AQUAFACT

Intertidal Habitat Assessment,

Renmore, Galway Bay

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Produced by

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On behalf of

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1. Introduction

AQUAFACT undertook a survey of the intertidal habitats at Renmore where it is proposed to expand the port of Galway to allow 24hr use of the harbour as it is currently restricted to operating only at high water. The expansion will require infilling an area of both intertidal and subtidal habitats of the Galway Bay cSAC. In the National Parks and Wildlife Service (NPWS, 2015) site synopsis for the Galway Bay cSAC, a complex of 2 intertidal habitats *i.e.* sand and mud flats exposed at low water (1140) and reefs (1170) is listed for the area in question.

2. Materials and methods

Sampling took place in November 2015. An intertidal walk over survey was carried out by three experiences marine ecologists to document the intertidal habitat types within the proposed development area. The surveyors determined biological zones based on differences in substrata and biological communities. A $0.25m^2$ quadrat was used to record the species present, their abundance and the substrate type. Abundance was recorded as percentage cover where possible. Photographs within each habitat were also taken. Where substrate allowed, 18cm diameter cores (to a depth of 15cm) were collected for faunal and sedimentary analysis.

Where sediment sampling was possible, 2 replicate faunal samples were collected and a third was collected for grain size and organic carbon analysis.

The contents of each core sampled was stored in a labelled container. On return to the laboratory, each sample was transferred portion by portion to a 1mm mesh sieve as a sediment water suspension. The sample was carefully and gently sieved and care was taken during the sieving process in order to minimise damage to taxa such as spionids, scale worms, phyllodocids and amphipods. The samples were then fixed with 4% buffered w/v formaldehyde solution and stained with Rose Bengal.

The samples were next sorted to pick out the fauna. All conspicuous fauna was extracted by hand, using forceps or pipette, first by eye to remove large specimens and then sorted using a stereo microscope at 6 to 10 times magnification. Following the removal of larger specimens, the samples

were placed in Petri dishes, approximately one half teaspoon at a time and sorted using a binocular microscope at x25 magnification. All fauna was sorted into four groups (Annelida, Crustacea, Mollusca and Others) and placed into suitable labelled containers and stored in 70-80% industrial methylated spirits. The faunal specimens were then identified to species level where possible using all relevant taxonomic keys and BEQUALM/NAMBQC guides.

A species list was then generated.

The sediment samples were stored in labelled plastic containers and these samples were frozen (<-18ºC) as soon as possible after acquisition.

The granulometric analysis was carried out by AQUAFACT using the traditional granulometric approach. Traditional analysis involved the dry sieving of approximately 100g of sediment using a series of Wentworth graded sieves. The process involved the separation of the sediment fractions by passing them through a series of sieves. Each sieve retained a fraction of the sediment, which were later weighed and a percentage of the total was calculated. Table 3.1 shows the classification of sediment particle size ranges into size classes. Sieves, which corresponded to the range of particle sizes (Table 3.1), were used in the analysis. Appendix 1 provides the detailed granulometric methodology.

Table 2.1: The classification of sediment particle size ranges into size classes (adapted from Buchanan, 1984).

Range of Particle Size	Classification	Phi Unit
<63µm	Silt/Clay	>4 Ø
63-125 µm	Very Fine Sand	4 Ø, 3.5 Ø
125-250 µm	Fine Sand	3 Ø, 2.5 Ø
250-500 µm	Medium Sand	2 Ø, 1.5 Ø
500-1000 µm	Coarse Sand	1 Ø, 1.5 Ø
1000-2000 µm (1 – 2mm)	Very Coarse Sand	0 Ø, -0.5 Ø
2000 – 4000 µm (2 – 4mm)	Very Fine Gravel	-1 Ø, -1.5 Ø
4000 -8000 µm (4 – 8mm)	Fine Gravel	-2 Ø, -2.5 Ø
8 -64 mm	Medium, Coarse & Very Coarse Gravel	-3 Ø to -5.5 Ø
64 – 256 mm	Cobble	-6 Ø to -7.5 Ø
>256 mm	Boulder	< -8 Ø

For organic carbon analysis, a sediment sample was taken at each station and stored in pre-labelled plastic bags, kept in cold freezer boxes onboard the vessel and frozen at -20°C on return to the lab. Organic carbon analysis was carried out by ALS laboratories using the Loss on Ignition (LOI) technique. This method involves oven drying the sediment sample in a muffle furnace (450°C for a period of 6 hours) after which time the organic content of the sample is determined by expressing as a percentage the weight of the sediment after ignition over the initial weight of the sediment.

