Intertidal Habitat Assessment,

Renmore, Galway Bay

June 2023

Produced by

AQUAFACT International Services Ltd

On behalf of

Galway Harbour Commissioners

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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. The intertidal area at Renmore was previously sampled in 2016 and the present survey was conducted to document the current status of the area.

2. Materials and methods

2.1. Survey methodology

The intertidal survey took place on the 15th and 16th June 2023. Weather was dry and overcast on both days and low water was at 9.52am on 15th and 10.35am on 16th June.

An intertidal walk over survey was carried out by three experienced 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. Table 2.1 lists the coordinates of the stations sampled by core and Figure 2.1 illustrates their location.

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

AQUAFACT has in-house standard operational procedures for benthic sampling, and these were followed for this project. Additionally, AQUAFACT follows the NMBAQC standard for benthic sampling and analysis (Worsfold and Hall*.*, 2010).

Table 2.1: Intertidal Core station locations, Renmore.

Station	Date	Latitude	Longitude
1	16/06/2023	53.26704	-9.04264
2	16/06/2023	53.26692	-9.04264
3	16/06/2023	53.2668	-9.04248
4	16/06/2023	53.26677	-9.04155
5	16/06/2023	53.2672	-9.04088
6	15/06/2023	53.26796	-9.0367
7	15/06/2023	53.26801	-9.03724
8	15/06/2023	53.26872	-9.03584
9	15/06/2023	53.2684	-9.03646
10	15/06/2023	53.26829	-9.0363

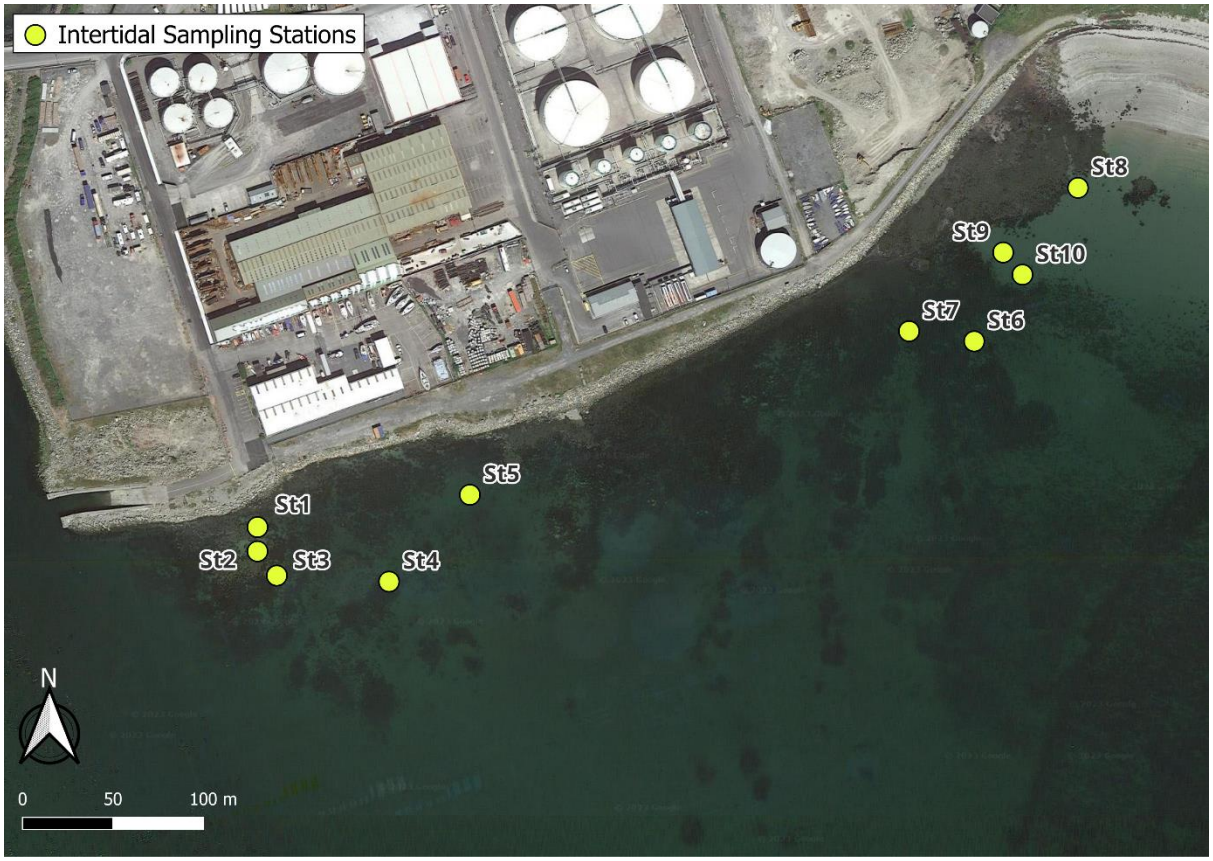

Table 2.2: Intertidal Core stations at Renmore.

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 Eosin dye.

For processing, each faunal sample was washed of formalin and placed in an illuminated shallow white tray and sorted first by eye to remove large specimens and then sorted under a stereo microscope (x 10 magnification). Following the removal of larger specimens, the samples were placed into Petri dishes, approximately one half teaspoon at a time and sorted using a binocular microscope at x25 magnification.

The fauna was sorted into four main groups: Polychaeta, Mollusca, Crustacea and others. The 'others' group consisted of echinoderms, nematodes, nemerteans, cnidarians and other lesser phyla. The fauna was maintained in stabilised 70% industrial methylated spirit (IMS) following retrieval and identified to species level where practical using a binocular microscope, a compound microscope and all relevant taxonomic keys. After identification and enumeration, specimens were separated and stored to major taxon level.

