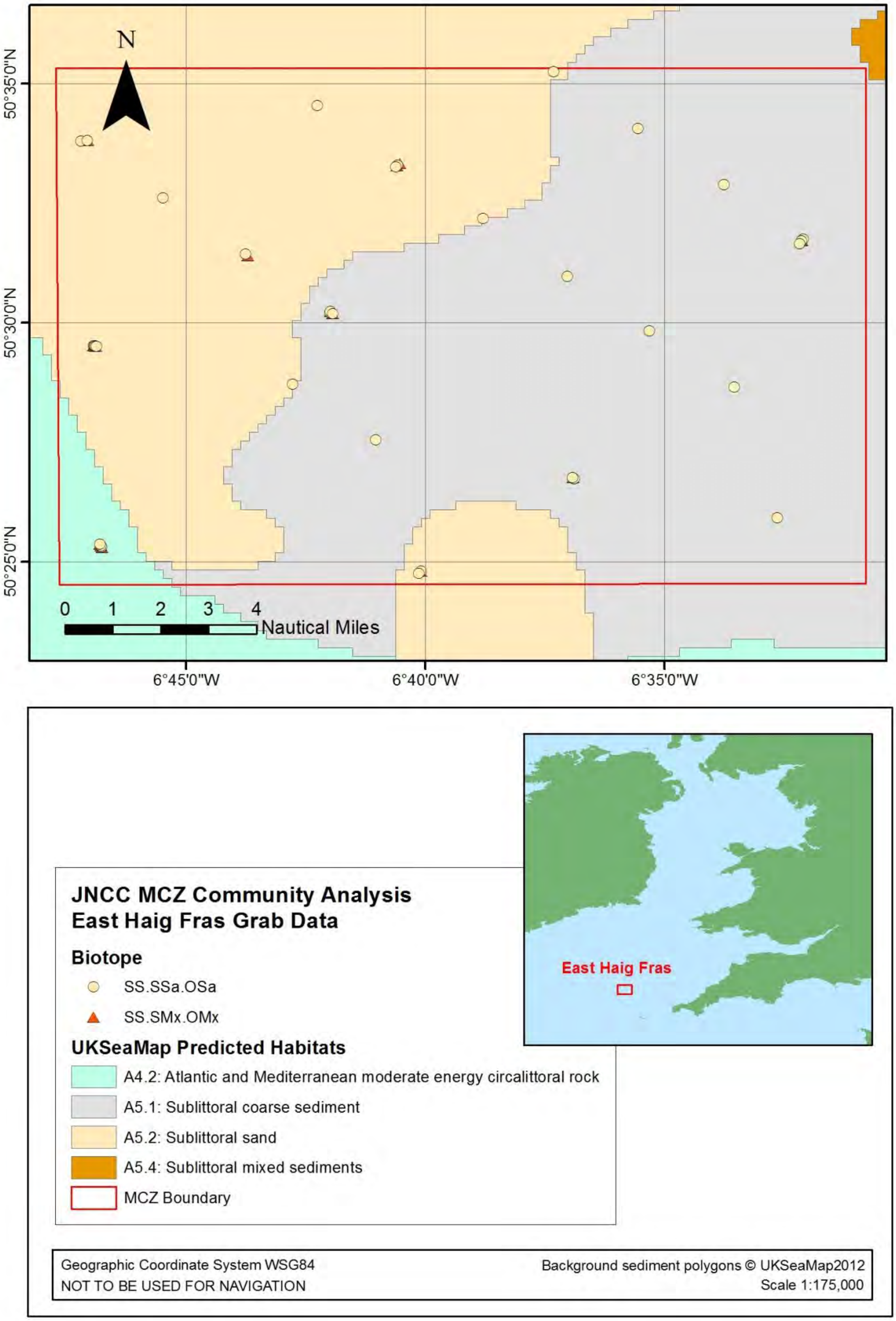


Figure 3.48. Geographical distribution of biotopes designated after multivariate analysis of CEND0312 video and still data, East of Haig Fras MCZ.

3.7 South-West Deeps MCZ – video and still data

3.7.1 Video data

3.7.1.1 Data rationalisation

The raw faunal data matrix was rationalised according to the methodology. For this particular data set, all fauna regarded as being pelagic, and therefore highly mobile, were removed from the data set prior to analysis. These taxa included Pisces, Gadidae, Pleuronectiformis, Triglidae and Cephalopoda. The rationalised data were then imported into PRIMER for statistical analysis.

3.7.1.2 Multivariate statistical analysis

Due to the data being based on SACFOR abundances, no data transformation was undertaken. A resemblance matrix using non-standardised, untransformed data was created using Bray Curtis similarity. Cluster analysis was then performed, and the resulting dendrogram plotted (Figure x).

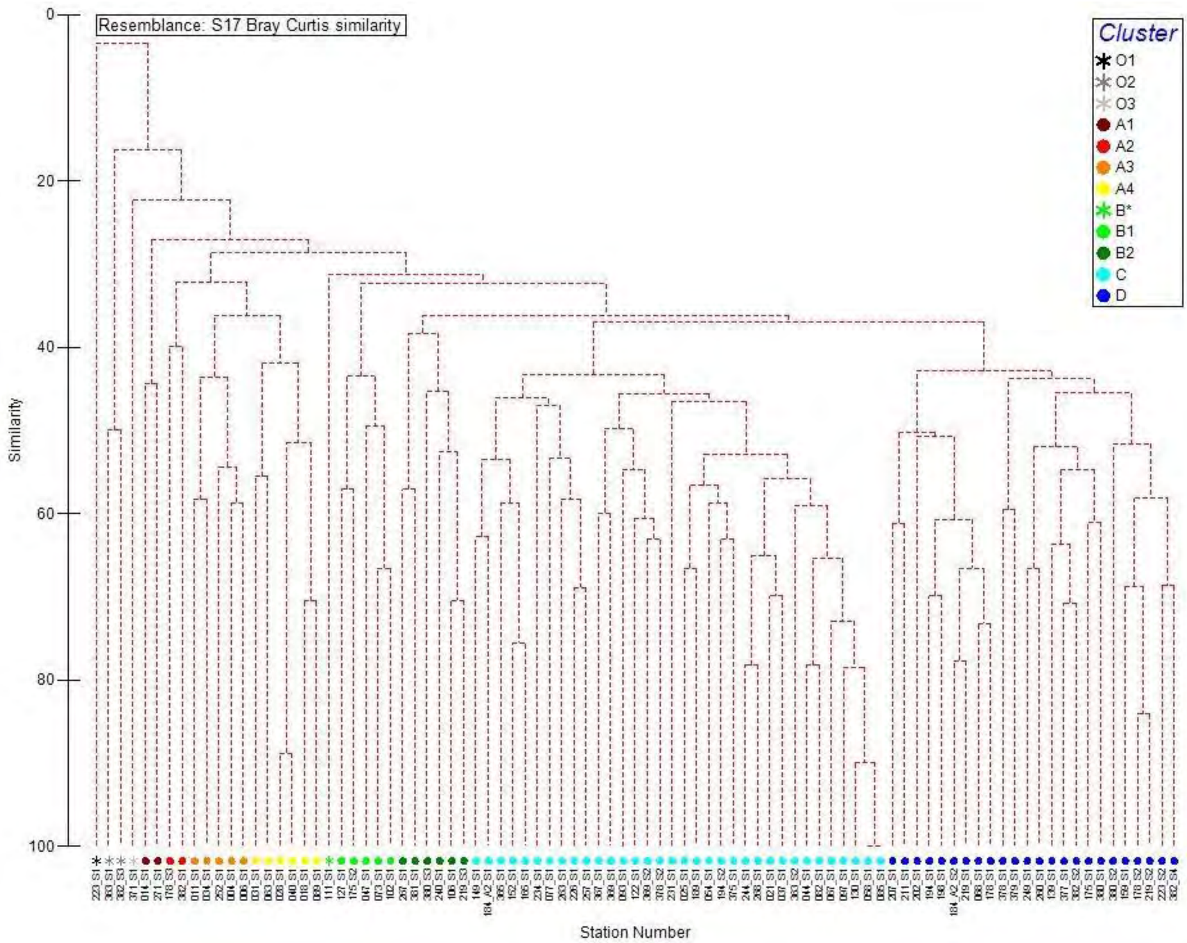


Figure 3.49. Dendrogram plot following cluster analysis of adjusted macrofaunal SACFOR data South-West Deeps (West) MCZ video data. Samples coloured according to assigned cluster groups.

There were four outlying video segments (O1 – O3). The first segment (223_S1) split off at ~4% similarity, followed by two segments at ~16% similarity (363_S1 and 382_S3). A final outlier (371_S1) split off at ~22% similarity. Group A consisted of four sub-groups. The first, sub-group A1, branched off at ~28% similarity, with sub-groups A2 – A3 branching off in one cluster at ~29% similarity. Sub-group A2 separated away at ~33% similarity, whilst sub-groups A3 and A4 split from each other at ~37% similarity. Between ~32% and ~37% similarity group B branched away. One outlier (111_S1, B*) split off at ~32% similarity. Sub-groups B1 and B2 contained five and six video segments respectively. At ~33% similarity sub-group B1 branched away, with sub-group B2 following at ~37% similarity. Groups C and D represented large clusters of video segments, containing 34 and 24 video sections respectively. These two groups split away from each other at ~38% similarity, with all video sections within cluster C ~43% similar, and those within group D ~41% similar.

Figure 3.50 shows a 2D MDS ordination plot of the cluster analysis. The stress value of 0.26 was relatively high, so too much reliance should not be placed on the exact details within the 2D MDS plot. Despite this, there appeared to be some good agreement between the dendrogram and MDS plot, with the different video segments roughly grouping together according to their assigned clusters.

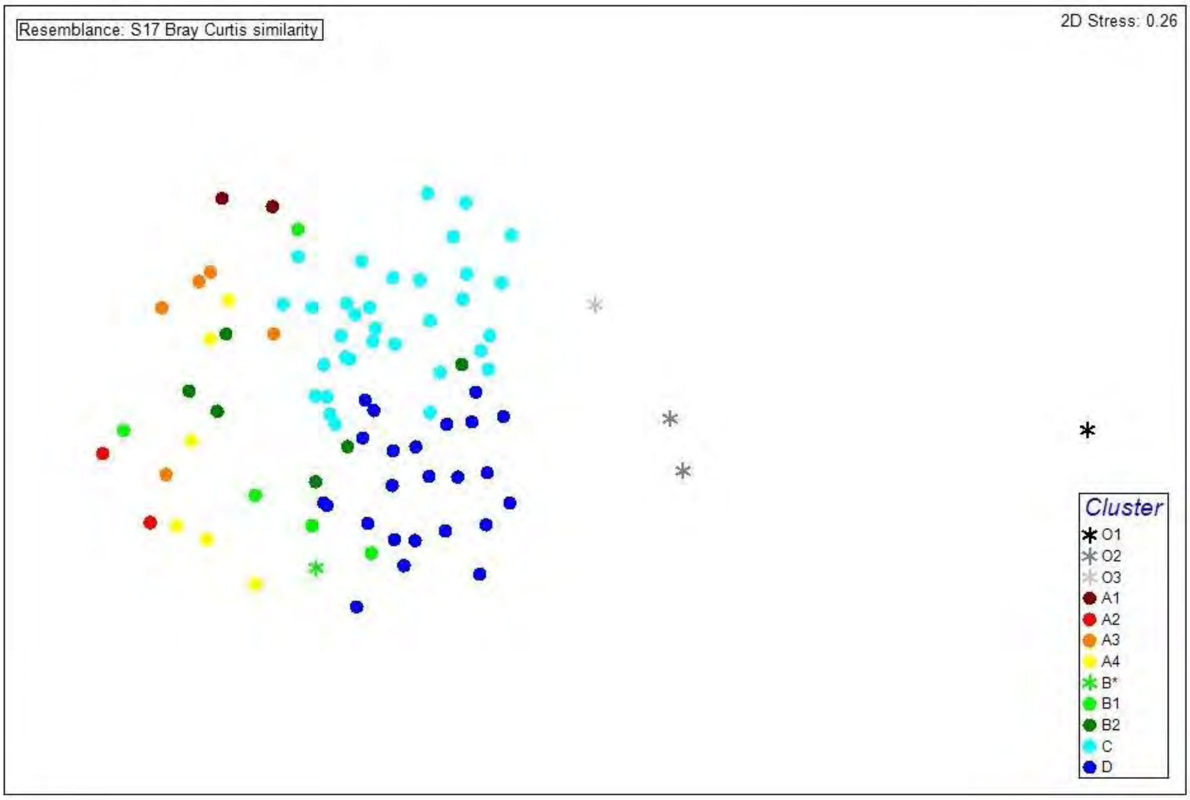


Figure 3.50. MDS ordination plot of South-West Deeps (West) MCZ video data.

Figure 3.51 shows the cluster analysis with the biotopes assigned to each station following the original video analysis. No overall pattern was discernible, with the exception of cluster group D containing more **SS.SMx.OMx** and **SS.SCS.OCS** biotopes than **SS.SSa.OSa.** However, other examples of both **OMx** and **OCS** are spread within the other cluster groups, with **OSa** stations spread across all clusters. This suggested that biotopes were principally assigned according to the sediment visible, probably because fauna were either rare or poorly distinguishable in the video footage. Alternatively, this clustering pattern may represent the ubiquitous nature of some of the identified fauna, such as hermit crabs, which can be found in a variety of different habitats.

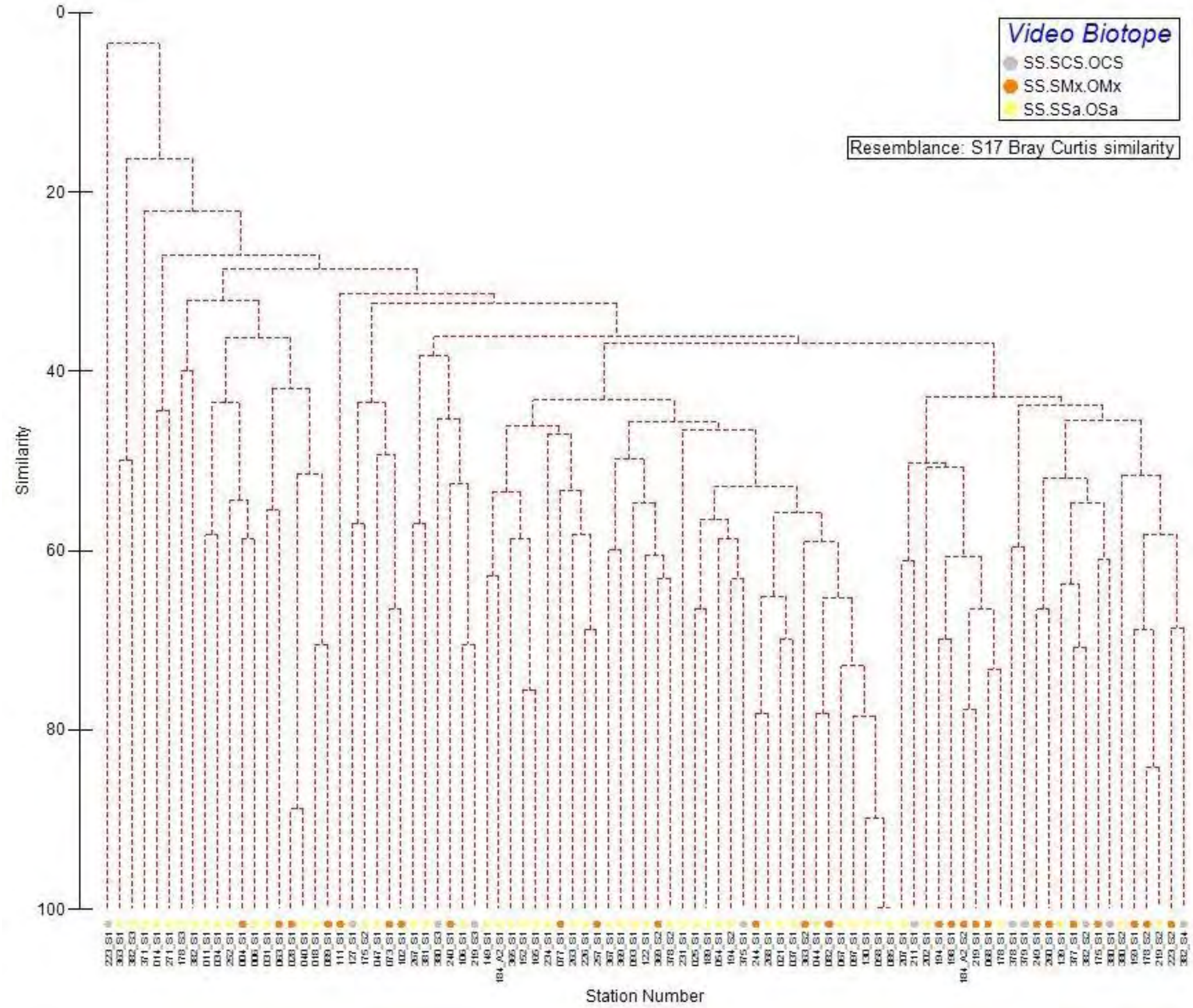


Figure 3.51. Dendrogram plot following cluster analysis of adjusted macrofaunal SACFOR data South-West Deeps (West) MCZ video data. Samples coloured according biotopes assigned from original analysis of data.

