Analysis of samples from the Hempton Turbot Bank

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National Parks & Wildlife

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1 INTRODUCTION

Aqua-Fact International Services Ltd was contracted by the Department of the Environment, Heritage and Local Government (DEHLG) to carry out the analysis of benthic samples collected in 2005 from the RV *Celtic Exploer* as part of the MESH sampling schedule. The samples in question were taken from the Hempton Turbot sandbank off the Co. Donegal coast.

2 METHODOLOGY

2.1 Sampling Procedure and Processing

Fifteen samples were collected from the Hempton Turbot sandbank on the 21st September 2005 during the MESH surveying schedule. Figure 1 shows the locations of the sampling stations and Table 1 shows the co-ordinates and depths of the sampling stations. A Shipek 0.04m^2 grab sampler was used and all faunal returns were sieved on a 0.1mm mesh sieve. The samples were stored in buffered formalin and subsequently sorted under a microscope (x 10 magnification), into four main groups: Polychaeta, Mollusca, Crustacea and others. The 'others' group consisted of echinoderms, nematodes, nemerteans, cnidarians and other lesser phyla. The taxa were then identified to species level where possible. Unfortunately, the faunal returns for station 57 could not be located and therefore this station was excluded from this assessment.

The MESH methodology for evaluating biomass was used to determine the total biomass for each faunal group. Faunal returns were blotted dry on absorbant paper prior to wet weighing. The Echinoidea and Holothurioidea were punctured to facilitate this process. Wet weight was determined to two decimal places using a Sartorious balance. All gastropods and bivalves were weighed in their shells. All hermit crabs and tubicolous species were removed from their shells/tubes prior to weighing.

An additional sample was taken at each station and used for granulometric analyses the results of which were made available for inclusion in this report. However, granulometric results were only available for stations HT63 to HT68.

