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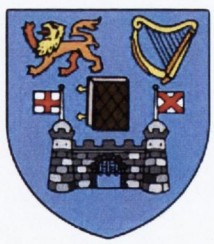
Benthic Habitat Mapping in the Southern Irish Sea

A dissertation submitted to the University of Dublin for the degree of Doctor of Philosophy

Fionnuala McBreen

26th April 2010



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Summary

Habitat mapping is an extremely important area in marine science. Before we can conserve areas or consider the potential impacts of industries such as fishing, aggregates, windfarms and wave or tidal turbines, we first need to learn about the environment and biology that exist in these areas. There are huge gaps in our knowledge of marine seabed habitats, with predictions often being based solely on the broad-scale physical environment, rather than on the fine-scale biological and chemical environment. Data need to be validated and the confidence with which one should look at data needs to be made clear. This project aimed to look at the physical and chemical aspects of sediment and to explore their relationship to the abundance, biomass and productivity of benthic macrofauna and to benthic foraminiferal assemblages.

The repeatability of the long armed continuous warped 0.1m^2 Van Veen grab sampler in sampling the chemical and physical characteristics of sediment in a homogenous environment was examined. The study looked at repeatability within a grab sample, within samples at a site and within sites in a homogenous habitat. Repeatable results were achieved for the chemical sediment characteristics of calcium carbonate, organic matter, organic carbon and organic nitrogen. There were differences between samples within grabs and within sites for mean grain size but not between samples within a site and within a habitat or within a grab and within a habitat. This was most likely due to the fact that the mud and gravel fractions would be unevenly dispersed throughout the grab, with a higher or lower percentage of mud or gravel in the top or bottom of the grab.

The physical and chemical characteristics of the HABMAP sediments of the southern Irish Sea were examined. Overall the HABMAP stations were dominated by 'gravelly sands'. The northerly stations in the Arklow Bank area were found to consist mainly of 'gravelly sands' and 'sandy gravels', while the southern stations consist of 'sands' and 'gravelly sands'. Caernarfon Bay contained a wide range of sediment types from 'muddy sandy gravels' to 'muddy sands'. Stations in Caernarfon Bay dominated by the bivalve *Modiolus modiolus* tended to be associated with 'slightly gravelly muddy sands' and 'gravelly muddy sands'. The Celtic Deep transect graduated from 'sandy gravels' and 'gravelly sands' in the north to 'muddy sands' and 'sandy muds' in the south. This study found that a combination of depth, gravel and the silt/claycontent best explained the separation of abundance-based macrofaunal assemblages in the southern Irish Sea (correlation = 0.546). High levels of calcium carbonate were found in the muddiest and gravelliest sediments, which were attributed to the presence of *Modiolus modiolus* shells in the more gravelly sediments and the presence of foraminifera in the 'muddy sands'. A strong positive correlation

between organic matter and silt/clay was obtained (r^2 = 93.3%, $p < 0.001$, n =61). A positive correlation between organic carbon and silt clay was also found (r^2 = 64.2%, $p = < 0.001$, n =61).

Two distinct groups of foraminiferal assemblages were recognised in the Celtic Deep in both the species and superfamily-based cluster analyses (stations 38 - 45 and stations 46 - 57), indicating that broad scale foraminiferal assemblages may be recognised by identification down to superfamily level only. Foraminiferal and macrofaunal assemblages in the Celtic Deep also appeared to group together at low levels of similarity in two distinct assemblages consisting of one group of the more southerly and muddier stations (stations 38 - 45) and a group consisting of the more northerly and sandier stations (stations 46 - 57). Formainiferal assemblage I was clearly associated with the more muddy sites and was dominated by calcareous foraminiferal species such as *Bulimina* sp., *Stainforthia fusiformis*, and *Hyalinea balthica*. Assemblage II was associated with coarser sediment and was dominated by *Cibicides* sp and agglutinated *Textularia* species. Canonical Correspondence Analysis (CCA) found that organic matter, calcium carbonate and depth were responsible for the majority of the variance in the species distribution at sites in the Celtic Deep. RELATE analysis found a correlation of 0.81 between foraminiferal species Bray-Curtis similarity matrix and the macrofaunal species Bray-Curtis similarity matrix for species from the Celtic Deep.

Forced-entry binary logistic regression was found to work well in predicting the presence or absence of abundance-based and biomass-based assemblages. It did not work very well in predicting the presence or absence of productivity-based assemblages. Multiple regressions worked well in predicting the continuous variables of total benthic macrofaunal biomass and productivity in the southern Irish Sea. The procedure could not be used for abundance-based assemblages.

An average benthic macrofaunal biomass of 370.9 AFDW g m^{-2} and an average benthic macrofaunal productivity of 61.1 AFDW g m^{-2} yr^{-1} were obtained for the whole of the southern Irish Sea. This resulted in an overall P:B value of 0.17. This P:B value is very low and is coupled with a high productivity value. This indicates that the high productivity is produced by larger animals such as *Modiolus modiolus* and *Glycymeris glycymeris*, which have low P:B values, rather than smaller species which have high P:B values. Large *M. modiolus* tend to be unavailable to predators, thus the low P:B value may be a better indication of the available food in the southern Irish Sea than the average productivity value. This may account for the lower fishing yields in the Irish Sea compared to the North Sea.

Acknowledgments

I would like to thank the following people for their help and support during the PhD.

- My supervisor, Prof. Jim Wilson, for his continued support and encouragement and for always pointing me in the right direction when needed.
- Dr. Andy Mackie, from the National Museum of Wales for allowing me to use macrofaunal abundance data from the BIOMÔR, SWISS and HABMAP projects and sediment data from BIOMÔR.
- Dr. Robin Edwards, my internal examiner, both for his initial suggestion that foraminifera samples should be taken during the survey and for his help with foraminiferal identification. As I had never identified a foram before the start of this project, his assistance and guidance both at the beginning and during the project were invaluable.
- Prof. Chris Frid, my external examiner, for his helpful advice and suggestions.
- Caitríona Nic Áonghusa, for allowing me to use her sediment data from the SWISS project.
- The HABMAP project partners, particularly Dr. Karen Robinson and Dr. Kirsten Ramsay and Charles Lindenbaum from the Council for the Countryside of Wales (CCW) and Dr. Andy Wheeler and Dr. Katrien Van Landeghem from University College Cork (UCC).
- The crew of the *RV Celtic Voyager* for their endless help when sampling in the field.
- The Centre for Microscopy and Analysis (CMA) for providing me with a bursary of €500 to take scanning electron microscope (SEM) photos of the Foraminifera.
- Dr. Mark Kavanagh from the Centre of the Environment (TCD), for his advice on sediment analysis.
- Katie Reeve-Arnold, for her help as a laboratory assistant to process sediment samples.
- The Zoology postgrads, in general, for always being there when needed and always ready to go for an emergency tea\coffee\lunch in a crisis. Lynsey & Gwen, in particular, helped me to get through the last week.
- My parents, Máirín & Owen McBreen, for their continued support, encouragement and understanding.
- Liam Doherty,

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Chapter 1

1 Introduction

1.1 *Background*

This study is a part of the larger EU Interreg IIIA funded project 'Habitat Mapping for conservation and management of the Irish Sea' (HABMAP) (Robinson et al., 2007). The joint Irish-Welsh project included partners from the Countryside Council of Wales (CCW) (lead partner), Trinity College Dublin (lead Irish partner), the National Museum of Wales and University College Cork (UCC). The aim of the HABMAP project was to integrate physical, environmental and biological information for the southern Irish Sea in order to produce predictive biotope maps for the area. By combining information and data from different disciplines we can further our understanding of marine ecosystems, thus enabling managers to produce more efficient and effective conservation and management plans for the marine environment. Further information about the HABMAP project can be obtained from the project report (Robinson et al., 2007) and from the HABMAP website: http://www.habmap.org.

1.2 *General overview*

This study examines in detail relationships between the biological, chemical and physical properties of the southern Irish Sea seabed. The integration of geology, physics, chemistry and biology is a key process to further knowledge of marine ecosystems. This study aims to test the relationships among benthic assemblages, both macrofaunal and foraminiferal, and physical and chemical environments in the southern Irish Sea. It also tests the possibility of using physical and chemical sediment characteristics as predictors of benthic macrofaunal abundance, biomass and productivity.

In order to conserve both marine species and spaces through enforcement and legislation, more information on marine habitats is required. Benthic marine habitat maps are traditionally based on physical sediment characteristics and, in more recent times, on geophysical data to produce broad-scale habitat maps (Kenny et al., 2003, Roff et al., 2003). These maps often have poor biological ground-truthing and thus are based more on physical sediment type and geology and their known associated communities, than on actual biological data (Roff and Taylor, 2000). Where biological data are available, there is a tendency to focus solely on macrofaunal data. Assumptions about the location, type and importance of biological communities and their boundaries are usually based on a combination of geophysical and sediment data, incorporating

some macrofaunal ground-truthing. Ground-truthing sometimes consists of qualitative data from trawls or dredges (Ellis and Rogers, 2000, Ellis et al., 2000, Ellis et al., 2002) rather than on quantitative data from grab samplers (Mackie et al., 1995a, Wilson et al., 2001, Robinson et al., 2007).

Bremner et al. (2006) emphasise the need for studies that look at different biotic components and ecological processes. This study aims to do that by studying macrofaunal community structure, both in terms of abundance and biomass, foraminiferal community structure and their relationships with the sedimentary environment. Exploring ecosystems and ecosystem dynamics, in terms of both habitats and communities, is necessary to further understand the importance of marine biotopes and the effect of disturbances both natural and anthropogenic, such as tides, storms, fishing, the extraction of aggregates and the construction of windfarms. Costanza et al. (1997) estimated the value of the marine environment as \$577 ha^{-1} yr^{-1} (€412 ha^{-1} yr^{-1}), showing the economic importance of the marine environment. In order to make the best use of and to best protect the marine environment, more information is needed on ecosystems dynamics in order to enable managers to decide how to optimise usage and conservation of the marine environment.

1.3 Concepts in benthic marine habitat mapping

Firstly, the concepts in marine benthic habitat mapping need to be clearly defined. The concepts of biotope, habitat and community vary greatly in the literature (Olenin and Ducrotoy, 2006). A marine 'habitat' is defined as the substratum, its topography and its conditions which contribute to the nature of the seabed (e.g. current, temperature and exposure) (Connor et al., 2004). A 'community' is an association of species which tends to have particular species in common (Connor et al., 2004). 'Biotope' was originally intended to mean the abiotic environment, which when combined with a 'biocenosis' (the biotic community) formed an 'ecosystem' (Olenin and Ducrotoy, 2006). Today, the word 'biotope' is used to define the combination of a habitat and an associated community of species (Connor et al., 2004, Olenin and Ducrotoy, 2006). The relationship between these abiotic and biotic conditions is fundamental to the structure of the Marine Nature Conservation Review (MNCR) (Connor et al., 2004) and the European Nature Information System habitat classification systems (Connor et al., 2004, Davies et al., 2004). These use hierarchical classifications to firstly identify habitats before including biological characteristics to define biotopes at higher levels of the classification systems (Connor et al., 2004, Davies et al., 2004). Confusion still exists, however, as the EC Habitats Directive uses the term 'habitat' in the same way that Connor (2004) and Olenin & Ducrotoy (2006) use the word

'biotope'. For the purpose of this thesis the terminology as adhered to by Connor (2004) and Olenin & Ducrotoy (2006) will be used.

1.4 *Reasons for benthic habitat mapping*

Benthic habitat mapping is necessary to identify existing, changing and damaged habitats. Marine benthic habitat maps are used by managers to identify conservation and management objectives for the marine environment. Some of the key areas in which marine benthic habitat maps can benefit users are outlined below.

- Identification of areas for conservation and protection in order to comply with international agreements and European Directives
- Identification of potential Special Areas of Conservation (SACs - Annex I of the Habitats Directive)
- Identification of potential Marine Protected Areas (MPAs - OSPAR)
- Identification of representative (typical) and distinct (atypical) habitats
- Assessment of the potential or ongoing impacts of industries on the marine environment (e.g. the fishing, windfarm or aggregate industries)
- Assessment of the impact of disasters, e.g. oil spills
- Assistance in carrying out a detailed assessment of the marine environment as required by the Marine Strategy Framework Directive.
- Assistance in Marine Spatial Planning

Habitat maps tend to be either broad-scale or fine-scale depending on the area covered and the requirements of the study. Fine-scale maps tend to involve intensive geophysical and biological surveying to produce biotope maps. Broad-scale maps usually involve modelling of abiotic variables to produce habitat maps. Both types of map are validated using existing biological data.

An excellent example of the need for benthic habitat mapping is illustrated by Stevens & Connolly (2005). Their study showed that by mapping a 2400km^2 area in Moreton Bay in Australia, only two of the nine habitats they found were located in a highly protected no-take zone and of these two habitats, less than 3% of their area was included in the no-take zone (Stevens and Connolly, 2005). Several habitats not previously known to exist in the area were also discovered (Stevens, 2002).

1.4.1 Legislation affecting the protection and conservation of benthic habitats in the southern Irish Sea

Southern Irish Sea habitats are protected under international Conventions, European Directives and national legislation. Conventions are international agreements between countries concerned with specific issues. European Directives are legislative and must be implemented by European Union (EU) Member States such as Ireland and the United Kingdom (U.K.). The Isle of Man (located in the Irish Sea) is a self-governing British Crown Dependency and thus is not obliged to enforce EU Directives or international conventions which it has not adopted.

1.4.1.1 International Conventions

Below is a list of international conventions which affect the Irish Sea. The names by which the conventions are usually known are highlighted in bold.

- The Convention on Wetlands of International Importance especially as Waterfowl Habitat **(Ramsar Convention adopted 1971, enforced 1975)**
- Convention for the Prevention of Marine Pollution by Dumping from Ships and Aircraft **(the Oslo Convention – adopted 1972)**
- Convention for the Prevention of Marine Pollution from Land-Based Sources **(the Paris Convention – adopted 1974)**
- The Convention on the Conservation of European Wildlife and Natural Habitats **(Bern Convention – adopted 1979, enforced 1982)**
- The Convention on the Conservation of Migratory Species of Wild Animals **(Bonn Convention – adopted 1979, enforced 1985)**
- The Convention on Biological Diversity **(CBD – adopted 1992, enforced 1993)**
- United Nations Framework Convention on Climate Change **(adopted 1992, enforced 1994)**
- The Convention for the Protection of the Marine Environment of the North-East Atlantic **(OSPAR – adopted 1992, enforced 1998)**

The main international convention affecting the Irish Sea is the 'Convention for the Protection of the Marine Environment in the North East Atlantic (OSPAR)' which was enforced in March 1998 (OSPAR Commission, 2009). Both Ireland and the U.K. are members of OSPAR. It replaced the 'Convention for the Prevention of Marine Pollution by Dumping from Ships and Aircraft '(the

Oslo Convention - 1972) and the 'Convention for the Prevention of Marine Pollution from Land-Based Sources' (the Paris Convention - 1974) both of which aimed to tackle marine pollution in the North-East Atlantic environment (OSPAR Commission, 2009).

OSPAR's mission is *'to conserve marine ecosystems and safeguard human health in the North-East Atlantic by preventing and eliminating pollution; by protecting the marine environment from the adverse effects of human activities; and by contributing to the sustainable use of the seas.'* (OSPAR Commission, 2009). OSPAR divides the North-East Atlantic into five regional seas. The Irish Sea comes under the Region III area known as the Celtic Seas (OSPAR Commission, 2009). OSPAR has six specific strategies it applies to the regional seas. It also considers the relevance of climate change to the regional seas.

OSPAR Strategies

1. Joint assessment and monitoring programmes
2. Biological Diversity and Ecosystems Strategy
3. Eutrophication Strategy
4. Hazardous Substances Strategy
5. Offshore Oil and Gas Industry Strategy
6. Radioactive Substances Strategy

The 'Biological Diversity and Ecosystems Strategy' has most relevance to the conservation of the Irish Sea benthic habitats. The strategy has four main elements: the setting of ecological quality objectives, assessments of threatened or declining species and habitats, the creation of 'an ecologically coherent network of well-managed marine protected areas (MPAs)' and the assessment of human activities which may affect the OSPAR area (OSPAR Commission, 2009).

1.4.1.2 European Directives

Below is a list of EU Directives which affect the Irish Sea Area,

- Council Directive 79/409/EEC on the conservation of wild birds **(Birds Directive)**
- Council Directive 92/43/EEC on the conservation of natural habitats and of wild fauna and flora **(Habitats Directive)**
- Directive 2000/60/EC of the European Parliament and of the Council establishing a framework for the community action in the field of water policy **(Water Framework Directive or WFD)**

- Directive 2008/56/EC of the European Parliament and of the Council of 17 June 2008 establishing a framework for community action in the field of marine environmental policy **(Marine Strategy Framework Directive or MSFD)**

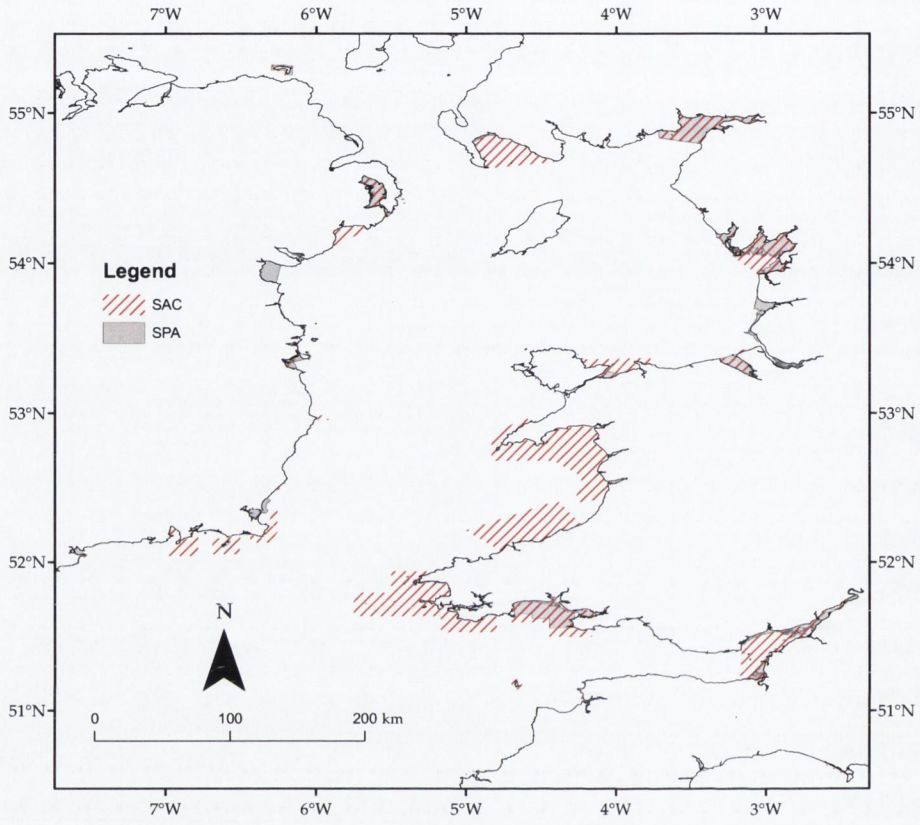


Figure 1.1: Special Areas of Conservation (Habitats Directive) and Special Protected Areas (Birds Directive) in the Irish Sea. Irish data from the National Parks and Wildlife Service. U.K. data from the Joint Nature Conservation Committee.

