Galway Harbour Extension
Subtidal Benthic Ecology Report

Produced by

AQUAFACT International Services Ltd
(APEM Group)

On behalf of

Galway Harbour Company

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1. Introduction

AQUAFACT was commissioned by Galway Harbour Company to carry out a benthic marine ecology survey of the seabed within Galway Bay in the vicinity of the proposed Galway Harbour Extension which will involve the infilling of *ca* 27ha including breakwaters and dredging of *ca* 46.5 ha of intertidal and subtidal habitat. The locations surveyed in the present study were previously surveyed in 2010 and this survey was to assess the current benthic habitats in comparison to the previous results.

2. Methodology

2.1. Benthic sampling

On the 4th May 2023, AQUAFACT surveyors carried out the benthic ecology and sediment physicochemical surveys in Galway Bay on board the AQUFACT RIB AQUAFACT1. Sampling was carried out using a 0.25m^2 Van Veen grab to collect faunal and sediment samples at the 6 locations shown in Figure 2.1 below. Table 2.1 shows the station coordinates.

Table 2.1: Station coordinates

Station	Latitude	Longitude
St 2	53.25	9.040277778
St 4	53.25629444	9.039097222
St 5	53.25615556	9.043027778
St 7	53.25935	9.037125
St 9	53.26395556	9.037736111
St 12	53.26611111	9.036222222

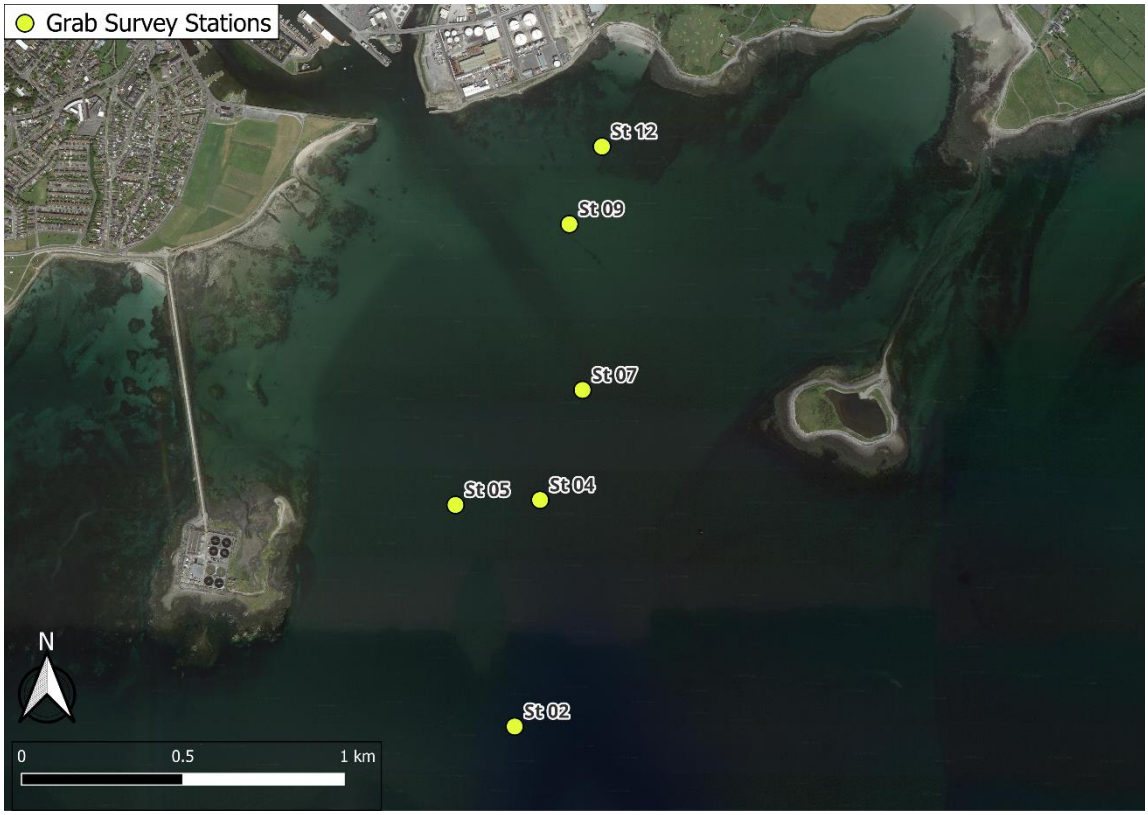

Figure 2.1: Location of the Galway Bay benthic survey stations.

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 *et al.,* 2010).

Three replicate samples were collected at each station, two grabs for benthic faunal analysis and a third grab sample was collected for sediment analysis including particle size analysis and organic carbon. Upon retrieval of the grab, penetration depth was measured and recorded in the sample data sheet. Only grab samples that contained a depth of >7cm for sand and >10cm for mud were retained. Re-sampling occurred until a sufficient depth of sediment was collected in the grab (the vessel repositioned between grab samples). Where cobbles or gravel was encountered, penetration depths were much shallower. All additional relevant data (sediment type, texture, grain size, colour, odour, layering, volume, presence of fauna, algae, surface features) were recorded in the sample data sheets. The grab sampler was cleaned between stations to prevent cross contamination.