Data Analysis

Prior to statistical evaluation, the dredge data was separated based into infaunal and epifaunal fractions and both were treated separately. Statistical evaluation of the faunal data was undertaken using PRIMER v.6 (Plymouth Routines in Ecological Research). Univariate statistics in the form of diversity indices are calculated. Numbers of species and numbers of individuals per sample will be calculated and the following diversity indices will be utilised:

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):

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

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 ith 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 Shannon-Wiener index incorporates both species richness and the evenness component of diversity (Shannon & Weaver, 1949).

The PRIMER programme (Clarke & Warwick, 2001) was used to carry out multivariate analyses on the station-by-station faunal data. All infaunal species/abundance data from the dredge and grab surveys were fourth root transformed and the epifaunal species/abundance data from the dredge surveys was reduced to presence/absence and used to prepare a Bray-Curtis similarity matrix in PRIMER The grab data was fourth root transformed and analysed separately from the dredge data. The fourth root transformation was used in order to allow the intermediate abundant and rarer species to play a part in the similarity calculation. (Other transformations *e.g.* square root, square root-1, were tested but had little effect of the spatial relationships between stations).

All species/abundance data from the samples was used to prepare a Bray-Curtis similarity matrix. The similarity matrix was then used in classification/cluster analysis. The 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 was 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. SIMPROF (Similarity Profile) permutation tests were incorporated into the CLUSTER analysis to identify statistically significant evidence of genuine clusters in samples which are *a priori* unstructured.

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 produced 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 & 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.

The species, which are responsible for the grouping of samples in cluster and ordination analyses, were identified using the PRIMER programme SIMPER (Clarke & Warwick, 1994). This programme determined the percentage contribution of each species to the dissimilarity/similarity within and between each sample group.

3. Results

3.1. *Granulometry and organic carbon.*

Table 3.1 presents the results of the granulometric analyses on the ten sediment samples collected at Renmore.

Station	Fine Gravel (>4mm)	Very Fine Gravel (2-4mm)	Very Coarse Sand (1-2mm)	Coarse Sand (0.5-1mm)	Medium Sand (0.25-0.5mm)	Fine Sand (125-250mm)	Very Fine Sand (62.5-125mm)	Silt-Clay (<63mm)
1	23.5	23.5	24.6	11	6.1	4.4	4.1	2.8
2	13.8	15.3	22.3	15.4	12.2	12.4	5.8	2.8
3	7.9	15.1	25.5	15.6	7.6	12.3	12	4.1
4	3	15.4	36	20.4	6.9	11.8	5.4	1
5	0.3	0.3	0.3	1.1	1.6	17.8	61.2	17.5
6	38.6	21.3	10.3	4.5	5.9	12.5	5.6	1.4
7	21.5	23.3	16.2	8	9.3	13	7.5	1.3
8	0	0.1	0.1	0.8	3.7	74.1	21	0.3
9	0	0	0.1	0.8	2.6	62.1	34	0.5
10	3	15.4	36	20.4	6.9	11.8	5.4	1

Table 3.1. Results of granulometric analyses of ten sediment samples collected at Renmore.

Except for St 5 where very fine sands predominated, sediments in the area are characterised gravels and coarse sand with low percentages of fine, very fine and silt clay fractions. Another characteristic aspect of the area surveyed was the presence of large numbers of mussel shells and shell debris particularly in the western half of the site. Many live mussels were also recorded and small number of juvenile native oysters, *Ostrea edulis.* Three bottom shells of the non-native Pacific Oyster *Crassostrea gigas* were also seen. Sediments throughout the area smelled strongly of hydrogen sulphide.