SIMPER analysis was undertaken to assess which species were characteristic for each of the sub-groups identified from the cluster analysis. Table 3.28 outlines the characteristic taxa for each sub-group, listing those taxa that contributed at least 90% similarity for each sub-group. Full SIMPER results showing all contributing species for each sub-group can be found in Appendix 13. The relatively short lists of characteristic species resulted from a restricted list of taxa identified from the video footage. The amount of higher level taxa within the lists suggested difficulty in accurate identification of fauna from the video footage. Extreme care must be taken when examining these results as entries such as Actiniaria, Anthozoa and *Actinauge richardi* could potentially all refer to the same taxon, with varying resolution within the video footage resulting in identification of the same fauna at different taxonomic levels.

After initial examination of the SIMPER results, *Lanice* could be seen to characterise every sub-group, contributing at least 22% to the similarity of stations within each group. Unfortunately *Lanice* can be found within the descriptions of coarse, mud, sand and mixed sediment biotopes. Bearing in mind comments concerning difficulties in resolution of taxonomic identification, the presence of Actiniaria, Anthozoa, Asteroidea, Ophiuroidea and Echinidae alongside fauna identified to species level that fall within these high level taxa, resulted in a low certainty to the basis of the clustering analysis. Other taxa that characterised sub-groups included relatively mobile species such as *Pagurus* and large echinoderms. Like *Lanice,* these species are characteristic of a range of biotope complexes.

Table 3.28. Results of SIMPER analysis of the sub-groups identified from cluster analysis of video faunal data, South-West Deeps (West) MCZ video data.

Group / Cluster	% Contribution of characterising species	
	Taxa / species	Contribution (%)
A1	Actiniaria	25
	Anthozoa	25
	Caridea	25
	Lanice	25
A2	*Lanice*	100
A3	*Lanice*	43.13
	Polychaeta	13.75
	Pagurus	11.22
	Chaetopterus	10.87
	Ophiuroidea	10.87
	Suberites carnosus	6.43
A4	*Lanice*	49.31
	Asteroidea	29.36
	Ophiuroidea	9.15
	Pagurus	6.13
B1	*Lanice*	37.48
	Astropecten irregularis	36.23
	Luidia sarsii	9.23
	Gracilechinus acutus	8.76
B2	*Lanice*	44.65
	Echinidae	26.6
	Ophiura	10.16
	Actinauge richardi	7.99
	Pagurus	6.97
C	*Actinauge richardi*	26.68
	Pagurus	25.6
	Lanice	22.44
	Actiniaria	14.51
	Polychaeta	3.27
D	*Lanice*	33.54
	Actinauge richardi	20
	Spatangus purpureus	15.43
	Echinidae	4.58
	Asteroidea	4.36
	Henricia	4.16
	Pagurus	3.88
	Gracilechinus acutus	3.33
	Ophiuroidea	2.59

Table 3.29 summaries the SIMPER results based on the biotopes assigned to each station from the original visual analysis of the video data. *Lanice, Actinauge richardi,* and *Pagurus* were characteristic of all three biotopes, whilst *Spatangus purpureus* and Echinidae characterised both **OCS** and **OMx** biotopes. Actiniaria characterised both **OMx** and **OSa.** The similarities between the characteristic fauna for each biotope suggested that the faunal community recognisable from the video analysis did not vary much across the different habitats observed.

Table 3.29. Results of SIMPER analysis of the biotopes assigned after visual analysis of data, South-West Deeps (West) MCZ video data.

Group / Cluster	% Contribution of characterising species	
	Taxa / species	Contribution (%)
SS.SCS.OCS	*Lanice*	34.18
	Actinauge richardi	24.5
	Echinidae	14.09
	Spatangus purpureus	6.27
	Pagurus	4.95
	Faunal turf	3.56
	Ophiura ophiura	2.62
SS.SMx.OMx	*Lanice*	46.36
	Actinauge richardi	15.15
	Pagurus	8.92
	Spatangus purpureus	6.92
	Asteroidea	5.38
	Gracilechinus acutus	3.81
	Actiniaria	3.32
	Echinidae	2.88
SS.SSa.OSa	*Lanice*	35.16
	Actinauge richardi	19.23
	Pagurus	19.14
	Actiniaria	10.77
	Polychaeta	2.97
	Ophiuroidea	2.11
	Faunal turf	1.57

3.7.2 Stills data

3.7.2.1 Data rationalisation

The raw faunal data matrix was rationalised according to the methodology. As per the South-West Deeps (West) video data, for this particular data set all fauna regarded as being pelagic, and therefore highly mobile, were removed prior to analysis. These taxa included Pisces, Gadidae, Pleuronectiformis, Triglidae and Cephalopoda. Still image data were combined for each parent video segment. Abundance of taxa were expressed as a percentage of the total images within each segment that they were present. The rationalised data were then imported into PRIMER for statistical analysis.

3.7.2.2 Multivariate statistical analysis

Due to the prior manipulation of data, no further transformations were undertaken. A resemblance matrix using non-standardised, untransformed data was created using Bray Curtis similarity. Cluster analysis was then performed, and the resulting dendrogram plotted (Figure 3.52).

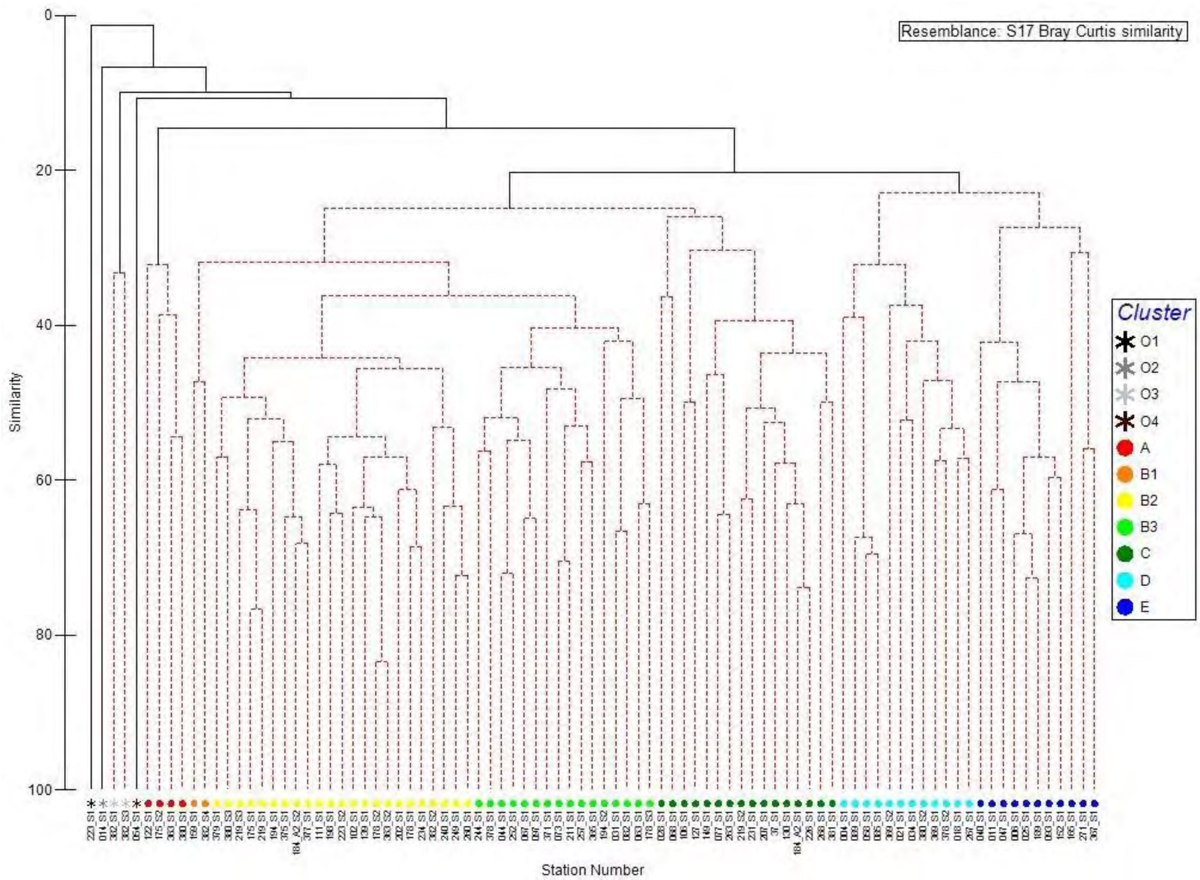


Figure 3.52. Dendrogram plot following cluster analysis of still image data, South-West Deeps (West) MCZ. Samples coloured according to assigned cluster groups.

The dendrogram showed five outlying points (O1 – O4) that branched away from the other data points between ~3% and ~11% similarity. Group A was a small cluster composed of four stations that split away at ~15% similarity. The remaining stations fell within two large clusters that branched from each other at ~20% similarity. The largest cluster split into two further groups at ~25% similarity.

The first larger group contained 41 stations (which were split into three sub-groups, B1 – B3), whilst the second smaller group contained 16 stations (Group C). Sub-group B1 separated away at ~33% similarity, whilst sub-groups B2 and B3 branched from each other at ~46% similarity. The second smaller cluster divided into two groups at ~23%. The first was group C, which contained 12 stations, and the second was group D, which contained 11 stations.

A 2D MDS ordination plot can be seen in Figure 3.53. Station 382_S2 was removed prior to plotting as it skewed the data set too much. The stress value of 0.22 was relatively high, suggesting that some caution should be used when examining patterns within the 2D plot. The stations clustered roughly together according to the groupings assigned from the dendrogram, but with a degree of overlap between some groups.

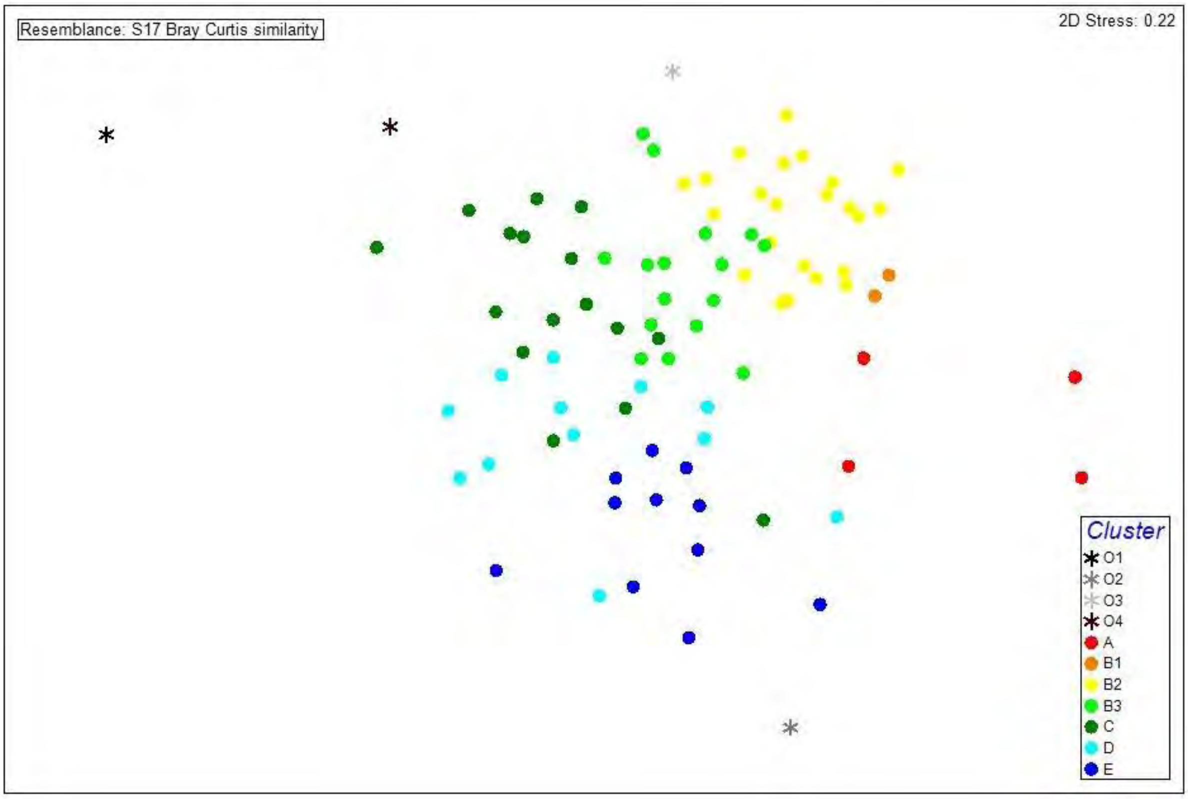


Figure 3.53. MDS ordination plot of South-West Deeps (West) MCZ video data.

Figure 3.54 shows the cluster analysis with the biotopes assigned to each station following the original video analysis. The patterns of clustering derived from the amalgamated stills data appeared to show a closer relationship to the video derived biotopes than was seen with the video footage data. Apart from a few exceptions, those video segments that were originally designated as mixed or coarse sediments were principally found within sub-groups B1 – B3.

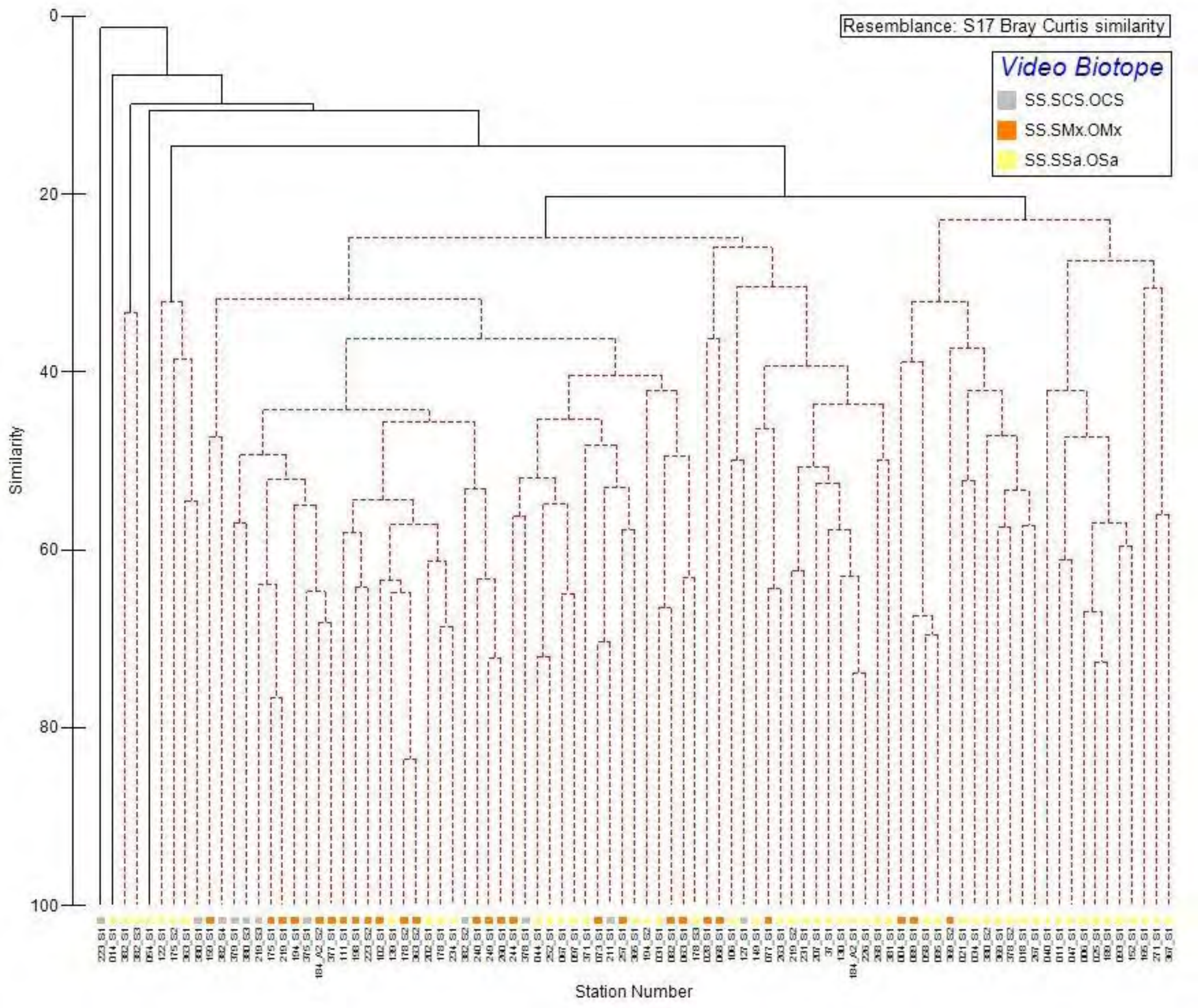


Figure 3.54. Dendrogram plot following cluster analysis of still image data, South-West Deeps (West) MCZ. Samples coloured according to biotopes assigned from original visual analysis of data.