The faunal grab samples were carefully and gently sieved on a 1mm mesh sieve as a sediment water suspension for the retention of fauna. Great care was taken during the sieving process to minimise damage to taxa such

as spionids, scale worms, phyllodocids and amphipods. The sample residue was carefully flushed into a pre-labelled (internally and externally) container from below. Each label contained the sample code and date. The samples were fixed immediately in with 6% w/v buffered formaldehyde solution. These samples were ultimately preserved in 70% alcohol upon return to the laboratory.

A sediment sample was retrieved from the grab and split into two, one sample for granulometric analysis and one sample for organic carbon. Sediment samples were placed in plastic sampling containers (granulometry and metals) and amber glass jars (hydrocarbons) and labelled internally and externally. These samples were frozen (<-18ºC) as soon as possible after acquisition. All faunal samples and sediment granulometry were analysed by AQUAFACT, while the organic carbon samples were analysed by the ALS labs Loughrea..

At one of the stations (St 12) the substrate consisted of cobbles and no sediment sample was suitable for analysis.

2.2. Sample processing

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 2.2: 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

2.3. Faunal Data Analysis

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

2.3.1. 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.

2.3.2. 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. Benthic Survey

The taxonomic identification of the benthic fauna across all 6 grab stations sampled at the Galway Bay sites yielded a total count of 110 taxa ascribed to 9 phyla. The 110 taxa consisted of 809 individuals. Of the 110 taxa recorded, 73 were identified to species level. The remaining 37 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 110 taxa present, 1 was a poriferan (sponge), 2 were cnidarians (anemone), 1 was a nematode (roundworm), 2 were nemerteans (ribbon worm), 54 were annelids (segmented worms including sipunculans and polychaetes), 21 were arthropods (crabs, shrimps, prawns), 24 were molluscs (mussels, cockles, snails *etc*.), 4 were echinoderms (brittlestars, urchins, *etc.*), and 1 were chordates (tunicates). The most dominant species were the gastropod *Turritellinella tricarinata* (formerly *Turritella communis*) (122 individuals), the polychaetes *Pholoe inornata* (sensu Petersen) (37 individuals), *Euclymene oerstedii* (30 individuals) and *Nephtys* spp. (22 individuals) and the bivalve *Thyasira flexuosa* (29 individuals) which together accounted for just over 46% of the total faunal abundance.

3.1.1. 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 3.1; 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 9 (St5) to 66 (St7). The total number of individuals ranged from 17 (St12) to 450 (St7). Richness ranged from 3.53 (S12) to 10.64 (St7). Evenness ranged from 0.41 (St5) to 0.93 (St9 & St12). Shannon-Wiener diversity ranged from 0.91 (St5) to 2.97 (St2). Effective number of species ranged from 2.48 (St5) to 19.45 (St2) indicating that station St2 is over 7.8 times more diverse than St5. Figure 3.1 shows these community indices (excluding Evenness) in graphical form.

Table 3.1: Univariate measures 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')
St 2	38	140	7.49	0.82	2.97	19.45
St 4	19	122	3.75	0.56	1.65	5.23
St 5	9	54	2.01	0.41	0.91	2.48
St 7	66	450	10.64	0.67	2.80	16.39
St 9	16	22	4.85	0.93	2.58	13.14
St 12	11	17	3.53	0.93	2.23	9.31