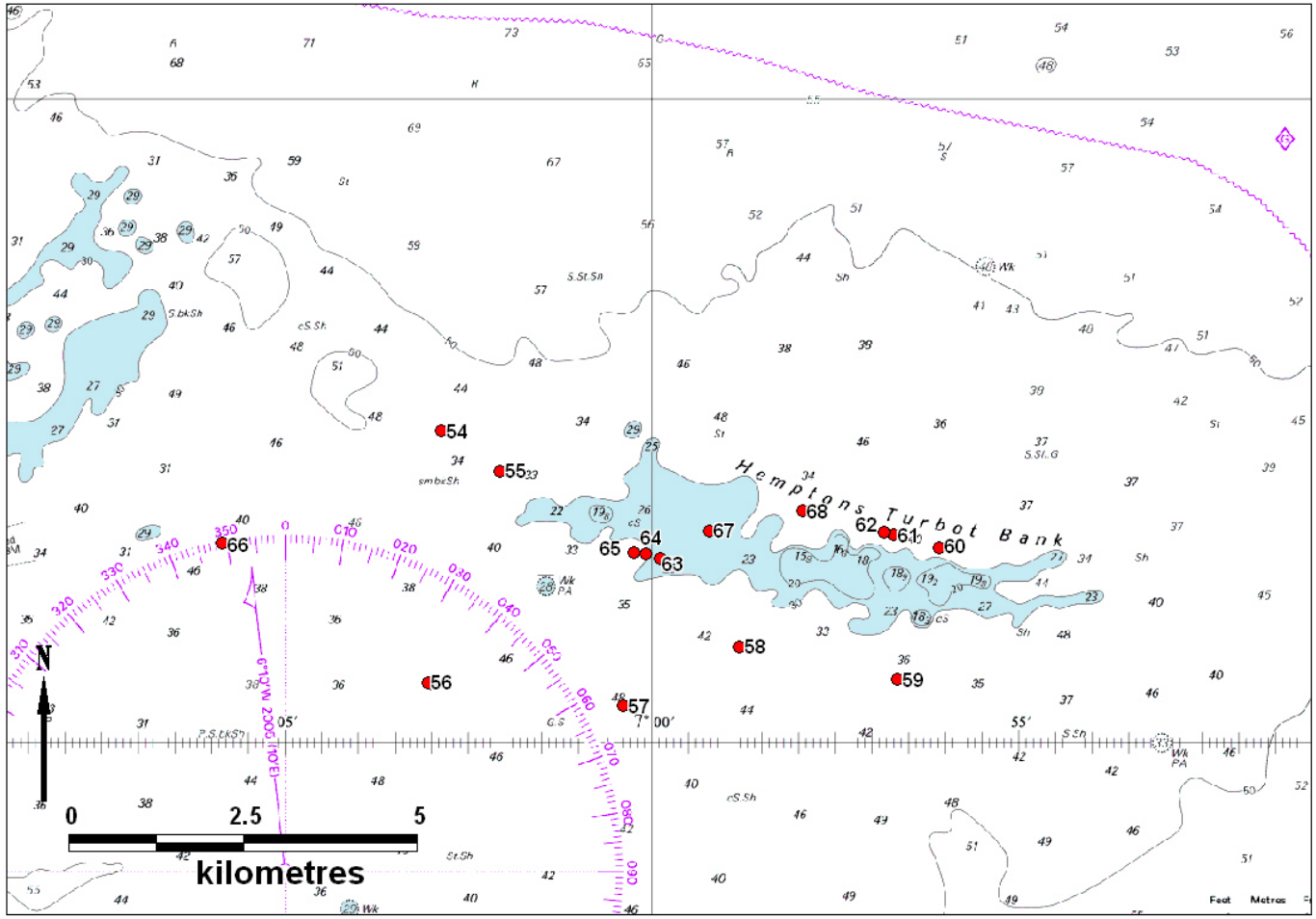

Figure 1: Station locations at the Hemptons Turbot Bank sampled on the 21st September 2005.

Table 1: Station coordinates for the 14 stations sampled at the Hempton Turbot Bank on the 21st September 2005.

Number	Latitude	Longitude	Depth
HT 54	55°27.4268	7°2.89	44
HT 55	55°27.1086	7°2.0891	38
HT 56	55°25.4724	7°3.0755	48
HT 58	55°25.7462	6°58.8249	43
HT 59	55°25.4917	6°56.6748	46
HT 60	55°26.5171	6°56.0959	42
HT 61	55°26.6192	6°56.7154	44
HT 62	55°26.6375	6°56.8546	44
HT 63	55°26.428	6°59.9	26
HT 64	55°26.4737	7°0.097	32
HT 65	55°26.4806	7°0.2682	31
HT 66	55°26.5524	7°5.883	33
HT 67	55°26.6445	6°59.2332	n/a
HT 68	55°26.8018	6°57.9622	49

2.2 Data processing

2.2.1 Fauna

As a Shipek grab, with a capacity of 0.04m² was used for the faunal sampling, all faunal returns were increased by a factor of 2.5 to make the results comparable to previous sandbank surveys carried out using 0.1m² grabs. Data matrices of all the faunal data were compiled and later used for statistical analyses using the Primer ® (Plymouth Routines in Multivariate Ecological Research) programme.

Univariate statistics in the form of diversity indices were calculated. The following diversity indices were calculated:
1) Margalef's species richness index (D), (Margalef, 1958).

$$D = \frac{S-1}{\log_2 N}$$

where: N is the number of individuals
S is the number of species

2) Pielou's Evenness index (J), (Pielou, 1977).

$$J = \frac{H' (observed)}{H'_{max}}$$

where: H'_{max} is the maximum possible diversity, which could be achieved if all

species were equally abundant (= $\log_2 S$)

3) Shannon-Wiener diversity index (H'), (Pielou, 1977).

$$H' = -\sum_{i=1}^{S} p_i(\log_2 p_i)$$

where: p_I is the proportion of the total count accounted for by the i^{th} taxa

Species richness is a measure of the total number of species present for a given number of individuals. Evenness is a measure of how evenly the individuals are distributed among different species. The diversity index incorporates both of these parameters. Richness ranges from 0 (low richness) to 12 (high richness), evenness ranges from 0 (low evenness) to 1 (high evenness), diversity ranges from 0 (low diversity) to 5 (high diversity).