SIMPER analysis was undertaken to assess which species were characteristic for each of the sub-groups identified from the cluster analysis. Table 3.30 outlines the characteristic taxa for each sub-group, listing those taxa that contributed at least 90% similarity for each sub-group. Full SIMPER results showing all contributing species for each sub-group can be found in Appendix 13.

As per the multivariate analysis of the video data, the still data clusters were based on very short lists of characteristic fauna. Many of the characteristic fauna were found within several of the clusters, such as *Lanice* and *Pagurus*. The problems seen in the video data with fauna being potentially counted under multiple taxa were again evident with the stills data.

Lanice was present as a characterising species in every sub-group except group A. The percentage contribution of *Lanice* to the similarity of stations within group E was only ~5%, much lower than within other sub-groups. The presence of Serpulidae as a characterising taxa in sub-groups B1 and B2 was somewhat supported by the prevalence of **OMx** and **OCS** biotopes assigned from the visual video analysis to stations within these sub-groups. However, Serpulidae also characterised group A, which were all **OSa**, and did not characterise sub-group B3, which also had many **OMx** and **OCS** stations.

As with the video data, many of the characteristic species of the sub-groups can be found from a range of different habitats (e.g. *Lanice* and *Pagurus*), and the presence of many high level taxonomic groups alongside fauna identified to species level resulted in a low certainty to the basis of the clustering analysis.

Table 3.30. Results of SIMPER analysis of the sub-groups identified from cluster analysis of still faunal data, South-West Deeps (West) MCZ video data.

Group / Cluster	% Contribution of characterising species	
	Taxa / species	Contribution (%)
A	Serpulidae	94.39
B1	Echinidae	42.25
	Serpulidae	35.21
	Lanice	22.54
B2	*Lanice*	66.71
	Serpulidae	14.53
	Actinauge richardi	4.56
	Ophiuroidea	4
	Gracilechinus acutus	2.13
B3	*Lanice*	66.7
	Pagurus	8.37
	Actiniaria	6.19
	Ophiuroidea	5.87
	Actinauge richardi	2.92
C	*Actinauge richardi*	40.43
	Lanice	30.61
	Faunal turf	12.25
	Pagurus	5.02
	Actiniaria	2.82
D	*Pagurus*	56.88
	Lanice	33.72
E	Actiniaria	61.38
	Pagurus	14.37
	Lanice	5.46
	Faunal turf	4.48
	Caridea	3.06
	Actinauge richardi	2.51

The SIMPER results based on the biotopes assigned to each station from the original visual analysis are in Table 3.31. The still image data showed that all three biotopes were characterised by *Lanice, Actinauge richardi* and Serpulidae. The **OCS** and **OMx** biotopes were both characterised by Ophiuroidea and *Gracilechinus acutus*, whilst OCS and OSa were characterised by Actiniaria and *Pagurus*. As with the video data, the faunal communities for each biotope were relatively similar. The characteristic taxa were not species typically representative of a particular habitat type.

Table 3.31. Results of SIMPER analysis of the biotopes assigned after visual analysis of data, South-West Deeps (West) MCZ still data.

Group / Cluster	% Contribution of characterising species	
	Taxa / species	Contribution (%)
SS.SCS.OCS	*Lanice*	42.91
	Serpulidae	27.11
	Ophiuroidea	10.39
	Gracilechinus acutus	3.63
	Anthozoa	3.34
	Actinauge richardi	1.96
	Faunal turf	1.86
SS.SMx.OMx	*Lanice*	62.6
	Serpulidae	11.04
	Ophiuroidea	4.12
	Actinauge richardi	3.88
	Pagurus	2.74
	Gracilechinus acutus	2.48
	Actiniaria	2.02
	Spatangus purpureus	1.99
SS.SSa.OSa	*Lanice*	38.74
	Pagurus	16.94
	Actinauge richardi	14.3
	Actiniaria	13.08
	Faunal turf	5.77
	Serpulidae	2.67

The rationalised combined still image data from South-West Deeps (West) resulted in a list of 64 taxa. As previously mentioned, the data set contained several possible examples where fauna maybe represented by multiple taxa (e.g. *Munida* and *Munida rugosa*; Ophiuroidea, Ophiuridae, *Ophiura* and *Ophiura albida etc*.). These uncertainties stemmed from the inability to sufficiently resolve taxonomic identifications to species level, due in part to the nature of the media, but also possibly the quality of the images taken. These uncertainties within the data can cause stations to cluster out inappropriately due to the presence of fauna potentially appearing within different taxa. Without examination of every image to ascertain the certainty of faunal identifications, these problems are difficult to resolve. Combining taxa under higher taxonomic levels may resolve some issues, but will reduce an already restricted list of taxa to even fewer entries.

3.7.3 Biotope designation

Table 3.32 summarises the biotopes assigned after analysis of the South-West Deeps (West) video and still data. Assessment of the epifaunal communities via cluster and SIMPER analysis suggested that there was insufficient data to accurately apply the multivariate statistical techniques to define biotopes for the South-West Deeps (West) video data. The low level of faunal identification possible from the video analysis resulted in potentially artificial clusters being created, especially with the possibility of fauna being represented under several different taxa. Therefore, the multivariate analysis could not identify any trends in the faunal community data that should over-rule the biotopes that were designated during the original visual analysis of the video footage. Analysts examining the video footage had a clearer view of any changes in habitat type reflected in the sedimentary environment. However, the presence of epifauna from the same taxa across all three biotopes identified during the video analysis may indicate that the faunal habitats were more similar than reflected by the biotope designations. The different habitats identified during the video analysis probably represented either patchiness or a transition between habitat types.

Some information about the survey area could be discerned from the epifaunal data. *Lanice* was ubiquitous all almost all video segments, suggesting an element of muddy sand present across the survey area. Many of the other taxa present such as hermit crabs and large echinoderms are characteristic of a range of biotope complexes. *Spatangus purpureus* was principally identified from videos originally assessed to be the biotope **SS.SMx.OMx** and **SS.SCS.OCS,** although no currently defined mixed sediment biotope contains *S. purpureus* as a characteristic species.

The South-West Deeps (West) data set contained 89 video segments. Of the 64 taxa recorded, 22 were identified only from a single video segment, and a further 22 from between two and nine segments. Two thirds of the taxa identified were present in only 10% or less of the video segments. This indicated that many of the taxa very relatively rare within the dataset, creating a lot of background 'noise'. Of the 20 taxa seen in more than 10% of the video segments, these were typically fauna such as Serpulidae, *Pagurus, Lanice,* Ophiuroidea, Hydrozoa, and faunal turf – relatively ubiquitous epifauna that can be found from a range of soft sediment environments with at least an element of gravel or shell. The data did allow for some generalisations to be made, such as the presence of *Lanice* suggested an element of muddy sand within the sediment, whilst Serpulidae suggested an element of larger substrata such as gravel, pebbles or shell material. However, this type of information gleaned from the faunal community does not provide any more information than would be visible to the original analyst of the video and still data.

Figure 3.55 shows the geographical distribution of the biotopes assigned to each station after the video and still multivariate analysis. **SS.SSa.OSa** biotopes were the most prevalent, generally occurring in areas predicted to be sandy sediments according to the UKSeaMap Project (McBreen *et al* 2011). The **SS.SCS.OCS** and **SS.SMx.OMx** biotopes tended to occur relatively close to areas that were predicted to be coarse sediments.

Table 3.32. Summary of biotopes assigned to video and still data, South-West Deeps (West) MCZ.

Biotope	Description	Original Biotope/s	Video Segment No.	Depth Range
A5.15 : Deep circalittoral coarse sediment **SS.SCS.OCS**	Faunal community data not informative enough to designate a different biotope from original visual analysis of video and still image data.	**SS.SCS.OCS**	127_S1, 211_S1, 219_S3, 223_S1, 375_S1, 378_S1, 379_S1, 380_S1, 380_S3, 382_S2, 382_S4	150 – 159m
A5.27 : Deep circalittoral sand **SS.SSa.OSa**	Faunal community data not informative enough to designate a different biotope from original visual analysis of video and still image data.	**SS.SSa.OSa**	006_S1, 011_S1, 014_S1, 018_S1, 021_S1, 025_S1, 031_S1, 034_S1, 037_S1, 040_S1, 047_S1, 054_S1, 058_S1, 067_S1, 085_S1, 093_S1, 097_S1, 106_S1, 122_S1, 130_S1, 139_S1, 149_S1, 152_S1, 165_s1, 175_S2, 178_S1, 178_S3, 184_A2_S1, 189_S1, 194_S2, 201_S1, 207_S1, 219_S2, 226_S1, 231_S1, 234_S1, 252_S1, 263_S1, 267_S1, 268_S1, 271_S1, 363_S1, 365_S1, 367_S1, 369_S1, 371_S1, 378_S2, 380_S2, 381_S1, 382_S1, 382_S3	131 – 170m
A5.45 : Deep circalittoral mixed sediments **SS.SMx.OMx**	Faunal community data not informative enough to designate a different biotope from original visual analysis of video and still image data.	**SS.SMx.OMx**	004_S1, 028_S1, 063_S1, 068_S1, 073_S1, 077_S1, 082_S1, 089_S1, 102_S1, 111_S1, 159_S1, 175_S1, 178_S1, 184_A2_S2, 194_S1, 198_S1, 219_S1, 223_S2, 240_S1, 244_S1, 249_S1, 257_S1, 260_S1, 363_S2, 369_S2, 377_S1	137 – 165m

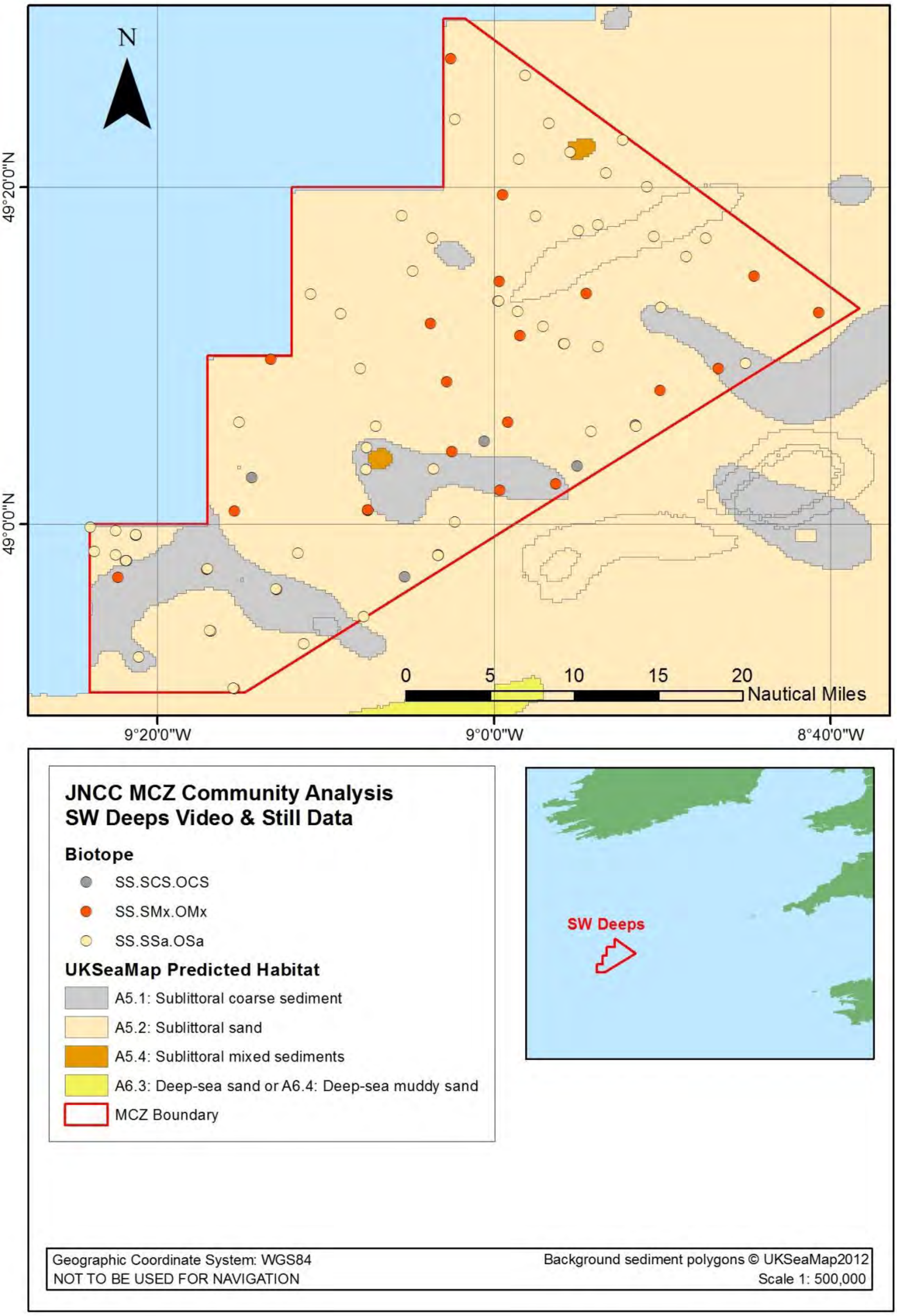


Figure 3.55. Geographical distribution of biotopes designated after multivariate analysis of video and still data, South-West Deeps (West) MCZ.

3.8 Swallow Sand MCZ – video and stills data

3.8.1 Video data

3.8.1.1 Data treatment

The raw faunal data matrix was rationalised according to the methodology. For this particular data set, all pelagic and highly mobile fauna were removed from the data set. These taxa included Ctenophora, and various fish such as *Myxine glutinosa,* Rajidae, *Lophius piscatorius,* Gadidae, Triglidae, and Ammodytidae. Any records of both adults and juveniles of the same taxa were merged. An error in species nomenclature was noted and corrected after confirmation of the identification in the raw data. The records of *Plumaria* (a red algae) were changed to *Plumularia* (a hydrozoan). This error was flagged and checked only due to sample depth being inappropriate for algae. The rationalised data were then imported into PRIMER for statistical analysis.

3.8.1.2 Multivariate statistical analysis

Due to the data being based on SACFOR abundances, no data transformation was undertaken. A resemblance matrix using non-standardised, untransformed data was created using Bray Curtis similarity. Cluster analysis was then performed, and the resulting dendrogram plotted (Figure 3.56).

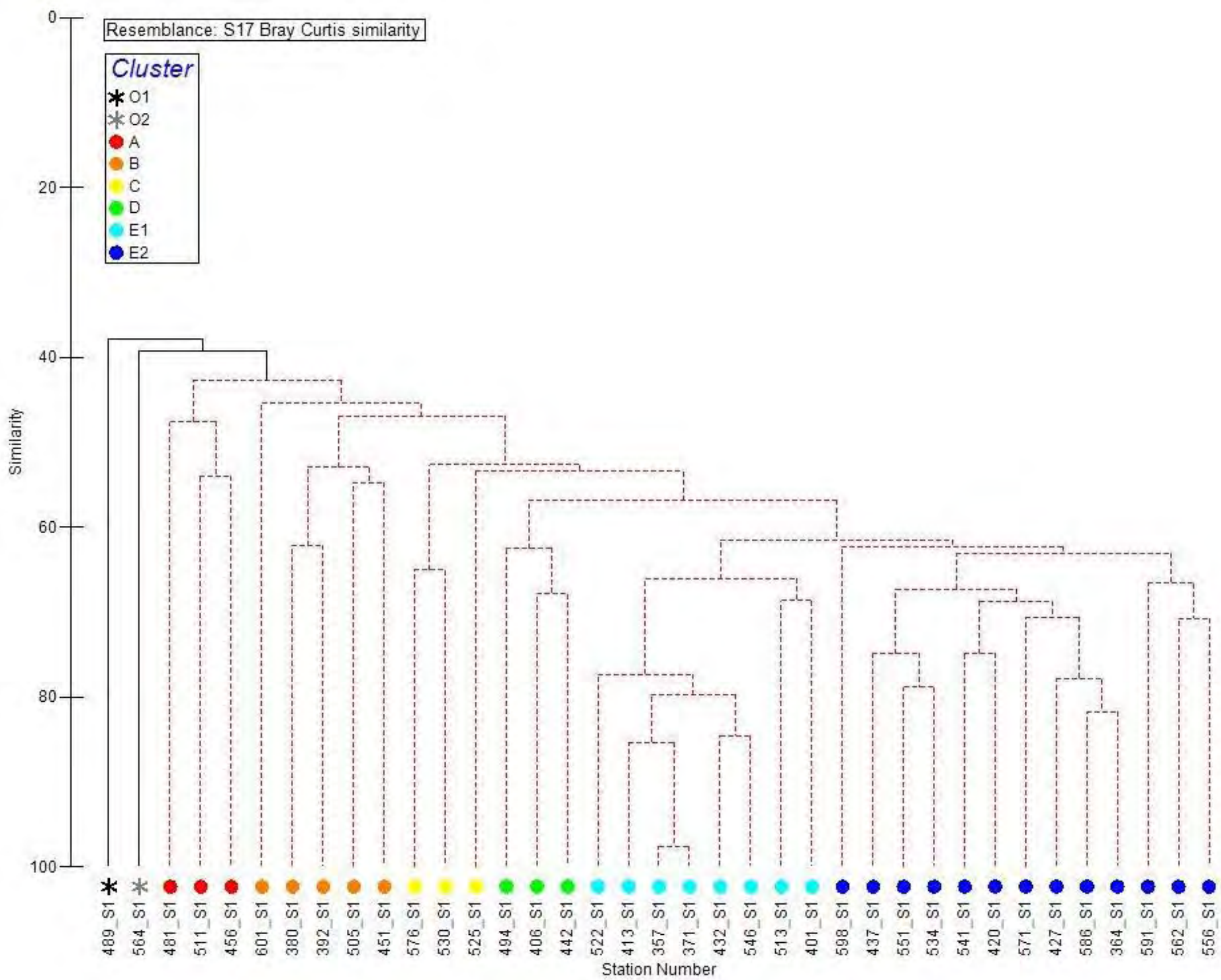


Figure 3.56. Dendrogram plot following cluster analysis of adjusted macrofaunal SACFOR data Swallow Sand MCZ video data. Samples coloured according to assigned cluster groups.