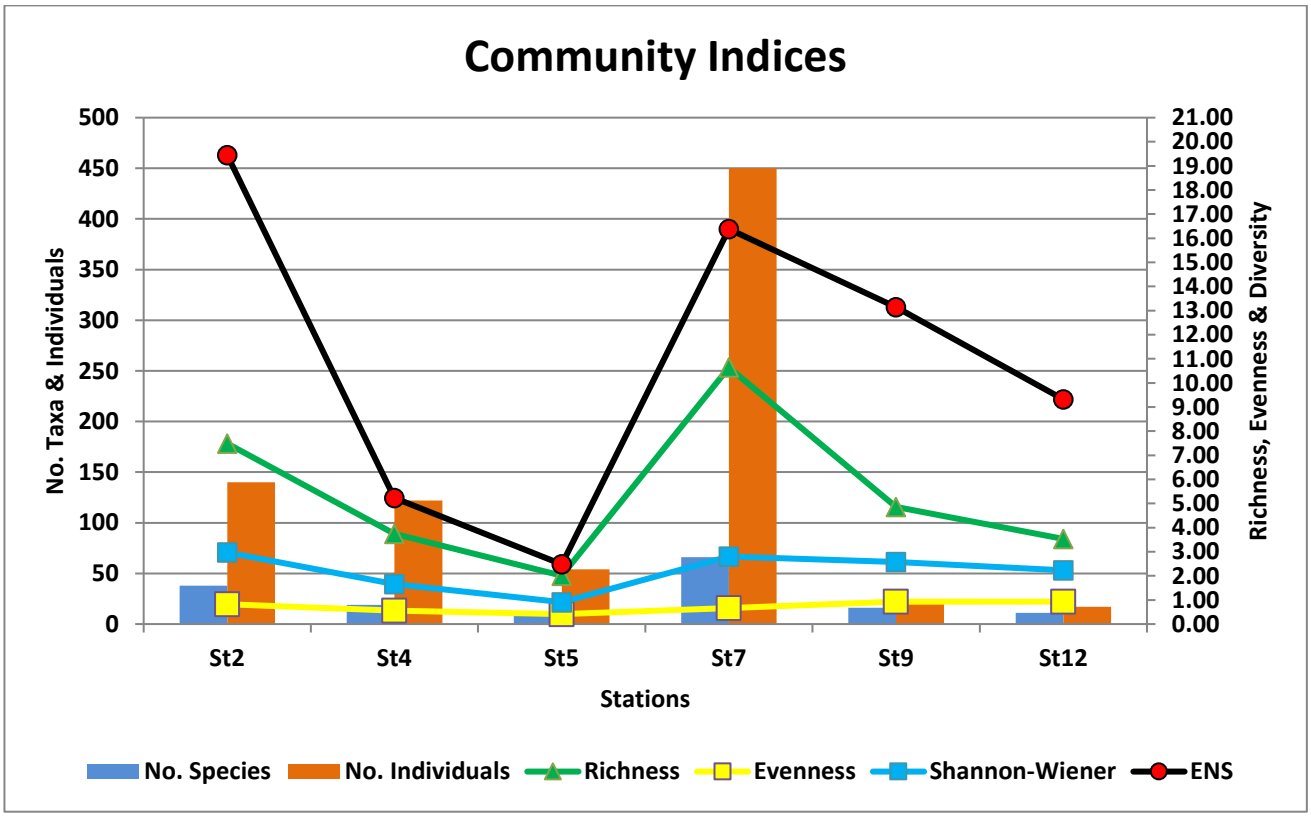

Figure 3.1: Community diversity indices. Diversity is expressed in Shannon-Wiener Diversity and Effective Number of Species (ENS).

3.1.2. 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 3.2 and 3.3 respectively. SIMPROF analysis revealed 4 statistically significant groupings between the 6 stations (the samples connected by red lines cannot be significantly differentiated). The stress level on the MDS plot indicates an excellent representation of the data with no prospect of misinterpretation.

A clear divide (97.58% dissimilarity) can be seen between **Group a** and all other groups. Additionally, a clear divide (83.75% dissimilarity) can be seen between **Group b** and **Groups c** and **d,** and an 80.81% dissimilarity between **Group c** and **d**.

Group a contains St12. This group separated from all other groups at a 97.58% dissimilarity level. The group contained 10 taxa comprising 16 individuals. Of the 10 taxa, 8 were present twice or less. Three taxa accounted for over 56% of the faunal abundance: the polychaetes *Sabellaria alveolata* (4 individuals, 25% abundance) and *Pygospio elegans* (2 individuals, 12.5% abundance) and the chiton *Lepidochitona cinerea* (3 individuals, 18.75% abundance). SIMPER analysis could not be carried out as the group only contained 1 station. *Sabellaria alveolata* is very sensitive to organic enrichment and is present in unpolluted conditions. *Lepidochitona cinerea* is indifferent to enrichment and are typically present in low densities with non-significant variations over time. *Pygospio elegans* is tolerant of disturbance, occurring under normal conditions, but their populations are stimulated by organic enrichment. No JNCC biotope could be assigned to this station and faunal returns we low, but the presence of *Sabellaria alveolata* is notable.

Group b contained 2 stations (St2 and St7) and separated from Groups c and d at a 83.75% dissimilarity level. This group had a within group similarity of 36.45%. Group b contained 75 taxa comprising 307 individuals. Of the 75 taxa, 44 were present twice or less. Five taxa accounted for over 40% of the faunal abundance: the polychaetes *Pholoe inornata* (*sensu* Petersen) (37 individuals, 12.05% abundance), *Euclymene oerstedii* (30 individuals, 9.77% abundance) and *Nephtys* sp. (15 individuals, 4.89% abundance), and the bivalves *Thyasira flexuosa* (27 individuals, 8.79% abundance) and *Thyasira* sp. (16 individuals, 5.21% abundance). SIMPER analysis could not be carried out as the group only contained 2 stations. *Pholoe inornata* and *Nephtys* sp. are indifferent to enrichment is tolerant of disturbance, occurring under normal conditions, but their populations are stimulated by organic enrichment. The stations of this group can be classified as belonging to the JNCC biotope SS.SMu.ISaMu.MelMagThy –

Melinna palmata with *Magelona* spp. and *Thyasira* spp. in infralittoral sandy mud (EUNIS Code A5.334) (De-Bastos, 2016).