The sediment 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 was later weighed and a percentage of the total was calculated. Table 2.2 shows the classification of sediment particle size ranges into size classes. Sieves, which corresponded to the range of particle sizes (Table 2.2), were used in the analysis.

A subsample of sediment was dried and passed through a 0.5mm sieve. This sample was delivered to ALS laboratories for organic carbon analysis (LOI@450˚C).

Table 2.3: 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

2.2. Faunal Data Analysis

Uni- and multi-variate statistical analysis of the faunal data was undertaken using PRIMER v.6 (Plymouth Routines in Ecological Research).

2.2.1. Univariate Indices

Using PRIMER, the faunal data were used to produce a range of univariate indices. Univariate indices are designed to condense species data in a sample into a single coefficient that provides quantitative estimates of biological variability (Heip *et al*., 1998; Clarke and Warwick, 2001). Univariate indices can be categorised as primary or derived indices.

Primary biological indices used in the current study include:

- number of taxa (S) in the samples and
- number of individuals (N) in the samples.

Derived biological indices, which are calculated based on the relative abundance of species in samples, used in the study include:

- Margalef's species richness index (d) (Margalef, 1958),

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

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

Margalef's species richness is a measure of the total number of species present for a given number of individuals.

- 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 (= $\log_2 S$)

Pielou's evenness is a measure of how evenly the individuals are distributed among different species.

- 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

Shannon-Wiener diversity index takes both species abundance and species richness into account quantify diversity (Shannon & Wiener, 1949).

- The Shannon-Wiener based Effective Number of Species (ENS) (Hill, 1973; Jost, 2006)

$$H = \exp(H')$$

where H' is the Shannon-Wiener diversity index.

The Shannon-Wiener index diversity index is converted to ENS to reflect 'true diversities' (Hill, 1973, Jost, 2006) that can then be compared across communities (MacArthur, 1965; Jost, 2006). The ENS is equivalent to the number of equally abundant species that would be needed in each sample to give the same value of a diversity index, *i.e.,* Shannon-Wiener Diversity index. The ENS behaves as one would intuitively expect when diversity is doubled or halved, while other standard indices of diversity do not (Jost, 2006). If the ENS of one community is twice that of another, then it can be said that that community is twice as more diverse than the other.

2.2.2. Multivariate Analysis

The PRIMER programme (Clarke & Warwick, 2001) was used to carry out multivariate analyses on the station-by-station faunal data. All species abundance data from the grab surveys was square root transformed and used to prepare a Bray-Curtis similarity matrix in PRIMER. The square root transformation allows the less abundant species to play a part in the similarity calculation. Various

ordination and clustering techniques can then be applied to the similarity matrix to determine the relationship between the samples.

Multidimensional scaling (MDS) is a technique that ordinates samples as points in 2D or 3D space based on similarity in species distribution data. MDS performed on the Bray-Curtis similarity matrix produce ordination maps whereby the placement of samples reflects the similarity of their biological communities, rather than their simple geographical location (Clarke & Warwick, 2001).

An indication of how well the similarity matrix is represented by the ordination is given by stress values calculated by comparing the interpoint distances in the similarity matrix with the corresponding interpoint distances on the ordinations. 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 (2001) 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 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 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 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.

Hierarchical Agglomerative Clustering (HAC) is used to cluster samples based on between-sample similarities into groups in dendrograms. Similarity Profiling (SIMPROF) is used to test if differences between HAC derived similarity-based clusters are significant. Similarity Percentages (SIMPER) analysis can be used to determine the characterising species of each cluster of stations identified either arbitrarily (by eye) from HAC dendrograms or statistically using SIMPROF testing (Clarke and Warwick, 2001; Clarke and Gorley, 2006; Anderson *et al*., 2008).

The species, which are responsible for the grouping of samples in CLUSTER 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 below presents the quantitative granulometric and organic carbon results of the sediment at the stations sampled in at Renmore. Highest levels of medium gravel and fine gravel were observed at St6 (48.3% and 22% respectively). Highest levels of very coarse sand and coarse sand were recorded at St3 (24.3% and 27.1% respectively). Highest levels of medium sand were observed at St1 (21.9%). Highest levels of fine sand were recorded at St7 (68.5%). Highest levels of very fine sand were recorded at St10 (58.3%) and highest levels of silt clay were recorded at St5 (4.5%). Figure 3.1 shows the breakdown of sediment composition at each station. Figure 3.2 illustrates the sediment type according to Folk (1954). Three of the 10 stations sampled were classified as gravelly sand (St1, St2 and St3), 3 statiosnwere classified as sandy gravel (St4, St6 and St10), 3 stations were classified as sand (St7, St9 and St10) and 1 station was classified as slightly gravelly sand (St5) t4 and St 5) according to Folk (1954).

Organic matter values ranged from 1.31% (St7) to 5.28% (St3).