Results of the organic carbon analyses are presented below in Table 3.2

Station	% LOI
1	8.16
2	4.28
3	4.26
4	3.96
5	2.24
6	3.36
7	2.18

8	1.15
9	1.12
10	1.22

Table 3.2 Results of granulometric analyses of ten sediment samples collected at Renmore.

Organic carbon levels ranged from 1.12 % at St.9 to 8.16% at St 1.

3.2. Flora and fauna

Lichen species (*Verrucaria maura*, *Lichina pygmaea, Xanthoria parietina* and *Caloplaca marina*) were recorded at High Water. Algal species recorded at the site included *Pelvetia canaliculata* in the highest parts of the upper shore, *Fucus spiralis* in the upper shore, *Ascophyllum nodosum* and its epiphytic red alga,*Vertebrata lanosa* along with *Fucus vesiculosus* in the mid shore area and *Fucus serratus* in the lower shore. Some red algae crusts were recorded from mid shore to lower shores areas.

With regard to infaunal invertebrates, 54 species were recorded (see Appendix II) represented by 1 nemertean, 28 annelids, 10 crustaceans, 2 chitons and 12 bivalve molluscs.

Results of the univariate statistical analyses are presented in Table 3.1 below. Stations 8, 9 and 10 returned the lowest number of species (8) while Station 4 returned the highest number (26). The lowest number of specimens was recorded at Stations 8 and 10 (8) and the highest number of specimens was recorded at St. 1 (1,549). Species richness was lowest (1.696092) at St. 9 and highest (4.235398) at St 4 while evenness was lowest (0.263671) at St 1 and highest (0.78269) at St 7. Diversity ranged from 0.789888 at St 1 to 2.45412 at St 7.

	S	N	d	J'	H'(loge)
ST1	20	1549	2.586665	0.263671	0.789888
ST2	15	963	2.03783	0.344377	0.932591
ST3	14	510	2.085201	0.455683	1.202574
ST4	26	366	4.235398	0.738705	2.406773
ST5	13	84	2.708304	0.754275	1.934676
ST6	24	309	4.011622	0.73269	2.328529
ST7	23	305	3.845944	0.78269	2.45412
ST8	8	45	1.838881	0.702141	1.460061
ST9	8	62	1.696092	0.655814	1.363727

ST10	8	45	1.838881	0.76063	1.581686

Table 3.1. Results of univariate statistical analyses. S: number of species, N: numbers of individuals, d: Margalef's species richness, J': Pielou's Evenness index and H'(log e): Shannon Weiner diversity.

Figures 3.1 and 3.2 present results of Cluster and Multidimensional Scaling (MDS) analyses.
The Cluster analysis revealed three groupings, Group A with St.5, 8 9 and 10, Group B with just 2 stations, 1 and 2 and the third with St.3,4,6 and 7. Group A separates from the other two groups at a similarity level of *ca* 30% while groups B and C separate from each other at a level of *ca* 45%.Stations 1 and 2 a quite similar to one another as they separate at a level of *ca* 75%.