All the video segments from the survey area had at least ~38% similarity to one another, suggesting some overall similarities between the observed faunal communities. Two outlying stations (489_S1 and 564_S1) split away at ~38% and ~39% similarity respectively. At ~43% similarity, three stations separated away and were assigned to group A. Group B contained five stations that split away at between ~45% and ~47% similarity. Three stations separated away at ~54 – 55% similarity, and were assigned to group C. At ~57% similarity the remaining stations split into two clusters. The smaller cluster (group D) contained three stations, whilst the larger cluster contained 21 stations. These 21 stations branched into sub-groups E1 and E2 at ~62% similarity, with E1 containing eight stations, whilst E2 continued 13 stations.

Figure 3.57 shows a 2D MDS ordination plot of the cluster analysis. The stress value of 0.22 was relatively high, suggesting that too much reliance should not be placed on the detail within the plot. There were generally good agreements between the MDS plot and dendrogram. Stations tended to cluster together in the same groupings as the dendrogram, with the exception of group C.

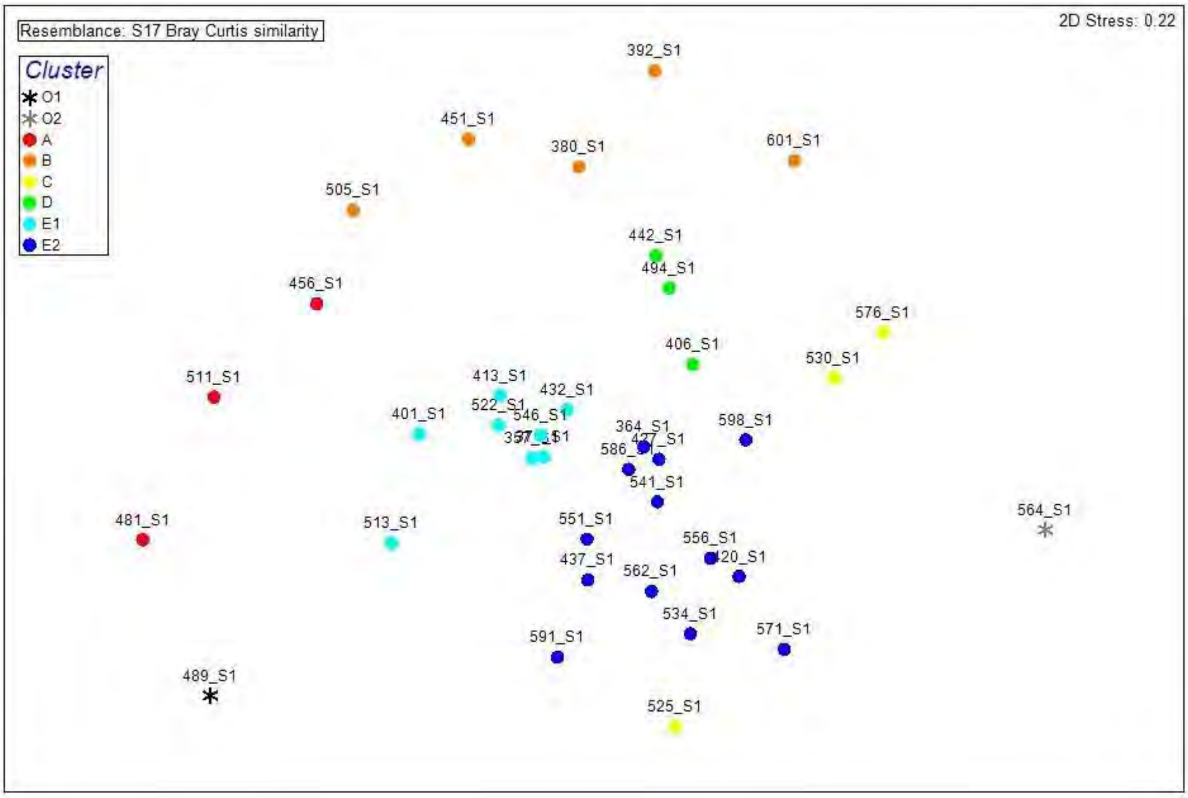


Figure 3.57. MDS ordination plot of Swallow Sand MCZ video data.

Figure 3.58 shows the cluster analysis with the biotopes assigned to each station following the original visual video analysis. There did not appear to be any trends between the structure of the station clustering within the dendrogram and the biotopes assigned to the stations following the original visual analysis of the video data. Those stations assigned the biotope **SS.SMx.CMx** tended to be less than 50% similar to the **CFiMu** and **CFiMu.SpnMeg** stations, although with some exceptions (e.g. 513_S1, 437_S1 and 541_S1).

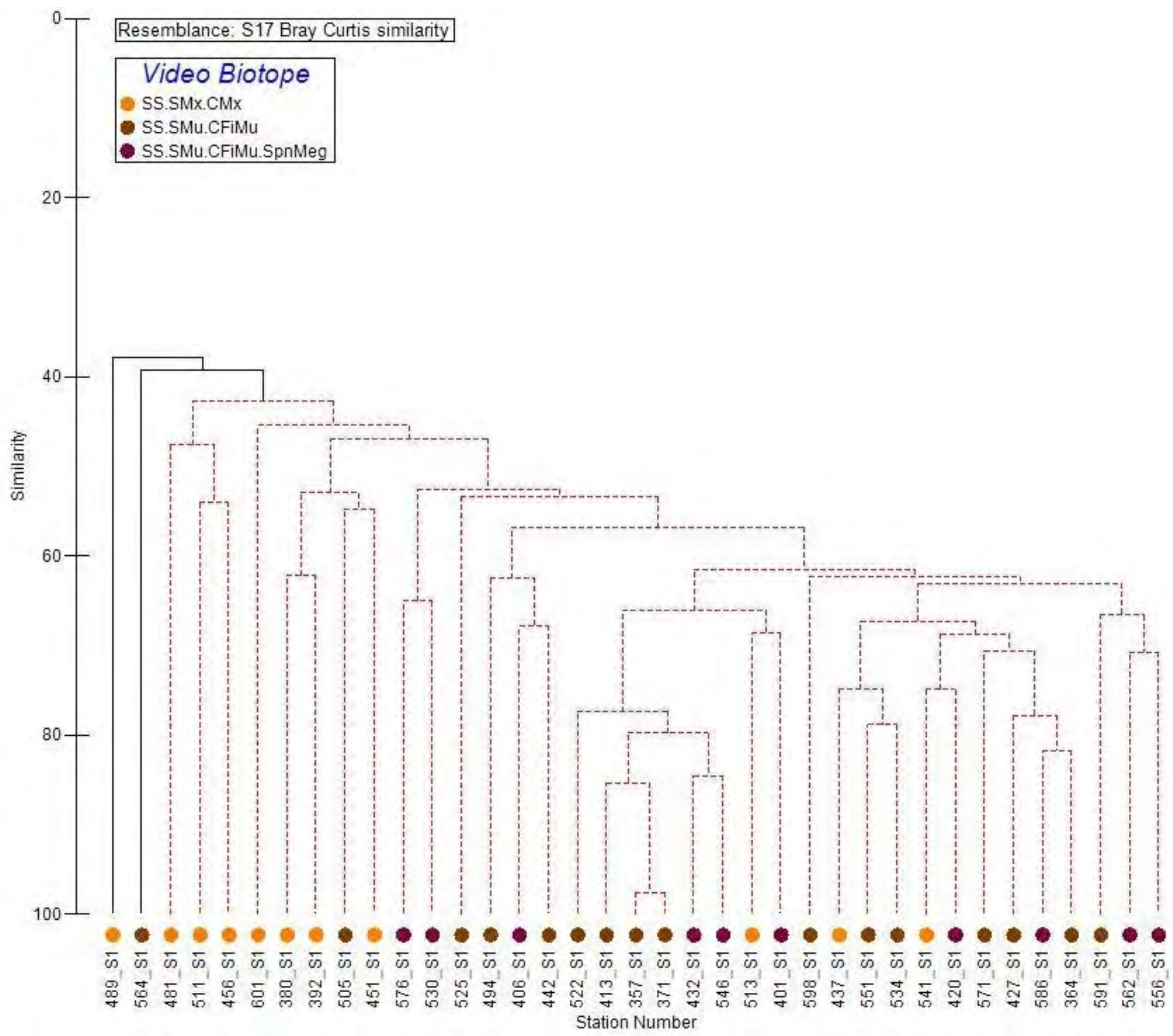


Figure 3.58. Dendrogram plot following cluster analysis of adjusted macrofaunal SACFOR data Swallow Sand MCZ video data. Samples coloured according biotopes assigned from original analysis of data.

SIMPER analyses were undertaken on both the groups assigned to stations after assessment of the cluster analysis, and on the biotopes assigned to each station by the original visual analysis of the data. Table 3.33 shows the characteristic taxa for each sub-group defined from the cluster analysis, listing those taxa that contributed at least 90% similarity for each sub-group. Full SIMPER results showing all contributing species for each sub-group can be found in Appendix 14.

Three species, *Alcyonium digitatum*, *Cerianthus lloydii* and *Pennatula phosphorea*, were characteristic of all groups, albeit with different percentage contributions. Other characteristic taxa that occurred across many of the groups included *Antalis entalis*, *Pagurus* and Asteroidea. These similarities between the characteristic species for each group suggested that the faunal community across the site was relatively ubiquitous, probably with some patchiness in sediment and species distributions. The presence of both *Cerianthus lloydii* and *Pennatula phosphorea* suggested a high component of fine-grained sediment. The average abundance of *P. phosphorea* in groups C, D, E1 and E2 was ‘Common’, whilst in groups A and B it was ‘Rare’ to ‘Occasional’. *Alcyoncium digitatum* indicated the presence of at least some hard substrata, such as pebbles or cobbles. However, examining the sediment metadata showed these to be a minority part of the sediment composition (<15%), which was principally sand or mud with some shell fragments.

Table 3.33. Results of SIMPER analysis of the sub-groups identified from cluster analysis of video faunal data, Swallow Sand MCZ video data.

Group / Cluster	% Contribution of characterising species	
	Taxa / species	Contribution (%)
A	*Asterias rubens*	34.83
	Cerianthus lloydii	23.22
	Alcyonium digitatum	11.61
	Bryozoa	11.61
	Pennatula phosphorea	7.87
	Pagurus	7.24
B	*Cerianthus lloydii*	17.79
	Pagurus	17.79
	Asteroidea	10.31
	Bryozoa	8.9
	Pennatula phosphorea	5.66
	Arenicola (Casts)	5.66
	Alcyonium digitatum	5.33
	Nephtys	5.15
	Antalis entalis	5.08
	Pagurus prideaux	5.01
	Nemertesia antennina	4.87
C	*Pennatula phosphorea*	30.03
	Cerianthus lloydii	23.32
	Asteroidea	23.32
	Alcyonium digitatum	9.99
	Antalis entalis	9.99
D	*Pennatula phosphorea*	19.31
	Cerianthus lloydii	14.94
	Pagurus	12.87
	Buccinidae	12.87
	Asteroidea	12.87
	Alcyonium digitatum	6.44
	Nephtys	6.44
	Antalis entalis	6.44
E1	*Asterias rubens*	18.9
	Pennatula phosphorea	18.41
	Spatangus purpureus	13.76
	Cerianthus lloydii	13.17
	Pagurus	8.75
	Antalis entalis	6.87
	Asteroidea	6.11
	Alcyonium digitatum	4.68
E2	*Pennatula phosphorea*	32.17
	Spatangus purpureus	15.8
	Cerianthus lloydii	12.68
	Alcyonium digitatum	8.39
	Asteroidea	8.04
	Antalis entalis	6.51
	Pagurus	6.45

A summary of the SIMPER analysis of the original visually assigned biotopes can be seen in Table 3.34. The three biotopes originally assigned were all characterised by some of the same taxa, including *Cerianthus lloydii, Pagurus, Alcyonium digitatum, Pennatula phosphorea,* Asteroidea and *Spatangus purpureus.* These similarities between the characteristic components of the faunal communities suggested that the originally assigned biotopes covered the same broad habitat. The assignment of **CFiMu** appeared to perhaps slightly conservative based on the multivariate data analysis. However, it is likely that the use of **CFiMu** as opposed to **CFiMu.SpnMeg** more accurately reflected the relative abundance of key species such as *Pennatula phosphorea* as seen during the original video analysis. The use of **CMx** probably reflected the relative abundance of certain taxa, in addition to highlighting visually observed differences in sediment composition.

Table 3.34. Results of SIMPER analysis of the biotopes assigned after original visual analysis of video data, Swallow Sand MCZ video data.

Biotope	% Contribution of characterising species	
	Taxa / species	Contribution (%)
SS.SMx.CMx	*Cerianthus lloydii*	20.61
	Pennatula phosphorea	13.59
	Pagurus	11.92
	Alcyonium digitatum	11.41
	Bryozoa	8.11
	Asterias rubens	7.79
	Spatangus purpureus	7.38
	Nephtys	6.55
	Asteroidea	4.34
SS.SMu.CFiMu	*Pennatula phosphorea*	24.61
	Spatangus purpureus	13.49
	Cerianthus lloydii	12.07
	Asteroidea	9.62
	Alcyonium digitatum	9.44
	Pagurus	8.54
	Antalis entalis	7.51
	Nephtys	4.45
	Bryozoa	3.52
SS.SMu.CFiMu.SpnMeg	*Pennatula phosphorea*	33.04
	Cerianthus lloydii	15.87
	Asteroidea	11.51
	Spatangus purpureus	8.95
	Pagurus	8.5
	Antalis entalis	7.64
	Alcyonium digitatum	5.83

3.8.2 Stills data

3.8.2.1 Data rationalisation

The raw faunal data matrix was rationalised according to the methodology. As per the video data for Swallow Sands, pelagic species were removed. These taxa were all fish, including *Lophius piscatorius,* Gadidae, Triglidae, Ammodytidae and *Pomatoschistus minutus* for example. Adult and juvenile entries of the same taxa were merged, and *Plumaria* was corrected to *Plumularia* as discussed in the video data treatment section. Still image data were combined for each parent video segment. Abundance of taxa were expressed as a percentage of the total images within each segment that they were present. The rationalised data were then imported into PRIMER for statistical analysis.

3.8.2.2 Multivariate statistical analysis

Due to the prior manipulation of data, no further transformations were undertaken. A resemblance matrix using non-standardised, untransformed data was created using Bray Curtis similarity. Cluster analysis was then performed, and the resulting dendrogram plotted (Figure 3.59). Cluster analysis of the still data showed that the parent video segments were less similar to each other overall than when compared to the dendrograms plotted using the video data (~23% similarity compared to ~38% similarity). This probably reflected the better resolution of faunal identification possible using still images versus video footage.

Station 456_S1 was an outlier, separating away at ~23% similarity. Group A contained three stations, and branched off at ~24% similarity. A small cluster of two stations (Group B) split off at ~28% similarity. Groups C and D both contained three stations, and separated off at ~33% and ~37% similarity respectively. Between ~37% similarity and ~39% similarity four stations branched off, three clustering together in group E, and one forming an outlier (392_S1; E*). At ~40% similarity group F separated away. Four stations clustered together within group H, which branched off at ~43% similarity. The remaining 15 stations clustered together in group G, with all stations within the group having ~52% similarity to each other.