Group c contains St9. This group separated from group d at an 80.81% dissimilarity level. The group contained 16 taxa comprising 22 individuals. Of the 16 taxa, 14 were present twice or less. Two taxa accounted for over 36% of the faunal abundance: the bivalve *Chamelea striatula* (5 individuals, 22.73% abundance) and the polychaete *Scoloplos armiger* (3 individuals, 13.64% abundance). SIMPER analysis could not be carried out as the group only contained 1 station. *Chamelea striatula* is very sensitive to organic enrichment and is present in unpolluted conditions. *Scoloplos armiger* is tolerant of disturbance, occurring under normal conditions, but their populations are stimulated by organic enrichment. This station exhibits elements of the JNCC biotope SS.SSa.IMuSa.FfabMag – *Fabulina fabula* and *Magelona mirabilis* with venerid bivalves and amphipods in infralittoral compacted fine muddy sand EUNIS code A5.242) (Tillen & Rayment, 2016).

Group d contained 2 stations (St4 and St5) and separated from group d at an 80.81% dissimilarity level. This group had a within group similarity of 37.96%. This group contained 23 taxa comprising 176 individuals. Of the 23 taxa, 15 were present twice or less. Three taxa accounted for over 78% of the faunal abundance: the gastropods *Turritellinella tricarinata* (117 individuals, 66.48% abundance) and *Hyala vitrea* (15 individuals, 8.52% abundance) and the polychaete *Nephtys* sp. (6 individudals, 3.41% abundance). SIMPER analysis could not be carried out as the group only contained 2 stations. *Hyala vitrea* is very sensitive to organic enrichment and are present in unpolluted conditions. *Turritellinella tricarinata* and *Nephtys* sp. are indifferent to enrichment and are typically present in low densities with non-significant variations over time. The stations in this group exhibit elements of the JNCC biotope SS.SMx.CMx.KurThyMx – *Kurtiella bidentata* and *Thyasira* spp. in circalittoral muddy mixed sediment (EUNIS code: A5.443) (De-Bastos & Marshall, 2016) as well as some elements of SS.SMu.ISaMu.MelMagThy – *Melinna palmata* with *Magelona* spp. and *Thyasira* spp. in infralittoral sandy mud (EUNIS Code A5.334).