The marine environment of the Irish Sea is covered by European Union (EU) legislation under several EU directives; the Birds directive (79/409/EEC), the Habitats Directive (92/43/EEC), the Water Framework Directive (2000/60/EC) and most recently the Marine Strategy Framework Directive (2008/56/EC). The Birds Directive led to the creation of Special Protection Areas (SPAs) for the conservation of wild birds. The Habitats Directive dealt with the conservation of 'natural habitats and of wild fauna and flora', focusing on the protection of habitats in Annex I and species in Annex II through the establishment of Special Areas of Conservation (SACs). The Habitats Directive led to the establishment of the Natura 2000 network, an EU wide network of nature protection areas comprising both SPAs and SACs, whose aim is to ensure the long-term survival of the EU's threatened habitats and species in both the terrestrial and the marine environment.

The Water Framework Directive aims to establish a framework to protect inland surface waters, coastal waters, transitional waters and groundwaters. While these three Directives are not specifically dedicated to the marine environment, they can lead to the establishment of SPAs or SACs in marine or coastal areas and the protection of water quality in coastal and transitional waters. While Ireland currently has no offshore SACs in the Irish Sea, it does have several inshore SACs and SPAs which are located in the Irish Sea (Figure 1.1).

The newly enacted Marine Strategy Framework Directive deals specifically with the marine environment and directs Member States to achieve or maintain good environmental status in the marine environment by 2011. Member States are required to develop marine strategies for their waters containing a detailed assessment of the marine environment and a definition of 'good environmental status' and to establish clear environmental targets and monitoring programmes.

1.4.1.3 National Legislation

The Irish Sea is covered by a wide range of acts and regulations from both the U.K. and Ireland. These often help to enshrine international conventions and European Directives in national legislation. Some of the main acts, orders and regulations are outlined below. The U.K. currently has a Marine and Coastal Access Bill at report stage, which will cover English and Welsh inshore waters and U.K. offshore waters. Northern Ireland and Scotland are also hoping to introduce Marine Bills in the near future.

Irish legislation

- Wildlife Act, 1976
- The Wildlife (Amendment) Act, 2000
- European Union (Natural Habitats) Regulations, S.I. 94/1997 (which have been amended twice with S.I. 233/1998 & S.I. 378/2005)

U.K. legislation

- The Wildlife (Northern Ireland) Order 1985
- Conservation (Natural Habitats, &c.) Regulations 1994
- Nature Conservation (Scotland) Act 2004
- The Offshore Marine Conservation (Natural Habitats, & c.) Regulations 2007

1.5 *Marine benthic habitat classification systems*

Today marine benthic communities are being much more rigorously defined, mostly in response to international conventions and EU legislation. The two main biological classification systems generally applied to the Irish Sea are the Marine Nature Conservation Review (MNCR) (Connor et al., 2004) and the European Nature Information System classification systems (Davies et al., 2004) (EUNIS: http://eunis.eea.europa.eu/). The MNCR system was originally designed with Britain & Ireland in mind, while EUNIS was designed to apply to the whole of north-eastern Europe and aimed to produce a network of protected sites across Europe known as Natura 2000. Both systems converge under the 'Mapping European Seabed Habitats' programme (MESH: www.searchmesh.net).

The EUNIS classification system classifies habitats on a 7 point hierarchical scale, in which level 2 identifies habitats based on stratum, permanent or non-permanent water cover, shelf, substrate type and presence of macro-algae (see **Error! Reference source not found.**) (Davies et al., 2004). Habitats are further subdivided at hierarchical levels, such as the sublittoral sediments classification at level 3 (see **Error! Reference source not found.**). Classifications go as far as Level 6 which can distinguish habitats from Level 5 by the presence of certain species such as *Nemertesia*, distinguishing habitat A5.441 at Level 5 from habitat A5.4411 at Level 6 (Level 5: A5.441 = [*Cerianthus lloydii*] and other burrowing anemones in circalittoral muddy mixed sediment and Level 6: A5.4411 = [*Cerianthus lloydii*] with [*Nemertesia*] spp. and other hydroids in circalittoral muddy mixed sediment).

Olenin and Ducrotoy (2006) recommend incorporating ecosystem functional characteristics at higher levels of biotope classification systems. The EU funded project 'Marine Biodiversity and Ecosystem Functioning' (MarBEF) focuses on the 'elusive link' between marine biodiversity and ecosystem functioning (MarBEF: http://www.marbef.org). Ecosystem functions are the processes and properties of habitats, biological communities and ecosystems (Costanza et al., 1997). Duarte (2000) suggests that increased biodiversity may increase the functional abilities of an ecosystem thereby leading to more efficient resource usage and thus increasing the stability of ecosystems and decreasing their vulnerability to disturbance but there is not as yet conclusive evidence of a link between biodiversity and ecosystem functioning.

1.6 *The development of broad-scale marine benthic habitat mapping*

Roff & Taylor (2000) adopted a hierarchical system for broad-scale habitat mapping of Canadian waters based on oceanographic and physiographic characteristics. They believed that the habitats level was the most appropriate unit for mapping at a broad national level where biological information is generally sparse (Roff and Taylor, 2000). Hierarchical habitat classification systems make it easier to identify both representative and distinct habitats for protection (Roff and Taylor, 2000).

Roff and Taylor (2000) used the term 'seascapes' to distinguish their benthic habitats. Seascapes were identified both for benthic and pelagic systems (see Table 1.1). Up to five hierarchical classes were used in the Canadian classification system. Oceanographic features considered included ice cover, salinity, temperature, water masses, light, nutrients, tidal amplitude, bottom slope and exposure (Roff and Taylor, 2000). Physiographic features included tectonic motion, latitude, depth and substrate particle size.

Table 1.1: Hierarchical classification system used by Roff & Taylor (2000) to identify Canadian benthic and pelagic habitats.

Classification Level	Seabed Habitats	Water Column
1	Geographic\temperature	Geographic\temperature
2	Benthic	Pelagic
3	Depth\Light	Depth\Light
4	Substrate Type	Stratification/mixing regime
5	Exposure\Slope	

A: EUNIS Habitat Classification: criteria for marine habitats (A) to Level 2

Note that the key to Level 1 shows two pathways to reach habitat type A: these are recombined here.
(number) refers to explanatory notes to the key (see following page).

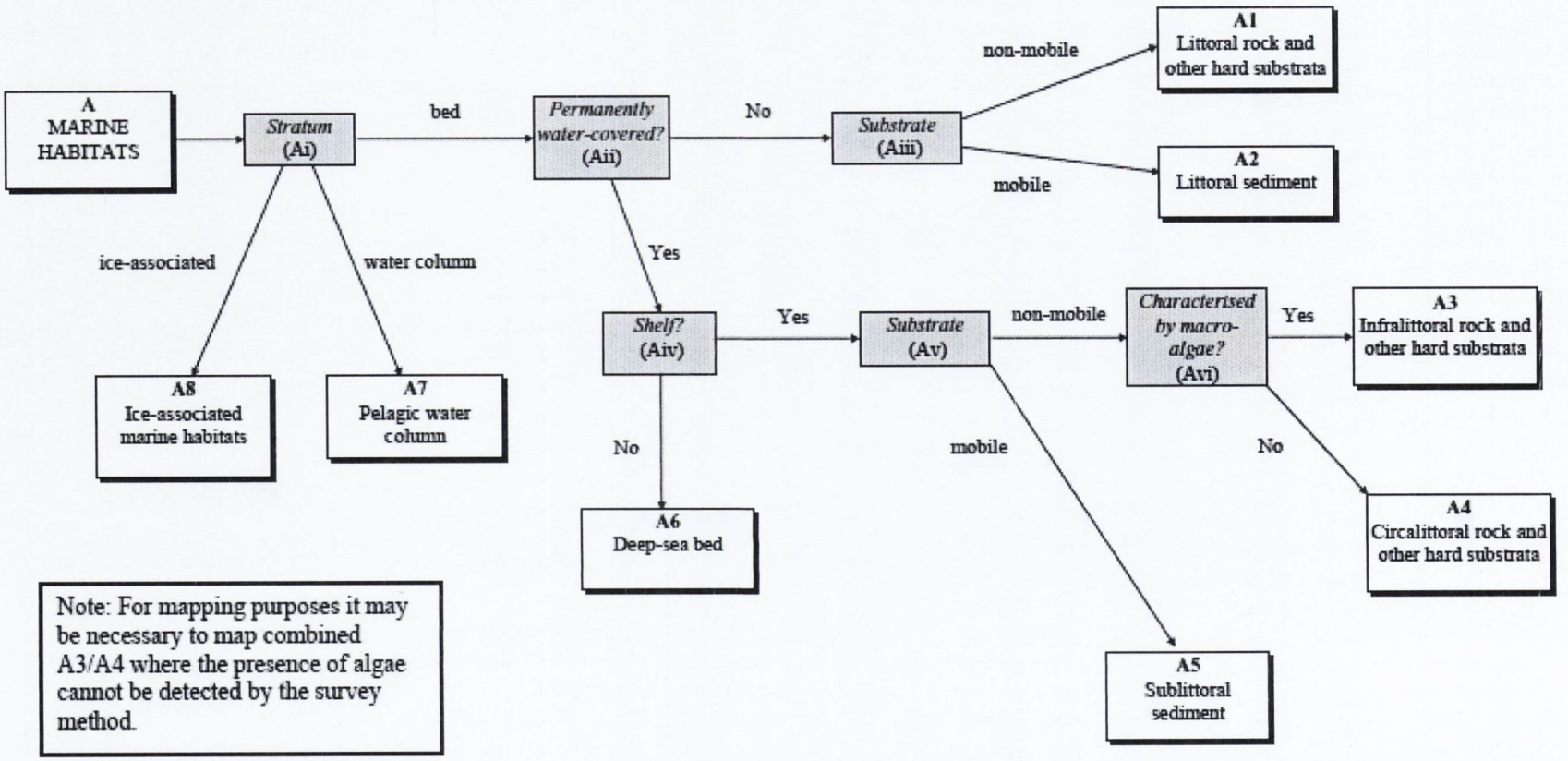
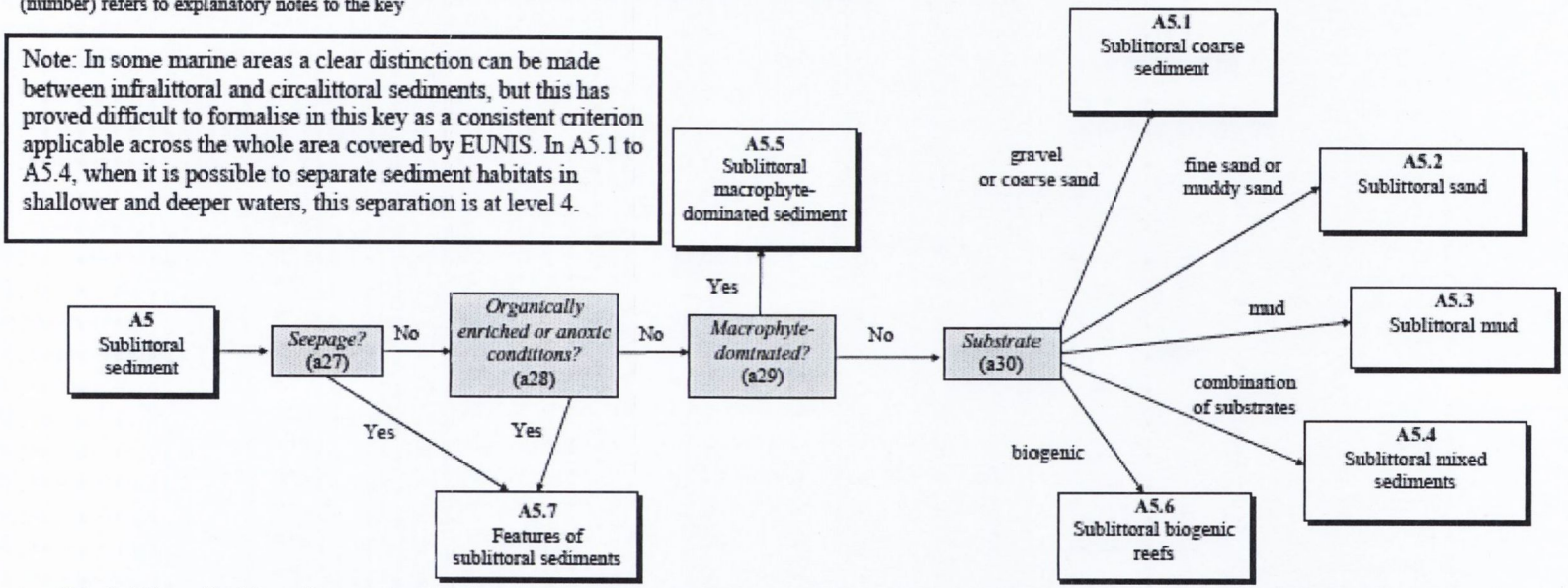


Figure 1.2: EUNIS guide to marine habitats (A) to level 2, (Davies et al. (2004)).

A5: EUNIS Habitat Classification: criteria for sublittoral sediment (A5) to Level 3
(number) refers to explanatory notes to the key



a27. Sublittoral habitats characterised by the presence of gases or liquids bubbling or seeping through sediments are distinguished (path = *Yes*).
a28. Sublittoral sediments which are organically-enriched or permanently or periodically anoxic are separated (path = *Yes*).
a29. Habitats dominated by aquatic angiosperm or algal macrophytes (path = *Yes*) are distinguished from those dominated by animal communities, with or without algae.
a30. Habitats are divided on the basis of the dominating particle size of the substrate. *Gravel or coarse sand* > 1 mm grain size (including shingle and mobile cobbles); *fine sand or muddy sand* <= 1 mm with <=30% silt (less than 0.063 mm grain size); *mud* >30% less than 0.063 mm grain size; *combination of substrates* - veneers or intimate mixtures of mobile substrates with different particle size; or *biogenic* structures on sediment. Note that sublittoral mosaics of mobile and non-mobile substrates are considered as complex X32 or X33 comprising units from A5 and A3 and/or A4.

Figure 1.3: EUNIS guide to sublittoral sediments (A5) to level 3 (Davies et al. (2004)).

Hierarchical marine benthic habitat classifications have been adopted in many areas, including Australia (Bax and Williams, 2001, Jordan et al., 2005, Stevens and Connolly, 2005, Harris, 2007), New Zealand (Snelder et al., 2007), East Antarctica (Beaman and Harris, 2005), the Baltic Sea (Leth, 2008), the Irish Sea (Vincent et al., 2004), the U.K. (Connor et al., 2006) and the North West Atlantic (Joint Nature Conservation Committee, 2007). Several broad-scale European marine benthic habitat mapping projects have included the southern Irish Sea area. The most relevant of these are outlined below.

1.6.1. Irish Sea Pilot (2002-2004)

The Irish Sea Pilot (ISP) applied the method of 'seascapes' proposed by Roff & Taylor (2000) to the Irish Sea regional sea. Seascapes were termed 'Marine Landscapes' for the purposes of the ISP. 'Marine landscapes' use geophysical and hydrographical data to identify habitats in the absence of biological data (Vincent et al., 2004). The coastal and marine seabed and water column landscapes were classified using environmental data. The maps were validated using biological data in order to test the ecological relevance of the maps (Vincent et al., 2004). The ISP divided the Irish Sea into five coastal and thirteen marine seabed landscape types (Vincent et al., 2004). The Irish Sea Pilot recommended that the marine landscape approach 'should be adopted as a key element for marine nature conservation and utilised in marine spatial planning and in the management of the marine environment' (Connor et al., 2006).

1.6.2. UKSeaMap (2004 - 2006)

UKSeaMap acted on the recommendation from the ISP to refine the marine landscape approach and apply it to all U.K. waters (Connor et al., 2006). UKSeaMap produced an ecologically relevant broadscale seabed map using available geological, physical and hydrographical data for U.K. waters (Connor et al., 2006) (see Figure 1.4). UKSeaMap used coastal physiographic, topographic feature and seabed data modelled using seabed substratum, depth and bed shear stress to identify forty-four marine seabed landscapes (Connor et al., 2006). The maps were validated using 32,000 biological samples classified using the MNCR classification system (Connor et al., 2006).

1.6.3. Mapping European Seabed Habitats (MESH) (2004 -2008)

MESH was a joint EU INTERREG funded project involving 12 project partners from the North East Atlantic Region (Joint Nature Conservation Committee, 2007). MESH produced predictive seabed habitat maps for the North-East Atlantic using level 3 of the EUNIS classification system and developed a framework for mapping European seabed habitats (see Figure 1.5 and Table 1.2) (Joint Nature Conservation Committee, 2007). National marine landscapes were also produced; however the same landscape classifications were not used for each country (Joint Nature Conservation Committee, 2007). In general, EUNIS maps were seen to be more biologically relevant than marine landscape maps. They also benefit from a hierarchical scale which can map habitats at a broad-scale level and biotopes at a finer scale depending on the level of available data.

Key outputs of the MESH project

- MESH guide to Marine Habitat Mapping
- Collated historical data for the MESH areas
- National marine landscape maps
- Predictive EUNIS classification habitat map for the North East Atlantic area.
- Predictions on the distributions of specific species and habitats

1.6.4. Habitat Mapping for Conservation and Management (HABMAP) (2004-2008)

HABMAP was an INTERREG IIIA project involving Irish and Welsh partners. The aim of HABMAP was to produce a predictive seabed map for the southern Irish Sea that could be used for conservation and management. The habitat maps were predicted down to level 5 of the 2004 Marine Nature Conservation Review (MNCR) habitat classification system (Connor et al., 2004). A combined predictive map for the southern Irish Sea was produced using a combination of level 3 and level 4 biotopes (see Figure 1.6 and Table 1.3). HABMAP produced a more detailed picture of the southern Irish Sea habitats than MESH or UKSeaMap. Sediment data from this study were used in the production of the HABMAP habitat maps.