The PRIMER ® programme (Clarke & Warwick, 2001) was used to carry out multivariate analyses on the station-by-station faunal data. This was done for all surveys individually and on the combined survey data. All species/abundance data were fourth root transformed and used to prepare a Bray-Curtis similarity matrix in PRIMER ®. The fourth root transformation was used in order to down-weigh the importance of the highly abundant species and to allow the mid-range and rarer species to play a part in the similarity calculation. The similarity matrix was then used in classification/cluster analysis. This aim of this analysis was to find "natural groupings' of samples, i.e. samples within a group that are more similar to each other, than they are similar to samples in different groups (Clarke & Warwick, *loc. cit.*). The PRIMER ® programme CLUSTER carried out this analysis by successively fusing the samples into groups and the groups into larger clusters, beginning with the highest mutual similarities then gradually reducing the similarity level at which groups are formed. The result is represented graphically in a dendrogram, the x-axis representing the full set of samples and the y-axis representing similarity levels at which two samples/groups are said to have fused.

The Bray-Curtis similarity matrix was also subjected to a non-metric multi-dimensional scaling (MDS) algorithm (Kruskal & Wish, 1978), using the PRIMER ® programme MDS. This programme produces an ordination, which is a map of the samples in two- or three-dimensions, whereby the placement of samples reflects the similarity of their biological communities, rather than their simple geographical location (Clarke & Warwick, 2001). With regard to stress values, they give an indication of how well the multi-dimensional similarity matrix is represented by the two-dimensional plot. They are calculated by comparing the interpoint distances in the similarity matrix with the corresponding interpoint distances on the 2-d plot. Perfect or near perfect matches are rare in field data, especially in the absence of a single overriding forcing factor such as an organic enrichment gradient. Stress values increase, not only with the reducing dimensionality (lack of clear forcing structure), but also with increasing quantity of data (it is a sum of the squares type regression coefficient). Clarke and Warwick (*loc. cit.*) have

provided a classification of the reliability of MDS plots based on stress values, having compiled simulation studies of stress value behaviour and archived empirical data. This classification generally holds well for 2-d ordinations of the type used in this study. Their classification is given below:

Stress value < 0.05: Excellent representation of the data with no prospect of misinterpretation.
Stress value < 0.10: Good representation, no real prospect of misinterpretation of overall structure, but very fine detail may be misleading in compact subgroups.
Stress value < 0.20: This provides a useful 2-d picture, but detail may be misinterpreted particularly nearing 0.20.
Stress value 0.20 to 0.30: This should be viewed with scepticism, particularly in the upper part of the range, and discarded for a small to moderate number of points such as < 50.
Stress values > 0.30: The data points are close to being randomly distributed in the 2-d ordination and not representative of the underlying similarity matrix.

Each stress value must be interpreted both in terms of its absolute value and the number of data points. In the case of this study, the moderate number of data points indicates that the stress value can be interpreted more or less directly. While the above classification is arbitrary, it does provide a framework that has proved effective in this type of analysis.

2.2.2 Sediment

A procedure similar to multi-dimensional scaling (MDS) was carried out on the sediment data. The procedure is known as principal component analysis (PCA) and it is a 2D/3D ordination. Like MDS, it is based on an underlying (dis)similarity matrix; however in this case it is a Euclidean distance dissimilarity matrix not a Bray-Curtis similarity matrix. The data matrix used for PCA included all of the environmental parameters, i.e. sediment particle size percentage distributions (% sand, %silt-clay etc). This dataset was transformed to prevent any outliers having a disproportionate influence on the results. The sediment particle size percentage distributions were square-root transformed. If any significant (pairwise correlation >0.95) correlations existed between variables, only one variable from that correlated group was included in the analysis, to prevent the correlation being exaggerated in the analysis. Following the transformations, the data were normalised to equalise the variance and standardise the contributory importance of each variable. The resulting data matrix was subjected to a correlation based PCA using the PRIMER® program PCA (Clarke & Warwick, 1994), to identify the parameters that accounted for a large proportion of the variance in the original data set. The variances of the principal components (eigen values), the proportion and cumulative proportion of the total variance, explained by each principal component, and the coefficients for each principal component (eigen vectors) were calculated. A two-dimensional PCA ordination of the data was constructed. The PCA plot defined the positions of samples in

relation to each axes, which represented the full set of variables. Each station acquired a place on this graph and the location depended on a number of variables significant to that station and which set it apart from all the rest.