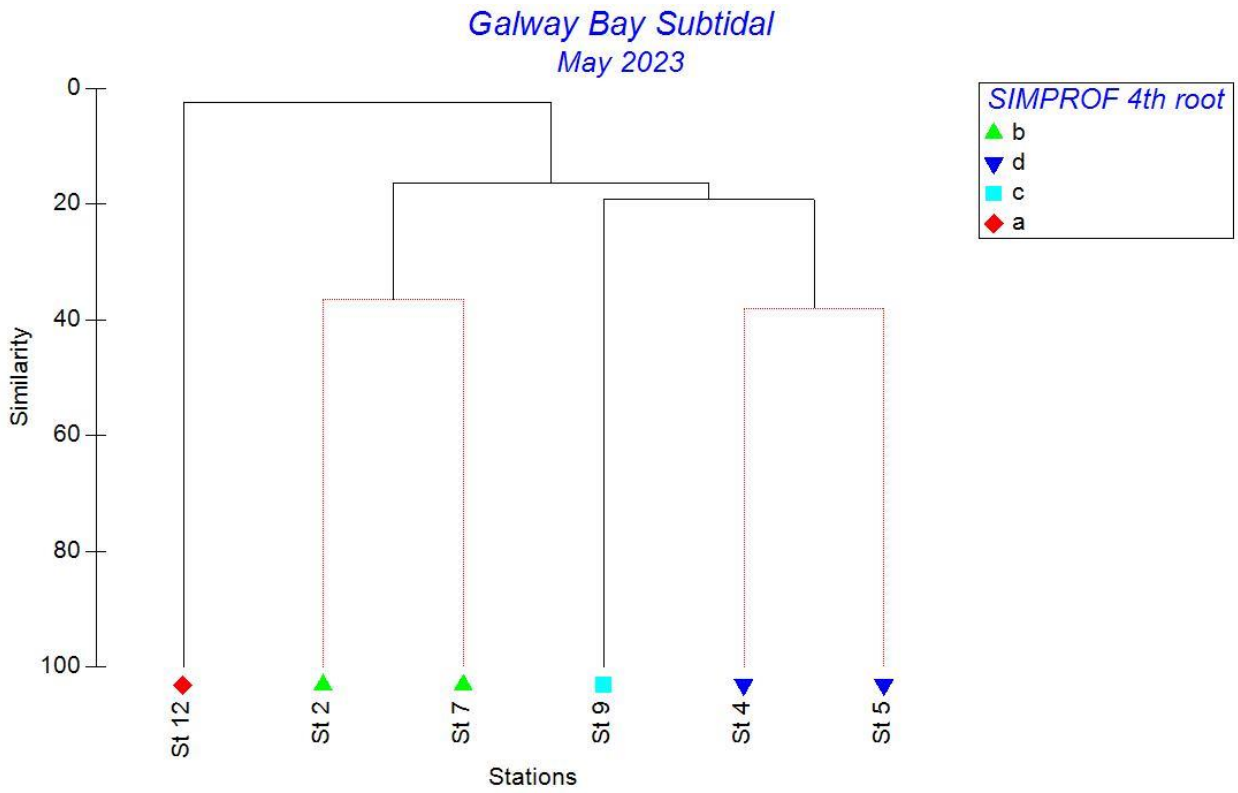

Figure 3.2: Dendrogram produced from Cluster analysis.

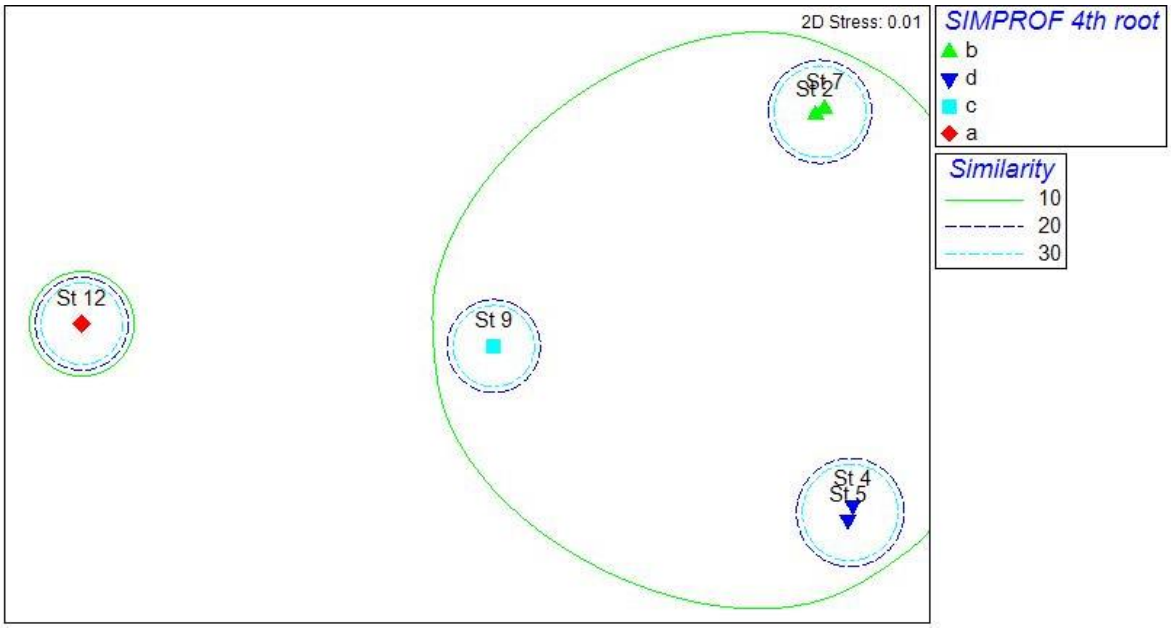

Figure 3.3: MDS plot.

3.2. Sediment results

Table 3.2 below presents the quantitative granulometric and organic carbon results of the sediment at the stations sampled in Galway Bay. No sample was available for analysis for station 12 as the substrate was of cobbles. Highest levels of medium gravel, fine gravel, very coarse sand, and coarse sand were observed at St 5 (1.3%, 8.5%, 18.5%, and 15% respectively). Highest levels of medium sand and fine sand were observed at St 9 (12.2% and 78.4% respectively). Highest levels of very fine sand were found at St 2 (64.5%) and highest levels of silt/clay were observed at St 4 (31.4%). Figure 3.4 shows the breakdown of sediment composition at each station. Figure 3.5 illustrates the sediment type according to Folk (1954). Two of the five stations sampled were classified as gravelly muddy sand (S t4 and St 5) according to Folk (1954), 2 were classified as slightly gravelly sand (St 7 and St 9) and one station (St 2) was classified as sand.

Organic matter values ranged from 1.41% (St 9) to 10.45% (St 5). As expected, the stations with a higher proportion of silt clay have the higher organic carbon content.

Table 3.2: Summary of the sediment granulometry results.