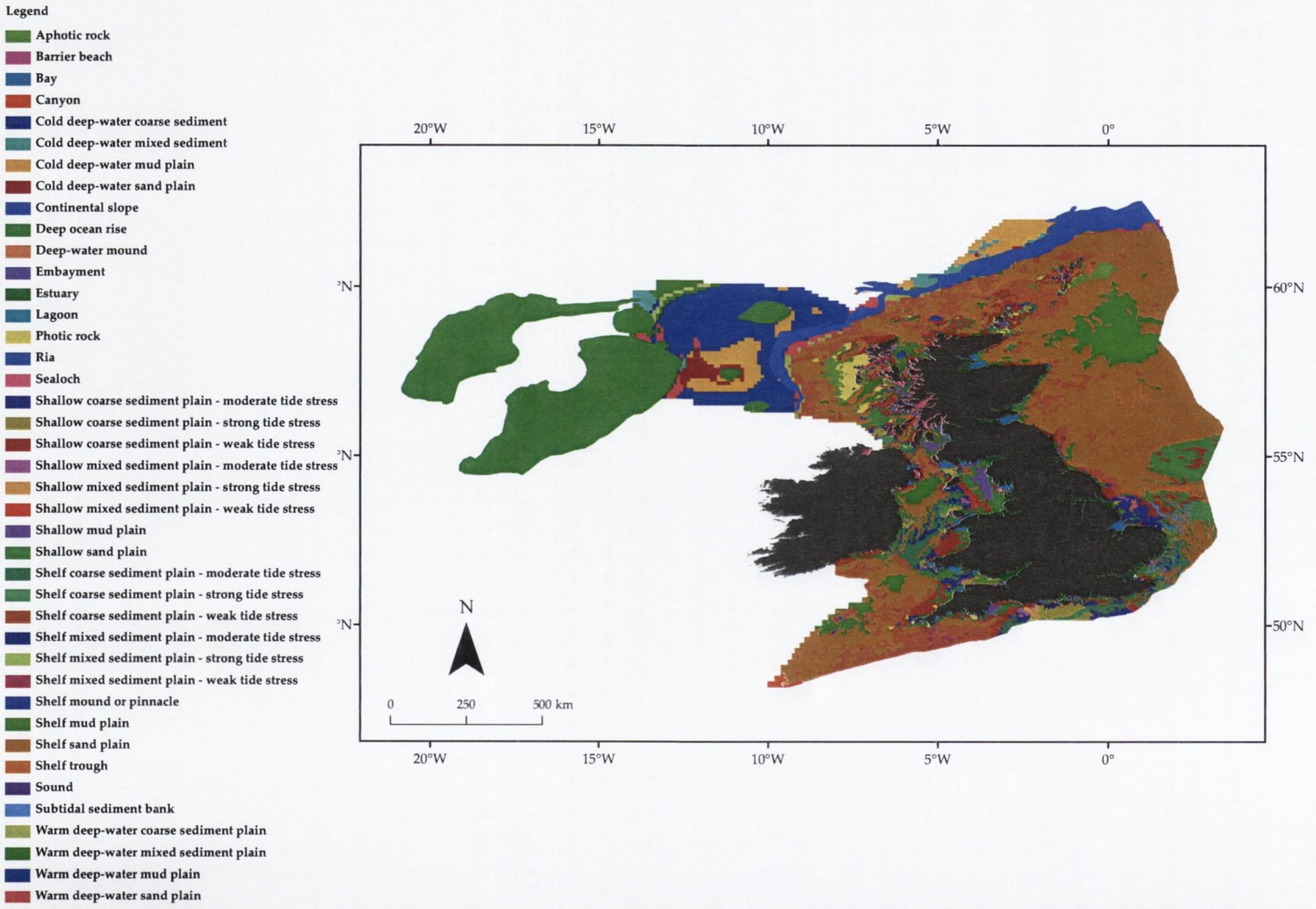


Figure 1.4: UKSeaMap marine landscapes for U.K. waters. (Connor et al., 2006)

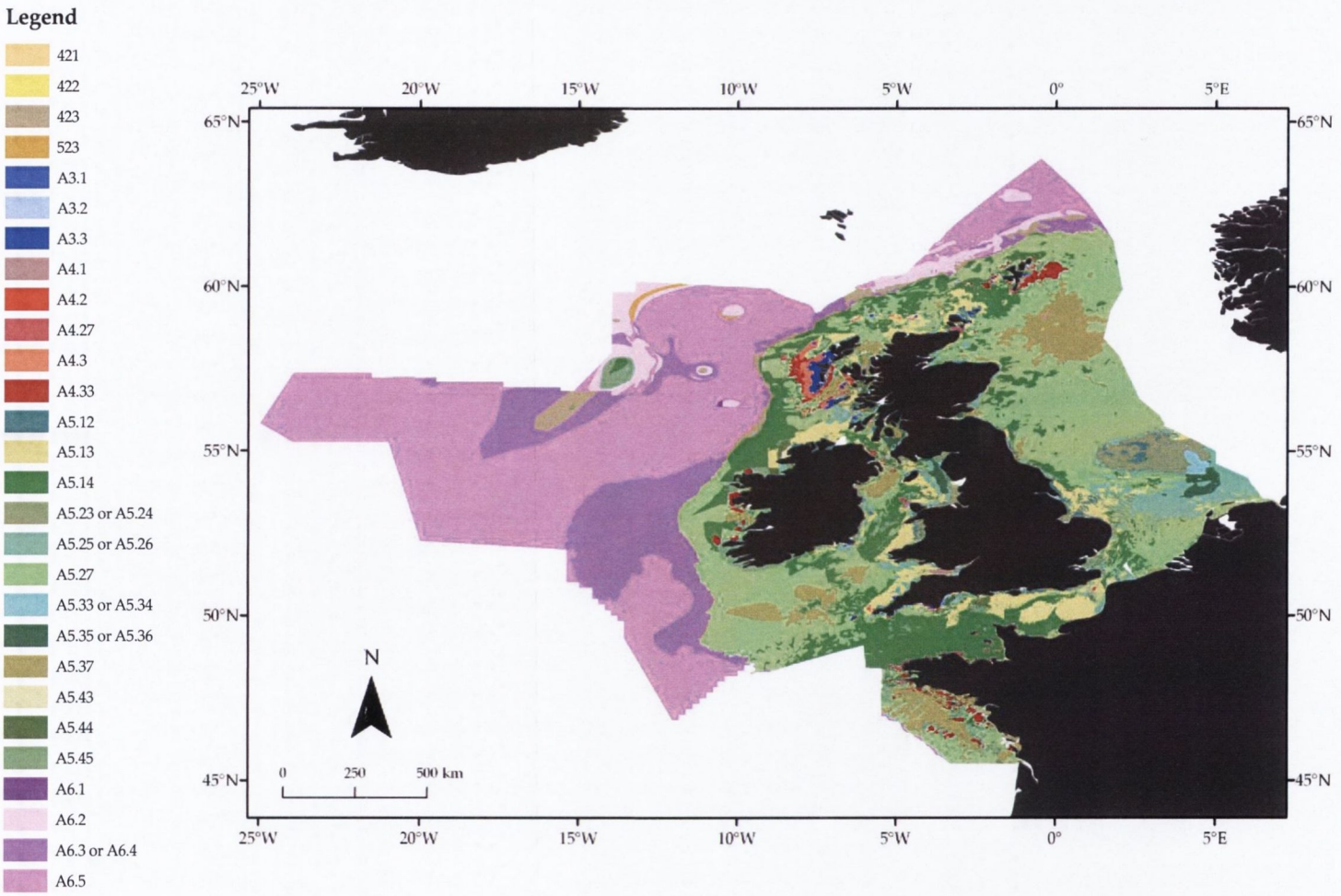


Figure 1.5: MESH predictive EUNIS habitat classification map for the North East Atlantic. Information contained here has been derived from MESH Consortium webGIS data (www.searchmesh.net) which received funding from the INTERREG IIIB NEW programme (www.nweurope.org).

Table 1.2: EUNIS codes predicted by the MESH project for the north-east Atlantic.

EUNIS level 3	EUNIS habitat code	EUNIS habitat description
No EUNIS code	421	Deep-sea coarse sediment
	422	Deep-sea coarse sediment
	423	Deep-sea coarse sediment
	523	Deep-sea coarse sediment
Infralittoral rock	A3.1	High energy infralittoral rock/reef
	A3.2	Moderate energy infralittoral rock/reef
	A3.3	Low energy infralittoral rock/reef
Circalittoral rock	A4.1	High energy circalittoral rock/reef
	A4.2	Moderate energy circalittoral rock/reef
	A4.27	Faunal communities on deep moderate energy circalittoral rock
	A4.3	Low energy circalittoral rock/reef
	A4.33	Faunal communities on deep low energy circalittoral rock
Sublittoral sediments	A5.12	Infralittoral coarse sediment
	A5.13	Circalittoral coarse sediment
	A5.14	Deep circalittoral coarse sediment
	A5.23 or A5.24	Infralittoral fine sand or infralittoral muddy sand
	A5.25 or A5.26	Circalittoral fine sand or circalittoral muddy sand
	A5.27	Deep circalittoral sand
	A5.33 or A5.34	Infralittoral sandy mud or infralittoral fine mud
	A5.35 or A5.36	Circalittoral sandy mud or circalittoral fine mud
	A5.37	Deep circalittoral mud
	A5.43	Infralittoral mixed sediments
	A5.44	Circalittoral mixed sediments
	A5.45	Deep circalittoral mixed sediments
Deep-sea	A6.1	Deep-sea rock and artificial hard substrata
	A6.2	Deep-sea mixed substrata
	A6.3 or A6.4	Deep-sea sand or deep –sea muddy sand
	A6.5	Deep-sea mud

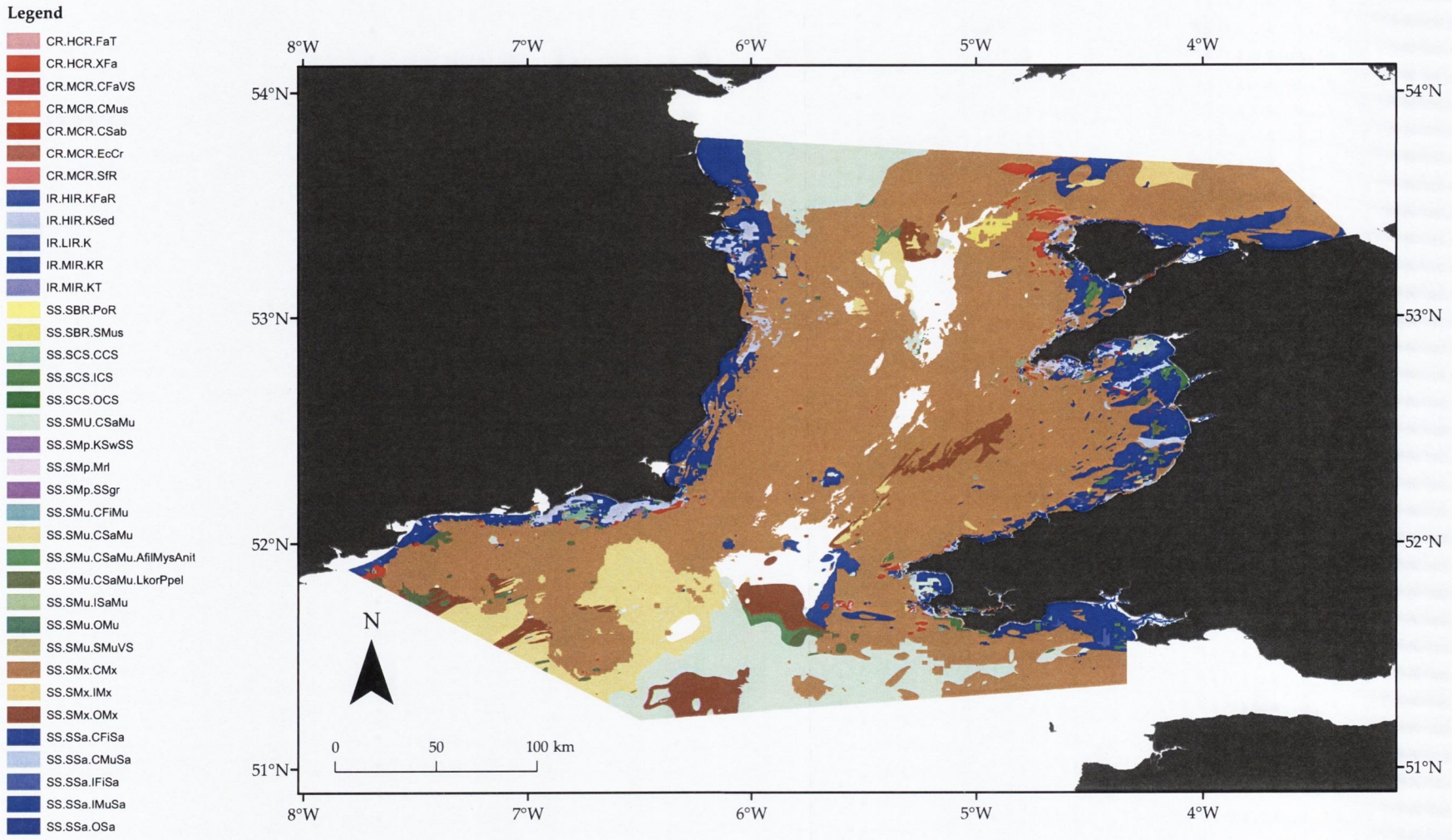


Figure 1.6: Combined HABMAP Level 3 and Level 4 MNCR biotope map (Robinson et al., 2007)

Table 1.3: Marine Habitat Classifictaion Review (MNCR) codes predicted for the southern Irish Sea by the HABMAP project.

MNCR Level 2	MNCR Biotope Code	MNCR Descriptions
High energy circalittoral rock	CR.HCR.Fat	Very tide swept faunal communities
	CR.HCR.XFa	Mixed faunal turf communities
Moderate energy circalittoral rock	CR.MCR.CFaVS	Circalittoral faunal communities in variable salinity
	CR.MCR.CMus	Circalittoral mussel beds on rock
	CR.MCR.CSab	Circalittoral *Sabellaria* reefs (on rock)
	CR.MCR.EcCr	Echinoderms and crustose communities
	CR.MCR.Sfr	Soft rock communities
High energy infralittoral rock	IR.HIR.KFar	Kelp with cushion fauna and/or foliose red seaweeds
	IR.HIR.KSed	Sediment-affected or disturbed kelp and seaweed communities
Low energy infralittoral rock	IR.LIR.K	Silted kelp communities (sheltered infralittoral rock)
Moderate energy infralittoral rock	IR.MIR.KR	Sediment-affected or disturbed kelp and seaweed communities
	IR.MIR.KT	Kelp and seaweed communities in tide-swept sheltered conditions
Sublittoral biogenic reefs on sediment	SS.SBR.PoR	Polychaete worm reefs (on sublittoral sediment)
	SS.SBR.SMus	Sublittoral mussel beds (on sublittoral sediment)
Sublittoral coarse sediment (unstable cobbles and pebbles, gravels and coarse sands)	SS.SCS.CCS	Circalittoral coarse sediment
	SS.SCS.ICS	Infralittoral coarse sediment
	SS.SCS.OCS	Offshore circalittoral coarse sediment
Sublittoral macrophyte-dominated communities on sediments	SS.SMp.Mrl	Maerl beds
	SS.SMp.SSgr	Sublittoral seagrass beds
Sublittoral cohesive mud and sandy mud communities	SS.SMu.CFiMu	Circalittoral fine mud
	SS.SMu.CSaMu	Circalittoral sandy mud
	SS.SMu.CSaMu.AfilMysAnit	*Amphiura filiformis, Mysella bidentata* and *Abra nitida* in circalittoral sandy mud
	SS.SMu.CSaMu.LkorPpel	*Lagis koreni* and *Phaxas pellucidus* in circalittoral sandy mud
	SS.SMu.ISaMu	Infralittoral sandy mud
	SS.SMu.OMu	Offshore circalittoral mud
	SS.SMu.SMuVS	Sublittoral mud in variable salinity (estuaries)

Table 1.3 (continued): Marine Habitat Classifictaion Review (MNCR) codes predicted for the southern Irish Sea by the HABMAP project.

MNCR Level 2	MNCR Biotope Code	MNCR Descriptions
Sublittoral mixed sediment	SS.SMx.CMx	Circalittoral mixed sediment
	SS.SMx.IMx	Infralittoral mixed sediment
	SS.SMx.OMx	Offshore circalittoral mixed sediment
Sublittoral sands and muddy sands	SS.SSa.CFiSa	Circalittoral fine sand
	SS.SSa.CMuSa	Circalittoral muddy sand
	SS.SSa.IFiSa	Infralittoral fine sand
	SS.SSa.IMuSa	Infralittoral muddy sand
	SS.SSa.OSa	Offshore circalittoral sand

1.7 Current European projects

Current projects in Europe involve an extension of UKSeaMap and a new project called EUSeaMap. The new UKSeaMap project aims to build on the earlier work of UKSeaMap and MESH to produce a single seabed habitat map for U.K. waters. This map will produce a EUNIS classified map based on improved environmental data and will be validated using more extensive biological data. This work is being carried out by the Joint Nature Conservation Committee (JNCC) and will be completed in 2010. EUSeaMap will use similar methods to produce updated seabed maps for European waters.

1.8 Ecological context

Physical, chemical and biological processes, both in the water column and the seabed, are fundamentally linked through highly complex systems (see Figure 1.7) (Gray and Elliott, 2009). Most marine benthic organisms rely on the water column for food or larval dispersion (Gray and Elliott, 2009). The main ecological processes are the same for organisms in either system (Gray and Elliott, 2009).

Figure 1.8 shows the main ecosystem functioning ecological processes affecting organisms. Gray and Elliott (2009) describe three kinds of interlinked relationships which create biological communities; environment–biology, biology–biology and biology-environment. Environment–biology relationships occur when physical and chemical characteristics (e.g. sediment type and water chemistry) provide the suitable conditions for biological organisms to colonize an area (Gray and Elliott, 2009). Biology-biology relationships alter the biological community structure

functioning through biological interactions such as competition and predation (Gray and Elliott, 2009). Finally, biology-environment relationships occur when the biological organisms alter the environment, e.g. through bioturbation (Gray and Elliott, 2009).

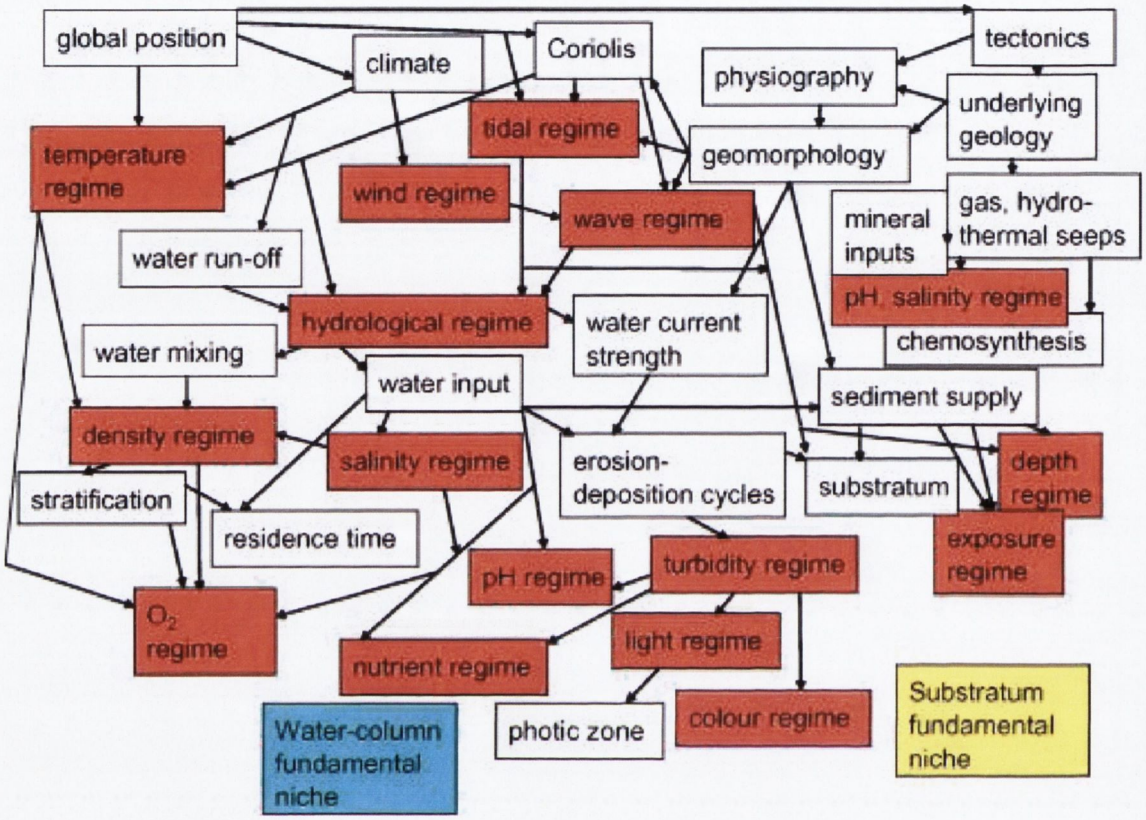


Figure 1.7: Links between physicochemical attributes resulting in the two main marine fundamental and overarching niches, for the water column and the substrate (Borja and Elliott, 2007, Gray and Elliott, 2009).