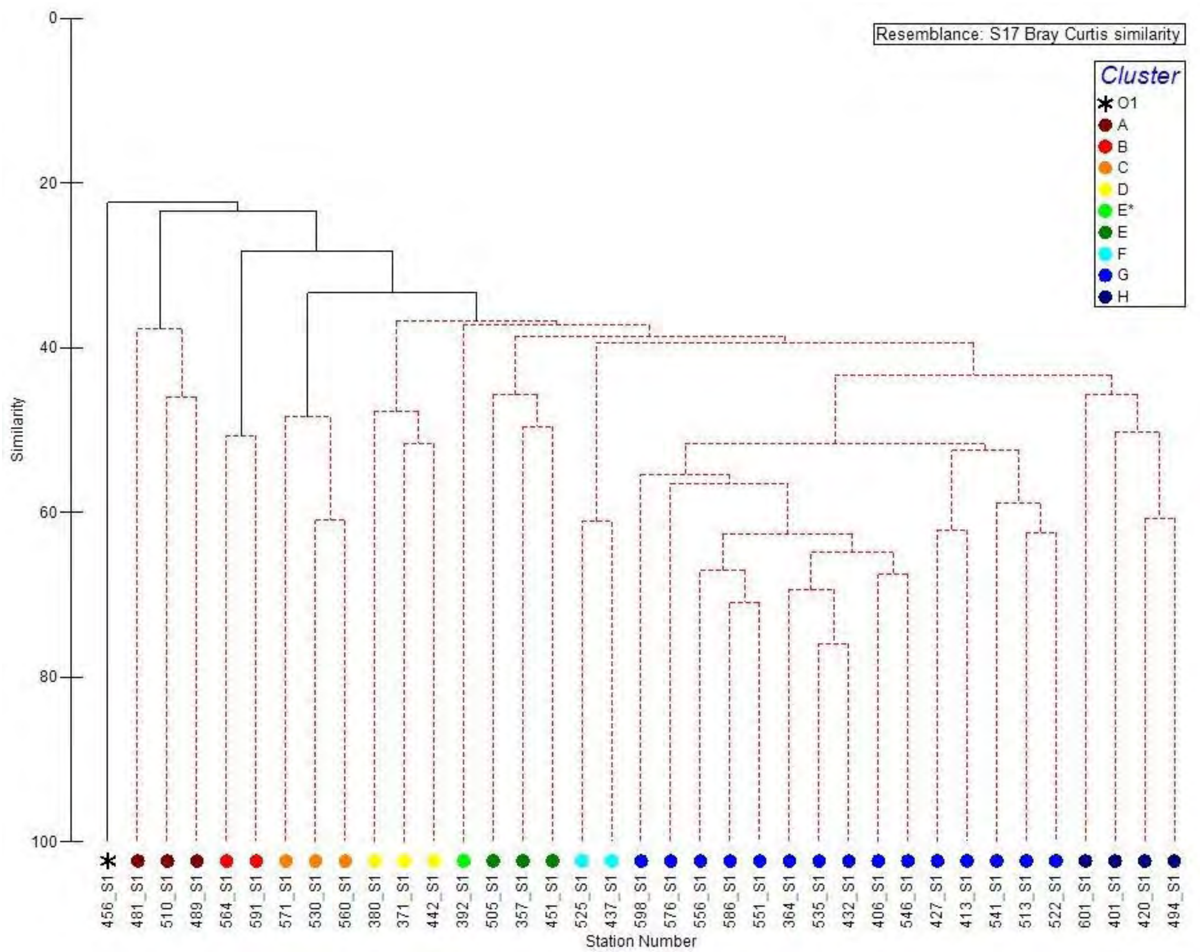


Figure 3.59. Dendrogram plot following cluster analysis of Swallow Sand MCZ still data. Samples coloured according to assigned cluster groups.

A 2D MDS ordination plot of the cluster analysis can be seen in Figure 3.60. The stress value was relatively high (0.22), indicating that too much reliance should not be placed on the details within the plot. The MDS plot showed some agreement with the dendrogram plot, with stations roughly clustering together according to the sub-groups assigned from the dendrogram.

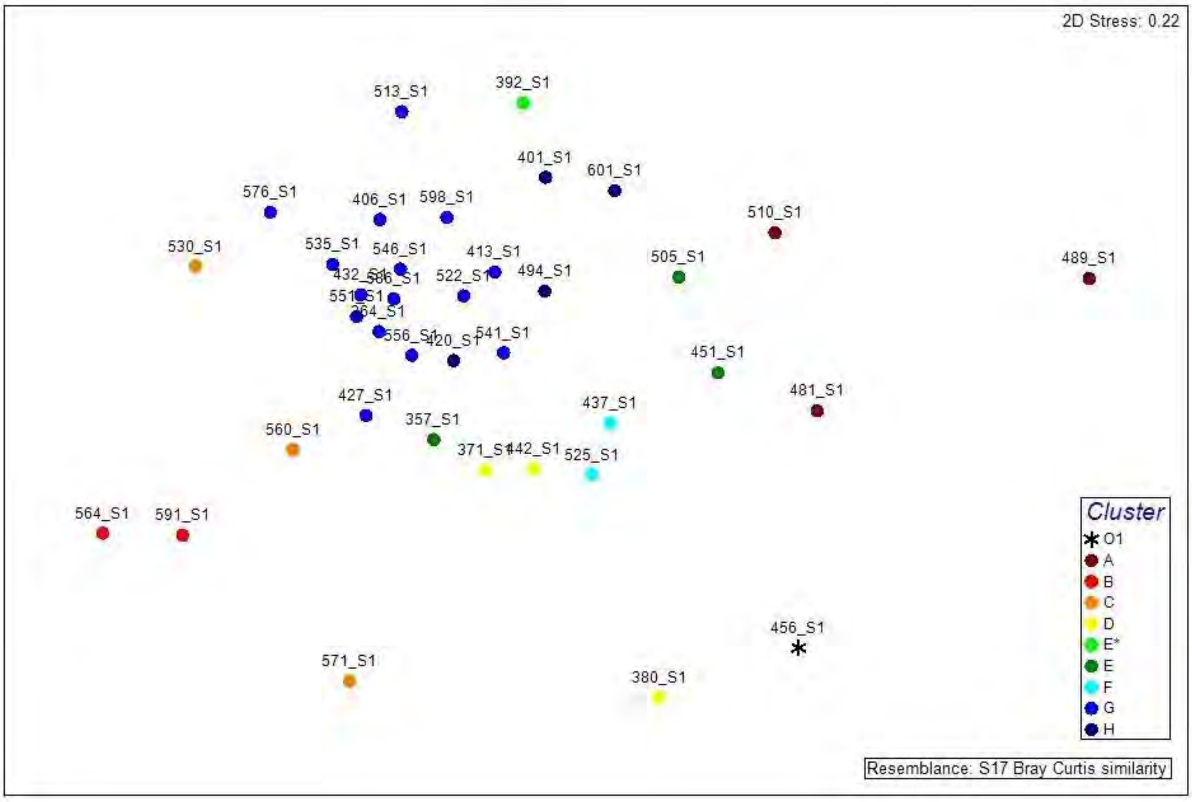


Figure 3.60. MDS ordination plot of Swallow Sand MCZ still data.

Figure 3.61 shows the cluster analysis with the biotopes assigned to each station following the original visual video analysis. The designation of biotopes did not seem to show any pattern when overlain on the clustering of stations. Although some of the smaller groups did tend to included stations designated the same biotope (e.g. group A and **SS.SMx.CMx**), most groups contained stations designated under two or more different biotopes.

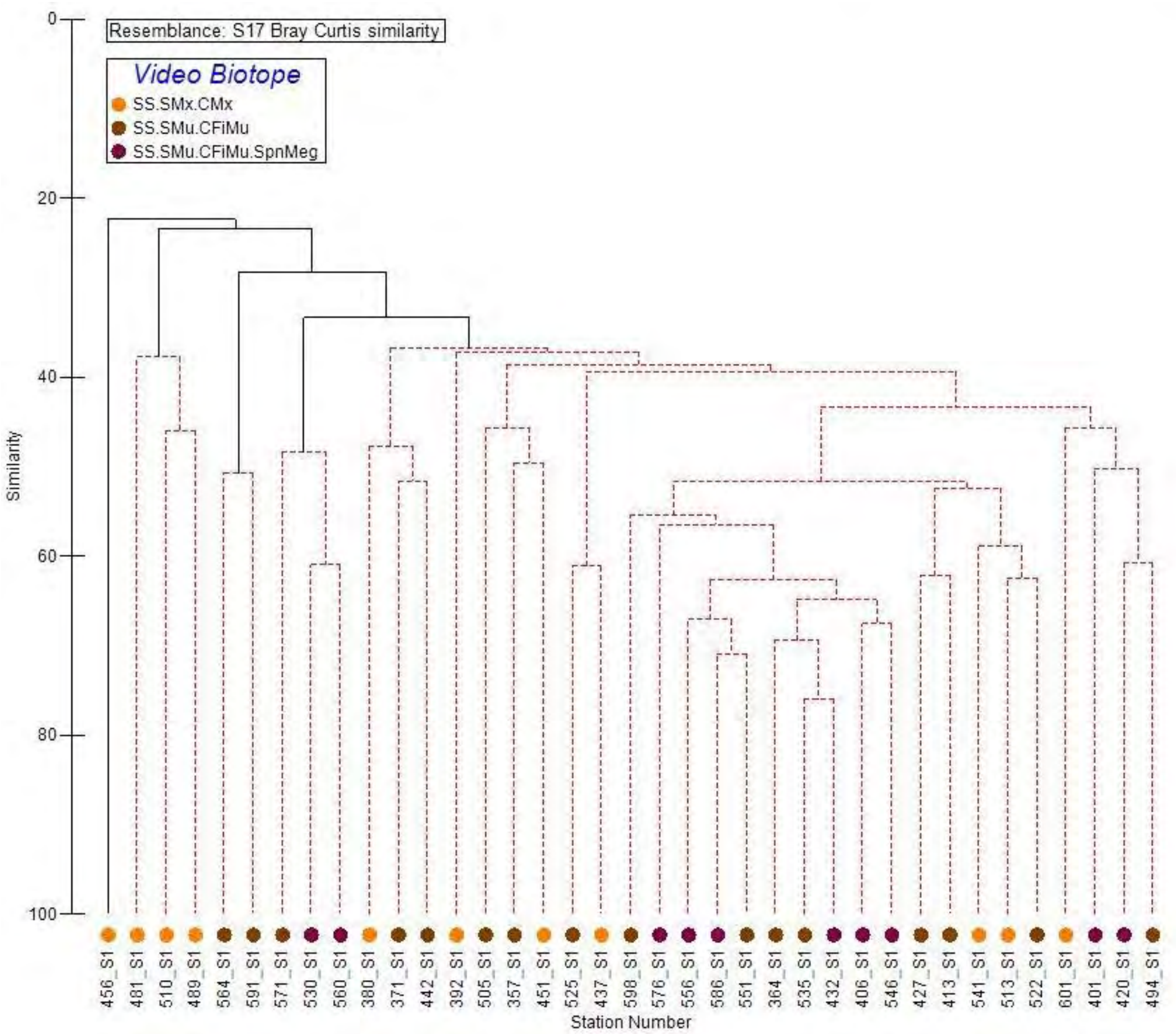


Figure 3.61. Dendrogram plot following cluster analysis of Swallow Sand MCZ still data. Samples coloured according to biotopes assigned from original visual analysis of data.

As per the video data, two different SIMPER analyses were undertaken. The first was undertaken on the groups assigned from the cluster analysis, whilst the second was performed using the visually assessed biotopes from the original analysis of the data. Table 3.35 outlines the characteristic taxa for each sub-group, listing those taxa that contributed at least 90% similarity for each sub-group. Full SIMPER results showing all contributing species for each sub-group can be found in Appendix 14.

The groups defined from the cluster analysis of the still data showed more differences than those defined by the video data. No species were characteristic of all groups, although some like *Alcyonium digitatum, Cerianthus lloydii* and *Pennatula phosphorea* characterised the majority of groups. The absence of *Pennatula phosphorea* in groups A and E possibly reflected the lack of any **CFiMu.SpnMeg** stations within these clusters. In general, the differences in the characteristic taxa for each group appeared to suggest local level patchiness, rather than significantly different faunal communities.

Table 3.35. Results of SIMPER analysis of the sub-groups identified from cluster analysis of still faunal data, Swallow Sand MCZ

Group / Cluster	% Contribution of characterising species	
	Taxa / species	Contribution (%)
A	Bryozoa	27.16
	Alcyonium digitatum	26.51
	Serpulidae	20.72
	Cerianthus lloydii	10.69
B	*Pennatula phosphorea*	84.34
	Spatangus purpureus	15.66
C	Polychaeta (burrows)	54.5
	Pennatula phosphorea	19.73
	Cerianthus lloydii	12.64
	Alcyonium digitatum	6.12
D	*Arenicola* (casts)	20.58
	Pennatula phosphorea	15.1
	Antalis entalis	14.18
	Cerianthus lloydii	12.25
	Hydractinia	11.57
	Bryozoa	9.39
	Pagurus	8.55
E	*Cerianthus lloydii*	22.72
	Alcyonium digitatum	15.97
	Antalis entalis	11.63
	Spatangidae	8.78
	Adamsia	8.52
	Pagurus prideaux	8.52
	Spatangus purpureus	8.52
	Epizoanthus	6.72
F	Porifera	15.87
	Pennatula phosphorea	12.7
	Cerianthus lloydii	12.7
	Spatangus purpureus	12.7
	Alcyonium digitatum	7.94
	Epizoanthus	6.35
	Pagurus	6.35
	Buccinidae	6.35
	Aequipecten opercularis	6.35
	Bryozoa	6.35
G	*Cerianthus lloydii*	38.84
	Pennatula phosphorea	25.83
	Spatangus purpureus	10.02
	Alcyonium digitatum	7.15
	Asterias rubens	6.09
	Epizoanthus	3.57
H	*Cerianthus lloydii*	54.64
	Pennatula phosphorea	22.94
	Alcyonium digitatum	10.3
	Antalis entalis	5.44

Table 3.36 shows the results of the SIMPER analysis of the biotopes assigned after the original visual analysis of the data. As with the video data, all three biotopes had many of the same characteristic species, including *Pennatula phosphorea, Asterias rubens, Alcyonium digitatum,* and *Cerianthus lloydii*. The main differences between the video and stills SIMPER analysis of biotopes appeared to the presence of taxa such as *Epizoanthus* that would not be visible during visual video analysis. *Spatangus purpureus* was not recognised as a characteristic taxon for the **CFiMu.SpnMeg** biotope, but this could reflect the species not being captured within an image, even though it was visible in the video footage.

Table 3.36. Results of SIMPER analysis of the biotopes assigned after visual analysis of data, Swallow Sand MCZ still data.

Biotope	% Contribution of characterising species	
	Taxa / species	Contribution (%)
SS.SMx.CMx	*Cerianthus lloydii*	35.15
	Bryozoa	18.01
	Alcyonium digitatum	9.08
	Pennatula phosphorea	8.35
	Asterias rubens	7.23
	Epizoanthus	5.57
	Spatangus purpureus	4.48
	Antalis entalis	2.56
SS.SMu.CFiMu	*Pennatula phosphorea*	31.82
	Cerianthus lloydii	25.26
	Spatangus purpureus	12.56
	Alcyonium digitatum	9.74
	Asterias rubens	3.69
	Pagurus	3.53
	Epizoanthus	3.42
SS.SMu.CFiMu.SpnMeg	*Cerianthus lloydii*	40.02
	Pennatula phosphorea	32.89
	Alcyonium digitatum	7.7
	Asterias rubens	5.74
	Antalis entalis	2.81
	Pagurus	2.09

3.8.3 Biotope designation

The multivariate analysis of the video and still data showed that the biotopes assigned from the original visual analysis of the data contained faunal communities characterised by many of the same taxa. The combination of species such as *Pennatula phosphorea, Cerianthus lloydii, Nephtys, Antalis entalis, Pagurus, Asterias rubens* and *Spatangus purpureus* were all suggestive of the **SS.SMu.CFiMu.SpnMeg** biotope. The species matrices also showed the presence of various faunal burrows, including *Nephrops norvegicus*. Assignment of this biotope may be considered a slight mismatch with regards to the depth. However, survey stations were sampled between 60 – 90m depth, which falls within the lower depth limit of circalittoral waters.

Bearing the similarities between the faunal communities in mind, the assignment of **SS.SMu.CFiMu** appeared to be conservative. However, as previously mentioned this probably reflected the relative abundance of key fauna like *Pennatula phosphorea* observed during the original visual analysis. The data examined had only captured faunal abundances semi-quantitatively using the SACFOR scale. The differences in the average abundance of *P. phosphorea* between the **CFiMu** and **CFiMu.SpnMeg** on the video footage was 'frequent – common' compared to 'common – abundant', representing an order of magnitude change.

The original visual assessment of the data would have been able to more effectively recognise these differences than the multivariate analysis. Therefore, the original assessment of these two different biotopes was retained.

The assignment of **SS.SMx.CMx** was also retained. Although the faunal communities were very similar to the **CFiMu** biotopes, the original visual analysis clearly defined these as being different due to sediment composition. The original analyst's descriptions of the **CMx** habitats also tended to suggest that these areas were more faunally sparse, which could be seen in the average abundance of certain taxa such as *Cerianthus lloydii* and *P. phosphorea*. The circalittoral depth was retained to match that used with the **CFiMu** biotopes, although again this may be regarded as a potential mismatch with the depth of the sample stations.