3 RESULTS

3.1 Fauna

The taxonomic identification of the benthic infauna across all 14 stations sampled in the Hempton Turbot Bank survey yielded a total count of 59 species, comprising 955 individuals, ascribed to 10 phyla. A complete listing of these species abundance is provided in Appendix II. Of the 59 species enumerated, 24 were polychaetes (segmented worms), 19 were crustaceans (crabs, shrimps, prawns), 6 were molluscs (mussels, cockles, snails etc.), 3 species were echinoderms (brittlestars, sea cucumbers), 1 species was a pycnogonid (sea spiders) and 1 species was a chordate (animals with a backbone). Five phyla were grouped as others; this group consisted of cnidarians (jellyfish, corals), nemerteans (ribbon worms), nematodes (round worms) and bryozoans (moss animals). As the cnidarians and bryozoans were recorded as presence/absence, they were removed from the statistical analysis.

UNIVARIATE ANALYSES

Univariate statistical analyses were carried out on the station-by-station faunal data. The following parameters were calculated and can be seen in Table 2; species numbers, number of individuals, richness, evenness and diversity. Biomass has also being included in this table. Stations 54, 55, 63, 65, 66 and 67 contained no fauna and as a result diversity indices could not be calculated for these stations. In addition, these stations were excluded from further analyses. Species numbers ranged from 1 (HT64) to 24 (HT61). Number of individuals ranged from 3 (HT64) to 435 (HT61). Richness ranged from 0 (HT64) to 3.79 (HT61). Evenness ranged from 0.36 (HT62) to 1 (HT58). Evenness could not be calculated for station HT64 due to the presence of only 1 species. Diversity ranged from 0 (HT64) to 3.73 (HT61). Biomass ranged from <0.01 (HT 58) to 7.78 (HT 61).

Table 2: Diveristy indices for the 14 stations sampled at the Hempton Turbot bank.

Station	Species Numbers	Number of Individuals	Richness	Evenness	Diversity	Biomass (g)
HT 54	0	0	n/a	n/a	n/a	0
HT 55	0	0	n/a	n/a	n/a	0
HT 56	15	105	3.01	0.72	2.81	1.78
HT 58	2	5	0.62	1	1	<0.01
HT 59	3	15	0.74	0.79	1.25	0.09
HT 60	10	33	2.59	0.98	3.24	7.72
HT 61	24	435	3.79	0.81	3.73	7.78
HT 62	13	285	2.12	0.36	1.31	2.45
HT 63	0	0	n/a	n/a	n/a	0
HT 64	1	3	0	n/a	0	3.78
HT 65	0	0	n/a	n/a	n/a	0
HT 66	0	0	n/a	n/a	n/a	0
HT 67	0	0	n/a	n/a	n/a	0
HT 68	8	75	1.6	0.56	1.67	4.03

MULTIVARIATE ANALYSES

The dendrogram and the MDS plot can be seen in Figures 2 and 3 respectively. Station HT64 split from all the other stations at a 0% similarity level i.e. it was 100% unlike any of the other stations sampled. This was due to the presence of only one species at this station, the lesser sand eel or sand lance *Ammodytes tobianus.* No infaunal benthic species were recorded from this station. Station HT58 split from the remaining stations at a similarity level of 2.91%. This station contained only two species, the polychaetes *Syllis* sp. and *Polygordius* sp.

The remaining stations formed at group at a similarity level of 10.71%. Within this group, stations HT60 and HT61 had a 19.32% similarity. Stations HT56 and HT62 had a similarity level of 24.63% and stations HT59 and HT68 had a similarity level of 37.51%. The latter two groupings, when combined had a similarity level of 15.79%.

In the coastal environment, groups formed below a 40% similarity level are usually statistically meaningless. All groupings at the stations sampled formed groups with a level of less than 40%. However, this has probably more to do with the fact that no replicate samples were taken rather than the fact that the stations were actually vastly different from each other.

These groupings were also preserved in the MDS plot. The stress value of the MDS ordination is 0.01; this is an excellent representation of the data with no prospect of misinterpretation. Figure 5 shows a close up of all stations with the exception of station HT64. The similarity percentages are superimposed on the plot.