As many macrobenthic species are sessile as adults, the communities are strongly influenced by the habitat selection preferences of the larvae (Gray, 1974). The settlement of the larvae is governed by a combination of (often interrelated) physical, chemical and biological factors, such as the structure and contours of the surface, sediment particle size, the presence of organic and inorganic compounds, bio-films and populations of the same species. In addition, the presence of the organisms themselves can lead to changes in the composition of sediments (Gray, 1974, Rhoads, 1974). Snelgrove & Butman (1994) have reviewed the relationship between sediments and infauna and have concluded that particle size alone was not sufficient to explain community structure. However, they did emphasise that particle size may be correlated to other factors, such as the passive transport of larvae with sediment particles, or the organic content of the sediments as food for deposivores (Snelgrove and Butman, 1994).

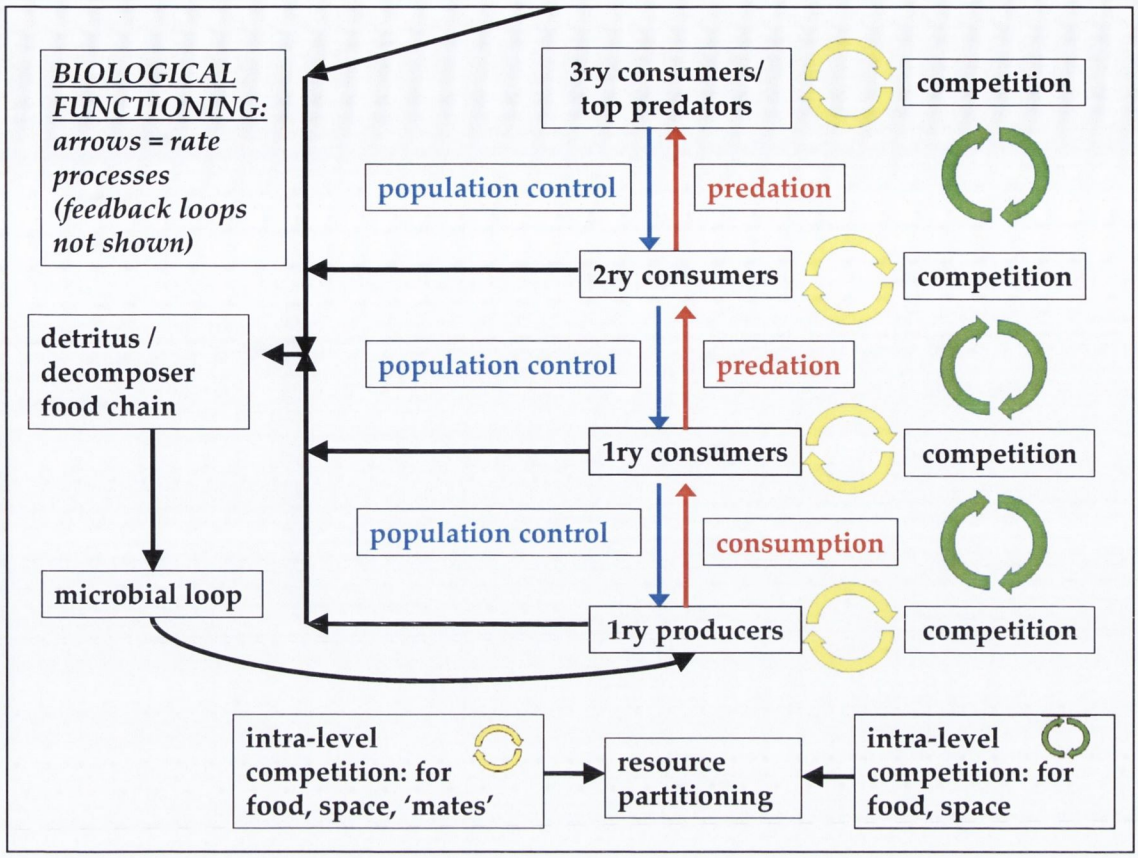


Figure 1.8: Ecosystem functioning - the main ecological processes (Gray and Elliott, 2009)

In areas with high densities and biomass of suspension feeders there is commonly a low density and biomass of epifaunal suspension feeders (Sanders, 1960, Rhoads and Young, 1970). Suspension feeders are more likely to be confined to sandy or firm mud substrates while deposit feeders are more likely to be found in abundance on soft muddy substrates (Rhoads and Young, 1970). Rhoads & Young (1970) suggested that reworking of a muddy bottom by deposit feeders produces a faecal rich surface that is easily re-suspended. This surface inhibits the colonization of the substrate by suspension feeders as suspended sediment clogs their filtering systems, newly settled larvae are buried and re-suspended, suspension feeder larvae are discouraged from settling and sessile epifauna are prevented from attaching to the unstable surface (Rhoads and Young, 1970).

1.9 *The southern Irish Sea*

The main study area (Chapter 3 - 6) was located in the southern Irish Sea. The study area was defined by the INTERREG IIIA area between Ireland and Wales stretching south from 54° 50'N to 51° 06'N between Ireland and Wales (see Figure 1.9). This area stretches from the southern Irish

Sea and across the boundary of the Irish Sea into the Celtic Sea. The southern Irish Sea consists of two shallow shelves on either side of St. George's Channel, which is over 100m deep (Bowden, 1955, Mackie et al., 1995a) (see Figure 1.9). The Irish platform, on the western side, is approximately 12-20km wide while the Welsh platform is up to 50km wide (James and Wingfield, 1987).

The study area is particularly important as it crosses the Celtic Front which acts as the boundary between southern Lusitanian species and northern Boreal species. The Celtic Front occurs at the boundary between the well-mixed waters of the Irish Sea and the highly stratified waters of the Celtic Sea (Boelens et al., 1999). The differences in seabed salinity and maximum seabed temperatures along the Celtic Front, from Carnsore Point on the Irish coast across to St. David's Head in Pembrokeshire, on the Welsh coast are shown in Figure 1.10 and Figure 1.11. The Celtic Front is generally established by mid-June and the greatest gradient in sea temperatures between the southern Irish and Celtic Seas occurs in mid-August (Boelens et al., 1999) (see Figure 1.11).

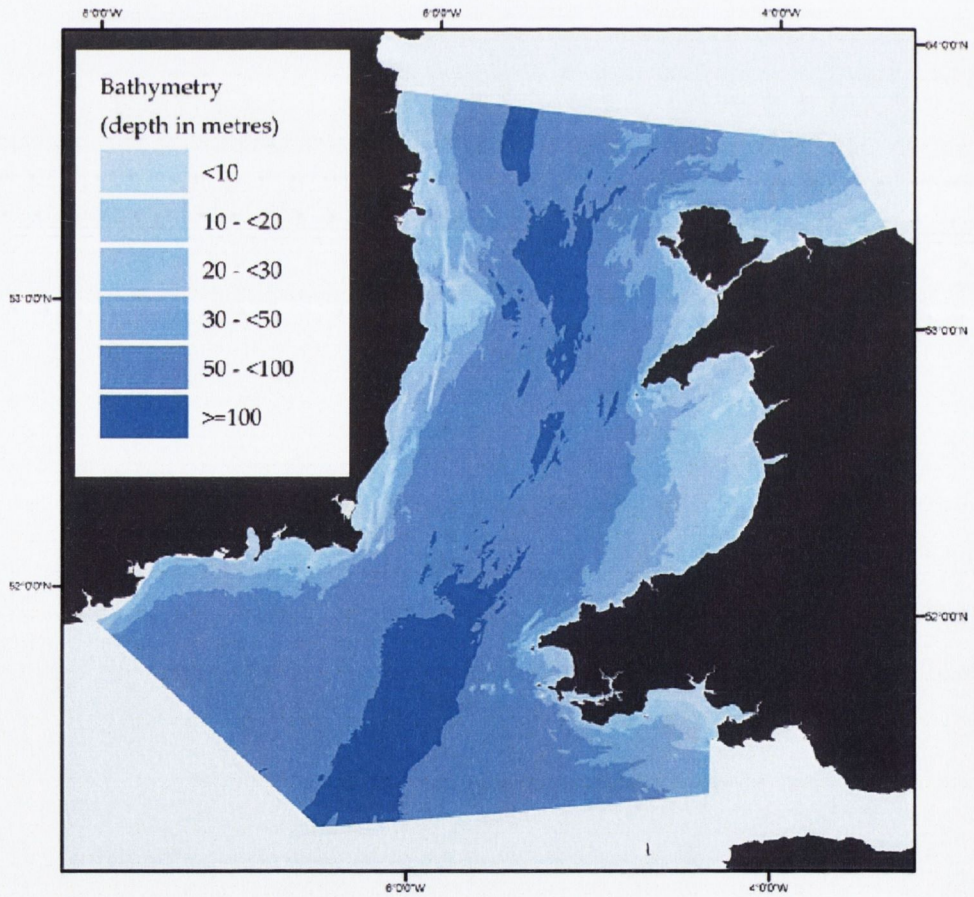


Figure 1.9: Bathymetry map of the HABMAP area (Robinson et al. (2007), Fig. 3.7, p 21,). Data derived from British Geological Survey (BGS) DIGIBATH250 data.

Tides, weather (such as surface waves and storm surges) and density differences are all major contributors to the circulation of water in the southern Irish Sea (Boelens et al., 1999). The tides move from the Atlantic northwards through St. George's Channel and southwards through the North channels, meeting to the south west of the Isle of Man with the majority of the tidal energy coming through St. George's Channel (Robinson, 1979). The mean tidal range varies from 1.75m at Carnsore Point to a mean spring tide of 8m on the Lancashire and Cumbrian coasts (Boelens et al., 1999).

Summer thermal stratification at the Celtic Front reduces mixing between the Irish and the Celtic Seas as saline Atlantic currents are directed across St. George's Channel westwards along the Irish Coast and southward into the Celtic Sea (Brown et al., 2003). A saline tongue can be seen stretching into the Irish Sea from the Celtic Sea on the seabed salinity map (see Figure 1.10). Water in the Irish Sea is thought to have a flushing cycle of one year (Gowen and Stewart, 2005). A density-driven cyclonic gyre operates in the western Irish Sea stratifying the cold bottom and warm surface waters in spring and summer (Boelens et al., 1999, Horsburgh and Hill, 2003) and material is retained within this gyre during those months (Boelens et al., 1999). Net long term circulation in the Irish Sea flows northwards along the British coast, exiting through the North channel, with a weaker return flow along the Irish coast (Boelens et al., 1999). Winds on the continental shelf can affect the interaction of water flows in the Irish Sea and affect the long term transport of material from the Irish Sea through the North channel (Xing and Davies, 2001).

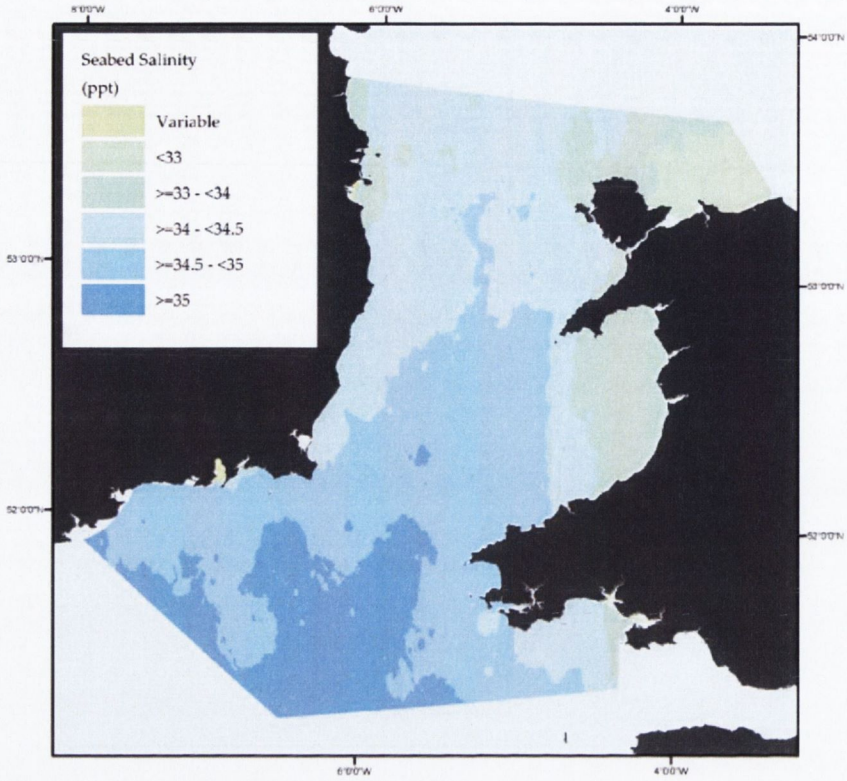


Figure 1.10: Annual mean seabed salinity map (ppt) for the HABMAP study area, (Robinson et al. (2007), Fig. 3.7, p 20).

The sea floor of the southern Irish Sea is predominantly sandy gravel, grading down through sand to mud in the deeper parts of the Celtic Sea and also in the shallower northern basin beyond Anglesey (see Figure 1.12) (Dobson et al., 1971, Robinson et al., 2007, Wilson et al., 2001) . Most marine sediments in the southern Irish Sea originate from glacial rather than riverine input (Mackie et al., 1995a). Southern Irish Sea sediments have been found to contain varying amounts of calcium carbonate derived from a range of sources such as calcareous algae, Foraminifera, sponges, Bryozoans, ostracods, cirripeds, malacostraceans, lamellibranchs, gastropods, scaphopods, asteroids, ophiuroids, echinoids and holothuroids (Dobson et al., 1971).

The Irish Sea has been divided into 9 different types of macrobenthic assemblage related to substrate and depth by Mackie (1990). A provisional map of the benthic assemblages in the Celtic Sea, based on an unpublished map by Cabioch, separated the Celtic Sea into seven different benthic assemblages based on sediment type (Boelens et al., 1999). These quantitative maps rely heavily on sediment types and provide different maps to those based on qualitative beam trawl data produced by Ellis et al. (2000) for the Irish Sea (six assemblage types) and by Ellis et al. (2002) for the Celtic Sea (two assemblage types) which rely more on epifaunal than infaunal data.

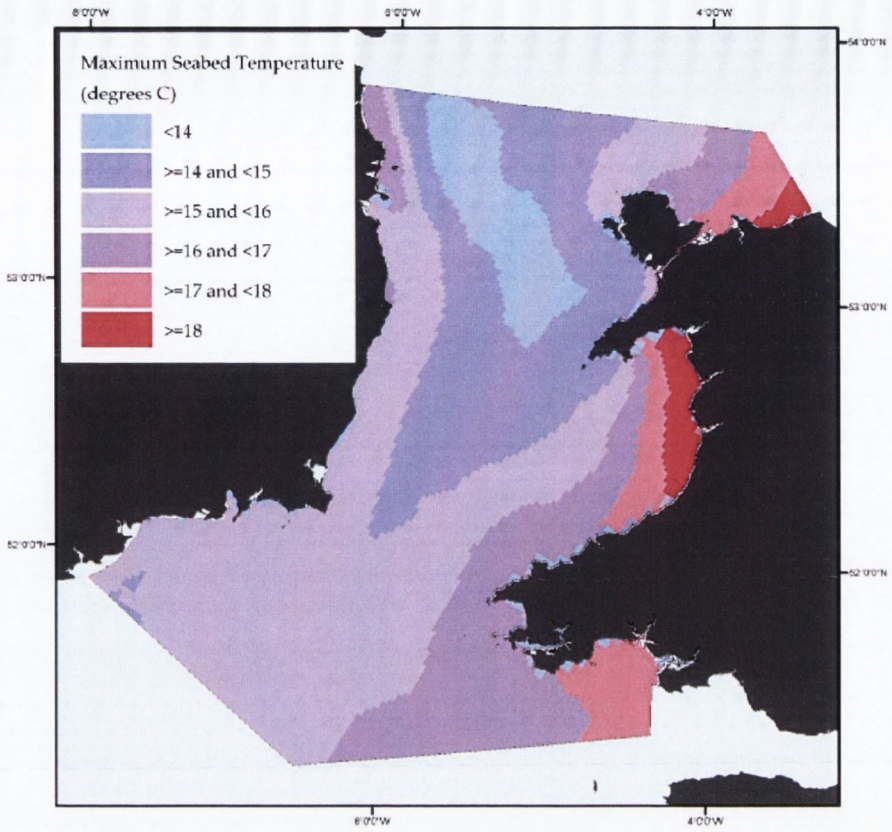


Figure 1.11: Maximum seabed temperature (°C) map of the HABMAP area derived by outputs from the ECOMSED model by Dabrowski (2005) (Robinson et al. (2007), Fig. 3.3, p 16).

Ecosystem function in the Irish Sea has been studied by Bremner et al. (2006) in their examination of some of the biological traits of benthic invertebrates (representing life history, morphology and behavioural characteristics) and environmental conditions in the Irish Sea, Bristol Channel and eastern English Channel. Using the RELATE procedure (Clarke and Ainsworth, 1993), biological traits were found to have the strongest correlation with the combination of salinity, sea surface temperature, average temperature range, weight of the shell in catch, fish taxon richness and the amount of fishing (ρ =0.417) (Bremner et al., 2006).

Lees and Mackinson (2007) used an Ecopath model to compare the whole Irish Sea ecosystem to the Ecopath models of the North Sea, English Channel and Western Channel ecosystems. The Ecopath model calculated a value of 33.71 for the ratio of total primary production to total biomass (PP:B) for the Irish Sea (Lees and Mackinson, 2007). The total PP:B was slightly higher than that of the English Channel (31.11) (Stanford and Pitcher, 2000) and substantially higher than those of the Western Channel (15.02) (Araújo et al., 2005) and the North Sea (3.82) (Mackinson and Daskalov, 2007). The Finn Cycling Index (FCI) which shows the total throughput percentage of

the system was compared between ecosystems and it was found that the North Sea (5.610) was the most developed of the four systems followed by the Western Channel (0.730), Irish Sea (0.590) and English Channel (0.140). The report notes however that caution is advised when comparing models as the ecosystems are sensitive to differences in how the models were specified (Lees and Mackinson, 2007).