The biotope designation of the video segments from the Swallow Sand MCZ data, based on both video and still multivariate analyses, is summarised in Table 3.37. In general terms, the faunal community data suggested that the survey area showed some patchiness in the density of fauna such as seapens, reflected in the assignment of **CFiMu** versus **CFiMu.SpnMeg** biotopes. In addition, patchiness in sediment composition was reflected by the assignment of the **SS.SMx.CMx** biotope where sediment had higher percentages of shell material, gravel and pebbles.

Figure 3.62 displays the geographical distribution of the biotopes designated after the multivariate statistical analysis of the Swallow Sand video and still data. The UKSeaMap 2010 (McBreen *et al* 2011) predictive sediment modelling suggested the survey area to be predominantly sand, with some patches of coarse sediment. The biotopes assigned suggested that the sediment was finer, probably either mud or sandy mud. The distribution of the **CFiMu** versus the **CFiMu.SpnMeg** showed some patchiness within the survey area. There did not appear to be a relationship between the predicted coarse sediment patches and the results of the data analysis, although some **CMx** biotopes were found around the large patch of predicated coarse sediment in the west of the MCZ site.

Table 3.37. Summary of biotopes assigned to video data, Swallow Sand MCZ

Biotope	Description	Original Biotope/s	Video Segment No.	Depth Range
A5.36 : Circalittoral fine mud **SS.SMu.CFiMu**	Characteristic fauna included *Pennatula phosphorea, Nephtys, Cerianthus lloydii, Asterias rubens* and faunal burrows. Verging on **CFiMu.SpnMeg**, but abundances of seapens lower. Some larger patches of gravel / pebbles with epifauna such as *Alcyonium digitatum.* **Potential depth boundary mismatch.**	**SS.SMu.CFiMu**	564_S1, 571_S1, 551_S1, 525_S1, 534_S1, 427_S1, 413_S1, 364_S1, 357_S1, 598_S1, 591_S1, 505_S1, 522_S1, 494_S1, 442_S1	65 – 80m
A5.361 : Seapens and burrowing megafauna in circalittoral fine mud **SS.SMu.CFiMu.SpnMeg**	As per **CFiMu** above, but with higher abundances of *Pennatula phosphorea.* **Potential depth boundary mismatch.**	**SS.SMu.CFiMu. SpnMeg**	576_S1, 586_S1, 530_S1, 562_S1, 556_S1, 420_S1, 401_S1, 406_S1, 432_S1, 546_S1	70 – 83m
A5.44 : Circalittoral mixed sediments **SS.SMx.CMx**	Areas of mixed sediment with shell material and soft sediment. Fauna generally sparse, but overall similar to other biotopes seen within the survey area. Fauna included *Cerianthus lloydii, Pennatula phosphorea, Alcyonium digitatum* and Bryozoa. **Potential depth boundary mismatch.**	**SS.SMx.CMx**	601_S1, 513_S1, 541_S1, 437_S1, 511_S1, 481_S1, 489_S1, 456_S1, 451_S1, 380_S1, 392_S1	99 – 104m

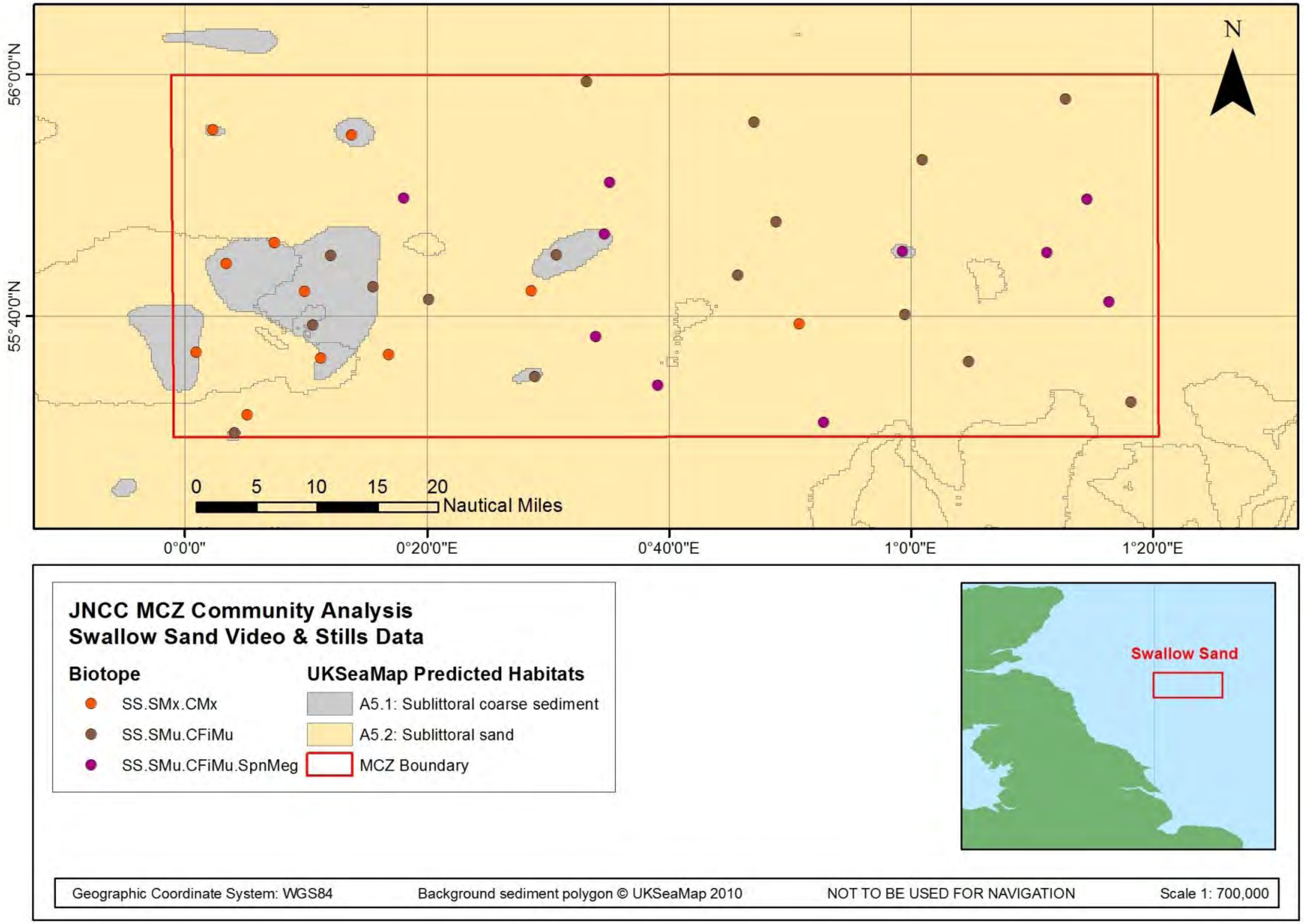


Figure 3.62. Geographical distribution of biotopes designated after multivariate analysis of video and still data, Swallow Sand MCZ.

4 Discussion

4.1 Summary of epifaunal and infaunal biotopes

For each MCZ area, the infaunal biotopes derived from the benthic grab analysis and the epifaunal biotopes from the video and still analysis are summarised below.

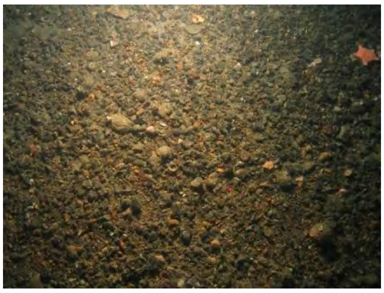
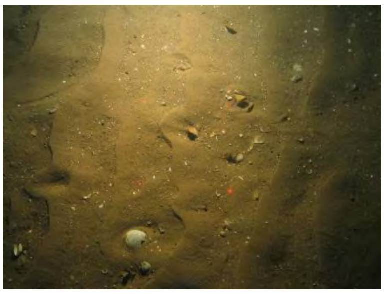
4.1.1 North East of Farnes Deep MCZ

The community analysis of the North East of Farnes Deep MCZ data assigned a total of four level 3 biotopes and four level 4 sub-biotopes, which are summarised in Table 4.1. Two circalittoral biotopes were assigned based on the components of the faunal communities matching specific biotopes. These occurred at the lower depth range of circalittoral sediments, and could be considered a depth mismatch. One new biotope was proposed, **SS.SSa.OSa.SpnMac, '**Seapens and burrowing macrofauna in fine deep circalittoral sand'. Although the biotope resembled **SS.SMu.CFiMu.SpnMeg**, the sediment clearly had a more significant sand contribution than that described for the **CFiMu.SpnMeg** biotope.

Table 4.2 summarises the biotopes assigned to stations where both benthic grab samples and video and still data were taken. Examining the level 3 biotope assigned to each station showed some good agreements between the different methodologies employed. The majority of mis-matches between grab and video data occurred when mixed sediments were identified from the faunal data, and not identified from the video and still analysis.

The multivariate analysis revealed that the epifaunal components of the communities observed were too similar to allow for differentiation between the habitats observed. The North East of Farnes Deep video and still data did not allow for biotopes to be assessed below level 3. The visual analysis of the video data was generally able to discern differences between the habitats in the MCZ at this level, supported by the assessment of the infaunal samples.

Table 4.1. Summary of biotopes assigned to North East of Farnes Deep MCZ data following community analysis. (a) indicates designation from grab data; (b) indicates designation from video and stills data.

EUNIS Level 3	EUNIS Level 4	EUNIS Level 5	Comments
A5.1 : Sublittoral coarse sediment	A5.15 : Deep circalittoral coarse sediment **SS.SCS.OCS** **(a, b)** 		
A5.2 : Sublittoral sand	A5.25 : Circalittoral fine sand **SS.SSa.CFiSa**	A5.251 : [Echinocyamus pusillus], [Ophelia borealis] and [Abra prismatica] in circalittoral fine sand **SS.SSa.CFiSa.EpusOborApri** **(a)** 	Potential depth mismatch
	A5.27 : Deep circalittoral sand **SS.SSa.OSa** **(b)** 	A5.272 : [Owenia fusiformis] and [Amphiura filiformis] in deep circalittoral sand or muddy sand **SS.SSa.OSa.OfusAfil** **(a)** 	

<table>
<tr><th>EUNIS Level 3</th><th>EUNIS Level 4</th><th>EUNIS Level 5</th><th>Comments</th></tr>
<tr><td></td><td></td><td>A5.27x : Seapens and burrowing megafauna in fine deep circalittoral sand
SS.SSa.OSaSpnMac **(b)**
</td><td>New biotope</td></tr>
<tr><td rowspan="2">A5.4 : Sublittoral mixed sediments</td><td>A5.44 : Circalittoral mixed sediments
SS.SMx.CMx **(a)**
</td><td></td><td>Potential depth mismatch; faunal suggested mixed sediments</td></tr>
<tr><td>A5.45 : Deep circalittoral mixed sediments
SS.SMx.OMx **(b)**
</td><td>A5.451 : Polychaete-rich deep [Venus] community in offshore mixed sediments
SS.SMx.OMx.PoVen **(a)**
</td><td></td></tr>
</table>

Table 4.2. Comparison between biotopes assigned to stations using grab data and video and still data, North East of Farnes Deep MCZ. Colour codes indicate whether biotopes agreed between methodologies at level 3. Green = match; Orange = partial match; Red = no match.

Station Code	Grab Sample Biotope	Video and Still Biotope	Level 3 Match?
RU_C_01	SS.SSa.CFiSa.EpusOborApri	SS.SSa.OSa	Green
RU_C_03	SS.SMx.OMx.PoVen	SS.SCS.OCS	Red
RU_C_15	SS.SSa.OSa.OfusAfil	SS.Ssa.OSa.SpnMac	Green
RU_C_18	SS.SMx.OMx.PoVen	SS.SMx.OMx	Green
RU_C_19	SS.SMx.OMx.PoVen	SS.SMx.OMx	Green
RU_C_20	SS.SMx.OMx.PoVen	SS.SMx.OMx	Green
RU_C_21	SS.SMx.OMx.PoVen	SS.SCS.OCS and SS.SSa.OSa	Red
RU_S_05	SS.SSa.CFiSa.EpusOborApri	SS.SMx.OMx and SS.SSa.OSa	Orange
RU_S_08	SS.SSa.CFiSa.EpusOborApri	SS.SCS.OCS and SS.SSa.OSa	Orange
RU_S_09	SS.SSa.OSa.OfusAfil / SS.SSa.CFiSa	SS.SSa.OSa	Green
RU_S_10	SS.SMx.CMx	SS.SSa.OSa	Red
RU_S_11	SS.SMx.OMx.PoVen	SS.SCS.OCS and SS.SMx.OMx	Orange
RU_S_13	SS.SSa.OSa.OfusAfil	SS.Ssa.OSa.SpnMac	Green
RU_S_16	SS.SSa.OSa.OfusAfil	SS.Ssa.OSa.SpnMac	Green
RU_S_18	SS.SSa.OSa.OfusAfil / SS.SSa.CFiSa	SS.SSa.OSa	Green
RU_S_24	SS.SSa.OSa.OfusAfil	SS.Ssa.OSa.SpnMac	Green

4.1.2 East of Haig Fras

The community analysis of the East of Haig Fras data assigned four level 3 biotopes and three level 4 biotopes, which are summarised in Table 4.3. The East of Haig Fras data included video and stills data analysed by two different contractors, with differing levels of precision made on faunal identifications. This potentially resulted in some areas of cobble/ boulder with epifauna being designated as **CR.HCR.DpSp** due to lower levels of faunal identification reached, whilst other were designated as **SS.SMx.OMx** as epifauna was only recorded as Hydrozoa, Bryozoa *etc*. These areas of cobble/boulder could be potential Annex I stony reef, possibly as part of a mosaic with muddy sand sediments.

Table 4.4 summaries the biotopes assigned to stations with both grab and video / stills data. There was a high level of disagreement between the biotope based on the infaunal communities and those based on the epifauna. In general, many stations where the fauna suggested sandy mud sediments (**SS.SMu.OMu**) were classified as sandy sediments from the visual analysis. The visual analysis of sediment composition is particularly hard when dealing with fine sediments. With the East of Haig Fras data there appears to have been difficulty distinguishing between sandy mud and muddy sand.

Table 4.3. Summary of biotopes assigned to East of Haig Fras MCZ data following community analysis. (a) indicates designation from grab data; (b) indicates designation from video and stills data.

EUNIS Level 3	EUNIS Level 4	EUNIS Level 5	Comments
A4.1 : Atlantic and Mediterranean high energy circalittoral rock	A4.12 : Sponge communities on deep circalittoral rock **CR.HCR.DpSp**	A4.121 : [Phakellia ventilabrum] and axinellid sponges on deep, wave-exposed circalittoral rock **CR.HCR.DpSp.(PhaAxi) (b)** 	Potential Annex I stony reef
A5.1 : Sublittoral coarse sediment	A5.15 : Deep circalittoral coarse sediment **SS.SCS.OCS (a, b)** 		Coarse sands with some gravel and cobbles
A5.2 : Sublittoral sand	A5.25 : Circalittoral fine sand **SS.SSa.CFiSa**	A5.251 : [Echinocyamus pusillus], [Ophelia borealis] and [Abra prismatica] in circalittoral fine sand **SS.SSa.CFiSa.EpusOborApri (a)** 	Potential depth mismatch
	A5.27 : Deep circalittoral sand **SS.SSa.OSa (a, b)** 		

EUNIS Level 3	EUNIS Level 4	EUNIS Level 5	Comments
A5.3 : Sublittoral mud	A5.37 : Deep circalittoral mud **SS.SMu.OMu (a)** 		
A5.4 : Sublittoral mixed sediments	A5.45 : Deep circalittoral mixed sediments **SS.SMx.OMx (b)** 	A5.451 : Polychaete-rich deep [Venus] community in offshore mixed sediments **SS.SMx.OMx.PoVen (a)** 	SS.SMx.OMx based on video uncertain – possibly CR.HCR.DpSp or CR.HCR.XFa biotopes based on review of images. Potential Annex I stony reef

Table 4.4. Comparison between biotopes assigned to stations using grab data and video and still data, East of Haig Fras MCZ. Colour codes indicate whether biotopes agreed between methodologies at level 3. Green = match; Orange = partial match; Red = no match.