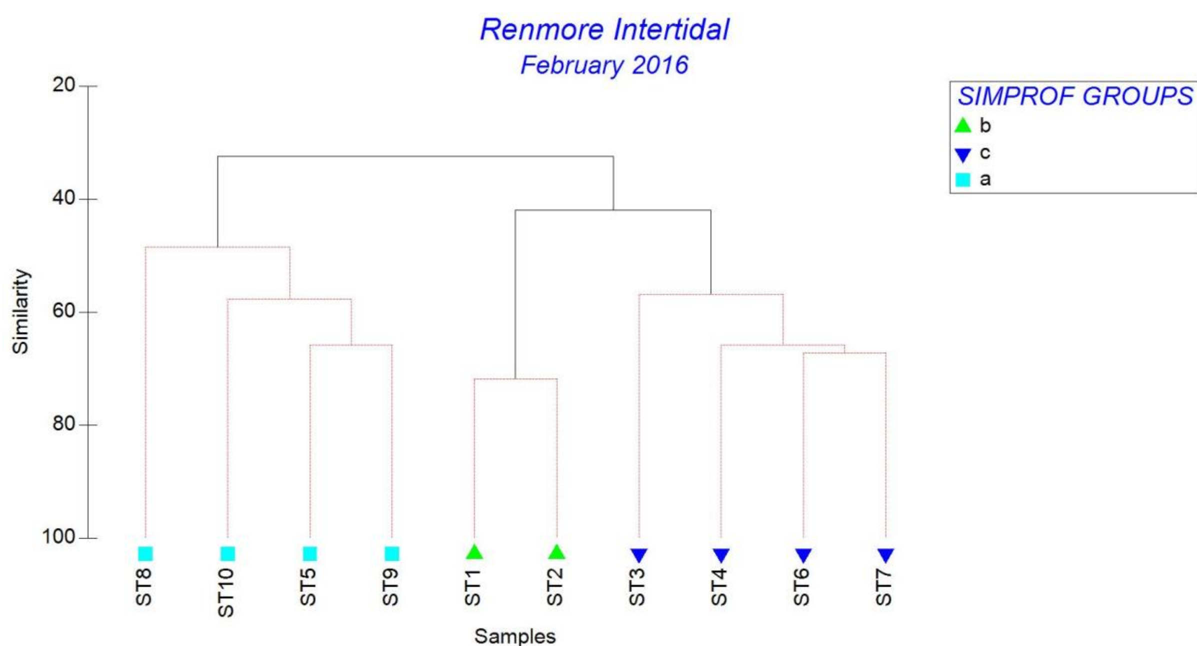


Figure 3.1 . Cluster analysis of quantitative faunal data from ten intertidal stations at Renmore.

Using the subroutine programme SIMPER in the PRIMER suite of analysis which selects the faunal species that characterise each cluster, the following species were identified.

Group A

Eteone longa agg., Capitella sp. complex, Pygospio elegans, Tellina fabula, Nephtys hombergii and *Tellina tenuis.*

Group B

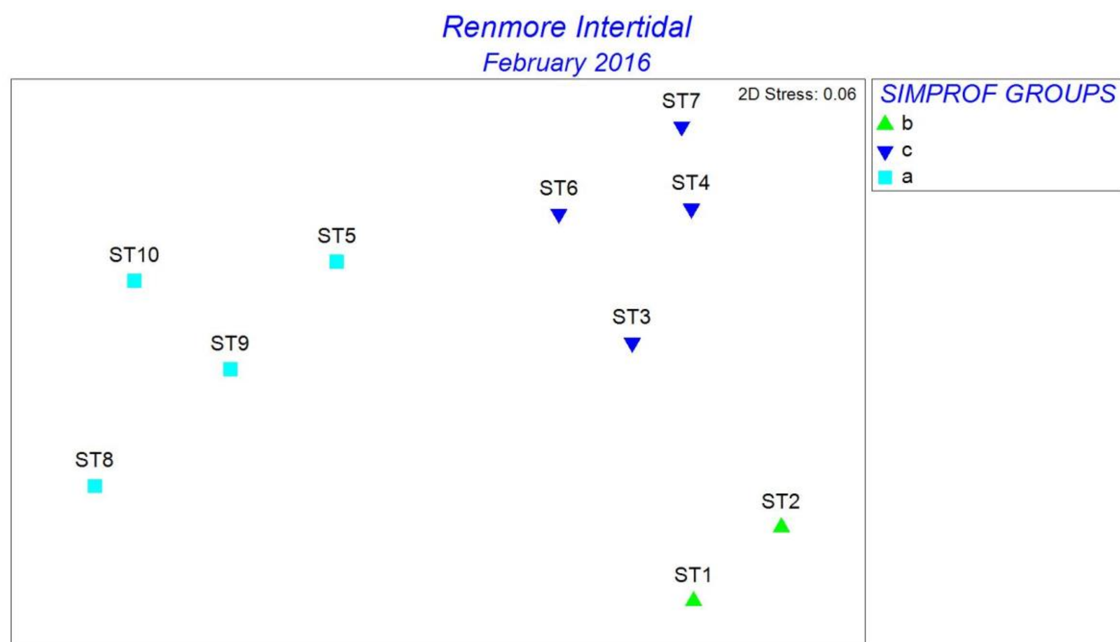
Tubificidae spp., *Eteone longa agg., Malacoceros fuliginosus, Hediste diversicolor, Brachyura, Macoma balthica, Melita palmata, Pygospio elegans, Venerupis corrugata* and *Tetrastemma*