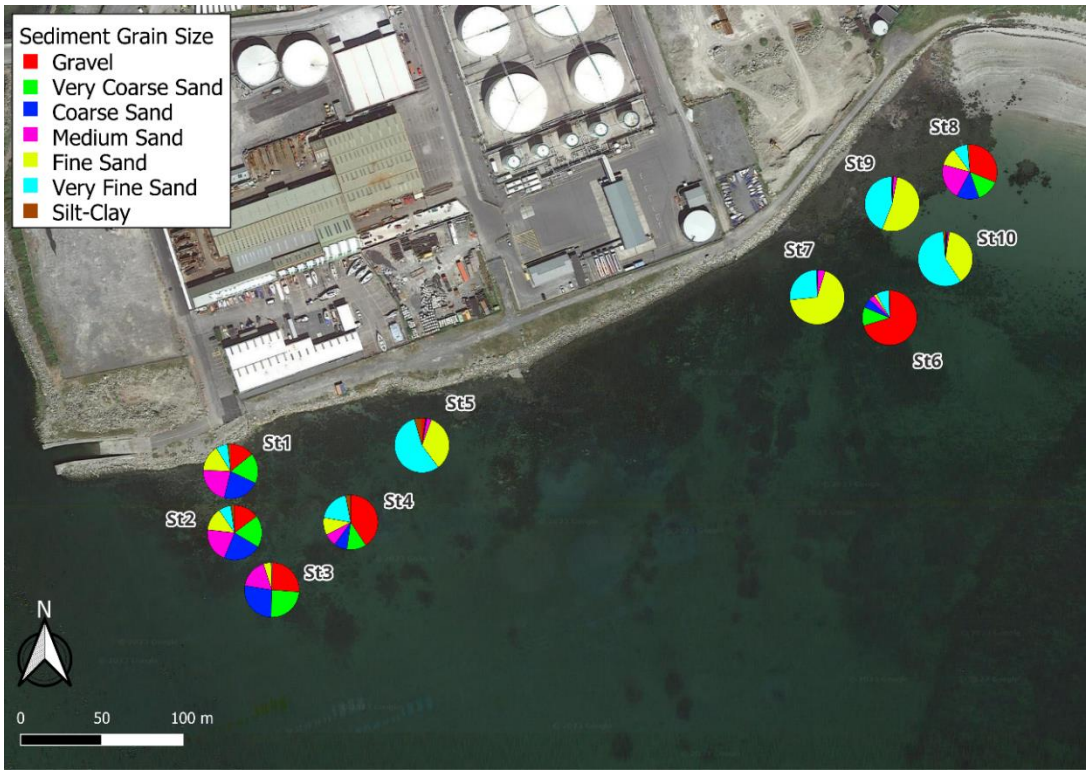

Figure 3.1: Sediment composition at the Renmore intertidal stations.

Table 3.1: Granulometry and Organic Carbon content from Renmore intertidal samples.

Station	>8mm	Medium Gravel (4-8mm) (%)	Fine Gravel (2-4mm) (%)	Very Coarse Sand (%)	Coarse Sand (%)	Medium Sand (%)	Fine Sand (%)	Very Fine Sand (%)	Silt-Clay (%)	Folk Classification	Organic Carbon (%)
Station 1	0	5.1	9.1	17.8	21.9	21.9	15.5	6.9	1.8	Gravelly sand	3.09
Station 2	0	6.3	8.5	18.9	22.6	20.5	13.6	7.3	2.3	Gravelly sand	4.12
Station 3	0	12.1	14.1	24.3	27.1	17.5	4.4	0.5	0	Gravelly sand	5.28
Station 4	0	21.4	19.4	11.6	7.7	7.4	10.4	19.1	3.1	Sandy gravel	3.15
Station 5	0	2.1	0.1	0.2	0.6	2.7	34.1	55.8	4.5	Slightly gravelly sand	1.45
Station 6	0	48.3	22	11	5.4	3.5	1.7	7.6	0.5	Sandy gravel	3.02
Station 7	0	0	0	0.1	0.5	4.2	68.5	26.4	0.2	Sand	1.31
Station 8	0	16.1	15.1	13.4	13.3	21.4	10.8	8.6	1.4	Sandy gravel	2.8
Station 9	0	0.1	0	0.1	0.6	2.2	53	43.6	0.4	Sand	1.33
Station 10	0	0	0.4	0.4	0.6	1	38.1	58.3	1.2	Sand	1.5