Stations HT59 and HT68 contained 9 species comprised of 90 individuals. The dominant species of this group was the common acorn barnacle

Semibalanus balanoides. This species accounted for 70% of the species abundance in this group. Other species present in this group included the barnacle *Elminuis modestus* and the polychaete *Eusyllis blomstrandi.*

Stations HT56 and HT62 contained 25 species comprised of 390 individuals. The dominant species of this group was the porcelain crab *Pisidia longicornis.* This species accounted for 73% of the species abundance in this group. Other species present in this group included the hermit crab *Pagurus prideaux*, the squat lobster *Galathea intermedia* and the common acorn barnacle *Semibalanus balanoides.*

Stations HT60 and HT61 contained 30 species comprised of 468 individuals. The dominants of this group included the mollusc *Muculus discors,* the amphipod *Parapleustes bicuspis,* the mollusc *Modiolula phaseolina,* the polychaetes *Autolytus alexandri* and *Autolytus inermis,* the amphipod *Parapleustes assimilis* and the polychaete *Trypanosyllis zebra.* These 7 species accounted for 72% of the species abundance in this group. Other species present in this group included the echinoderm *Ophiopholis aculeata,* the amphipod *Gammaropsis maculata,* the hermit crab *Pagurus pubescens* and *Nematoda* sp.

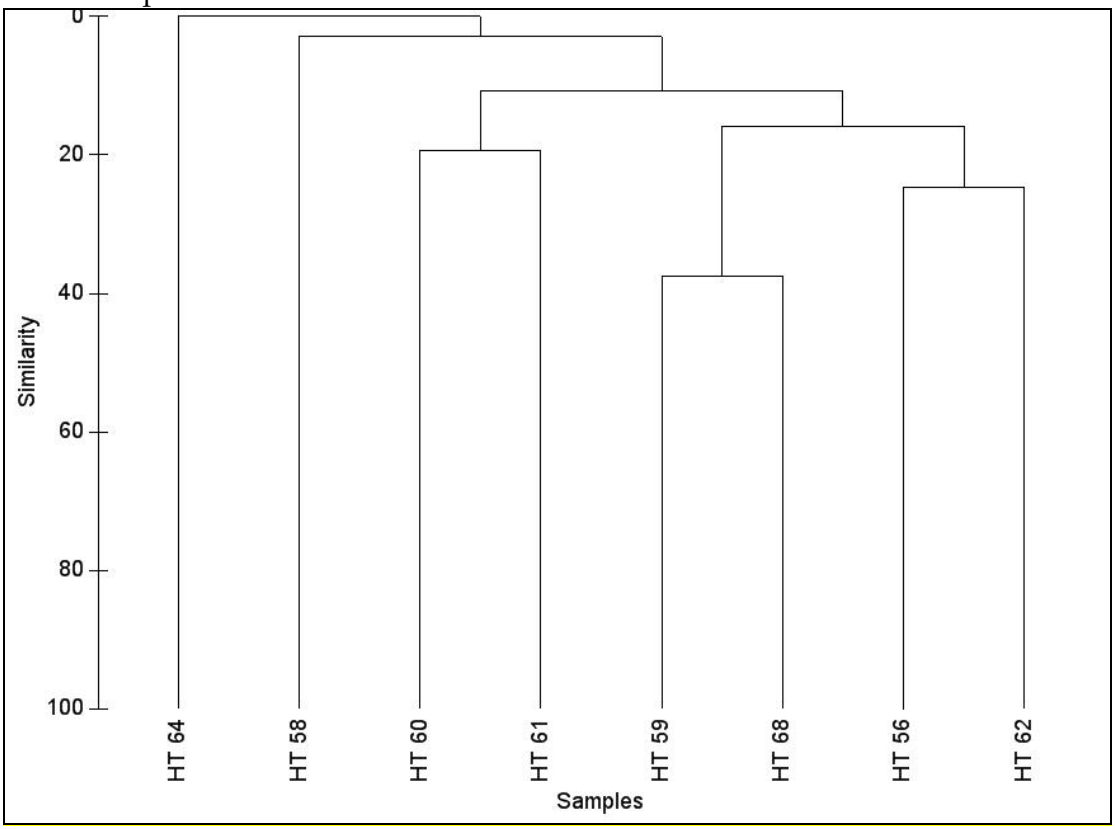

Figure 2: Dendrogram showing the 8 fauna containing stations sampled at the Hempton Turbot Bank on the 21st September 2005.