Station	Medium Gravel (4-8)	Fine Gravel (2-4)	Very Coarse Sand (%)	Coarse Sand (%)	Medium Sand (%)	Fine Sand (%)	Very Fine Sand (%)	Silt-Clay (%)	Folk Classification	TOC (%)
St 2	0	0.7	0.7	2.7	3.4	23.1	64.5	4.9	Sand	4.77
St 4	1.2	4.4	8.9	8.5	8.9	10.6	26.1	31.4	Gravelly muddy sand	7.32
St 5	1.3	8.5	18.5	15	11.1	5.5	13.4	26.6	Gravelly muddy sand	10.45
St 7	0.8	0.8	1.2	1.2	4.5	61.4	26.8	3.4	Slightly gravelly sand	2.33
St 9	0.6	1.2	1	1.4	12.2	78.4	5.1	0.2	Slightly gravelly sand	1.41

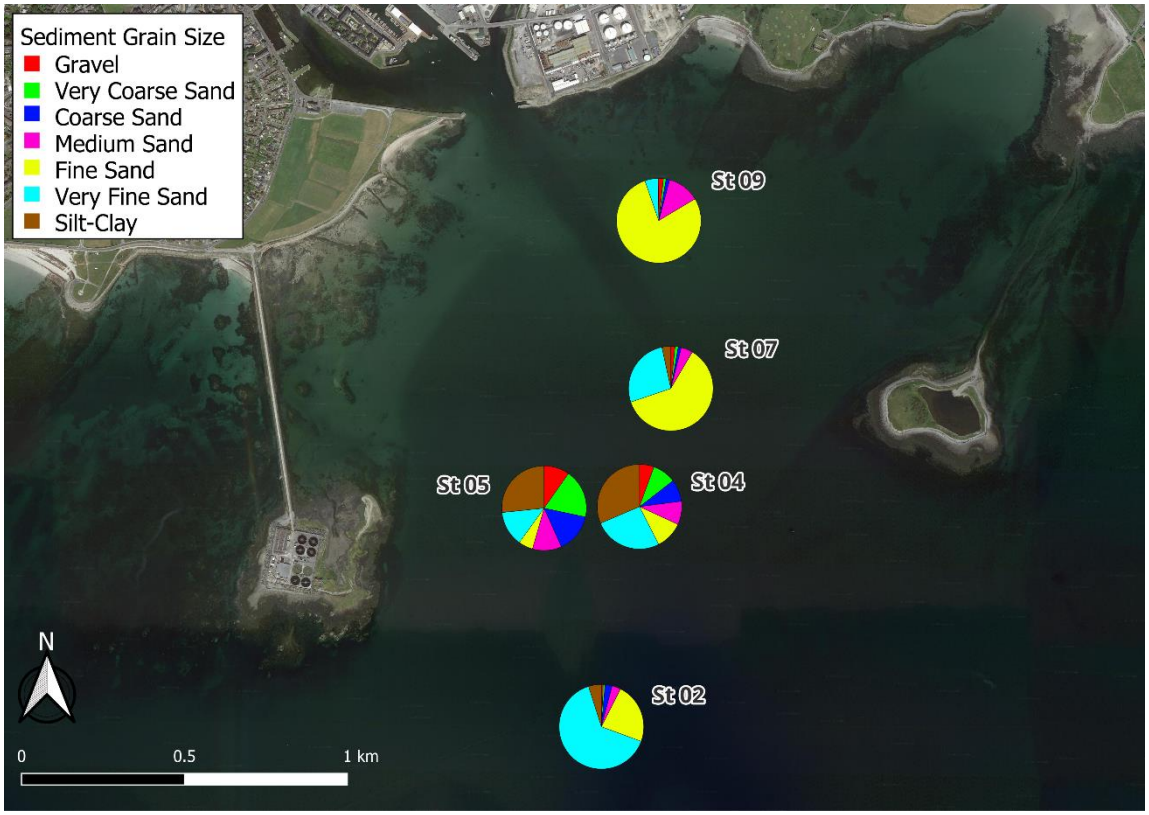

Figure 3.4: Sediment composition at Galway Bay stations.