melanocephalum.

Group C

Tubificidae spp., *Pygospio elegans, Heteromastus filiformis, Eteone longa agg., Tetrastemma melanocephalum, Macoma balthica, Glycera tridactyla, Nephtys hombergii, Scoloplos armiger, Melinna palmata, Prionospio sp., Protodorvillea kefersteini, Leptochiton asellus, Parvicardium scabrum* and *Parvicardium minimum.*

The occurrence of the pioneering polychaete genus *Capitella* and high numbers of tubificid oligochaetes, in Cluster A (Stations 1 and 2 which are closest to the plume of the River Corrib) indicates a high level of organic carbon and a low level of oxygen in the sediment.



3.3. Distribution of intertidal communities.

The result of the walk over of the intertidal area at Renmore and the documentation of the intertidal communities recorded are shown in Figure 3.3 below.

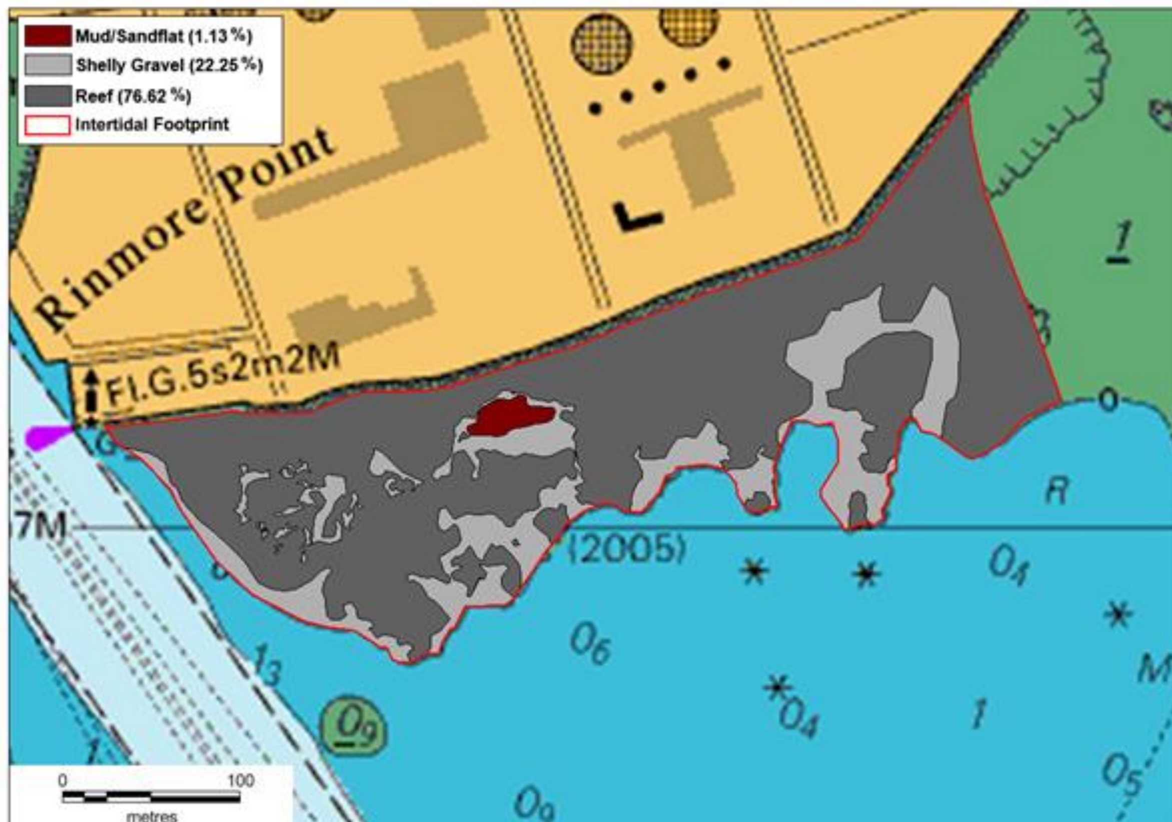


Figure 3.3.Distribution of intertidal communities recorded at Renmore.

As can be seen from this figure, the reef and shelly gravel habitats together make up *ca* 98.8% of the habitat type with mud/sand flat only comprising a little over 1%. There is a large area of mud and sand flat just to the east of the red line marked above at Ballyloughan Beach.

4. Discussion

The intertidal habitat at the Renmore area has historically been impacted by organic enrichment from loadings in the River Corrib which on an ebbing tide, flows over the western parts of the area. Before the Mutton Island treatment plant was commissioned in the early years of this century, untreated sewage effluent was disposed of to the sea either in the river itself or via a disposal pipe south of Nimmo's Pier for many many decades giving rise to sediments with low levels of oxygen, high levels of sedimentary hydrogen sulphide and therefore reduced numbers of infaunal invertebrates. Besides the untreated effluent as a source of organic enrichment, the catchment of the Corrib particularly along the eastern section and to a lesser extent, the southern section, drains lands that are intensively farmed. These areas also have a number of towns, *e.g.* Tuam, Headford, Oughterard that only have secondary treatment works, the effluent of which is disposed of to rivers