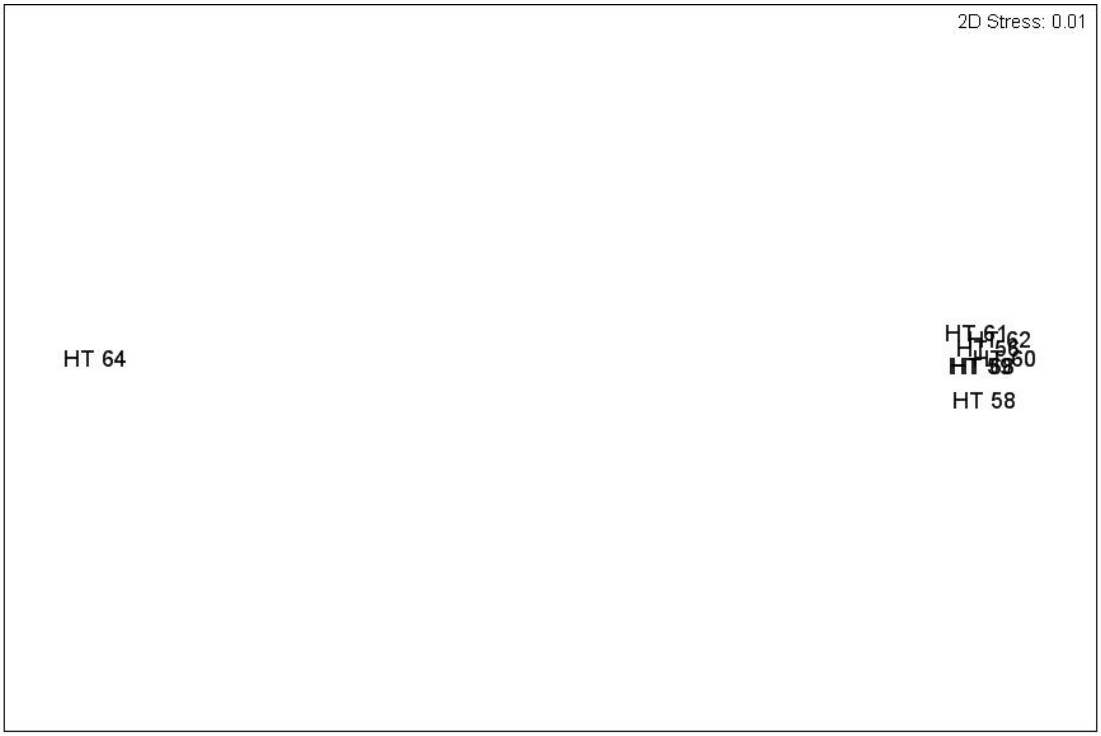

Figure 3: MDS plot of all 8 fauna containing stations sampled at the Hempton Tuurbot on the 21st September 2005.