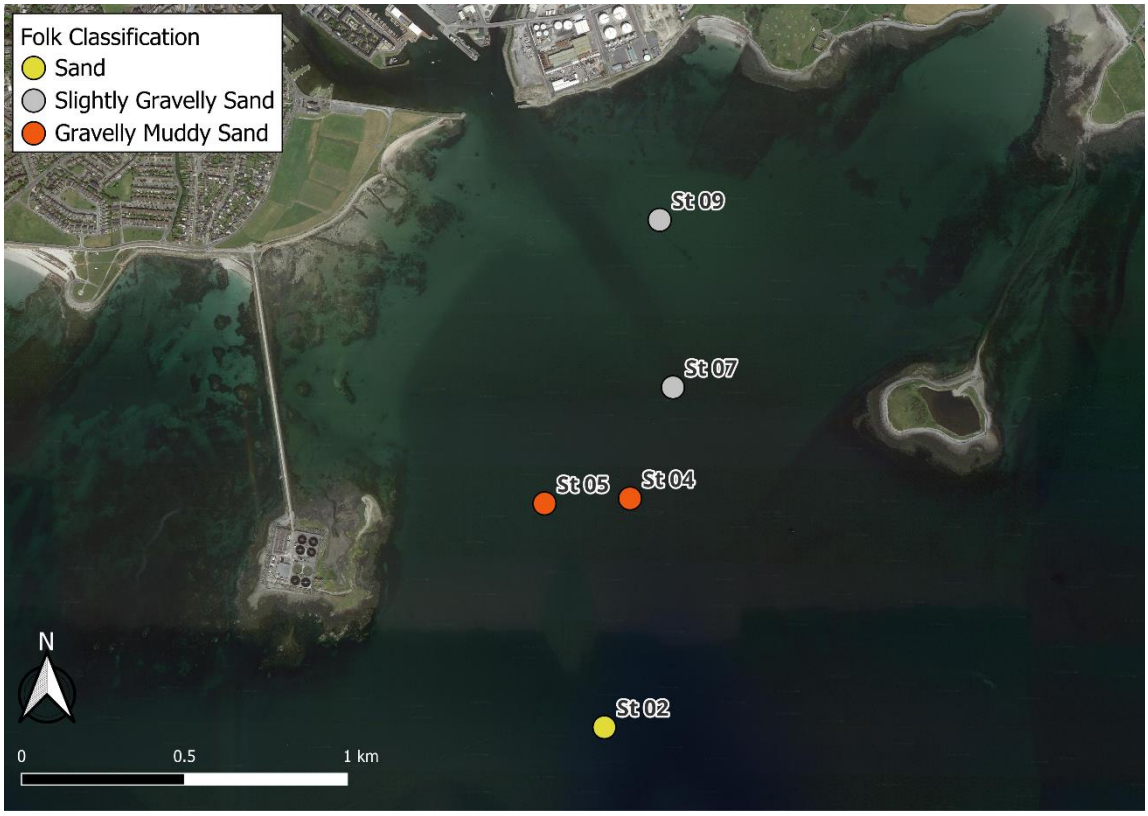

Figure 3.5: Folk classification of sediment samples.

4. Discussion

In the 2010 subtidal survey the dominating macrofaunal subtidal species were the bivalve *Kurtiella bidentata,* the tube-dwelling polychaete *Melinna palmata,* the amphipod *Ampelisca brevicornis* and the bivalve mollusc *Thracia phaseolina*. Other dominants included the polychaete *Phyllochaetopterus anglicus*, the amphipod *Crassicorophium crassicorne*, the polychaetes *Nephtys* spp. and *Euclymene oerstedii*, the bivalves *Fabulina fabula, Venus casina* and *Thyasira flexuosa*, the gastropod *Turritellinella tricarinata* and the ophiuroid *Amphiura filiformis*. These species are quite common for this area and are typical of species that inhabit muddy sand areas. Their characteristics identify them with previously recorded communities in the area: the *Melinna palmata* association reported by Keegan *et al.* (1976), Groups A and C recorded by Shin *et al*. (1982) and is an equivalent to the *Tellina fabula* sub-community described by Spärck (1935).

The groupings identified by the 2010 CLUSTER analysis represented slight variations of the above community between stations, but overall, the faunal assemblage of the area was homogenous. *Kurtiella bidentata* is a common species in this area and *Melinna palmata* is tolerant to organic enrichment. These species are typical of the study area, which is a shallow, moderately exposed site and the species inhabiting it are adapted to on-going natural stresses and disturbances (*i.e.,* fluctuations in salinity, strong waves, tides and storms, periodic high turbidity). No unusual species were observed during the 2010 study.

In the present study, the dominant species included a number of taxa that were dominant in the 2010 survey: the gastropod *Turritellinella tricarinata*, the polychaetes *Pholoe inornata* (*sensu* Petersen), *Euclymene oerstedii,* and *Nephtys* spp. and the bivalve *Thyasira flexuosa*.
The CLUSTER analysis of the fauna recorded revealed 4 significant groupings. Three of the groups exhibited many of the elements of JNCC biotopes:

- SS.SMu.ISaMu.MelMagThy – *Melinna palmata* with *Magelona* spp. and *Thyasira* spp. in infralittoral sandy mud (Groups b and d),
- SS.SSa.IMuSa.FfabMag – *Fabulina fabula* and *Magelona mirabilis* with venerid bivalves and amphipods in infralittoral compacted fine muddy sand (Group c), and
- SS.SMx.CMx.KurThyMx – *Kurtiella bidentata* and *Thyasira* spp. in circalittoral muddy mixed sediment.

Group a (St 12) could not be assigned to a biotope and had sparse faunal returns. The presence of *Sabellaria alveolata* is notable and reefs of this tube building polychaete worm are known along the nearby coastline, particularly intertidally at Silver Strand, Galway Bay.

In 2010, the majority of the stations were dominated by silt clay (8 of the 12 stations including 3 stations resurveyed in 2023: St 2, St 4, and St 5). The remaining stations were dominated by very fine sand (4 stations including St 7, St 9, and St 12, resurveyed in 2023).