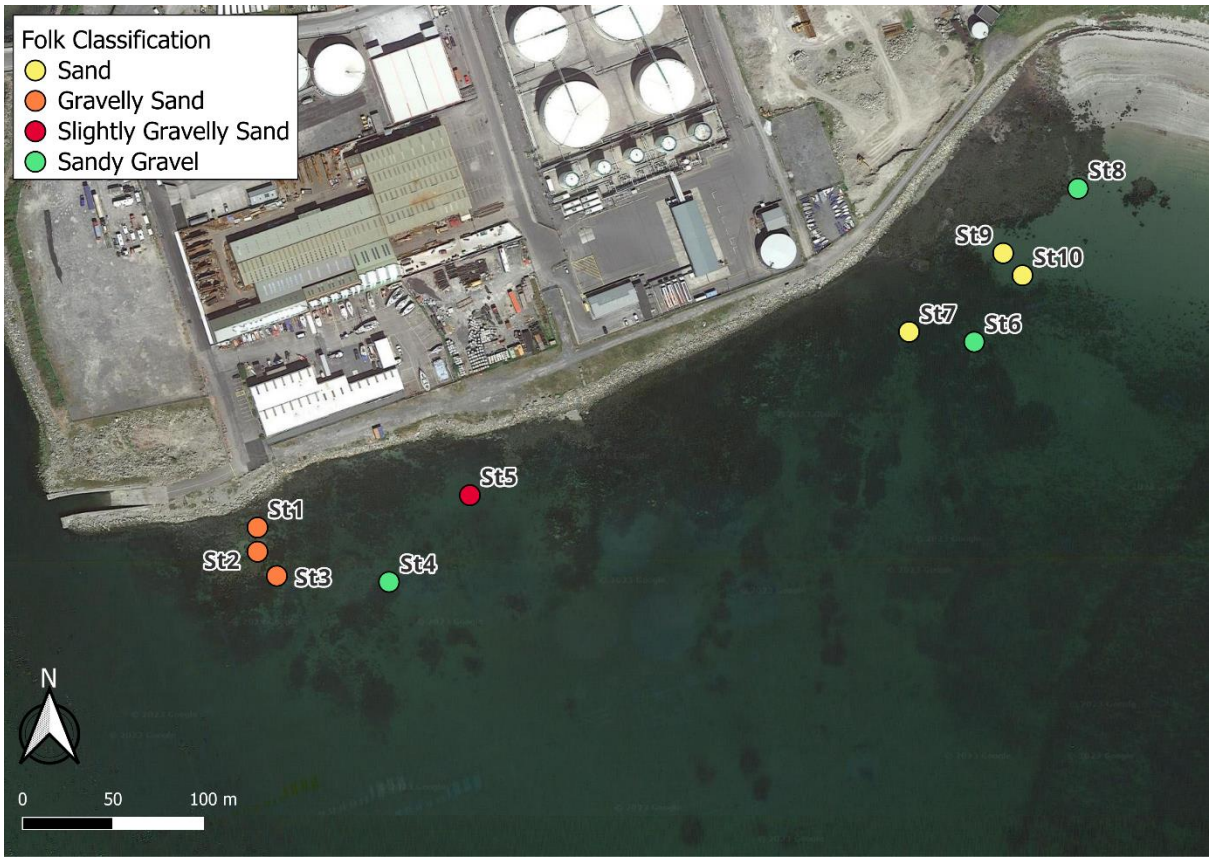

Figure 3.2: Folk Classification of the sediment at the Renmore intertidal stations.

3.2. Flora and fauna

3.2.1. Littoral Rock biotopes

Lichen species (*Hydropunctaria maura* (formerly *Verrucaria maura*), *Xanthoria parietina* and *Caloplaca marina*) were recorded on the rock armour above 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. *Ulva* spp. were recorded through the shore. *Arenicola marina* (Lugworm) were extensive in the lower shore (at St1, St2, St3, St8, St9, and St10) and were recorded at at density of 3/m^2. The intertidal reef community remains the same as the previous survey and can be seen in Figure 3.3 below.

The upper shore and bedrock can be classified as the JNCC biotope LR.MLR.BF.PelB – *Pelvetia canaliculata* and barnacles on moderately exposed littoral fringe rock (EUNIS code: A1.211) (Perry, 2016). The mid shore can be classified as the the JNCC biotope LR.LLR.F.Asc.FS – *Ascophyllum nodosum*

on full salinity mid eulittoral rock (EUNIS code: A1.3141) (Perry and Hill, 2020) in the reef/boulder areas. The lower shore can be classified as the JNCC biotope LR.MLR.BF.Fser.R – *Fucus serratus* and red seaweeds on moderately exposed lower littoral eulittoral rock (EUNIS code: A1.2141) (d'Avack and Tyler-Walters, 2015). The biotopes in the sand, shell and mud substrates are determined by their infaunal species as outlined in section 3.22 below.

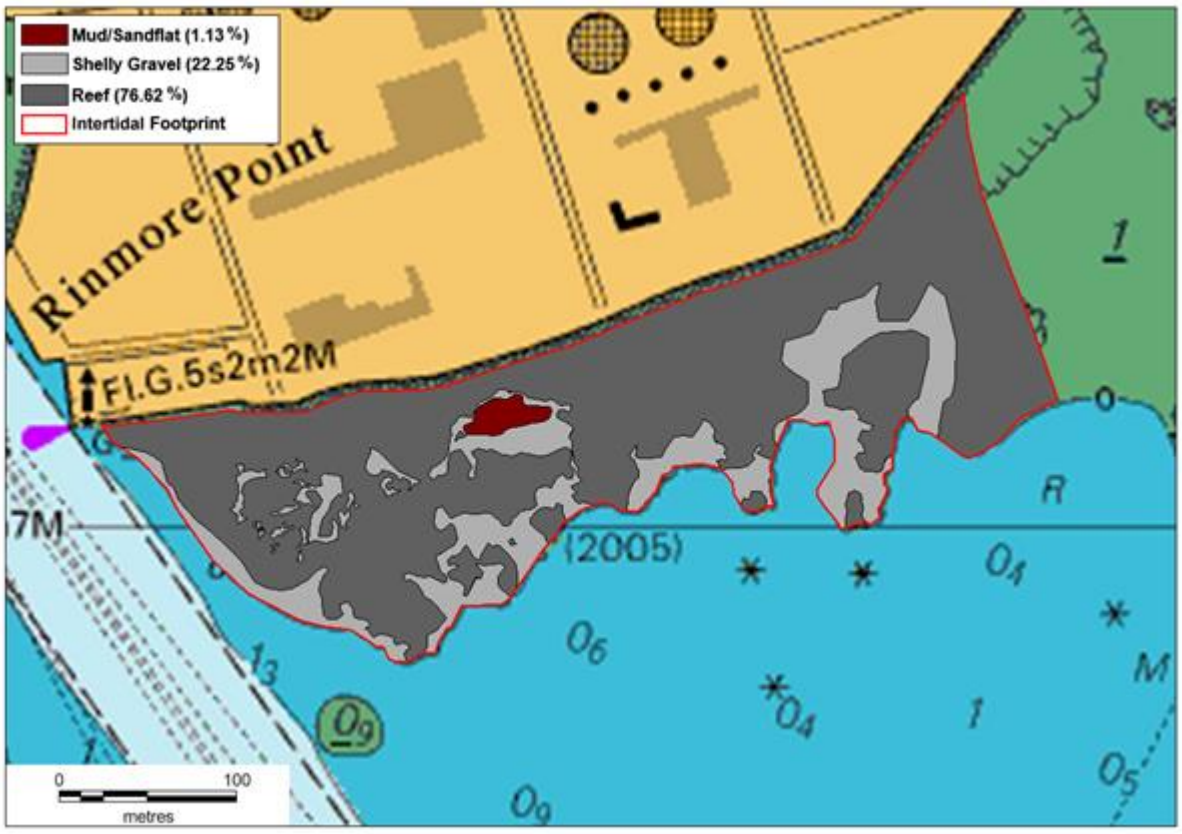

Figure 3.3: Intertidal substrate habitats at Renmore.