Wragg (2006) in his network analysis of the Irish Sea concluded that the stability and recycling within the Irish Sea was largely dependent on benthic fauna, which contained two major fisheries of *Nephrops norvegicus* and *Buccinum undatum* (Ball et al., 2000, Fahy, 2001). Fishery extraction in the Irish Sea was estimated to affect benthic faunal biomass substantially more than pelagic or demersal fisheries, extracting 11.30% of the benthic biomass, compared to 0.66% of pelagic biomass and 0.85% of demersal biomass (see Table 1.4), thus indicating that benthic fauna could be very vulnerable to over-fishing (Wragg, 2006). However, both pelagic and demersal fisheries extracted higher percentages of the productive fauna than benthic fisheries, indicting that perhaps benthic fauna may be more resistant to fishing than pelagic or demersal fisheries (see Table 1.4).

Table 1.4: Percentage of fisheries extract from trophic compartments in the Irish Sea (Wragg, (2006): p 52).

Trophic compartment	Fishery Extracts g C m^{-2} yr^{-1}	Biomass %	Respiration %	Production %
Benthic	0.048	11.30	3.11	0.42
Pelagic	0.017	0.66	6.68	0.70
Demersal	0.015	0.85	6.15	1.03

Otter trawls, *Nephrops* trawls (modified otter trawls), beam trawls and scallop dredges are deemed to be the methods of fishing which cause the most physical disturbance to large areas of the Irish Seabed (Kaiser et al., 1996). The Irish Sea supports less fishing than the North Sea as fish yields are lower thus leading to fewer disturbances by fishing vessels in the Irish Sea (Brander and Dickson, 1984, Kaiser et al., 1996). Many of the areas fished heavily in the Irish Sea are in areas adapted to regular natural disturbances, therefore these habitats are less disturbed by overfishing, however, *Modiolus* communities have been highlighted as being particularly vulnerable to overfishing (Kaiser et al., 1996). Kaiser and Spencer (1996) and Hiddink et al. (2006) have found that fishing reduces benthic macrofaunal abundance and biomass respectively in the Irish Sea.

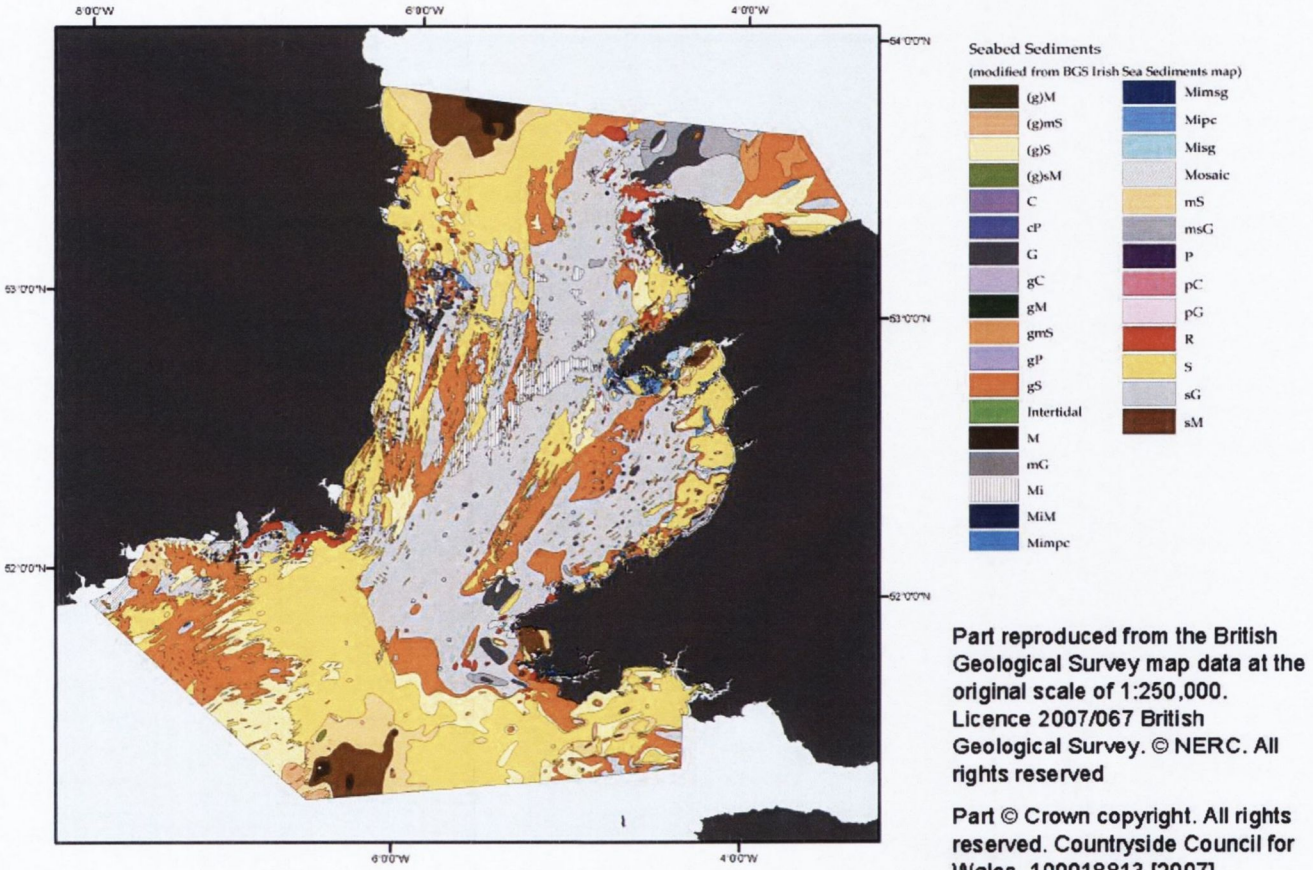


Figure 1.12: Sediment map for the southern Irish Sea based on the BGS Irish Sea Sediments map, Robinson et al. (2007), Fig. 3.18, p 34.

1.10 *BIOMÔR, SWISS & HABMAP*

This study incorporates sediment and macrofaunal data from three Irish Sea projects, BIOMÔR (Mackie et al., 1995a), SWISS (Wilson et al., 2001) and HABMAP (Robinson et al., 2007) which all focus on the benthic diversity of the southern Irish Sea (see Figure 1.13). The BIOMÔR, SWISS and HABMAP projects have used sediment particle size, organic matter, total organic carbon and nitrogen along with benthic macrofaunal abundance to define habitats and biological communities in the southern Irish Sea. The physical gradient in particle size is correlated with organic content and also with biological communities. There are, however, marked discrepancies between boundaries defined by the classical sediment characterisation trigon, by the chemical characteristics of the sediments and by biological communities.

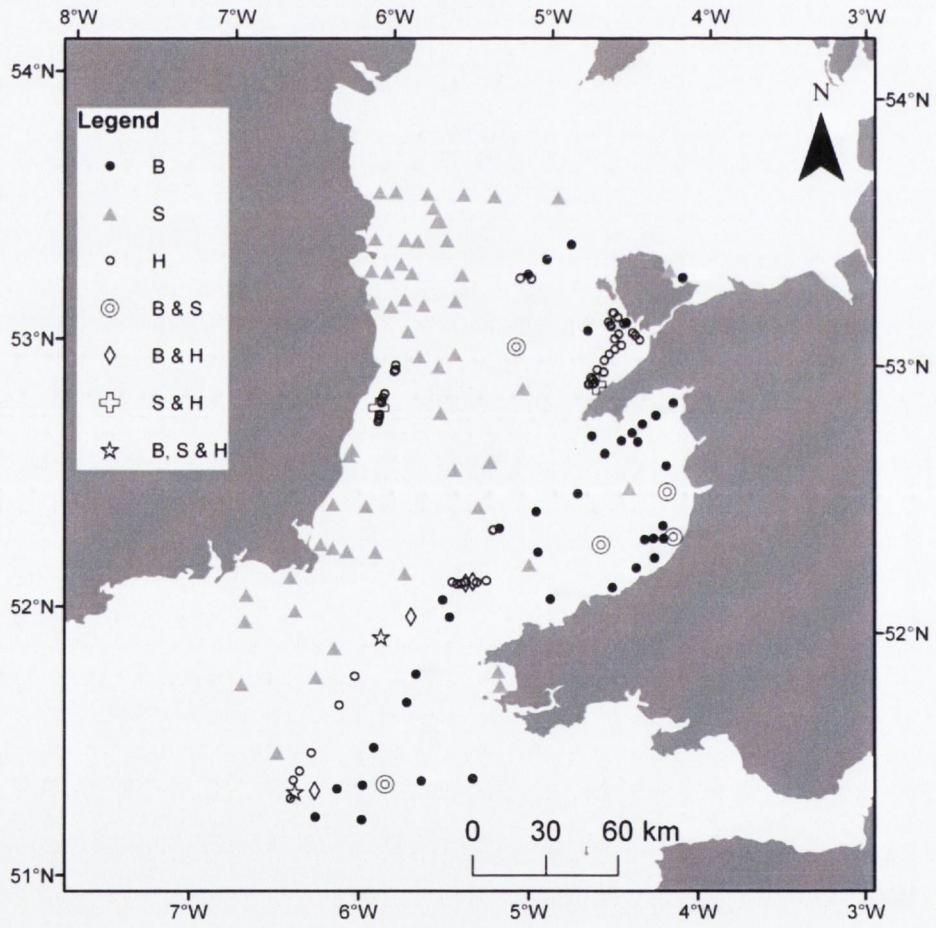


Figure 1.13: Location of BIOMÔR (B), SWISS (S) and HABMAP (H) sites.

Sediment data from the BIOMÔR project and macrofaunal data for all three projects were kindly provided by Dr. Andrew S.Y. Mackie from the National Museum of Wales (Mackie et al., 1995a, Wilson et al., 2001, Robinson et al., 2007). Sediment data from the SWISS project were provided by Trinity College Dublin (Nic Aonghusa, 1999). Sediment data from the HABMAP project were

sampled and analysed during this study (see Chapter 3). BIOMÔR (1989-91) was a Welsh project led by the National Museum of Wales which studied benthic sites on the Welsh side of the Irish Sea (Mackie et al., 1995a). It aimed to obtain invertebrates for taxonomic and bio-geographic purposes and to obtain quantitative data for the southern Irish Sea (Mackie et al., 1995a). The South West Irish Sea (SWISS), a joint Irish-Welsh project followed on from BIOMÔR in 1997-98 and aimed to further knowledge of the benthic environment on the Irish side of the Southern Irish Sea (Wilson et al., 2001). HABMAP followed in 2004-2007 aiming to build on the previous work of BIOMÔR & SWISS by focusing on the fine scale to produce biotope maps for the southern Irish Sea (Robinson et al., 2007).

1.11 Chapter Outlines & Aims

This study aims to explore different benthic properties which could be used in seabed mapping. Traditional benthic mapping projects focus on abiotic variables or macrofaunal data to produce habitat and biotope maps. The integration of increased biological data (e.g. meiofauna) and ecosystem properties (e.g. secondary production) could lead to more ecosystem-orientated seabed maps.

1.11.1. Chapter 2

This chapter examines the repeatability of the Van Veen grab sampler. Ground-truthing is an important process in marine benthic habitat mapping. Both broad-scale and fine-scale maps need to be ground-truthed so that sediment data can be used to validate interpolated and predictive marine benthic habitat maps. Maps are only as good as the underlying data. It is essential that scientists can have confidence in the ground-truth data that they use to validate their maps.

The repeatability of quantitative sampling in the marine environment is important in situations where replicate sampling can be limited due to time and monetary constraints. This issue is examined in Chapter 2 which looks at the spatial variability of the chemical and physical properties of Van Veen grab sediment samples at three different spatial scales in a homogenous environment in Dublin Bay. A modified long armed continuous warped 0.1m^2 Van Veen grab was used to quantitatively sample the sediments, foraminifera and macrofauna discussed in chapters 2 - 6. It was decided that further investigation was required to assess the repeatability of the Van Veen grab in sampling physical and chemical sediment characteristics.

Aim

- To quantify the variability of samples at three different spatial scales: within a single Van Veen grab, at a site and within a homogenous biotope.

1.11.2. Chapter 3

This chapter aims to provide sediment data which can improve marine benthic habitat maps for the HABMAP survey areas. The sediment data will ground-truth the geophysical data and will be used to assign habitats and biotopes for the areas. It will provide information about the habitats that the biological organisms inhabit. The sediment data will be compared to existing British Geological Survey maps for the areas in question to see whether improvements can be made. The sediment properties examined in this chapter will also facilitate analyses in subsequent chapters.

The physical and chemical sediment characteristics of the HABMAP sites in the southern Irish Sea are explored in Chapter 3. Particle size and the sediment chemical characteristics of organic content, calcium carbonate and organic carbon are measured for each station. This chapter facilitates the testing of hypotheses in this and subsequent chapters in order to test the relationship between sediment characteristics and biological assemblages at sites in the southern Irish Sea.

Aims

- Investigate the physical and chemical properties of the sediments at the HABMAP stations in the southern Irish Sea.
- Explore the relationship between particle size and the chemical characteristics of the sediment at these stations.
- Test the relationship between sediment characteristics and biological assemblages in the southern Irish Sea.
- Compare HABMAP particle size data with British Geological Survey (BGS) data.

1.11.3. Chapter 4

Chapter four examines foraminiferal assemblages of the Celtic Deep. The chapter tests the relationship between foraminiferal assemblages and sediment characteristics and compares site classifications of foraminiferal and macrofaunal assemblages. The data will be used to construct foraminiferal biotope maps for the area. The assemblages will be compared to those from

previous projects in the area. Macrofauna and meiofauna exist in the same sedimentary habitats. Comparisons will be made to see if the patterns of total (live & dead) benthic foraminiferal assemblages follow similar patterns to those of benthic macrofaunal assemblages. Previous work by Le Calvez (1958), Murray (1979) and Scott et al. (2003) focused on the foraminifera of the Celtic Sea but did not draw links between macrobenthic and foraminiferal assemblages. Unlike macrofauna, benthic foraminifera do not have swimming abilities and thus they cannot actively enter the water column of their own accord (Alve, 1999). Thus foraminifera cannot actively select preferred habitats over wide distances. This could be useful in reconstructing historical macrofaunal environments.

Aims

- Identify foraminiferal assemblages in the Celtic Deep.
- Explore the potential of using foraminifera tools in habitat mapping
- Discriminate among assemblages at different taxonomic levels.
- Compare site classifications of foraminiferal & macrofaunal assemblages.
- Test the relationship of environmental variables with foraminiferal assemblages.
- Compare this study with previous work.

1.11.4. Chapter 5

This chapter examines the possibility of using logistic and multiple regression analyses as tools for predictive marine benthic habitat mapping. It focuses on the validity of using physical and sediment characteristics to predict benthic macrofaunal assemblages in the southern Irish Sea. While physical properties of the seabed and water column are often incorporated into habitat classification systems, sediment chemical characteristics and ecosystem function (e.g. biomass or productivity), community structure and meiofaunal data (e.g. foraminifera) are not incorporated into these classifications. As it is impossible to survey and ground-truth every inch of the seabed, predictive tools for habitat mapping are extremely useful in helping us to understand more about marine benthic environments. Regression analysis has previously been used to predict the presence or absence of benthic species. This chapter explores whether the same methods are useful in predicting benthic habitats. This chapter will also examine the possibility of incorporating sediment characteristics into habitat classification systems such as EUNIS or the MNCR.

Aim

- Evaluate the validity of using binary logistic regression to predict benthic macrofaunal community distributions from physical and sediment characteristics.

1.11.5. Chapter 6

The validity of using multiple regression and binary logistic regression to predict benthic macrofaunal community function, in terms of benthic macrofaunal biomass and productivity, from physical and sediment characteristics is tested in this chapter. Maps are produced interpolating benthic macrofaunal biomass and productivity using the BIOMÔR (Mackie et al., 1995a), SWISS (Wilson et al., 2001) and HABMAP (Robinson et al., 2007) datasets. With increasing emphasis on the ecosystem approach to management, benthic habitat mapping will increasingly have to take account of biological structuring and system function and may be more accurately based on process-relevant parameters rather than on the traditional particle size classification schemes. Duarte (2000) suggests that ecosystem function depends on the type of species in the ecosystem rather than on the abundance of species in the ecosystem.

It is important to understand the processes which take place in benthic habitats. Habitat maps are extremely useful, but once you know what exists you need to look in greater detail at the structure and function of the habitats to understand how the individual components of the ecosystem affect each other. Benthic macrofaunal productivity is an important component in the structure and function of an ecosystem. It is an area which has not been fully explored in the southern Irish Sea. It provides vital information on the availability of food and health of a habitat.

Aim

- Evaluate the validity of using binary logistic regression to predict benthic macrofaunal community function from physical and sediment characteristics.
- Map benthic macrofaunal biomass and productivity in the southern Irish Sea.

Chapter 7

This chapter aims to draw together the recommendations and conclusions of the study as a whole and examine their benefit to benthic habitat mapping.

Chapter 2

2 Spatial variability of Van Veen grab samples

2.1 Introduction

2.1.1 Overview

On a research cruise factors such as time and money are of extreme importance, especially when multiple research projects are taking place on the same cruise. There may not be enough time to do extensive ground-truthing. Modern marine benthic habitat mapping usually involves using a combination of acoustic mapping (e.g. through multibeam or sidescan sonar) and ground-truthing (e.g. through grab sampling or video sampling) to produce benthic habitat and biotope maps (Magorrian et al., 1995, Brown et al., 2004, Kendall et al., 2005, Ierodiaconou et al., 2006). On the HABMAP sampling cruise, for example, areas in the southern Irish Sea were surveyed using multibeam sonar, video sampling, sediment profile imagery, macrofaunal, foraminiferal and sediment sampling. The geophysical survey was used to stratify areas to be ground-truthed on the sampling survey.

Underwood & Chapman (2005) state that clear objectives are needed when undertaking quantitative sampling, both in terms of the variables to be measured and the hypotheses to be tested. Benthic assemblages are patchy both in their distribution and their abundance (Underwood and Chapman, 2005); the same is true of sedimentary habitats. Robinson et al. (2007) in their modelling of benthic species and habitats used 63 sediment classes in order to account for the patchiness of sediments. Mosaics (areas of rocks and sediment) and mixtures (areas containing a mix of pebbles or cobbles and Folk sediments) were used in addition to the Folk classification and a new gravel classification (Robinson et al., 2007). Broad-scale habitat mapping generally does not account for the fine-scale patchiness of sediments.

2.1.2 Sampling design

The appropriate sampling design for a survey depends on the questions being asked (Bale and Kenny, 2005, Gray and Elliott, 2009). A systematic grid approach involves making no judgements about an area in advance (Gray and Elliott, 2009). Today, however, with the advent of modern technology, a stratified random design which results in a similar amount of effort being exerted in each stratum may be more appropriate.