that eventually flow into Lake Corrib. The fact that the water of the Corrib River has its own organic loading contributes to the impact that the intertidal habitat at Renmore is experiencing.

5. References

Folk, R.L. 1954. The distinction between grain size and mineral composition in sedimentary rock nomenclature. *Journal of Geology* 62 (4): 344-359.

Appendix 1

Grain Size Methodology

Granulometry

1. Approximately 25g of dried sediment is weighed out and placed in a labelled 1L glass beaker to which 100 ml of a 6 percent hydrogen peroxide solution was then added. This was allowed to stand overnight in a fume hood.
2. The beaker is placed on a hot plate and heated gently. Small quantities of hydrogen peroxide are added to the beaker until there is no further reaction. This peroxide treatment removes any organic material from the sediment which can interfere with grain size determination.
3. The beaker is then emptied of sediment and rinsed into a. 63µm sieve. This is then washed with distilled water to remove any residual hydrogen peroxide. The sample retained on the sieve is then carefully washed back into the glass beaker up to a volume of approximately 250ml of distilled water.
4. 10ml of sodium hexametaphosphate solution is added to the beaker and this solution is stirred for ten minutes and then allowed to stand overnight. This treatment helps to dissociate the clay particles from one another.
5. The beaker with the sediment and sodium hexametaphosphate solution is washed and rinsed into a 63µm sieve. The retained sampled is carefully washed from the sieve into a labelled aluminium tray and placed in an oven for drying at 100ºC for 24 hours.
6. When dry this sediment is sieved through a series of graduated sieves ranging from 4 mm down to 63µm for 10 minutes using an automated column shaker. The fraction of sediment retained in each of the different sized sieves is weighed and recorded.
7. The silt/clay fraction is determined by subtracting all weighed fractions from the initial starting weight of sediment as the less than 63µm fraction was lost during the various washing stages.