In 2023, the granulometry results showed some changes. Two stations were dominated by silt clay (St 4 and St 5) as they were in 2010; St2 was dominated by very fine sand (previously dominated by silt clay); 2 stations (St 7 and St 9) were dominated by fine sand where they were previously dominated by very fine sand; one station (St 12) was composed of large cobbles in 2023 and a sediment sample couldn't be collected, whereas in 2010 this station was dominated by very fine sand.

While the groupings within the present study vary when compared to the 2010 survey, the biotopes recorded are typical of the study area and to be expected in the shallow, moderately exposed site.

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Appendix 1

Galway Bay Survey Species List

May 2023

Station	2A	2B	4A	4B	5A	5B	7A	7B	9A	9B	12A	12B
Cliona								1				
Clytia hemisphaerica							1					
Actiniaria	1	1					1					
Nemertea	1							1				
Tubulanus polymorphus						1				1		
Nematoda		1										
Golfingiidae juvenile								1				
Golfingia elongata	1											
Phascolion strombus								3				
Thalassema thalassema								2				
Harmothoe							1					
Pholoe juvenile							1	1				
Pholoe baltica (sensu Petersen)	1						3					
Pholoe inornata (sensu Petersen)		1					4	32				
Sigalion mathildae									1			
Phyllodocidae								2				
Eteone longa								1				
Eumida sanguinea		1										
Glycera tridactyla										1		
Hesionidae			1									
Podarkeopsis capensis				1								
Syllidae juvenile							1					
Syllis armillaris								1				

Station	2A	2B	4A	4B	5A	5B	7A	7B	9A	9B	12A	12B
Parexogone hebes		2					2					
Platynereis dumerilii								3				
Nephtys	1	2	3	1	1	1	6	6		1		
Nephtys hombergii	3			1			2	3				
Lumbrineris cingulata		3										
Scoloplos armiger									3			
Paraonidae		1										
Aricidea cerrutii	2						1					
Paradoneis lyra							1					
Poecilochaetus serpens	1											
Spionidae									frag			
Polydora cornuta											1	
Prionospio			1	3			4					
Prionospio fallax												1
Pygospio elegans											2	
Magelona		2							1			
Magelona alleni	1						1					
Magelona filiformis	1	2					1		1			
Spiochaetopterus		1				3			1			
Cirratulidae							1					1
Cirratulus cirratus							1					
Tharyx	2	5					1					
Capitella				1	1							
Notomastus		1										
Maldanidae									frag			
Euclymene oerstedii	21	6					1	2				

Station	2A	2B	4A	4B	5A	5B	7A	7B	9A	9B	12A	12B
Pectinariidae		1										
Sabellaria alveolata											4	
Sabellaria spinulosa							1	8				
Ampharetidae								1				
Melinna palmata	2		2	1			1	3				
Ampharete							3					
Terebellides							1					
Serpulidae		1					20	10				
Hydroides norvegica								1				
Spirobranchus	1											
Spirobranchus lamarcki	5	2					65	80				
Tubificoides amplivasatus						1						
Tubificoides diazi							1	2				
Austrominius modestus								37			1	
Balanus crenatus							18	38				
Calanoida						1			1			
Leucothoe lilljeborgi	1			1								
Urothoe elegans								1				
Harpinia antennaria	5	5										
Nototropis guttatus												1
Ampelisca brevicornis		1					1					
Ampelisca tenuicornis	1	2										
Abludomelita obtusata	3											
Microprotopus maculatus										1		
Aoridae								1				
Microdeutopus anomalus								3				

Station	2A	2B	4A	4B	5A	5B	7A	7B	9A	9B	12A	12B
Monocorophium sextonae								2				
Zeuxo holdichi							1					
Chondrochelia savignyi							2	13				
Tanaopsis graciloides	2	2					1	1				
Diastylis laevis						1						
Paguridae juvenile								1				
Pagurus bernhardus			1				1					
Pisidia longicornis								1				
Lepidochitona cinerea											3	
Bittium reticulatum											1	
Turritellinella tricarinata			63	11	35	8	4		1			
Hyala vitrea			2	12	1							
Tritia juvenile				1			1	2				
Tritia incrassata			1	1			1					
Sorgenfreispira brachystoma							3					
Odostomia			3	1			3					
Nudibranchia juvenile												1
Bivalvia				1								
Ostrea edulis								1				
Thyasira	5	5		2			3	3				
Thyasira sarsii							1	1				
Thyasira flexuosa	13	11	1	1			3					
Kurtiella bidentata	3	1		2				2				
Tellinidae juvenile		1					2	1				
Macomangulus tenuis							1		1			1
Fabulina fabula										1		

Station	2A	2B	4A	4B	5A	5B	7A	7B	9A	9B	12A	12B
Abra juvenile							2					
Abra alba								1				
Abra nitida			3			1						
Chamelea striatula									1	4		
Thracia juvenile		1								1		
Thracia phaseolina							1		1			
Asterias rubens								1				
Amphiura filiformis	1											
Amphipholis squamata							1					
Ophiura juvenile										1		
Dendrodoa grossularia								2				