There are several different sampling designs which can be used; simple random, proportional random and optimal random sampling (Gray and Elliott, 2009). Simple random sampling involves allocating the same sampling effort per area (Gray and Elliott, 2009). In a study area that has had been mapped using acoustic methods where different strata have been identified, simple random sampling would mean that the same sampling effort would be applied to each different area (Gray and Elliott, 2009). Proportional sampling involves applying the same sampling density to each area identified by the geophysical mapping, e.g. by overlaying a grid over the whole survey area and taking one sample per grid unit (Gray and Elliott, 2009). Optimal sampling takes more samples in variable strata (Gray and Elliott, 2009).

Replicate sampling results in a better statistical power to pick up differences between areas but results in less spatial coverage (Gray and Elliott, 2009). Underwood and Chapman (2005) state that sample replication is mandatory in any benthic study in order to estimate the natural variation. However, Gray and Elliot, (Gray and Elliott, 2009) state that single samples can be useful to describe the characteristics of areas (Gray and Elliott, 2009). Each sampling method has pros and cons depending on whether the statistical differences within a site, between sites, between strata or between sampling occasions are most important (Gray and Elliott, 2009).

2.1.3 Van Veen Grab sampler

The repeatability of samples in the marine environment poses a problem. Due to environmental factors such as wind, waves and tides, repeatable grab samples at a site or within a habitat can be difficult to achieve. Mackie (2004): corrected in Mackie et al. (2006), has found that replicate macrofaunal samples using the modified 0.1m^2 long armed continuous warp Van Veen grab sampler agreed with each other, but there are no data on the repeatability of the chemical and physical sediment characteristics from samples taken using the modified 0.1m^2 Van Veen grab.

In response to these variability and repeatability issues, it was decided to conduct a preliminary survey in Dublin Bay before the main HABMAP fieldwork took place to examine the variability of the modified Van Veen grab which would be used during the summer field work when sampling sediment characteristics. The aims were to examine the consistency of replicate sediment sampling using the Van Veen grab sampler in terms of the physical and chemical characteristics of the sediment and to establish the variability within a site and a supposed designated 'biotope' which is expected to be homogenous in nature, with sediment samples from the area having the same characteristics.

Previous studies on the repeatability of the Van Veen grab have focused on sediment volume (Lie and Pamatmat, 1965), comparisons of the Van Veen with other benthic samplers in terms of sampling epibenthic marine benthos (Wigley, 1967) and infaunal marine benthos (Beukema, 1974, Gage, 1975, Heip et al., 1977, Riddle, 1989b, Riddle, 1989a). Lie and Pamatmat (1965) examined the repeatability of the Van Veen grab in terms of sediment volume and infauna. They found the coefficient of variation for sediment volume to range from 7.4% to 20.3%. Riddle (1989b) examined the bite profile of six benthic grab samplers; the Petersen grab, a chain-rigged Van Veen, a short arm warp rigged Van Veen, a long arm warp rigged Van Veen, a Day grab and a Smith-McIntyre grab. The long arm warp rigged Van Veen was found to sample 100% of the sediment in the 40-50mm depth range. The long arm warp rigged Van Veen had the largest bite profile and the greatest depth penetration.

The Van Veen grab used in this project was a modified $0.1m^2$ long armed continuous warp Van Veen grab sampler (see Figure 2.1) used regularly by workers from the National Museum of Wales. The grab sampler had been modified with an L-frame to improve digging efficiency and to make the sampler more stable on the seabed (Riddle, 1989b, Mackie et al., 2006). The modifications also made the grab safer for personnel to use (Wilson et al., 2001). It had been used successfully in 5 earlier studies; in the Irish Sea (Wilson et al., 2001), in Carmarthen Bay in southwest Wales (Woolmer, 2003), on Welsh sandbanks (Darbyshire et al., 2002), in the Seychelles (Mackie et al., 2005) and in the Outer Bristol Channel (Mackie et al., 2006).

Figure 2.1: The modified long-arm continuous warp $0.1m^2$ Van Veen grab onboard the RV Celtic Voyager, July 2005.

2.1.4 Study area

Dublin Bay is a shallow bay on the eastern side of Ireland, surrounded on three sides by Dublin city with a general clockwise circulation of water (Spencer, 1972). Three main rivers, the Tolka, the Liffey and the Dodder flow into the Bay. Rees & Walker (1974) established the presence of a residual gyre in Dublin Bay. The tidal range in Dublin is 3.80m with the flood tide running north and the ebb tide running south (Harris, 1980). The flood tide enters from the south, flows clockwise through the bay mixing with water from the Liffey and exits the Bay at Howth Head (Harris, 1980). Sea-bed temperature ranges from 13 - 15° C (Harris, 1980).

Harris (1980) describes the sediment of Dublin Bay as primarily sands, ranging from very fine sand to medium sands (see Figure 2.2). Dublin Bay has been divided into 6 different zones, categorised by macrofaunal community type, as shown by Wilson & Magennis (1985) and Wilson (1987) (see Figure 2.3). The study area for Chapter 2 is located in the fine sand '*Venus* community' in south Dublin Bay (see Figure 2.4) (Harris, 1980, Wilson and Magennis, 1985, Wilson, 1987) . This area was chosen as a homogenous area was required for sampling and it avoided the busy shipping lanes of Dublin Port. Sediment samples taken by Harris (1980) using a 2km grid had indicated that the area was comprised of poorly to moderately sorted fine sands with a median grain size of 3.0 phi and approximately 10% calcium carbonate content (Harris, 1980). Wilson & Magennis (1985) found the study area was dominated by a '*Venus*' community.

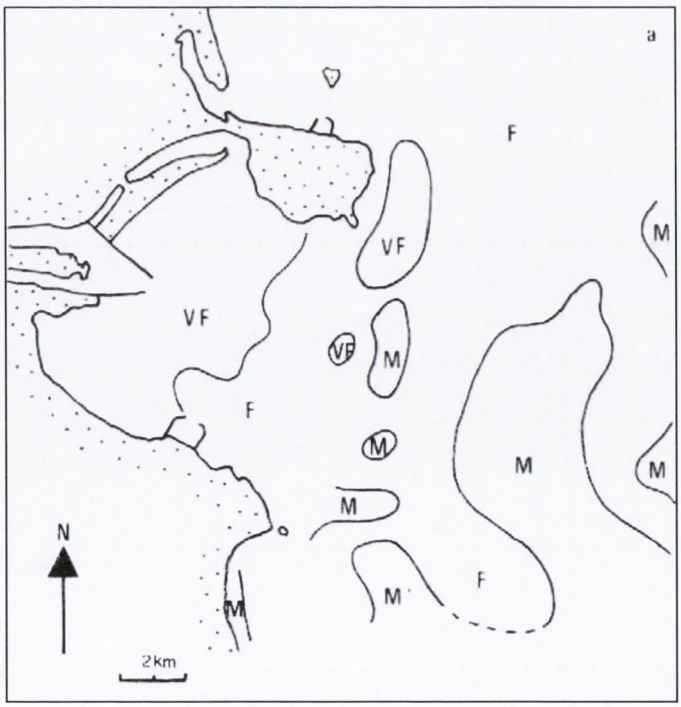


Figure 2.2: Modal distribution of sediment particle size in Dublin Bay. VF = very fine sand, F = fine sand and M = medium sand. Figure taken from Harris (1980), Fig. 5, p 46.

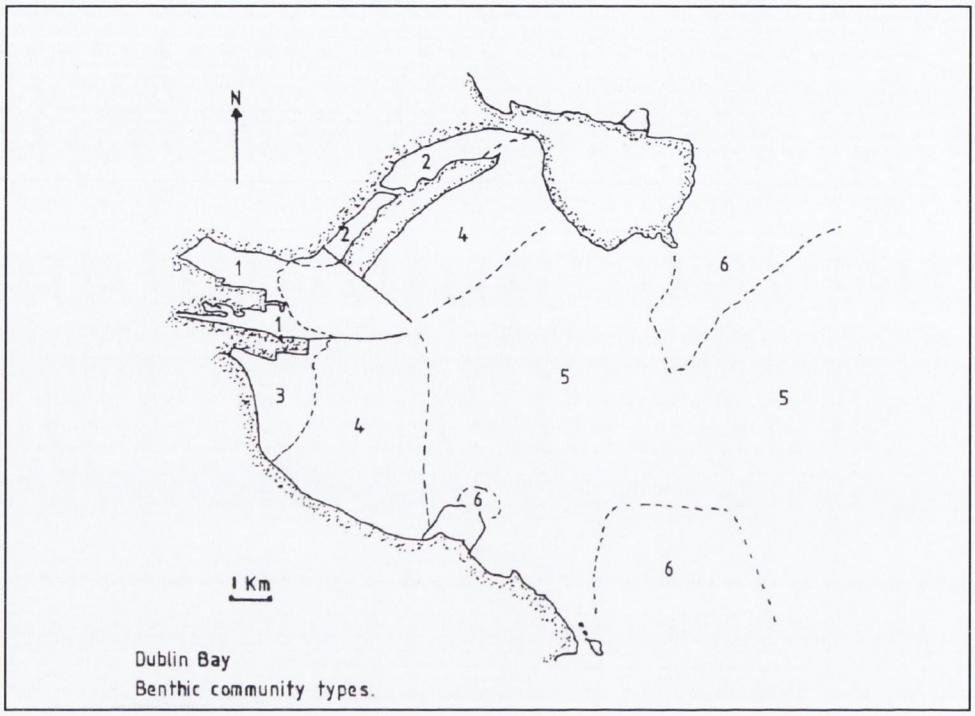


Figure 2.3: Dublin Bay zoned by community type. 1 = Abnormal, 2 = muddy *Macoma*, 3 = sandy *Macoma*, 4 = *Tellina*, 5 = *Venus* and 6 = *Abra* (Wilson and Magennis, 1985, Wilson, 1987).

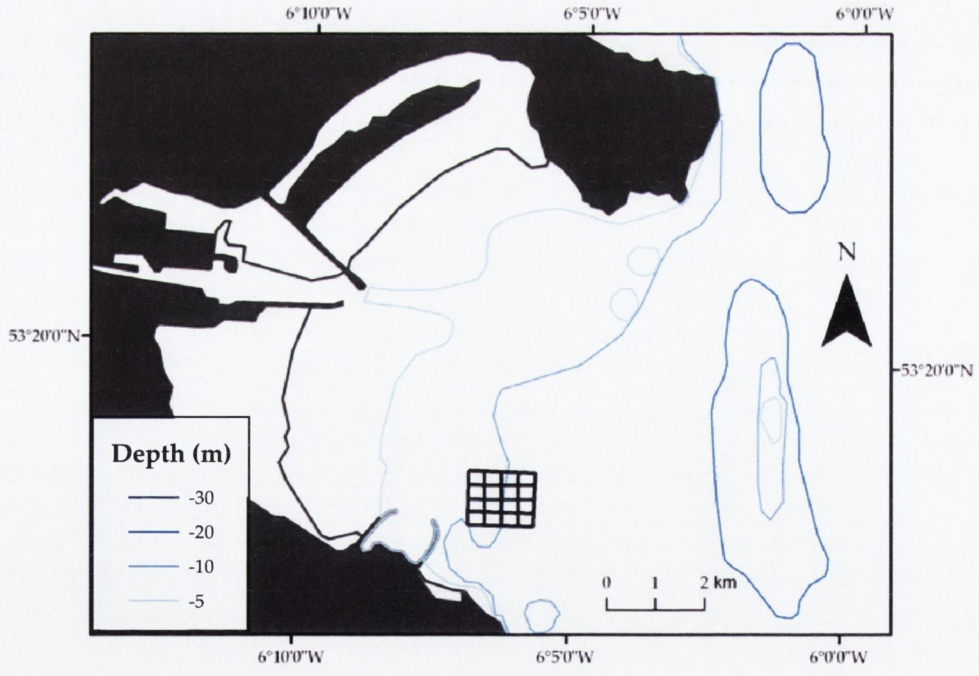


Figure 2.4: The Dublin Bay sampling area located in the fine sand '*Venus*' community (Harris, 1980, Wilson and Magennis, 1985, Wilson, 1987).

2.1.5 Aims of Dublin Bay study

This chapter focuses on the spatial variability of the physical and chemical sediment characteristics of samples taken using the Van Veen grab in Dublin Bay by quantifying the variability of sediment samples at three different spatial scales: within a single Van Veen grab, at a site and from several sites within a homogenous biotope. A homogenous biotope is a biotope made of the same elements, e.g. a biotope which has consistent abiotic and biotic conditions such as depth, temperature, current, tide, salinity, substrate and a single macrofaunal community. A heterogeneous biotope could, for example, contain different substrates such as rock and muddy sand and different infaunal and epifaunal communities. The aims of this chapter are as follows:

- Test the repeatability of samples in a single Van Veen grab sample
- Test the repeatability of samples taken with the Van Veen grab at a single site
- Test the repeatability of samples taken with the Van Veen grab at different sites within a homogenous biotope

2.2 *Methods*

2.2.1 Field work

Using historical data from Dublin Bay (Harris, 1980, Wilson and Magennis, 1985, Wilson, 1987), a homogenous biotope of fine sand, 10m water depth and a *Venus* community was selected in Dublin Bay (see Figures 2.3 and 2.4). The initial location of the sampling area had to be changed on board the vessel *RV Celtic Voyager* due to the close proximity of the initial sampling area to shipping lanes in the area. The final location of the grid is shown in Figure 2.4.

The experiment examined the variability within a sampler (GS), the variability of a sampler at a site (SS) and the variability of the sampler at different sites within a biotope (BS). A 4 x 4 grid, with 16 rectangles of equal size was constructed in the biotope using the computer program ArcMap (see Figure 2.5). A random number generator was used to decide which box each sample would be located in (Haahr, 2007). Samples were taken at random locations within the designated boxes. The ship was positioned within each designated box and the samples taken.

1	2	3	4
5	6	7	8
9	10	11	12
13	14	15	16

Figure 2.5: Grid of Dublin Bay sampling areas.

On the 27th April 2005, sediment samples were taken in Dublin Bay on the *R.V. Celtic Voyager* to test the variability of a modified 0.1m^2 long-arm continuous warp Van Veen grab (Figure 2.1). Approximately 100g of sediment was taken for each sample. Samples were placed in polythene bags, labelled and frozen. For the GS samples, ten samples were taken from a single Van Veen grab sample, ten separate Van Veen grab samples were taken from an individual site (SS) and nine separate Van Veen grab samples were taken from individual sites within a homogenous biotope (BS). Sediment samples were taken by hand from the surface of the grab through the hatch of the sampler. To complete the experiment properly it was necessary to take all the samples in the same habitat and at the same time; this enabled the variability of factors such as tide, wind, current and the accuracy of positioning systems to be reduced.

As the grab samples (GS) were all contained within the one grab, there are differences between the ways in which these samples were taken as opposed to the site (SS) and biotope (BS) samples. The sediment samples taken for site (SS) and biotope (BS) were the only samples taken from each grab. As the grab samples (GS) were taken from a single grab, the samples would be taken at different depths to the site (SS) and biotope (BS) samples. These sampling differences could have an effect on the final results.

2.2.2 Laboratory work

Sediment analysis in the laboratory was completed with the help of technical assistant Katie Reeves-Arnold in Trinity College Dublin. Sediment samples were dried at 105°C in the oven. Sediment samples were analysed for organic content, total organic carbon, total organic nitrogen, calcium carbonate and particle size.

2.2.2.1 Particle size analysis (PSA)

Particle size analysis followed procedures of Buchanan (1984). The sediment (25-30g) was pre-treated with 100ml of 30% hydrogen peroxide to remove organic matter. The samples were left overnight to allow the oxidation of organic matter. The next day they were heated gently and hydrogen peroxide was added till no further reaction occurred. The contents were washed onto no. 50 Whatman filter paper using a Buchner filter and distilled water. After filtration, the sediment was washed from the filter paper using 200-300ml of distilled water. Ten millilitres of the dispersant sodium hexametaphosphate (6.2g/l) was added. The mixture was stirred for 15 minutes and left overnight. The next morning the sediment was stirred again and washed through a 500μm sieve into a basin. The sieve was agitated and puddled to separate the finer sediments. The two fractions were washed into containers and placed to dry in the oven at 105°C. The 8mm to 500μm fractions were mechanically sieved through 8mm, 4mm, 2mm, 1mm and 500μm sieves. Each fraction was weighed and any sediment less then 500μm in size was added to the finer sediment.

The finer fraction was analysed using a Malvern Mastersizer E laser particle size machine. The less than 500μm fraction was weighed and a sub-sample of it was mixed in a conical flask with a solution of 10% sodium hexametaphosphate (to ensure even dispersal of particles throughout the solution). The solution was placed on a shaker overnight. The next morning the samples were added to water in the Malvern laser particle size machine & analysed. The samples were kept on

the shaker until they were ready to be analysed. A printout of the percentage size fractions of the sample was obtained from the machine. A minimum of three readings were taken for each sample. Percentages of sediment fractions over 500, 250, 125, 63 and 31μm were converted into percentages of the total sediment weight.

2.2.2.2 Organic content

The procedure for organic content followed that of the SWISS project (Buchanan, 1984, Wilson et al., 2001). Organic content was determined by weighing 2g of dried sediment into a pre-weighed, oven-dried crucible. The crucible was placed in a muffle furnace and the temperature was slowly raised to 550 °C. The samples were left at 550 °C for 3 hours. Crucibles were placed in a desiccator to cool, and then reweighed. Loss-on-ignition was used to calculate the percentage of organic content in the sample using the following formula:

$$\text{Organic Content (\%)} = \frac{\text{Weight loss of sample (g)}}{\text{Oven dry weight of sample (g)}} \times 100$$

2.2.2.3 Total organic carbon & nitrogen

The procedures for total organic carbon and nitrogen also followed those of the SWISS project (Verardo et al., 1990, Wilson et al., 2001). The samples were pre-sieved through a 1mm sieve before pre-treatment with sulphurous acid overnight to remove inorganic carbon (Bale and Kenny, 2005). The samples (0.1 – 0.2g) were then analysed in the LECO elemental analyser. Blanks, standards and sample weights were entered into the analyse menu and then loaded onto the carousel. Five EDTA standards are used to calibrate for drift of the LECO. A printout of the percentage of carbon and nitrogen was obtained for each sample. The results were corrected to take into account both the standards and any increases in weight due to the sulphurous acid treatment.

2.2.2.4 Calcium carbonate

Calcium carbonate samples were analysed using an acid digestion method (Buchanan, 1984, Mackie, 1990). Oven-dried samples were weighed and then digested in hydrochloric acid to remove the calcium carbonate. The next day the samples were filtered through pre-weighed glass

fibre filter paper. The sample and filter paper were washed into a pre-weighed dish and placed in the oven at 105°C. The dish was placed in a desiccator to cool and the total weight of the filter paper, dish and treated sediment was taken. The carbonate content was expressed as a percentage of the difference in weight between the untreated & treated sediment.

2.2.3 Statistical analysis

Barcharts and graphs were constructed in SPSS 15.0.

2.3 *Results*

The results were first examined using descriptive statistics in Minitab 15 (see Table 2.1). The coefficient of variation measures the ratio of the standard deviation to the mean; this means that it can be used to compare variables. Coefficients of variation were largest for percentage gravel (1.08 – 3.30), sand (1.89 – 4.24), mud (1.09 – 4.24) and clay (0.93 – 3.27) (see Table 2.1). Gravel can be affected by a large piece of stone or a cobble in a sample which can make a huge difference between the percentage gravel from one sample to another. Thus it was decided to use mean grain size in any further analysis which showed much lower coefficients of variation than categorized sediments. Coefficients of variation were very low for total organic carbon and total organic nitrogen, however caution is advised in relying on coefficients of variation when the mean approaches zero.