3.2.2. Intertidal Core Infaunal analysis

The taxonomic identification of the benthic fauna across all 10 grab stations sampled at the Renmore intertidal stations yielded a total count of 54 taxa ascribed to 6 phyla. The 55 taxa consisted of 2,110 individuals. Of the 54 taxa recorded, 29 were identified to species level. The remaining 25 could not be identified to species level as they were either juveniles, partial/damaged or indeterminate. Appendix 1 shows the faunal abundances from the sampled sites.

Of the 55 taxa present, 1 was a cnidarian (anemone), 1 was a nematode (roundworm), 1 was a nemertean (ribbon worm), 21 were annelids (segmented worms including sipunculans and polychaetes), 14 were arthropods (crabs, shrimps, prawns), and 16 were molluscs (mussels, cockles, snails *etc*.). The most

dominant species were the oligochaetes *Tubificoides benedii* (932 individuals) and *Tubificoides pseudogaster* (141 individuals), Nematoda (317 individuals) and the polychaete *Capitella* sp. complex (141 individuals) which together accounted for just almost 73% of the total faunal abundance.

3.2.2.1. Univariate Analysis Results

Univariate statistical analyses were carried out on the combined replicate station-by-station infaunal data. Colonial and epifaunal species were removed from the dataset for the analyses. The following parameters were calculated and can be seen in Table 3.2; Total number of taxa, total number of individuals, richness, evenness, Shannon-Wiener diversity, and Effective Number of Species (ENS). Total number of taxa ranged from 3 (St9) to 19 (St1). The total number of individuals ranged from 7 (St9) to 842 (St3). Richness ranged from 1.03 (St2) to 3.27 (St3). Evenness ranged from 0.35 (St2) to 0.87 (St9). Shannon-Wiener diversity ranged from 0.86 (St10) to 1.86 (St6). Effective number of species ranged from 2.36 (St10) to 6.44 (St6) indicating that station St6 is over 2.7 times more diverse than St10. Figure 3.3 shows these community indices (excluding Evenness) in graphical form.

Table 3.2: Univariatemeasures of community structure.

Station	No. Taxa	No. Individuals	Richness	Evenness	Shannon-Wiener Diversity	Effective Number of Species
	S	N	d	J'	H'(loge)	EXP(H')
St1	19	337	3.09	0.61	1.80	6.04
St2	15	397	2.34	0.35	0.95	2.59
St3	23	842	3.27	0.41	1.28	3.59
St4	7	18	2.08	0.84	1.64	5.17
St5	11	114	2.11	0.62	1.48	4.39
St6	14	157	2.57	0.71	1.86	6.44
St7	12	89	2.45	0.71	1.76	5.84
St8	7	36	1.67	0.73	1.41	4.11
St9	3	7	1.03	0.87	0.96	2.60
St10	8	107	1.50	0.41	0.86	2.36

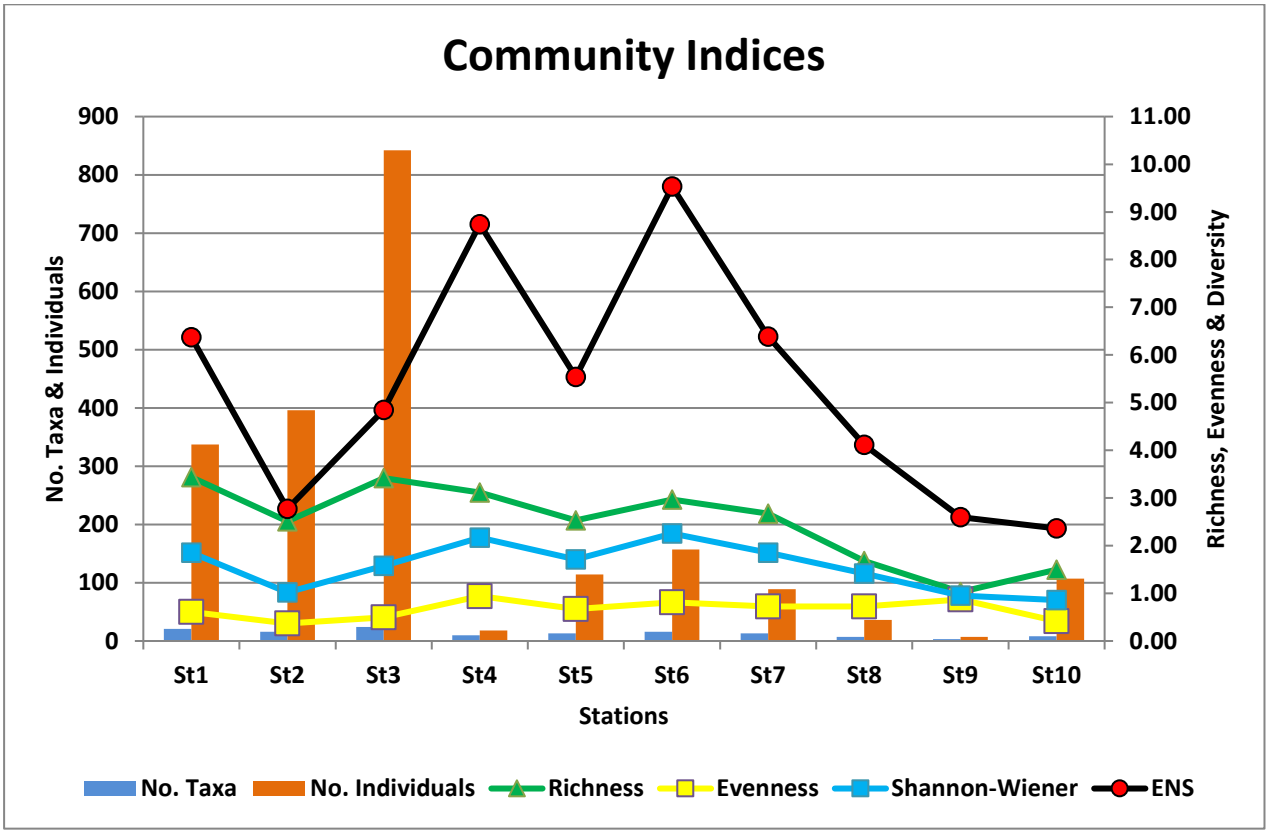

Figure 3.4: Community diversity indices. Diversity is expressed in Shannon-Wiener Diversity and Effective Number of Species (ENS).