Appendix II

Species list

	ST1	ST2	ST3	ST4	ST5	ST6	ST7	ST8	ST9	ST10
Tetrastemma melanocephalum	1	8	5	13	3	5	8	0	1	0
Pholoe sp.	0	0	0	0	0	0	1	0	0	0
Eteone longa agg.	73	87	48	9	37	31	75	13	27	23
Phyllodoce mucosa	0	0	0	4	1	0	9	0	0	0
Glycera sp.	0	1	0	0	0	1	0	0	0	0
Glycera tridactyla	2	0	10	4	0	3	6	1	1	0
Hediste diversicolor	43	18	0	0	0	0	0	0	0	0
Eunereis longissima	0	0	0	0	1	0	0	0	0	0
Nephtys sp.	2	0	0	0	0	0	0	0	0	0
Nephtys hombergii	0	0	5	1	9	28	11	0	2	4
Protodorvillea kefersteini	0	0	2	9	0	0	2	0	0	0
Scoloplos armiger	0	0	4	15	1	1	9	0	0	0
Scoloplos sp.	0	0	0	0	3	0	0	0	0	0
Aonides oxycephala	0	0	0	11	0	0	0	0	0	0
Malacoceros fuliginosus	61	40	4	0	0	0	0	0	0	0
Microspio sp.	0	0	0	17	0	0	0	0	0	0
Polydora sp.	0	0	0	0	0	1	0	0	0	0
Prionospio sp.	0	0	0	5	0	13	8	0	0	0
Pygospio elegans	4	10	51	49	7	24	26	2	4	2
Spiochaetopterus sp.	0	0	0	0	0	3	2	0	0	0

Cirratulus cirratus	0	0	0	2	0	0	0	0	0	0
Capitella sp. complex	3	0	0	10	7	41	0	21	23	3
Heteromastus filiformis	1	1	11	86	3	56	57	0	0	0
Mediomastus fragilis	0	0	0	0	0	2	0	0	0	0
Notomastus latericeus	0	0	0	0	0	0	0	1	0	0
Arenicola marina	0	0	0	0	1	0	0	4	0	0
Melinna palmata	0	0	1	15	0	1	4	1	0	0
Manayunkia aestuarina	1	0	0	0	0	0	0	0	0	0
Tubificidae spp.	1292	753	353	90	4	72	29	0	1	0
Calliopius laeviusculus	0	0	0	0	0	0	1	0	0	0
Gammarus salinus	0	0	0	0	0	0	1	0	0	0
Melita palmata	29	5	0	0	0	0	0	0	0	0
Microdeutopus anomalus	2	0	0	2	0	3	0	0	0	0
Corophium sp.	0	0	0	1	0	0	0	0	0	0
Lekanesphaera monodi	3	0	0	0	0	0	0	0	0	0
Jaera albifrons	11	0	0	0	0	0	0	0	0	0
Crangon crangon	0	0	0	0	0	1	3	0	0	2
Brachyura	6	10	0	0	0	0	0	0	0	0
Liocarcinus sp.	1	0	0	0	0	0	0	0	0	0
Leptochiton asellus	0	0	0	1	0	12	25	0	0	0
Lepidochitona (Lepidochitona) cinerea	0	1	0	0	0	0	0	0	0	0
Mytilus edulis spat	0	0	0	0	0	2	0	0	0	0
Kellia suborbicularis	0	0	0	0	0	0	1	0	0	0
Kurtiella bidentata	0	0	3	5	0	0	0	0	0	0

Parvicardium minimum	0	0	0	1	0	1	3	0	0	0
Parvicardium scabrum	4	1	0	4	0	1	12	0	0	0
Tellina tenuis	0	0	0	3	0	3	0	2	0	2
Tellina fabula	0	0	0	0	7	0	0	0	3	7
Macoma balthica	6	20	11	3	0	3	10	0	0	2
Abra sp.	0	0	2	0	0	0	0	0	0	0
Abra alba	0	0	0	2	0	0	2	0	0	0
Timoclea ovata	0	4	0	0	0	0	0	0	0	0
Venerupis corrugata	4	4	0	4	0	1	0	0	0	0