Standard deviations for the percentage gravel content of the grab (GS) and biotope (BS) samples were greater than the mean, indicating high variance between the samples. This could occur where large pieces of shell occur in some samples and not in others. Pebbles or cobbles in one sample could also explain the high standard deviation and variance in the percentage gravel variable for the grab sample (GS).

The boxplots show that there were outliers for the calcium carbonate content of the samples from within a grab (GS), with stations 6 and 10 having substantially higher values than the other stations (see Figures 2.3 -2.7). This outlier is most likely due to a piece of shell in the sample. The ranges are larger for samples from grabs within biotopes indicating that there is more variation in these samples with the possible exception of total organic carbon content (see Figure 2.7).

Table 2.1: Descriptive statistics for all 29 sediment samples from Dublin Bay (Minitab 15.0.1.1). S.E. = Standard Error, S.D. = Standard deviation, Var = Variance, Min. = Minimum, Med. = Median, Max. = Maximum and C.V. = Coefiiceint of Variation.

Variable	Type	N	Mean	S.E.	S.D.	Var	Min.	Med.	Max.	C.V.
Calcium carbonate (%)	Grab	10	14.64	0.50	2.48	10.76	12.80	14.25	17.40	1.57
	Site	10	14.39	0.27	0.75	6.02	13.30	14.30	15.90	0.87
	Biotope	9	13.86	0.49	2.16	10.60	12.20	14.00	16.70	1.47
Total organic carbon (%)	Grab	10	0.17	0.03	0.01	47.07	0.09	0.14	0.31	0.08
	Site	10	0.25	0.02	0.00	23.78	0.18	0.23	0.34	0.06
	Biotope	9	0.22	0.03	0.01	37.86	0.10	0.24	0.34	0.08
Total organic nitrogen (%)	Grab	10	0.03	0.00	0.00	37.73	0.02	0.04	0.06	0.01
	Site	10	0.04	0.00	0.00	26.68	0.02	0.04	0.06	0.01
	Biotope	9	0.05	0.01	0.00	35.59	0.02	0.05	0.07	0.02
Total organic matter (%)	Grab	10	1.86	0.05	0.02	7.70	1.62	1.87	2.08	0.14
	Site	10	1.69	0.07	0.05	13.19	1.46	1.61	2.12	0.22
	Biotope	9	1.66	0.12	0.13	22.07	1.20	1.66	2.19	0.37
Gravel (%)	Grab	10	2.45	1.05	10.93	134.74	0.66	1.59	11.75	3.30
	Site	10	1.25	0.34	1.17	86.56	0.23	0.88	3.14	1.08
	Biotope	9	1.54	0.45	1.78	86.41	0.14	1.44	4.05	1.33
Sand (%)	Grab	10	92.00	0.86	7.36	2.95	84.59	92.62	94.32	2.71
	Site	10	89.65	0.60	3.57	2.11	86.16	89.55	92.05	1.89
	Biotope	9	88.53	1.41	17.92	4.78	79.64	89.46	93.56	4.24
Mud (%)	Grab	10	5.55	0.34	1.19	19.61	3.67	5.41	7.17	1.09
	Site	10	9.10	0.49	2.36	16.90	7.22	8.83	11.40	1.54
	Biotope	9	9.93	1.41	17.92	42.64	5.61	10.10	18.61	4.24
Silt (%)	Grab	10	1.65	0.07	0.05	13.30	1.36	1.69	1.91	0.22
	Site	10	2.41	0.15	0.22	19.50	1.88	2.29	3.11	0.47
	Biotope	9	2.43	0.34	1.05	42.17	1.08	2.28	4.20	1.03
Clay (%)	Grab	10	3.90	0.29	0.87	23.84	2.24	3.73	5.29	0.93
	Site	10	6.69	0.37	1.35	17.37	5.25	6.29	8.29	1.16
	Biotope	9	7.50	1.09	10.65	43.53	4.01	7.82	14.41	3.27
Mean grain size	Grab	10	2.35	0.03	0.01	3.79	2.19	2.33	2.52	0.09
	Site	10	2.61	0.04	0.02	5.00	2.45	2.65	2.80	0.13
	Biotope	9	2.48	0.08	0.06	10.04	2.20	2.46	2.96	0.25
Median grain size	Grab	10	2.40	0.02	0.00	2.09	2.32	2.39	2.51	0.05
	Site	10	2.54	0.02	0.00	2.75	2.44	2.57	2.63	0.07
	Biotope	9	2.45	0.04	0.02	5.03	2.31	2.42	2.65	0.12

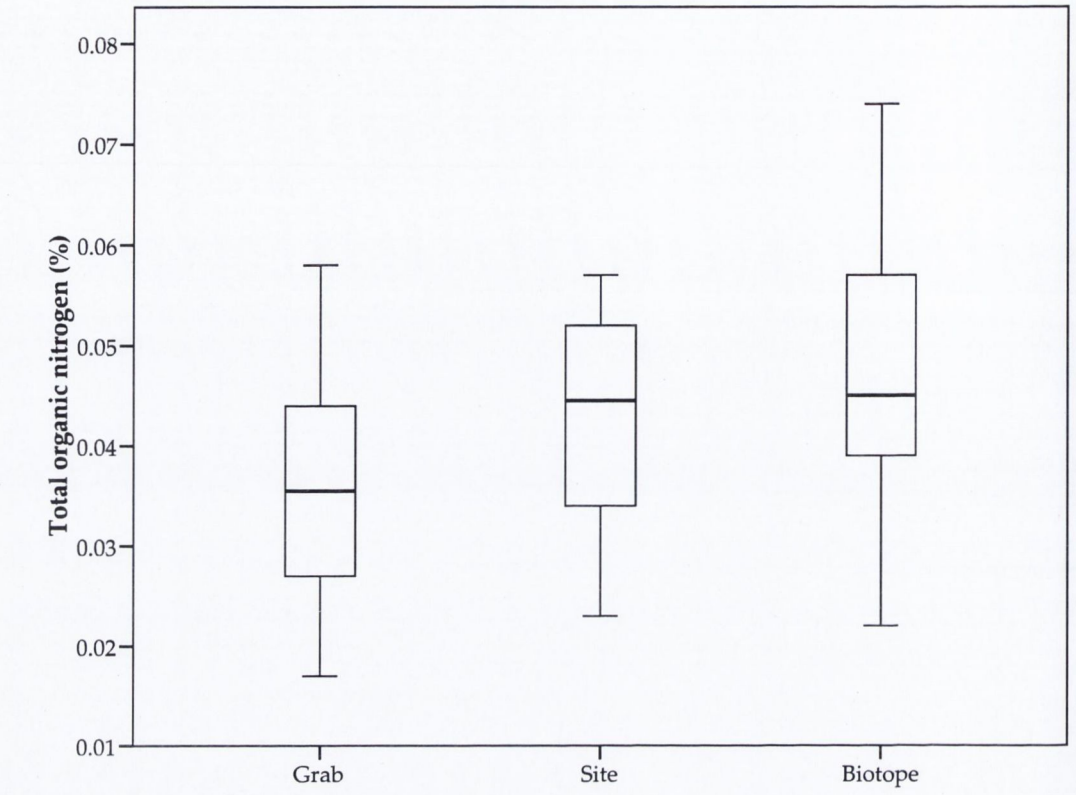


Figure 2.6: Boxplots of total organic nitrogen (%) for grab, site and biotope samples in Dublin Bay (Minitab 15.1.1.0).

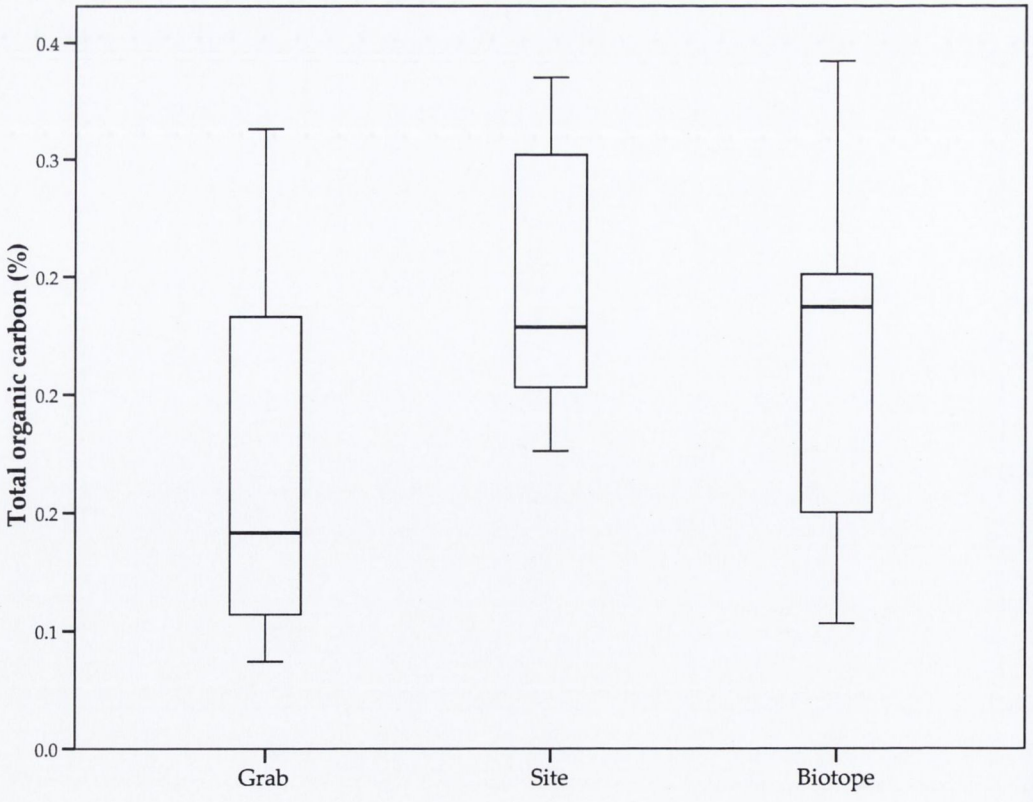


Figure 2.7: Boxplots of total organic carbon (%) for grab, site and biotope samples (SPSS 15.0).

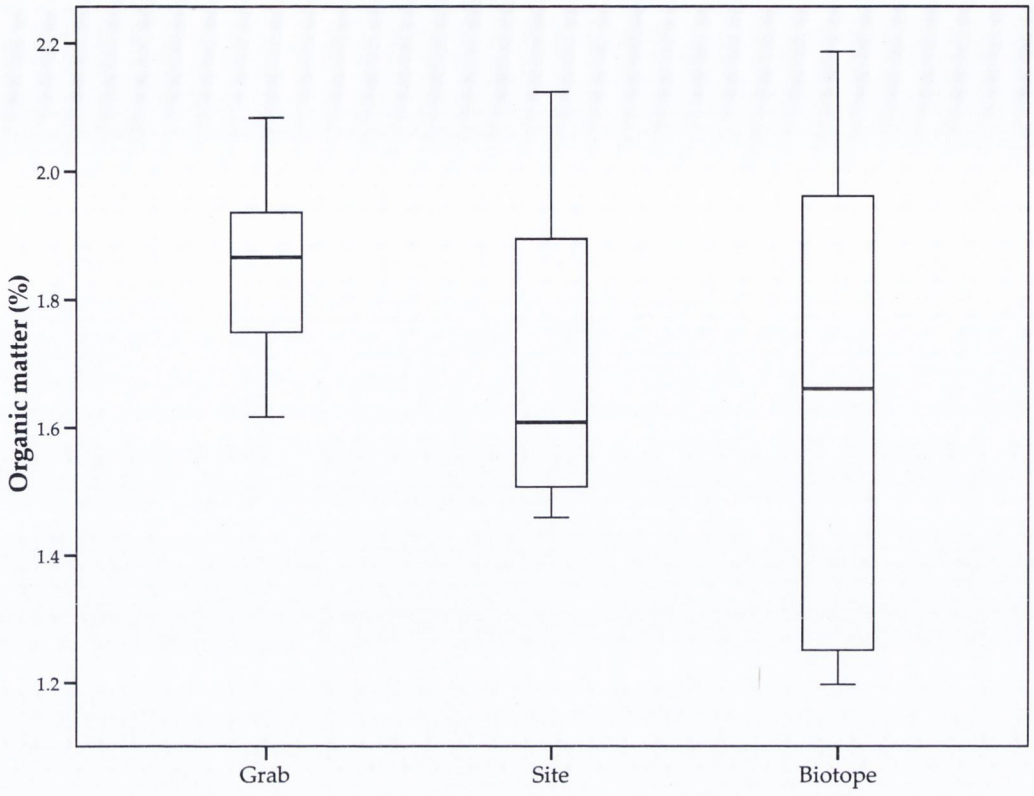


Figure 2.8: Boxplots of total organic matter (%) for grab, site and biotope samples in Dublin Bay (SPSS 15.0).

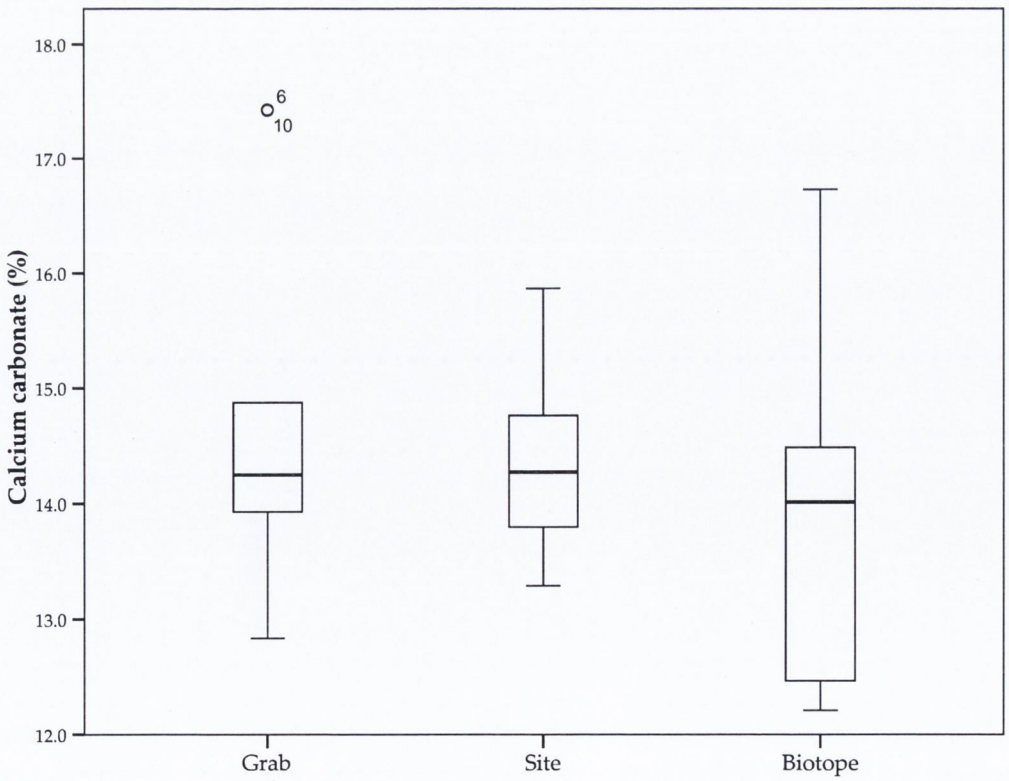


Figure 2.9: Boxplots of calcium carbonate (%) for grab, site and biotope samples ((SPSS 15.0).

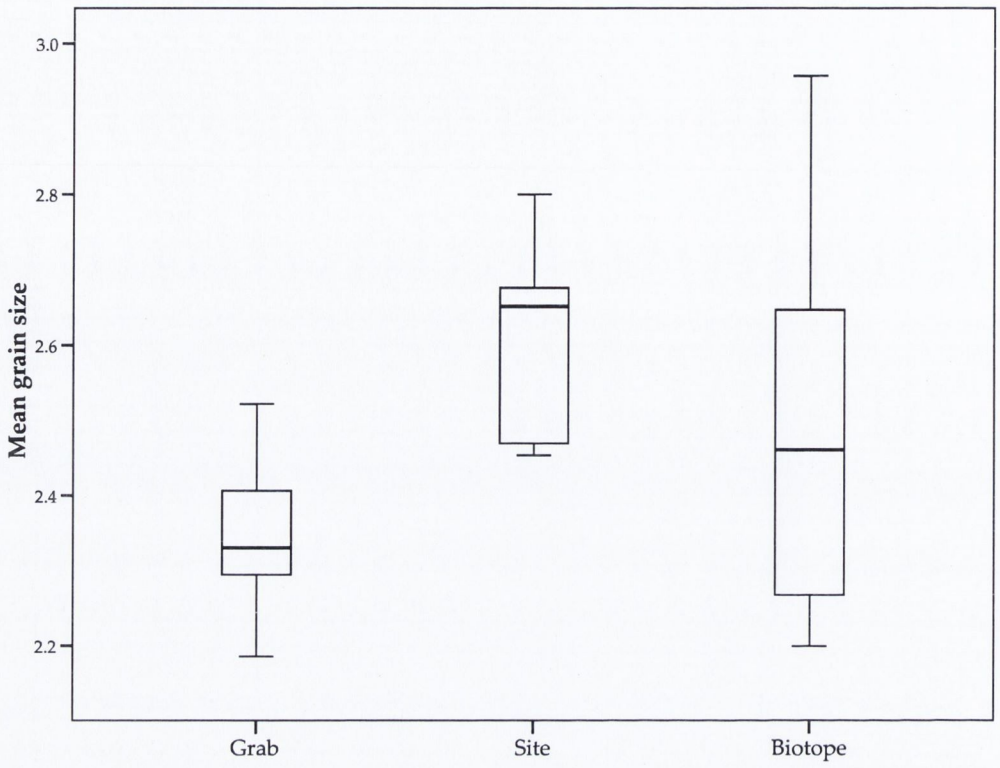


Figure 2.10: Boxplots of mean grain size (ϕ units) for grab, site and biotope samples in Dublin Bay (SPSS 15.0).

The particle size statistics for the samples show that all of the samples had a mean grain size of fine sand (see Table 2.1). However, Folk classifications for the samples included 'gravelly sand', 'slightly gravelly sand', 'slightly gravelly muddy sand' and 'muddy sand'. The samples from with a grab (GS) were all 'slightly gravelly sand' with the exception of 5GS which was 'gravelly sand'. The samples from within a site (SS) included two 'slightly gravelly muddy sand' stations and eight 'slightly gravelly sand' stations. The samples from within a biotope (BS) consisted of a mixture of 'slightly gravelly sand' (4 stations), 'slightly gravelly muddy sand' (4 stations) and one 'muddy sand' station. Samples were either poorly or moderately sorted, leptokurtic or very leptokurtic and ranged from one very coarse skewed sediment to very finely skewed sediments.

Table 2.2: Table of particle size characteristics for the GS, SS and HS samples.