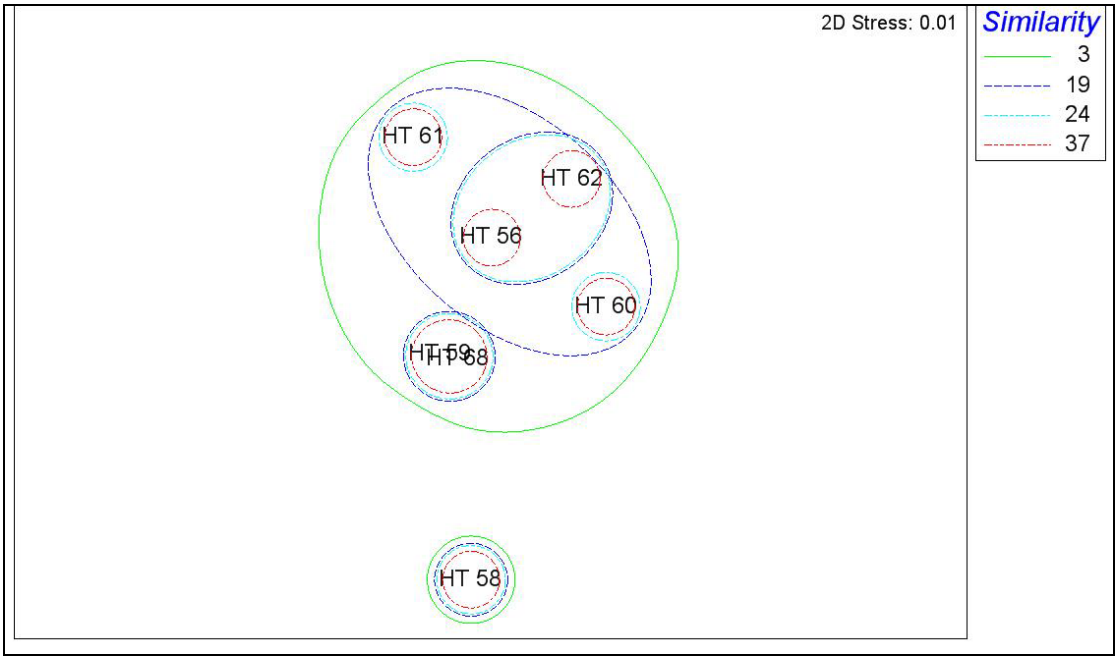

Figure 4: MDS plot of all 8 fauna containing stations sampled at the Hempton Tuurbot on the 21st September 2005.

3.2 Sediment

The results from the traditional granulometric analysis can be seen in Table 3. The sediment sampled along the Hempton Turbot Bank ranged from gravel at stations HT 66 and HT 67, very coarse sand at station HT 68, coarse sand at station HT 63 and medium sand at stations HT 64 and HT 65. Fine sand was very low at these stations and no very fine sand or silt-clay was present. Figure 5 shows the PCA ordination of the sediment data analysed from the Hempton Turbot Bank. The variation seen in the 2-D ordination accounted for 92.3% of the overall variation, PC1 accounted for 61.6% of the variation, whereas PC2 accounted for 30.8% of the variation. Stations HT 64 and HT65 were classified as medium sand, however station HT64 contained more coarse sand than station HT65 and as a result HT 65 grouped closed to HT 63 (the station dominated by coarse sand). Both stations HT 66 and HT 67 were classified as gravel, however as station HT 66 contained almost equal fractions of both gravel and very coarse sand, it grouped towards the very coarse sand area of the plot. HT 68 group alone, due to its high fraction of very coarse sand.

Table 3: Granulometry results for the 6 stations sampled at the Hempton Turbot Bank on the 21st September 2005.

Station	Gravel (%)	Very Coarse Sand (%)	Coarse Sand (%)	Medium Sand (%)	Fine Sand (%)	Very Fine Sand (%)	Silt-Clay (%)
HT 63	8.38	17.99	37.97	34.46	1.19	0	0
HT 64	14.82	13.02	16.84	51.63	3.69	0	0
HT 65	4.25	19.61	26.96	48.70	0.48	0	0
HT 66	30.96	29.51	14.69	23.98	0.86	0	0
HT 67	46.21	5.14	7.41	38.13	3.12	0	0
HT 68	15.89	33.73	32.12	18.10	0.16	0	0