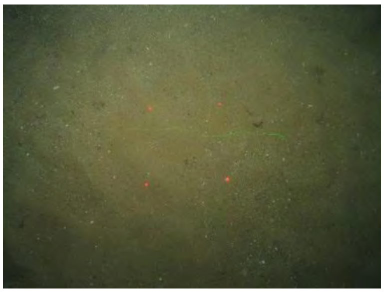
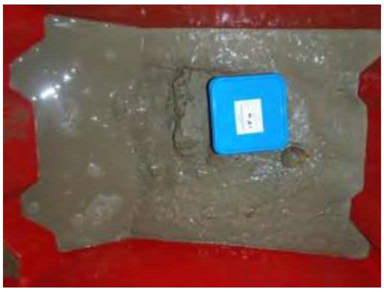
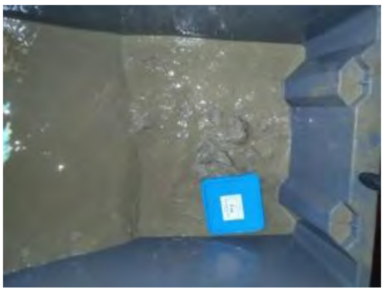
Station Code	Grab Sample Biotope	Video and Still Biotope	Level 3 Match?
EHF_C01	SS.SMx.OMx.(PoVen)	SS.SMx.OMx	Green
EHF_C03	SS.SMx.OMx.(PoVen)	SS.SSa.OSa	Red
EHF_C06	SS.SCS.OCS	SS.SMx.OMx and SS.SSa.OSa	Red
EHF_C10	SS.SMu.OMu	SS.SSa.OSa	Red
EHF_C13	SS.SMu.OMu	SS.SSa.OSa	Red
EHF_C14	SS.SSa.OSa	SS.SSa.OSa	Green
EHF_C18	SS.SMu.OMu	SS.SSa.OSa	Red
EHF_C20	SS.SMu.OMu	SS.SMx.OMx and SS.SSa.OSa	Red
EHF_C22	SS.SSa.OSa	SS.SSa.OSa	Green
EHF_C24	SS.SCS.OCS	SS.SMx.OMx and SS.SSa.OSa	Red
EHF_C25	SS.SSa.OSa	SS.SSa.OSa	Green
EHF_C27	SS.SMu.OMu / SS.SMx.OMx	SS.SSa.OSa	Red
EHF_C29	SS.SMu.OMu	SS.SSa.OSa	Red
EHF_R01	SS.SSa.OSa	SS.SMx.OMx and SS.SSa.OSa	Orange
EHF_S01	SS.SMu.OMu / SS.SMx.OMx	SS.SMx.OMx and SS.SSa.OSa	Orange
EHF_S06	SS.SSa.OSa	SS.SMx.OMx and SS.SSa.OSa	Orange
EHF_S09	SS.SMu.OMu	SS.SMx.OMx and SS.SSa.OSa	Red
EHF_S11	SS.SMu.OMu	SS.SSa.OSa	Red
EHF_S13	SS.SMu.OMu	SS.SMx.OMx and SS.SSa.OSa	Red
EHF_S15	SS.SMu.OMu	SS.SMx.OMx and SS.SSa.OSa	Red
EHF_S17	SS.SSa.OSa	SS.SSa.OSa	Green
EHF_S19	SS.SSa.OSa	SS.SSa.OSa	Green

4.1.3 South-West Deeps (West)

Table 4.5 summarises the biotopes assigned to the South-West Deeps (West) data sets. A total of four level 3 biotopes were assigned (including SS.SMu.OMu as part of the stations designated SS.SSa.OSa / SS.SMu.OMu after analysis of the infaunal communities). Four level 4 sub-biotopes were assigned, three of which were newly proposed – **SS.SSa.OSa.(Ech)**, **SS.SSa.OSa.(Pex)** and **SS.SMx.OMx.Csmi**.

The South-West Deeps (West) MCZ was principally dominated by sandy sediment habitats. These sand habitats varied in coarseness of particle size and the degree of gravel and shell present. Comparison between stations where both grab and video/still data were collected showed general consensus at biotope level 3 (Table 4.6). The majority of partial biotope matches between the different methodologies appeared to stem from the infaunal community indicating finer sediment than was visible from the video/still data.

Table 4.5. Summary of biotopes assigned to South-West Deeps (West) MCZ data following community analysis. (a) indicates designation from grab data; (b) indicates designation from video and stills data.

EUNIS Level 3	EUNIS Level 4	EUNIS Level 5	Comments
A5.1 : Sublittoral coarse sediment	A5.15 : Deep circalittoral coarse sediment **SS.SCS.OCS (a, b)** 		
A5.2 : Sublittoral sand	A5.27 : Deep circalittoral sand **SS.SSa.OSa (a, b)** 	A5.27x : Deep circalittoral sand with *Paraphellia expansa* **SS.SSa.OSa.(Pex) (a)** 	New biotope, uncertain
		A5.27x : Deep circalittoral sand with heart urchins **SS.SSa.OSa.(Ech) (a)** 	New biotope, uncertain
A5.3 : Sublittoral mud	A5.37 : Deep circalittoral mud **SS.SMu.OMu (a)** 		Faunal communities suggested a mix of SS.SSa.OSa / SS.SMu.OMu

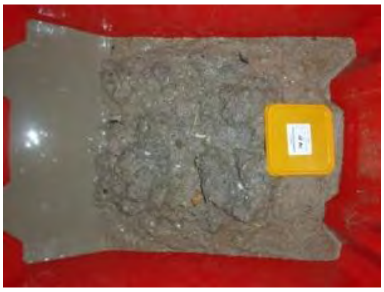
<table>
<tr><th>EUNIS Level 3</th><th>EUNIS Level 4</th><th>EUNIS Level 5</th><th>Comments</th></tr>
<tr><td rowspan="2">A5.4 : Sublittoral mixed sediments</td><td rowspan="2">A5.45 : Deep circalittoral mixed sediments
SS.SMx.OMx (a, b)
</td><td>A5.451 : Polychaete-rich deep [Venus] community in offshore mixed sediments
SS.SMx.OMx.PoVen (a)
</td><td></td></tr>
<tr><td>A5.45x : Deep circalittoral mixed sediment with Caryophyllia smithii
SS.SMx.OMx.Csmi (a)
</td><td>New biotope</td></tr>
</table>

Table 4.6. Comparison between biotopes assigned to stations using grab data and video and still data, South-West Deeps (West) MCZ. Colour codes indicate whether biotopes agreed between methodologies at level 3. Green = match; Orange = partial match; Red = no match.

Station Code	Grab Sample Biotope	Video and Still Biotope	Level 3 Match?
SWDW_AddGT01	SS.SSa.OSa / SS.SMx.OMx	SS.SSa.OSa	Orange
SWDW_AddGT02	SS.SSa.OSa	SS.SSa.OSa	Green
SWDW_AddGT03	SS.SSa.OSa	SS.SSa.OSa	Green
SWDW_AddGT05	SS.SSa.OSa / SS.SMu.OMu	SS.SSa.OSa	Orange
SWDW_AddGT06	SS.SSa.OSa / SS.SMx.OMx	SS.SMx.OMx and SS.SSa.OSa	Green
SWDW_AddGT07	SS.SSa.OSa / SS.SMx.OMx	SS.SMx.OMx and SS.SSa.OSa	Green
SWDW_AddGT08	SS.SSa.OSa / SS.SMx.OMx	SS.SSa.OSa	Orange
SWDW_AddGT09	SS.SMx.OMx.PoVen	SS.SCS.OCS	Red
SWDW_AddGT10	SS.SSa.OSa / SS.SMx.OMx	SS.SMx.OMx	Orange
SWDW_C02	SS.SSa.OSa / SS.SMu.OMu	SS.SSa.OSa	Orange
SWDW_C05	SS.SSa.OSa	SS.SMx.OMx and SS.SSa.OSa	Orange
SWDW_C10	SS.SSa.OSa / SS.SMx.OMx	SS.SSa.OSa	Orange
SWDW_C13	SS.SSa.OSa	SS.SMx.OMx and SS.SSa.OSa	Orange
SWDW_C17	SS.SSa.OSa	SS.SSa.OSa	Green
SWDW_C18	SS.SSa.OSa	SS.SSa.OSa	Green
SWDW_C22	SS.SSa.OSa / SS.SMx.OMx	SS.SSa.OSa	Orange
SWDW_C27	SS.SMx.OMx.PoVen	SS.SMx.OMx	Green
SWDW_C30	SS.SMx.OMx.Csmi	SS.SMx.OMx	Green
SWDW_C31	SS.SSa.OSa	SS.SSa.OSa	Green
SWDW_C36	SS.SMx.OMx.PoVen	SS.SMx.OMx	Green
SWDW_C37	SS.SSa.OSa / SS.SMx.OMx	SS.SSa.OSa	Orange
SWDW_GT05	SS.SSa.OSa	SS.SSa.OSa	Green
SWDW_GT08	SS.SSa.OSa	SS.SSa.OSa	Green
SWDW_GT09	SS.SSa.OSa	SS.SMx.OMx	Red
SWDW_GT13	SS.SSa.OSa	SS.SSa.OSa	Green
SWDW_GT15	SS.SSa.OSa	SS.SCS.OCS and SS.SSa.OSa	Orange
SWDW_GT17	SS.SSa.OSa	SS.SSa.OSa	Green
SWDW_GT20	SS.SSa.OSa	SS.SCS.OCS and SS.SSa.OSa	Orange
SWDW_GT24	SS.SSa.OSa	SS.SSa.OSa	Green
SWDW_GT28	SS.SSa.OSa	SS.SSa.OSa	Green
SWDW_GT34	SS.SSa.OSa	SS.SCS.OCS	Red
SWDW_GT37	SS.SSa.OSa	SS.SMx.OMx	Red
SWDW_GT39	SS.SSa.OSa / SS.SMu.OMu	SS.SSa.OSa	Orange
SWDW_GT40	SS.SSa.OSa / SS.SMu.OMu	SS.SSa.OSa	Orange
SWDW_GT41	SS.SSa.OSa	SS.SSa.OSa	Green
SWDW_S002	SS.SSa.OSa	SS.SMx.OMx and SS.SSa.OSa	Orange
SWDW_S005	SS.SSa.OSa	SS.SMx.OMx and SS.SSa.OSa	Orange
SWDW_S012	SS.SSa.OSa.(Pex)	SS.SSa.OSa	Green
SWDW_S013	SS.SSa.OSa	SS.SSa.OSa	Green
SWDW_S015	SS.SSa.OSa / SS.SMx.OMx	SS.SMx.OMx	Orange

Station Code	Grab Sample Biotope	Video and Still Biotope	Level 3 Match?
SWDW_S016	SS.SSa.OSa / SS.SMx.OMx	SS.SMx.OMx	
SWDW_S018	SS.SSa.OSa / SS.SMu.OMu	SS.SSa.OSa	
SWDW_S019	SS.SSa.OSa.(Ech)	SS.SSa.OSa	
SWDW_S022	SS.SSa.OSa.(Pex)	SS.SSa.OSa	
SWDW_S027	SS.SSa.OSa / SS.SMu.OMu	SS.SSa.OSa	
SWDW_S033	SS.SSa.OSa	SS.SSa.OSa	
SWDW_S037	SS.SSa.OSa / SS.SMx.OMx	SS.SMx.OMx and SS.SCS.OCS	
SWDW_S039	SS.SSa.OSa / SS.SMx.OMx	SS.SMx.OMx	
SWDW_S042	SS.SSa.OSa / SS.SMx.OMx	SS.SCS.OCS	
SWDW_S046	SS.SSa.OSa	SS.SSa.OSa	
SWDW_S047	SS.SSa.OSa	SS.SMx.OMx and SS.SCS.OCS	
SWDW_S050	SS.SSa.OSa	SS.SSa.OSa	
SWDW_S052	SS.SMx.OMx.Csmi	SS.SCS.OCS	
SWDW_S053	SS.SSa.OSa / SS.SMx.OMx	SS.SSa.OSa	
SWDW_S055	SS.SSa.OSa	SS.SCS.OCS and SS.SSa.OSa	
SWDW_S056	SS.SSa.OSa	SS.SMx.OMx	
SWDW_S058	SS.SMx.OMx.PoVen	SS.SMx.OMx	
SWDW_S066	SS.SSa.OSa	SS.SSa.OSa	
SWDW_S069	SS.SMx.OMx.(PoVen)	SS.SMx.OMx	
SWDW_S073	SS.SSa.OSa	SS.SSa.OSa	
SWDW_S076	SS.SSa.OSa / SS.SMx.OMx	SS.SMx.OMx	
SWDW_S077	SS.SSa.OSa / SS.SMx.OMx	SS.SMx.OMx	
SWDW_S080	SS.SSa.OSa / SS.SMu.OMu	SS.SSa.OSa	
SWDW_S084	SS.SSa.OSa	SS.SSa.OSa	
SWDW_S086	SS.SSa.OSa	SS.SSa.OSa	
SWDW_S089	SS.SMx.OMx.(PoVen)	SS.SMx.OMx	
SWDW_S093	SS.SSa.OSa	SS.SMx.OMx	
SWDW_S096	SS.SSa.OSa	SS.SSa.OSa	
SWDW_S100	SS.SMx.OMx.PoVen	SS.SMx.OMx	
SWDW_S103	SS.SSa.OSa	SS.SSa.OSa	
SWDW_S104	SS.SSa.OSa.(Pex)	SS.SSa.OSa	
SWDW_S112	SS.SSa.OSa	SS.SSa.OSa	
SWDW_S113	SS.SSa.OSa	SS.SMx.OMx	

4.1.4 Swallow Sand

Table 4.7 summarises the biotopes assigned to the Swallow Sand data after community analysis. A total of four level 3 biotopes were assigned. Two of these, **SS.SMu.CFiMu** and **SS.SMx.CMx**, had potential depth mismatches, found at the lower end of the circalittoral depth boundary. Four level 4 sub-biotopes were also assigned. One of these (**CFiMu.SpnMeg**) again had a potential depth mismatch. Another was a newly proposed biotope, representing deep circalittoral muddy sand with *Ditrupa arietina* (**SS.SSa.OSa.Dari**).

Comparison between biotopes at stations where data were collected using grabs and drop-down camera systems showed a high number of partial matches (Table 4.8). The infaunal community included taxa that represented a transition from muddy sand to sandy mud. This fine sediment category covered both **SS.SSa.OSa** and **SS.SMu.OMu** biotopes (and related sub-biotopes), but visually would be very difficult to separate. Area designated as mixed sediments from the visual analysis tended not to agree with the infaunal data, perhaps suggesting that the 'mixed' aspect of the sediment was restricted to a surface layer of shell and gravel, with the greater part of the infaunal community present within the sediment and thus not influenced by the coarser material.

Table 4.7. Summary of biotopes assigned to Swallow Sand MCZ data following community analysis. (a) indicates designation from grab data; (b) indicates designation from video and stills data

EUNIS Level 3	EUNIS Level 4	EUNIS Level 5	Comments
A5.2 : Sublittoral sand	A5.27 : Deep circalittoral sand **SS.SSa.OSa** **(a)** 	A5.271 : Maldanid polychaetes and [Eudorellopsis deformis] in deep circalittoral sand or muddy sand **SS.SSa.OSa.MalDef** **(a)** 	Uncertain
		A5.27x : Deep circalittoral muddy sand with *Ditrupa arietina* **SS.SSa.OSa.Dari** **(a)** **No image**	New biotope
A5.3 : Sublittoral mud	A5.36 : Circalittoral fine mud **SS.SMu.CFiMu** **(b)** 	A5.361 : Seapens and burrowing megafauna in circalittoral fine mud **SS.SMu.CFiMu.SpnMeg** **(b)** 	Potential depth mismatch

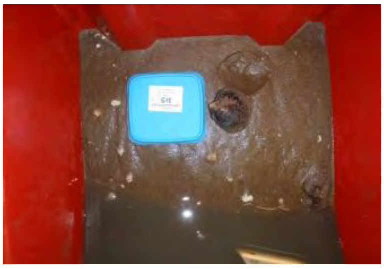
EUNIS Level 3	EUNIS Level 4	EUNIS Level 5	Comments
	A5.37 : Deep circalittoral mud **SS.SMu.OMu** **(a)** 	A5.376 : [Paramphinome jeffreysii], [Thyasira] spp. and [Amphiura filiformis] in offshore circalittoral sandy mud **SS.SMu.OMu.PjefThyAfil** **(a)** 	
A5.4 : Sublittoral mixed sediments	A5.44 : Circalittoral mixed sediments **SS.SMx.CMx** **(b)** 		Potential depth mismatch

Table 4.8. Comparison between biotopes assigned to stations using grab data and video and still data, Swallow Sand MCZ. Colour codes indicate whether biotopes agreed between methodologies at level 3. Green = match; Orange = partial match; Red = no match

Station Code	Grab Sample Biotope	Video and Still Biotope	Level 3 Match?
SS02	SS.SMu.OMu.PjefThyAfil	SS.SMu.CFiMu.SpnMeg	
SS04	SS.SMu.OMu.PjefThyAfil	SS.SMx.CMx	
SS07	SS.SSa.OSa.(MalEdef) / SS.SMu.OMu	SS.SMu.CFiMu	
SS10	SS.SSa.OSa.(MalEdef) / SS.SMu.OMu	SS.SMu.CFiMu.SpnMeg	
SS13	SS.SSa.OSa.(MalEdef) / SS.SMu.OMu	SS.SMu.CFiMu	
SS16	SS.SSa.OSa / SS.SMu.OMu	SS.SMx.CMx	
SS18	SS.SSa.OSa / SS.SMu.OMu.(PjefThyAfil)	SS.SMu.CFiMu.SpnMeg	
SS20	SS.SMu.OMu.PjefThyAfil	SS.SMx.CMx	
SS21	SS.SMu.OMu.PjefThyAfil	SS.SMu.CFiMu	
SS24	SS.SSa.OSa / SS.SMu.OMu.(PjefThyAfil)	SS.SMu.CFiMu.SpnMeg	
SS25	SS.SSa.OSa / SS.SMu.OMu.(PjefThyAfil)	SS.SMu.CFiMu	
SS26	SS.SSa.OSa.(MalEdef) / SS.SMu.OMu	SS.SMx.CMx	