3.2.2.2. Multivariate Analysis Results

The same infaunal dataset used above for the univariate analyses was also used for the multivariate analyses. The dendrogram and the MDS plot can be seen in Figures 3.4 and 3.5 respectively. SIMPROF analysis revealed 4 statistically significant groupings between the 10 stations (the samples connected by red lines cannot be significantly differentiated). The stress level on the MDS plot indicates a good representation, no real prospect of misinterpretation of overall structure, but very fine detail may be misleading in compact subgroups.

A clear divide (83.68% dissimilarity) can be seen between **Group a** and all other groups. Additionally, a clear divide (76.5% dissimilarity) can be seen between **Group b** and **Groups c** and **d,** and an 60.27% dissimilarity between **Group c** and **d**.

Group a contains St9. This group separated from all other groups at an 83.68% dissimilarity level. The group contained only 3 taxa comprising 7 individuals: Nematoda (4 individuals, 57.14% abundance) and

the polychaetes *Nephtys* sp. (2 individuals, 28.57% abundance) and *Etone longa* (1 individual, 14.29% abundance). *Nephtys* sp. are indifferent to enrichment and are typically present in low densities with non-significant variations over time. Nematoda and *Eteone longa* aretolerant of disturbance, occurring under normal conditions, but their populations are stimulated by organic enrichment. No JNCC biotope could be assigned to this station based on the low faunal returns.

Group b contained 3 stations (St4, St8 and St10) and separated from Groups c and d at a 76.5% dissimilarity level. This group had a within group similarity of 45.14%. Group b contained 16 taxa comprising 161 individuals. Of the 16 taxa, 8 were present twice or less. Two taxa accounted for over 77% of the faunal abundance: the polychaetes *Capitella* sp. complex (107 individuals, 66.46% abundance) and *Eteona longa* (17 individuals, 10.56% abundance. SIMPER analysis further revealed *Tubificopides benedii* and Nematoda as characterising taxa of this group. Nematoda and *Eteone longa* are tolerant of disturbance, occurring under normal conditions, but their populations are stimulated by organic enrichment. *Capitella* sp. complex and *Tubificoides benedii* are first order opportunistic taxa that proliferate in reduced sediments. The stations of this group can be classified as belonging to the JNCC biotope LS.Lsa.MuSa.HedMacEte – *Hediste diversicolor, Macoma balthica* and *Eteona longa* in littoral muddy sand (EUNIS code: A2.243) (Ashley, 2016).

Group c contains 3 stations (St1, St2 and St3). This group separated from group d at a 60.27% dissimilarity level. This group had a within group similarity of 50.03%. Group c contained 45 taxa comprising 1,575 individuals. Of the 45 taxa, 14 were present twice or less. Five taxa accounted for over 87% of the faunal abundance: the oligochaetes *Tubificoides benedii* (801 individuals, 50.86% abundance) and *Tubificoides pseudogaster* agg. (104 individuals, 6.6% abundance), Nematoda (267 individuals, 16.95% abundance), and the polychaetes *Pygospio elegans* (120 individuals, 7.62% abundance) and *Eteona longa* (86 individuals, 5.46% abundance). SIMPER analysis revealed the bivalve *Macoma balthica* as an additional characterising species of this group. Nematoda, *Pygospio elegans, Eteone longa,* and *Macoma balthica* are tolerant of disturbance, occurring under normal conditions, but their populations are stimulated by organic enrichment. *Tubificoides benedii* and *Tubificoides pseudogaster* agg. are first order opportunistic taxa that proliferate in reduced sediments. This group can also be classified as the JNCC biotope LS.Lsa.MuSa.HedMacEte – *Hediste diversicolor, Macoma balthica* and *Eteona longa* in littoral muddy sand (EUNIS code: A2.243).

Group d contained 3 stations (St5, St6 and St7). This group separated from group c at a 60.27% dissimilarity level. This group had a within group similarity of 51.42%. Group d contained 28 taxa

comprising 360 individuals. Of the 28 taxa, 14 were present twice or less. Five taxa accounted for over 76% of the faunal abundance: the oligochaetes *Tubificoides benedii* (126 individuals, 35% abundance) and *Tubificoides pseudogaster* agg. (35 individuals, 9.72% abundance), the polychaetes *Mediomastus fragilis* (47 individuals, 13.06% abundance) and *Eteona longa* (24 individuals, 6.67% abundance) and Nematoda (42 individuals, 11.67% abundance). SIMPER analysis revealed the bivalve *Macoma balthica* as an additional characterising species of this group. Nematoda, *Mediomastus fragilis, Eteone longa,* and *Macoma balthica* are tolerant of disturbance, occurring under normal conditions, but their populations are stimulated by organic enrichment. *Tubificoides benedii* and *Tubificoides pseudogaster* agg. are first order opportunistic taxa that proliferate in reduced sediments. This group can also be classified as the JNCC biotope LS.Lsa.MuSa.HedMacEte – *Hediste diversicolor, Macoma balthica* and *Eteona longa* in littoral muddy sand (EUNIS code: A2.243).