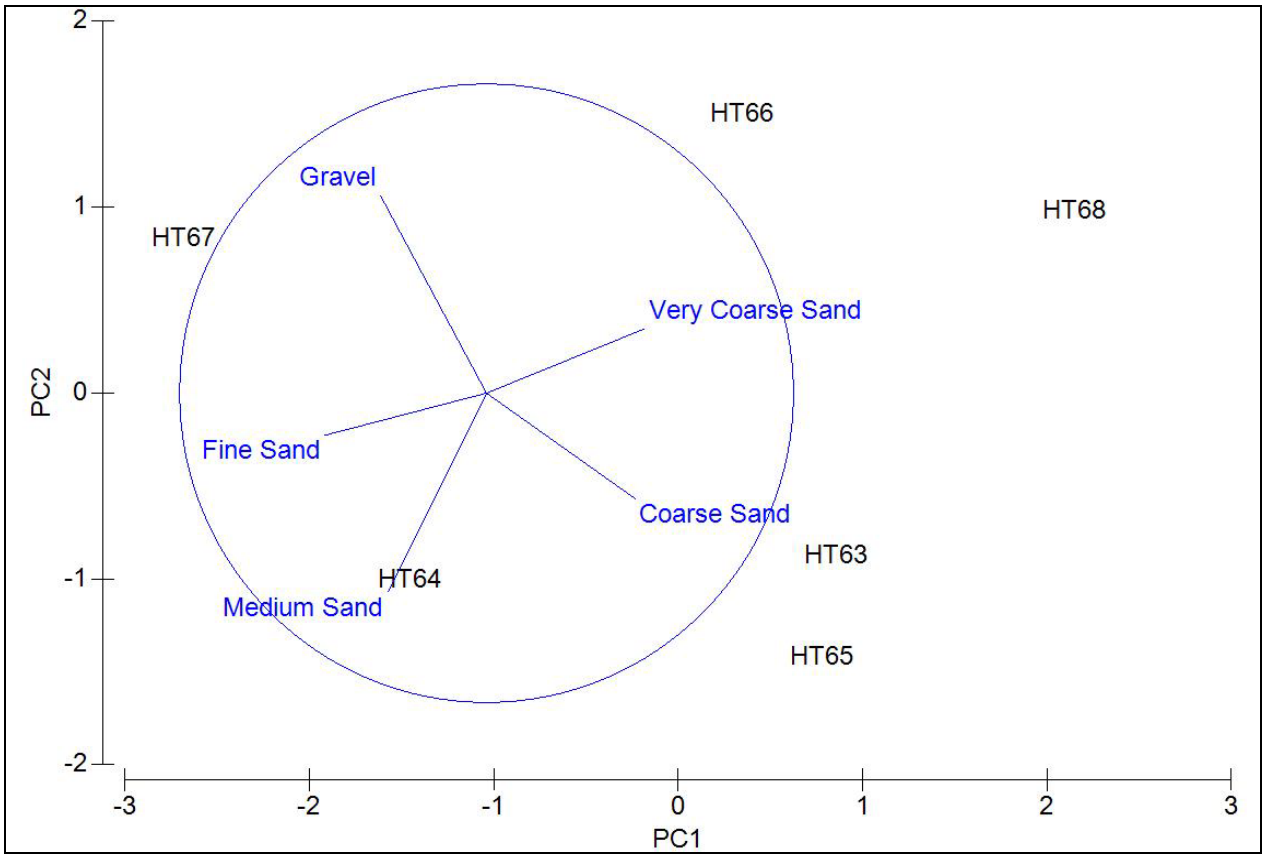

Figure 5: PCA plot of 6 stations sampled at the Hempton Tuurbot on the 21st September 2005.

4 DISCUSSION

It should be noted that due to the lack of replicate samples, the faunal returns and in turn the statistical analyses do not give an accurate picture of the benthic faunal assemblages at the Hempton Turbot Bank. Additionally, the use of Shipek grab resulted in smaller quanities than are typical or expected from faunal grab sampling. The Shipek grab would also have affected the integrity of the surficical layers which are typically badly disturbed during sampling with this device. This and the lack of replicates may explain the low numbers of faunal returns and the complete absense of fauna at 6 stations from this sandbank. While the faunal abundance values were increased to a level similar to that expected from a van Veen or Day grab, it is likely that a lot of species within the area remained unsampled and unaccounted for and no predictions could be made regarding the 6 stations that completely lacked fauna. As faunal returns were low, the determination of biotopes would have been inaccurate and as a result biotopes were not determined. Granulometric data were only available for two the the stations successfully sampled for fauna (HT64 and HT68). In the absence of sedimentary data, the determination of biotopes is inaccurate. Finally, only three of the sampling locations were actually sampled from with the sandbank (HT63, HT64 and HT67 See Figure 1) area.

Two of the stations sampled (HT64 and HT58) contained two species or less. These species were the lesser sand eel or sand lance *Ammodytes tobianus* (HT64) and the polychaetes *Syllis* sp. and *Polygordius* sp. These species are typically of sandy environments. Stations HT59 and HT68 contained the common acorn barnacle *Semibalanus balanoides*, the barnacle *Elminuis modestus* and the polychaete *Eusyllis blomstrandi*. Stations HT56 and HT62 contained the porcelain crab *Pisidia longicornis,* the hermit crab *Pagurus prideaux*, the squat lobster *Galathea intermedia* and the common acron barnacle *Semibalanus balanoides*. Stations HT60 and HT61 contained the mollusc *Muculus discors,* the amphipod *Parapleustes bicuspis,* the mollusc *Modiolula phaseolina,* the polychaetes *Autolytus alexandri* and *Autolytus inermis,* the amphipod *Parapleustes assimilis* and the polychaete *Trypanosyllis zebra.*

While the species recorded from the area are typical of coarse gravely sands, a complete picture of the benthic infaunal assemblage is lacking for the reasons outlined above. In order to accurately determine the assemblages, it is recommended that further sampling be carried out at predetermined sample locations within the sand bank and a minimum of three replicates be taken including one for granulometry using a 0.1m² Day grab.

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