Station Code	Grab Sample Biotope	Video and Still Biotope	Level 3 Match?
SS28	SS.SSa.OSa / SS.SMu.OMu	SS.SMu.CFiMu	
SS31	SS.SSa.OSa.(MalEdef) / SS.SMu.OMu	SS.SMu.CFiMu.SpnMeg	
SS35	SS.SSa.OSa.(MalEdef) / SS.SMu.OMu	SS.SMu.CFiMu	
SS40	SS.SSa.OSa.(MalEdef) / SS.SMu.OMu	SS.SMu.CFiMu.SpnMeg	
SS41	SS.SSa.OSa.(MalEdef) / SS.SMu.OMu	SS.SMu.CFiMu.SpnMeg	
SS43	SS.SMu.OMu.PjefThyAfil	SS.SMu.CFiMu.SpnMeg	
SS46	SS.SSa.OSa / SS.SMu.OMu	SS.SMu.CFiMu	
SS54	SS.SSa.OSa.(MalEdef) / SS.SMu.OMu	SS.SMu.CFiMu	
SS59	SS.SSa.OSa.(MalEdef) / SS.SMu.OMu	SS.SMu.CFiMu	
SS62	SS.SSa.OSa / SS.SMu.OMu	SS.SMu.CFiMu	
SS63	SS.SSa.OSa / SS.SMu.OMu	SS.SMu.CFiMu	
SS64	SS.SSa.OSa / SS.SMu.OMu.(PjefThyAfil)	SS.SMu.CFiMu	
SS66	SS.SMu.OMu.PjefThyAfil	SS.SMx.CMx	
SS67	SS.SMu.OMu.PjefThyAfil	SS.SMx.CMx	
SS70	SS.SSa.OSa / SS.SMu.OMu	SS.SMu.CFiMu	
SS79	SS.SSa.OSa / SS.SMu.OMu	SS.SMx.CMx	
SS81	SS.SSa.OSa / SS.SMu.OMu.(PjefThyAfil)	SS.SMu.CFiMu	
SS88	SS.SSa.OSa / SS.SMu.OMu.(PjefThyAfil)	SS.SMx.CMx	
SS91	SS.SSa.OSa / SS.SMu.OMu	SS.SMu.CFiMu	
SS92	SS.SSa.OSa / SS.SMu.OMu	SS.SMu.CFiMu	
SS96	SS.SSa.OSa / SS.SMu.OMu.(PjefThyAfil)	SS.SMx.CMx	
SS99	SS.SSa.OSa / SS.SMu.OMu.(PjefThyAfil)	SS.SMu.CFiMu.SpnMeg	
SS100	SS.SSa.OSa / SS.SMu.OMu.(PjefThyAfil)	SS.SMx.CMx	
SS101	SS.SMu.OMu.PjefThyAfil	SS.SMx.CMx	
SS102	SS.SSa.OSa.(MalEdef) / SS.SMu.OMu	SS.SMu.CFiMu.SpnMeg	

4.2 Limitations

As mentioned in the methodology and within the results section, there were several limitations encountered during the course of this project. Some issues such as errors in metadata transcription were easily solved. Differences in species nomenclature could also be largely ignored in terms of the overall impact they made on the data analysis, provided a single taxon was not represented twice within the same data set.

A more-significant limitation was the level of taxonomic identification possible from the video footage and still images. The majority of the stations within the MCZs surveyed were soft sediments, which tended not to be particularly rich in epifauna. Those epifauna recorded tended to be more mobile, and not necessarily diagnostic of the habitat where they were recorded. Therefore, the video and still data sets tended to be very restricted in terms of the amount of faunal abundance data they contained. Only two data sets had a small portion of the available still images analysed (three images per video segment), which further reduced the amount of available data. Still images generally allow a more accurate identification of the fauna present; attempts to resolve biotopes to level 4 or below were prevented by the lack of data.

In addition, the level of faunal identification from the video and still data was limited due to the nature of the media. Most data sets contained faunal identifications to higher taxonomic levels (typically family or higher). This presented problems when taxa from several levels within the same taxonomic hierarchy were recorded (e.g. Anthozoa, Actiniaria and *Actinauge richardi*), as it was not certain whether this represented genuinely different taxa, or possibly the same taxon recorded under multiple entries depending on the resolution of the image/ video. This is not an easy problem to resolve as it reflects the nature of the media used. A potential method could be to use a greater number of qualifiers on faunal records. For example, rather than just recording ‘Porifera’, colour and/or morphology could be added i.e. ‘Porifera, yellow crust’. Uncertain identifications could also be made clearer (i.e. *Munida*, probably *M. rugosa*), thus allowing for more certainty in combining/leaving taxa separate at the data rationalisation stage. Although some of these qualifiers were present, they were not used constantly within and between data sets.

The combination of high level identifications along with scarcity of data meant that taxa such as Hydrozoa and Serpulidae tended to dominate the faunal communities based on the number of observations. For many of the data sets, the faunal community did not vary much between areas defined as different sediment types during the original visual analysis.

The results of the multivariate analysis based on the video and stills data did not reveal much more information about the benthic communities that could not ascertained by visual analysis of the data alone. This may not be the case if more rock/hard substrata communities were assessed, as these tend to have more epifauna than is typically seen on soft sediments. The best results were achieved when examining data that included obvious epifauna that had a strong link to the sedimentary environment (e.g. seapens) or a greater degree of cobbles and pebbles (**CR.HCR.DpSp** biotopes in East of Haig Fras).

One additional concern noted from the video and still data was that some identification appeared to be overly ambitious given the type of media. For example, two different species of the small gastropod genus *Euspira* were identified from still images in the East of Haig Fras CEND0513 data set. It is highly unlikely to be able to discern species level differences for these taxa using still images alone. Over confident identification can lead to problems with the artificial separation of groups.

Differentiation between muddy sand and sandy mud was not always clear within the infaunal community data. However, these are clearly split into two different biotopes in deep circalittoral water (**SS.SMu.OMu** and **SS.SSa.OSa**). It could be argued that muddy sand and sandy mud habitats are more similar in terms of component infaunal species than the muddy sand and medium sand habitats that are both covered under **OSa**. One solution may be to follow the sub-divisions used for infralittoral and circalittoral sediments (e.g. **OMu.OSaMu** and **OSa.OMuSa**) to distinguish between these habitats. However, the community analysis has shown that estimating the level of fine sediment from video and still data is not very accurate, and such sub-divisions could potentially lead to more mis-matches between different survey methodologies. The presence of surface gravel and shell can also lead to a mis-match between biotopes assigned from infaunal data compared to what is assigned from a visual analysis of the sediment.

When dealing with the faunal abundance data it is important to note that a different approach to the data rationalisation step could potentially lead to different results from those obtained within this report. A good example was the removal of juvenile echinoderms from the South-West Deeps (West) data set. The high abundances of these ephemeral seasonal taxa masked the patterns of clustering based on the other fauna. The clusters created as a result of the multivariate analysis are usually based on a small section of the whole data set employed. There is some redundancy, with some taxa present within the data not contributing to the patterns of station clustering observed within the dendrogram structure. These taxa could be removed or merged with others at higher taxonomic levels without changing the structure of station clustering. However, identifying which taxa are 'redundant' in the overall patterns between stations can be very time consuming, requiring multiple re-runs of analyses.

A number of different contractors were used during the initial analysis of the benthic grab samples and video/still data. This resulted in data sets with varying levels of conservatism in faunal identifications and biotope designations. Each data set was treated independently to mitigate this as much as possible, but the two East of Haig Fras video/still data sets from different cruises demonstrated some of the potential problems. The CEND0513 data set contained many low taxonomic faunal identifications (possibly forced – see comments above), whilst the CEND0312 fauna was generally only identified to higher taxonomic levels. Reviewing the assigned biotopes based on the community data in Table 4.3 suggested that one data set allowed cobble and boulder substratum to be recognised as **CR.HCR.DpSp** biotope, whilst the other data set did not pick out the epifauna sufficiently, so these areas were assigned to **SS.SMx.OMx**. Upon reviewing several still images, the amount of cobbles within these 'mixed' sediment areas may be sufficient to suggest a potential Annex I stony reef. Comparisons between data sets should therefore be made with extreme caution.

One way to improve comparisons between data sets would be to rationalise faunal lists between survey areas. Survey areas to be compared should both have the same list of faunal species. Care should be taken to account for any differences between data sets due to taxonomic name changes, differences in taxonomic opinon, taxonomic hierarchies, recording of juveniles and adults and any other factors that could potential mask any genuine community differences. These rationalistaion steps can be particularly important if surveys have been conducted at different time periods, since taxonomic reorganisation of species can lead to changes in nomenclature. Examining data sets from different analysts may increase the level of rationalisation required to make the data sets comparable. Appropriate QA of data sets may lessen the amount of work involved with the rationalistaion of data sets between different surveys. Benthic faunal samples analysed by contractors operating under the NMBAQC scheme should theorectically be more comparable due to the QA protocols that exist under the scheme. However, no such scheme currently exists for assessment of video and still image data. When comparing between data sets, consistency in sampling methods, equipment and techniques are also very important to consider before undertaking any analyses.

Although multivariate statistical techniques were used to assess the faunal communities, the assignment of biotopes still required some subjectivity on behalf of the analyst. It is therefore recommended that text descriptions of faunal communities should be read carefully before using any of the biotopes designated within this contract.

5 References

CLARKE, K.R. & WARWICK, R.M. 2001. *Change in Marine Communities: an approach to statistical analysis and interpretation, 2nd edition*. PRIMER –E, Plymouth.

COGGAN, R., MITCHELL, A., WHITE, J. & GOLDING, N. 2007. *Recommended Operating Guidelines (ROG) for Underwater Video and Photographic Imaging Techniques.* Available from http://www.searchmesh.net/default.aspx?page=1915.

CONNOR, D.W., ALLEN, J. H., GOLDING, N., HOWELL, K. L., LIEBERKNECHT, L. M., NORTHEN, K. O. & REKER, J. B. 2004. *The National Marine Habitat Classification for Britain and Ireland. Version 04.05.* Joint Nature Conservation Committee, Peterborough. ISBN: 1 861 07561 8 (internet version).

FOWLER, J. & COHEN, J. 1992. *Practical Statistics for Field Biology*. John Wiley & Sons, Chichester, England, 227 pages.

GAGE, J.D. & TYLER, P.A. 1991. *Deep-Sea Biology: A Natural History of Organisms at the Deep-sea Floor*. Cambridge University Press, 504 pages.

MCBREEN, F., ASKEW, N., CAMERON, A., CONNOR, D., ELLWOOD, H. & CARTER, A. 2011. *UKSeaMap 2010: Predictive mapping of seabed habitats in UK waters*. *JNCC Report No. 446*. JNCC, Peterborough.

PARRY, M.E.V. 2014. *Guidance on Assigning Benthic Biotopes using EUNIS or the Marine Habitat Classification of Britain and Ireland.* JNCC, Peterborough. Unpublished internal report.

WoRMS. 2014. World Register of Marine Species. Available from: http://www.marinespecies.org at VLIZ.

Appendix 1. Offshore MCZ survey data

Details of survey metadata including station identifiers, position, and depth can be found in the attached file:

Appendix 1 – Offshore MCZ Community Analysis – Survey Data.xls

Data is arranged according to the following worksheets within the spreadsheet:

- 1. North East of Farnes Deep grab
- 2. North East of Farnes Deep video
- 3. East of Haig Fras grab
- 4. East of Haig Fras 0312 video
- 5. East of Haig Fras 0513 video
- 6. South-West Deeps (West) grab
- 7. South-West Deeps video
- 8. Swallow Sand grab
- 9. Swallow Sand video

Appendix 2. Raw benthic grab faunal matrices

The raw faunal data matrices from the identification and enumeration of benthic grab samples can be found in the attached file:

Appendix 2 – Offshore MCZ Community Analysis – Grab Raw Fauna.xls

Data is arranged according to the following worksheets within the spreadsheet:

- 1. North East of Farnes Deep
- 2. East of Haig Fras
- 3. South-West Deeps (West)
- 4. Swallow Sand

Appendix 3. Rationalised benthic faunal matrices

The rationalised faunal data matrices from the benthic grab samples can be found in the attached file:

Appendix 3 – Offshore MCZ Community Analysis – Grab Rationalised Fauna.xls

Data is arranged according to the following worksheets within the spreadsheet:

- 1. North East of Farnes Deep
- 2. East of Haig Fras
- 3. South-West Deeps (West)
- 4. Swallow Sand

Appendix 4. Video and still image proformas

The video and still images proformas completed by analysts under different contracts can be found in the attached file:

Appendix 4 – Offshore MCZ Community Analysis – Video and Still Porformas.xls

Data is arranged according to the following worksheets within the spreadsheet:

- 1. North East of Farnes Deep Video
- 2. North East of Farnes Deep Still
- 3. East of Haig Fras 0312 Video
- 4. East of Haig Fras 0312 Still
- 5. East of Haig Fras 0513 Video
- 6. East of Haig Fras 0513 Still
- 7. South-West Deeps (West) Video
- 8. South-West Deeps (West) Still
- 9. Swallow Sand Video
- 10. Swallow Sand Still

Appendix 5. Video and still raw faunal matrices

The raw faunal abundances can be found as data matrices within in the attached file:

Appendix 5 – Offshore MCZ Community Analysis – Video and Still Raw Fauna.xls

Data is arranged according to the following worksheets within the spreadsheet:

- 1. North East of Farnes Deep Video
- 2. North East of Farnes Deep Still
- 3. East of Haig Fras 0312 Video
- 4. East of Haig Fras 0312 Still
- 5. East of Haig Fras 0513 Video
- 6. East of Haig Fras 0513 Still
- 7. South-West Deeps (West) Video
- 8. South-West Deeps (West) Still
- 9. Swallow Sand Video
- 10. Swallow Sand Still

Appendix 6. Video and still rationalised faunal matrices

The rationalised faunal abundances can be found as data matrices within in the attached file:

Appendix 6 – Offshore MCZ Community Analysis – Video and Still Rationalised Fauna.xls

Still images have been amalgamated and assigned to their parent video section as detailed in the methodology section. Data is arranged according to the following worksheets within the spreadsheet:

- 1. North East of Farnes Deep Video
- 2. North East of Farnes Deep Still
- 3. East of Haig Fras 0312 Video
- 4. East of Haig Fras 0312 Still
- 5. East of Haig Fras 0513 Video
- 6. East of Haig Fras 0513 Still
- 7. South-West Deeps (West) Video
- 8. South-West Deeps (West) Still
- 9. Swallow Sand Video
- 10. Swallow Sand Still

Appendix 7. North East of Farnes Deep Grab PRIMER Analyses

All outputs from the PRIMER analyses of the North East of Farnes Deep grab data can be found in the attached file:

Appendix 7 – Offshore MCZ Community Analysis – North East of Farnes Deep Grab Analyses.xls

Appendix 8. East of Haig Fras Grab PRIMER Analyses

All outputs from the PRIMER analyses of the East of Haig Fras grab data can be found in the attached file:

Appendix 8 – Offshore MCZ Community Analysis – East of Haig Fras Grab Analyses.xls

Appendix 9. South-West Deeps (West) Grab PRIMER Analyses

All outputs from the PRIMER analyses of the South-West Deeps (West) grab data can be found in the attached file:

Appendix 9 – Offshore MCZ Community Analysis – South-West Deeps (West) Grab Analyses.xls

Appendix 10. Swallow Sand Grab PRIMER Analyses

All outputs from the PRIMER analyses of the Swallow Sand grab data can be found in the attached file:

Appendix 10 – Offshore MCZ Community Analysis – Swallow Sand Grab Analyses.xls

Appendix 11. North East of Farnes Deep Video and Still PRIMER Analyses

All outputs from the PRIMER analyses of the North East of Farnes Deep video and still data can be found in the attached file:

Appendix 11 – Offshore MCZ Community Analysis – North East of Farnes Deep Video and Still Analyses.xls

Appendix 12. East of Haig Fras Video and Still PRIMER Analyses

All outputs from the PRIMER analyses of the East of Haig Fras video and still data can be found in the attached file:

Appendix 12 – Offshore MCZ Community Analysis – East of Haig Fras Video and Still Analyses.xls

Appendix 13. South-West Deeps (West) Video and Still PRIMER Analyses

All outputs from the PRIMER analyses of the South-West Deeps (West) video and still data can be found in the attached file:

Appendix 13 – Offshore MCZ Community Analysis – South-West Deeps (West) Video and Still Analyses.xls

Appendix 14. Swallow Sand Video and Still PRIMER Analyses

All outputs from the PRIMER analyses of the Swallow Sand video and still data can be found in the attached file:

Appendix 14 – Offshore MCZ Community Analysis – Swallow Sand Video and Still Analyses.xls