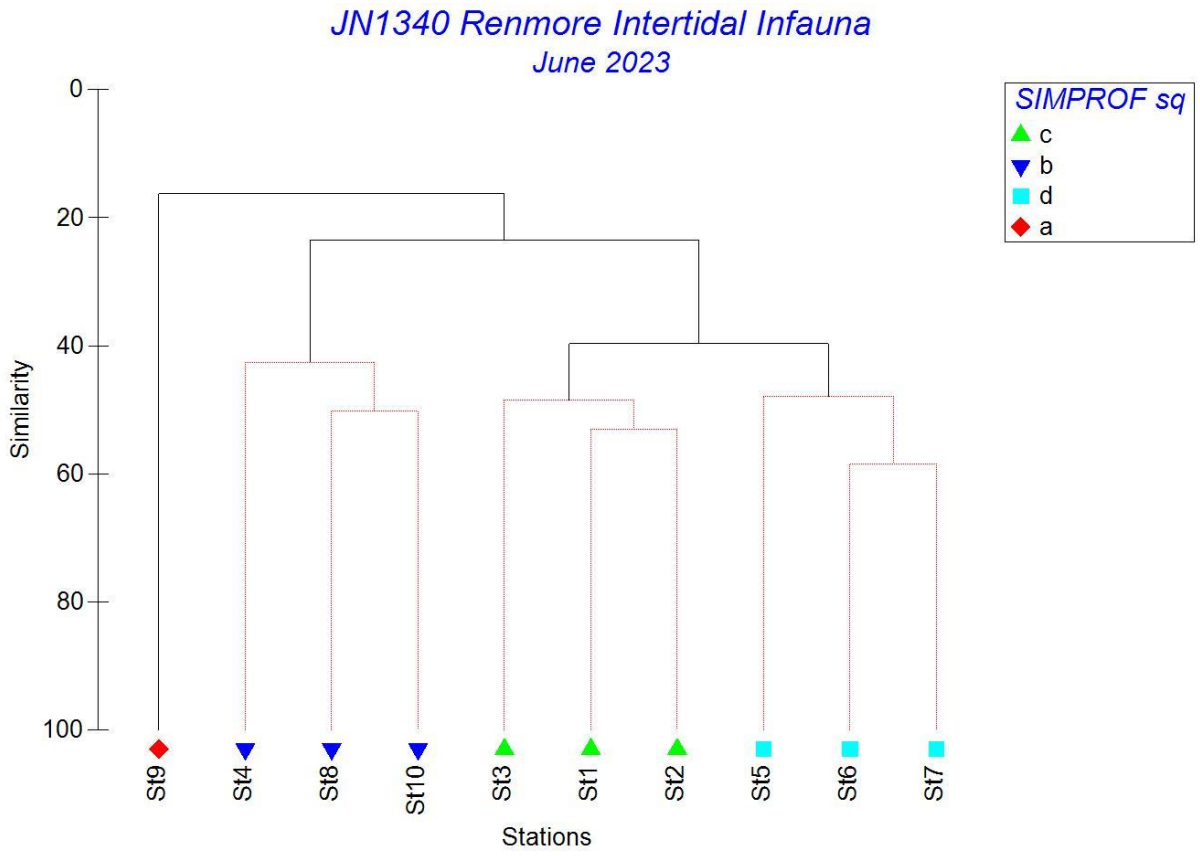

Figure 3.5: Dendrogram produced from Cluster analysis.

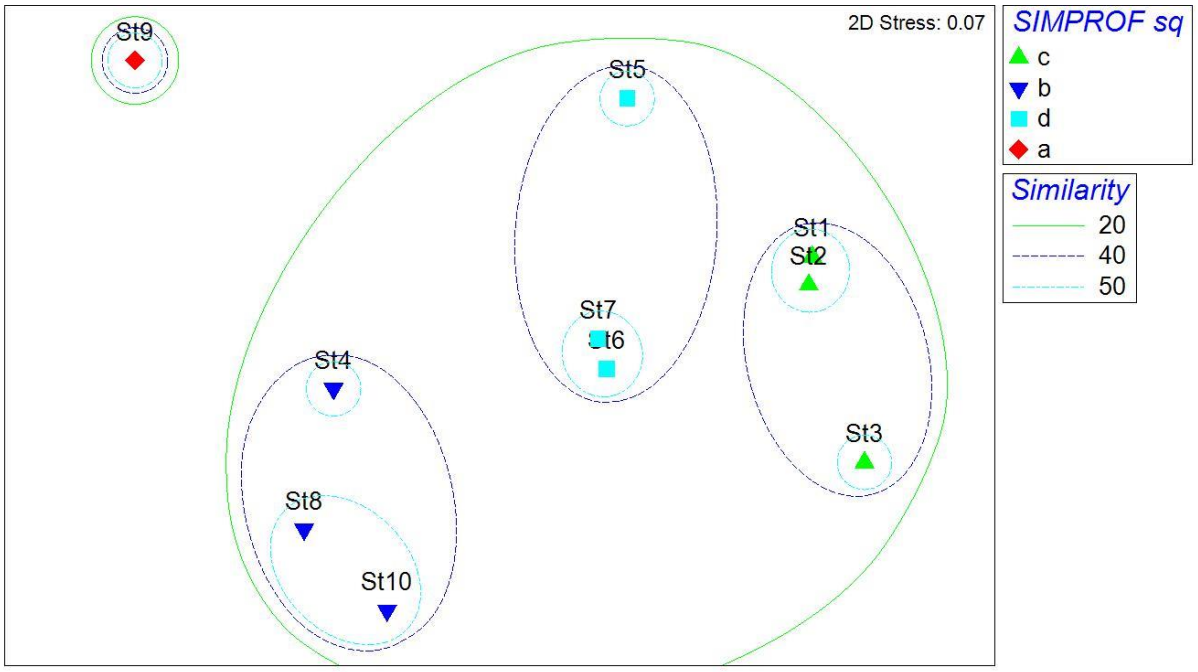

Figure 3.6: MDS plot.

The biotope LS.LSa.MuSa.HedMacEte - *Hediste diversicolor, Macoma balthica* and *Eteona longa* in littoral muddy sand (EUNIS code: A2.243) is described by Connor *et al.* (2004) as fine to very fine muddy sand on the mid shore at the lower extreme of estuaries, and in moderately exposed and sheltered bays and marine inlets, sometimes subject to variable salinity. The infauna is characterized by the polychaetes *Eteone longa*, *Hediste diversicolor* (ragworm) and *Pygospio elegans*, oligochaetes (mostly *Tubificoides benedii* and *Tubificoides pseudogaster*), the crustaceans *Corophium volutator* and *Crangon crangon*, the spire shell *Peringia ulvae* and the baltic tellin *Macoma balthica*. The cockle *Cerastoderma edule* may be abundant, and the sand gaper *Mya arenaria* may be superabundant, though these species are not always present, or may be missed in core samples due to their large size. The polychaetes *Arenicola marina, Polydora cornuta* and *Capitella*, and the mussel *Mytilus edulis* are sometimes present. The three main groups accounting for 9 of the 10 stations can be classified as belonging to this group, though with less mud content, with separations into the 3 groups as a result in variations in abundances of the fauna.

The occurrence of the first order opportunistic taxa *Tubificoides benedii* and *Tubificoides pseudogaster* agg. and *Capitella* in high numbers across all of the 3 main groups points to the influence of organic enrichment along the Renmore intertidal stations as a result of its close proximity to the mouth of the Corrib River.

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.

The littoral rock biotopes remain the same as they were in the 2016 survey and include LR.MLR.BF.PelB – *Pelvetia canaliculata* and barnacles on moderately exposed littoral fringe rock in the upper shore and rock armour, LR.LLR.F.Asc.FS – *Ascophyllum nodosum* on full salinity mid eulittoral rock in the midshore reef/boulder areas and LR.MLR.BF.Fser.R – *Fucus serratus* and red seaweeds on moderately exposed lower littoral eulittoral rock in the lower shore.

The littoral sand biotope can be classified as LS.LSa.MuSa.HedMacEte - *Hediste diversicolor, Macoma balthica* and *Eteona longa* in littoral muddy sand though there was less mud than typically associated with this biotope. The species found in the present survey are typical of this biotope and were also recorded in the 2016 survey. In the present survey, as in 2016 the opportunistic species (*Capitella, Tubificoides* spp.) were most abundant in those stations closest to the mouth of the Corrib.

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Appendix 1

Renmore Intertidal Species List

	AphiaID	1_1	1_2	2_1	2_2	3_1	3_2	4_1	4_2	5_1	5_2	6_1	6_2	7_1	7_2	8_1	8_2	9_1	9_2	10_1	10_2
Actiniaria	1360												1								
Nemertea unidentifiable	152391				2				1	1											
Nematoda	799		51	26	1	118	71		1	3	19	12	4		4	2		1	3		1
Eteone longa	130616	18	30	20	14	1	3	2	1		1	3	11	4	5	3	5	1		5	1
Phyllodoce mucosa	334512					1						2									
Hediste diversicolor	152302	1		2	2		4														
Nephtys	129370									1								1			
Nephtys hombergii	130359							1	1		1										
Scoloplos armiger	130537									3											
Spionidae	913		1	3		2	27					1	3		1	1				frag	
Malacoceros	129614					3	5					2									
Pygospio elegans	131170	3	117									2	11	5							
Cirratulidae	919										7										
Capitella	129211		1			10	17	1	3			4	2			7	11			35	50
Mediomastus fragilis	129892						1			11	5	4	8	9	10						
Arenicola marina	129868																1				
Euclymene	129347										1										
Terebellidae	982													1							
Manayunkia aestuarina	130926											2									
Serpulidae	988				1																
Baltidrilus costatus	743898								2			3									
Tubificoides	137393	1		2				1			1										
Tubificoides benedii	137571	28	43	159	142	248	181	2		16	35	10	28	21	16	1				2	
Tubificoides diazi	137574										7										

	AphiaID	1_1	1_2	2_1	2_2	3_1	3_2	4_1	4_2	5_1	5_2	6_1	6_2	7_1	7_2	8_1	8_2	9_1	9_2	10_1	10_2
Tubificoides pseudogaster	137582		3		4	71	26	2				23	10	2							
Austrominius modestus	712167						3														
Balanus crenatus	106215						2														
Perioculodes longimanus	102915														1						
Gammarus	101537						2														
Melitidae	101397						1														
Abludomelita obtusata	102788					1															
Melita palmata	102843			1			18														
Lekanesphaera hookeri	118953		1				1														
Jaera female	118364		1				4														
Crangon allmanni	107551															2	3				
Brachyura juvenile	106673	5			1	1															
Liocarcinus	106925						3														
Carcinus maenas juvenile	107381			4																	
Chironomidae larva	118100																			1	
Lepidochitona cinerea	152774		1				2														
Bittium reticulatum	139054							1													
Peringia ulvae	151628	11	1										2								
Hyala vitrea	140129	1																			
Tritia	246140	1																			
Mytilidae juvenile	211																			7	
Kurtiella bidentata	345281			2						1			1								
Cardiidae juvenile	229				1									1							
Parvicardium pinnulatum	181343													1	1						

	AphiaID	1_1	1_2	2_1	2_2	3_1	3_2	4_1	4_2	5_1	5_2	6_1	6_2	7_1	7_2	8_1	8_2	9_1	9_2	10_1	10_2
Cerastoderma edule	138998	1				1	2														
Tellinidae juvenile	235			1																	
Macomangulus tenuis	878470						1	1					1							2	
Macoma balthica	880017	8	4		3	3	3				2	5	3	1	2					3	
Veneridae juvenile	243		2	4	2	2	3														
Ruditapes juvenile	231748	2																			
Ruditapes decussatus	231749		1			2	3							2	2						