Sample	Folk	Mean	Sorting	Skewness	Kurtosis
1GS	(g)S	Fine Sand	Moderately Sorted	Symmetrical	Leptokurtic
2 GS	(g)S	Fine Sand	Moderately Sorted	Symmetrical	Leptokurtic
3 GS	(g)S	Fine Sand	Moderately Sorted	Symmetrical	Leptokurtic
4 GS	(g)S	Fine Sand	Moderately Sorted	Symmetrical	Leptokurtic
5 GS	gS	Fine Sand	Poorly Sorted	Very Coarse Skewed	Very Leptokurtic
6 GS	(g)S	Fine Sand	Poorly Sorted	Fine Skewed	Very Leptokurtic
7 GS	(g)S	Fine Sand	Poorly Sorted	Symmetrical	Leptokurtic
8 GS	(g)S	Fine Sand	Poorly Sorted	Fine Skewed	Very Leptokurtic
9 GS	(g)S	Fine Sand	Moderately Sorted	Symmetrical	Very Leptokurtic
10 GS	(g)S	Fine Sand	Moderately Sorted	Symmetrical	Leptokurtic
11SS	(g)S	Fine Sand	Poorly Sorted	Fine Skewed	Very Leptokurtic
12SS	(g)S	Fine Sand	Poorly Sorted	Very Fine Skewed	Very Leptokurtic
13SS	(g)S	Fine Sand	Poorly Sorted	Fine Skewed	Very Leptokurtic
14SS	(g)mS	Fine Sand	Poorly Sorted	Very Fine Skewed	Very Leptokurtic
15SS	(g)S	Fine Sand	Poorly Sorted	Fine Skewed	Very Leptokurtic
16SS	(g)S	Fine Sand	Poorly Sorted	Fine Skewed	Very Leptokurtic
17SS	(g)S	Fine Sand	Poorly Sorted	Fine Skewed	Very Leptokurtic
18SS	(g)S	Fine Sand	Poorly Sorted	Fine Skewed	Very Leptokurtic
19SS	(g)S	Fine Sand	Poorly Sorted	Fine Skewed	Very Leptokurtic
20SS	(g)mS	Fine Sand	Poorly Sorted	Fine Skewed	Very Leptokurtic
22BS	mS	Fine Sand	Poorly Sorted	Fine Skewed	Very Leptokurtic
23BS	(g)mS	Fine Sand	Poorly Sorted	Fine Skewed	Very Leptokurtic
24BS	(g)S	Fine Sand	Poorly Sorted	Fine Skewed	Very Leptokurtic
25BS	(g)mS	Fine Sand	Poorly Sorted	Fine Skewed	Very Leptokurtic
26BS	(g)S	Fine Sand	Poorly Sorted	Symmetrical	Very Leptokurtic
27BS	(g)mS	Fine Sand	Poorly Sorted	Fine Skewed	Very Leptokurtic
28BS	(g)S	Fine Sand	Moderately Sorted	Symmetrical	Leptokurtic
29BS	(g)S	Fine Sand	Poorly Sorted	Symmetrical	Leptokurtic
30BS	(g)mS	Fine Sand	Poorly Sorted	Very Fine Skewed	Very Leptokurtic

2.3.1 Parametric statistics

Before using parametric statistical tests it was necessary to first see if the continuous variables were normally distributed. The results were first tested for normality using the Kolmogorov-Simirnov test which can be used on small sample numbers (Dytham, 2003). If a significance < 0.05 is found for the test, the data are not normally distributed (Dytham, 2003). All the variables tested were found to be normally distributed (see Table 2.3).

Table 2.3: Significance levels for Kolmogorov-Simirnov test of normality for sediment samples from Dublin Bay (SPSS 15.0.1).

Variable	Grab	Site	Habitat
Calcium carbonate	0.386	0.931	0.973
Total organic carbon	0.712	0.710	0.990
Total organic nitrogen	0.997	0.979	0.995
Total organic matter	0.994	0.760	0.861
Mean grain size	0.953	0.690	0.955

One-way Analysis of Variance (ANOVA) is a parametric test which tests the null hypothesis that groups have the same mean (Dytham, 2003). ANOVA assumes that data are normally distributed and also that the variance of each group is homogenous (Dytham, 2003). All categories were proven to be normally distributed using the Kolmogorov-Simirnov test (see Table 2.3). The assumption that the variances were equal was tested using the Levene test for homogeneity (Pallant, 2007).

The Levene test found that five variables had equal variances with a significance level greater than 0.05 (see Table 2.4). Calcium carbonate, organic carbon, organic nitrogen, gravel and sand were found to have equal variances. Organic matter and mean grain size did not have equal variances and thus could not be tested using one-way ANOVA.

One-way ANOVA was used to test the hypothesis that the means for samples from a grab, site and biotope are the same for calcium carbonate, organic carbon and organic nitrogen (see Table 2.5) (Dytham, 2003). As calcium carbonate, organic carbon and organic nitrogen all had significance levels greater than 0.05, the between-group variance for each variable is deemed to be the same as the within-group variation.

Table 2.4: Levene Test of homogeneity of variance for sediment samples from Dublin Bay (SPSS 15.0.1).

	Levene Statistic	df1	df2	Sig.
Calcium carbonate	1.210	2	26	0.314
Organic carbon	0.800	2	26	0.460
Organic nitrogen	0.960	2	26	0.396
Organic matter	4.203	2	26	0.026
Mean grain size	5.140	2	26	0.013

Table 2.5: One-way ANOVA for calcium carbonate, organic carbon, organic nitrogen, organic matter, gravel and sand (SPSS 14.0).

		Sum of Squares	df	Mean Square	F	Sig.
Calcium carbonate	Between Groups	3.055	2	1.528	0.86	0.435
	Within Groups	46.199	26	1.777		
	Total	49.254	28			
Organic carbon	Between Groups	0.03	2	0.015	2.707	0.086
	Within Groups	0.144	26	0.006		
	Total	0.174	28			
Organic nitrogen	Between Groups	0.001	2	0	2.301	0.12
	Within Groups	0.005	26	0		
	Total	0.006	28			

2.3.2 Non-parametric statistics

The Kruskal-Wallis test is a non-parametric test, which tests the null hypothesis that all groups have the same median (Dytham, 2003). Non-parametric tests such as the Kruskal-Wallis test assume that samples are random and that the observations are independent (Pallant, 2007). The Kruskal-Wallis test does not assume that either the data are normally distributed or that the variances are equal. The Kruskal-Wallis test showed that mean grain size ($\chi^2 = 2.971$, $p = 0.004$, $df = 2$) had significance levels less than 0.05 indicating that there was a difference between grab, site and biotope for this category. Organic matter showed no difference between grab, site and biotope ($\chi^2 = 10.831$, $p = 0.226$, $df = 2$).

The Mann-Whitney U test is a non-parametric test which tests the differences between two groups (Dytham, 2003, Pallant, 2007). It does not assume normality or equal variances (Dytham, 2003). Mann-Whitney U tests were conducted for mean grain size to discover which groups differed from each other. Samples from the grab were compared to samples from sites and biotopes and samples from sites were compared to samples from biotopes. There was found to be no difference between site and biotope ($p = 0.121$) or between grab and biotope ($p = 0.253$) but the differences between grab and site were found to be significant ($p = 0.001$).

2.4 *Discussion*

In a homogenous environment, repeatable results were achieved for the chemical sediment characteristics of calcium carbonate, organic matter, organic carbon and organic nitrogen using the long armed continuous warped 0.1m² Van Veen grab. The Dublin Bay samples displayed no difference between groups (e.g. grab and site) and within groups (e.g. grab) for calcium carbonate, organic carbon and organic nitrogen using one-way ANOVA. These results indicate that there is no difference between the means of samples from within the grab, from grabs within a single site and from different sites within a homogenous biotope. The non-parametric Kruskal Wallis test also found that there was no difference between grab, site and biotope samples for organic matter. Mann Whitney U tests did find differences between grab and site for mean grain size but not between site and biotope or grab and biotope.

For the site (SS) and biotope samples (BS), the sediment was taken from the surface sediment of the Van Veen grab. For the grab sediment samples (GS), sediment was taken from throughout the grab; this may have resulted in the difference in the means between the grab mean grain size values and the site mean grain sizes. The mud and gravel fractions could be unevenly dispersed throughout the grab with a higher or lower percentage of mud or gravel\shell in the top or the bottom of the grab. The lack of difference between the means for the site and habitat sediment results for all categories, where sediment samples were taken from the surface of the grab sample, shows that in a homogenous environment there should be little difference in the chemical and physical sediment properties of replicate sediment samples. No comparable studies analysing the repeatability of marine sediment samplers in obtaining chemical sediment information were found in the literature to compare with this study's data, as previous studies tended to focus on the repeatability of marine sediment samplers in sampling macrofauna or sediment volume.

It was interesting to note, that although differences were found between samples from within a grab (GS) and samples within a site (SS), the same mean grain size of fine sand was achieved for every sample from each of the three categories. This confirms that the sediments in the area have not changed since 1980 (Harris, 1980). Folk categories did vary between the samples, perhaps indicating that mean grain size would be a better classification for areas than the British Geological Survey (BGS) modified Folk classification.

It is logistically impossible to survey every square centimetre of seabed. Information from acoustic systems and photographic devices can help to determine the homogenous or

heterogeneous nature of the seabed. Without these additional sources of information one has to rely on information from point samplers. The point samplers are an indication of what occurs at a single location; however this is often taken to be an indication of seabed habitat or biotope over a general area. Information should only be generally applied to whole areas where other information such as previous studies, acoustic data (e.g. multibeam, backscatter or side scan), photographic evidence (e.g. video or still photos) or diving surveys can give substance to the conclusions. Without the assistance of these other sources of information, grab sampling surveys should be extremely well planned, numerous and taken at regular intervals.

For macrofaunal samples, it is deemed that one sample may be sufficient for surveys designed to map the benthic macrofaunal assemblages of an area (Cuff and Coleman, 1979, Cuff, 1980, Green, 1980, Mackie et al., 2007). In broad scale studies, at least two macrofaunal replicates are recommended (Mackie et al., 1995a, Mackie et al., 2007). In order to compare biological and sediment data, it is recommended that sediment samples are taken for particle size but that separate grab samples are used for particle size and macrofaunal samples, although this may mean that in heterogeneous areas the sediment samples used for particle size analysis may be slightly different to the sediment in the macrofaunal grab samples (Mackie et al., 2007).

In the HABMAP survey, separate grab samples were used for sediment and macrofauna (see Chapter 3). However, sediment and foraminiferal samples were taken from the same grab (see Chapter 4). Taking sediment samples from the same grab as the macrofaunal samples would mean that species could be removed from the macrofaunal sample and comprise the sample. As the size range of foraminifera identified (63 - 500μm) is so much smaller than that of the macrofauna (>1mm), a sub-sample of sediment was used for foraminiferal sample. In a Van Veen sediment grab sample there is sufficient room to take approximately 100g of surface sediment for analysis and to also fill a 120ml tub full of surface sediment for foraminiferal analysis.

Stratified random sampling was recommended for the HABMAP sampling survey. Two replicate sediment samples at each station were taken for the HABMAP cruises. The collection of other data such as multibeam, sediment profile imagery and video during the HABMAP cruises, meant that these could be referred to if there were questions about the repeatability of the sediment samples. Also, as the replicate sediment samples were to be compared to replicate macrofaunal samples taken from the same location and at the same time on the HABMAP cruises, it was deemed that these comparisons would be valid.

In hindsight, replicate samples, from each stratum, which were more widely spaced apart may have been a better choice. Ideally replicates would be proportionally random, applying the same sampling density to each stratum and using a gridded pattern to decide where to take the samples rather than taking replicates from the same sites (Gray and Elliott, 2009). This would be the best method of replicate sampling for the production of broad-scale seabed habitat maps. If there is a lot of information available before a survey indicating where areas are more likely to be variable, optimal sampling may be more appropriate (Gray and Elliott, 2009). However, due to time restrictions this was not logistically possible during the HABMAP surveys. Single samples rather than replicate samples may have been enough to provide a characterisation of each stratum (Gray and Elliott, 2009).

Chapter 3

3 HABMAP sediments of the southern Irish Sea

Parts of the methods (3.2) and results (3.3) sections of this chapter have previously been published in the sediment methods (4.2) and sediment results (4.3.2) section of the HABMAP project report (Robinson et al., 2007).

3.1 Introduction

Both physical and biological boundaries can often be extremely arbitrary. Physical classification systems such as the Folk sediment trigon (Folk, 1954) generally do not take into account chemical characteristics, biological structuring or ecosystem functioning. This is problematic when physical sediment maps are used as the basis for biological habitat maps. This chapter will not only examine particle size but also the chemical characteristics of the sediments in order to test the relationship between sediment characteristics and benthic macrofaunal assemblages in the southern Irish Sea. Particle size, organic matter content, total organic carbon content and calcium carbonate content are analysed for each HABMAP station. This chapter also facilitates the analysis of HABMAP sediment data together with BIOMÔR (Mackie et al., 1995a) and SWISS (Wilson et al., 2001) data in later chapters.

3.1.1 Factors influencing marine sediments

Sediments can be categorized by particle size (e.g. gravel, sand, mud, median grain size), by their origin (e.g. glacial) and by their material (e.g. carbonates) (Gray and Elliott, 2009). The substrate which macrofauna live on or in is not only affected by the sediment type but by a range of environmental conditions. The locations of sublittoral sediments are influenced by the hydrographical conditions which can re-suspend, move and re-deposit the sediments (Gray and Elliott, 2009). Wave action can have an influence on substrata up to depths of 100m (Gray and Elliott, 2009). The deeper the area the less effect waves will have, and current action then becomes the dominant factor in the dispersion of sediments (Gray and Elliott, 2009).

Sediment deposits are mainly affected by three key factors: settling velocity, roughness of the sediment and the threshold velocity (Gray and Elliott, 2009). The settling velocity is governed by Stokes' Law, which states that a particle in a viscous environment reaches a terminal velocity when the frictional and buoyant forces match the gravitational forces (Gray and Elliott, 2009). The roughness of sediments also affects sediment transport as rough particles are more easily picked

up by the currents flowing over the sediments (Gray and Elliott, 2009). The threshold velocity is the force needed to pick up a particle of sediment (Gray and Elliott, 2009). This means that if the settling velocity is greater than the threshold velocity then the particle will fall to the seabed, however, if the threshold velocity is greater, the particle will be picked up by the current and transported.

Particles 0.18mm in size (this size corresponds to a fine sand) are the easiest to move (Gray and Elliott, 2009). Finer particles compact more tightly and are thus more difficult to move, while coarser particles are heavier and therefore also difficult to move (Gray and Elliott, 2009). Large areas of fine sediments therefore tend to occur in areas with low current and wave action (Gray and Elliott, 2009). While grain size is an important factor in the presence of macrofauna, it is not the only factor affecting the distribution of macrofaunal assemblages. A hard-packed clay may be composed of very fine grains, but due to the cohesiveness of the sediment, it will act more like a hard substrate to macrofauna (Gray and Elliott, 2009). Porosity, the size of the pore space between grains, affects the amount of water in sediment while permeability defines the amount of water which can flow through the sediment (Gray and Elliott, 2009). The porosity and permeability of sediment influence the salinity, oxygen content and redox potential of sediment, all of which in turn affect the ability of animals to survive in or on the sediments (Gray and Elliott, 2009).

3.1.2 Sedimentary environments and macrofaunal communities

Species are affected not only by sediment type but by a combination of environmental factors such as currents, waves, sediment type and structure. Species are thought to have two niches, a fundamental niche and a realised niche (Gray and Elliott, 2009). The fundamental niche is the entire spectrum of environmental conditions which a species can occupy, while the realised niche is the area in which the species actually does exist (Gray and Elliott, 2009). Factors such as competition can prevent a species from occupying the full range of its fundamental niche (Gray and Elliott, 2009).

The idea that communities are dependant on the sedimentary environment is widely accepted today. Thorson (1957) showed that similar species occuring across geographical regions were restricted to similar sediment types. Both macrofaunal communities and individual macrofaunal species have been shown to have a strong affinity for certain sediment types. Sanders (1960) in his benthic macrofaunal study of Buzzard Bay, Massachusetts found two main faunal assemblages, a *Nucula proxima* and *Nephyts incisa* dominated community found in muddy sediments and a *Ampelisca* dominated community found in sandier sediments. Sanders (1960) also found filter-

feeders to be more abundant in muddy sediments and suspension-feeders to be more abundant in sandier sediments.

Most marine sedimentary animals live in an aphotic environment, dependant on organic matter sinking down through the water column to provide food (Snelgrove, 1999). In photic shallow waters, photosynthetic organisms such as phytoplankton and kelp provide food (Snelgrove, 1999). Organisms in the aphotic environment depend on the water column not only for their food but also for their supply of oxygen (Snelgrove, 1999). In areas with large amounts of organic matter areas can quickly become anoxic and uninhabitable (Snelgrove, 1999). As animals respire, they also use up oxygen enabling areas to become anoxic (Snelgrove, 1999). Most organisms cannot live in anoxic environments and so they need to live close to the surface of the sediment or in burrows making them more vulnerable to predators and environmental conditions (Snelgrove, 1999).

Grain size has been shown to be of great importance to species living in interstitial spaces (infauna) (Gray, 1974). However it is possible that for interstitial species, grain size acts as proxy for other factors such as porosity, permeability or oxygen content. Indeed, some larvae have been found to be very restrictive in their settlement with the larvae of *Opheila bicornis*, for example, found to prefer medium sands (200 -450 μm) as opposed to coarse or fine sands (Wilson, 1948) and the larvae of *Protodrilus rubropharyngeus* preferring grain sizes of 0.5 – 1 mm (Gray, 1967).

Glémarec (1973) described the environment of the European North Atlantic. Areas were firstly divided into three étages based on temperature and thermal stability in the water column: an infralittoral étage, a coastal étage and an open sea étage. Within these étages, macrofaunal communities associated with sediment types were described for the north Gascony shelf and the European north Atlantic Plateau which included areas such as the Celtic, Irish and North Seas, the English Channel, the Danish Straits and the British, French, Dutch and German coasts (Glémarec, 1973).

There is a long tradition of associating sediment type with macrofaunal assemblages in the North Sea. From Petersen's (1913) early studies of the Kattegat and Skagerrak, through to the studies of Glémarec (1973), Kingston & Rachor (1982), Duinveld (1991), Heip et al (1992), Daan & Mulder (2005) and Rees et al. (2007) to name but a few, macrofaunal assemblages are consistently shown to have a significant association with either sediment type or grain size. Heip et al. (1992) found macrofaunal biomass to be associated with sediment type in the North Sea. Increased biomass

was found in fine sediments with high chlorophyll-a content, while diversity was not associated with sediment type.

The practice of identifying habitats based on environmental conditions and substrate type is still used today by the MNCR and EUNIS classification systems (Connor et al., 2004, Davies et al., 2004). They use sediment type in combination with hydrographical parameters to distinguish habitats at coarse levels before integrating biology to identify biotopes at higher levels (Connor et al., 2004, Davies et al., 2004). MNCR habitats and biotopes were used in predictive models of the southern Irish Sea during the HABMAP project (Robinson et al., 2007), while the European habitat classification system EUNIS was used to make predictive models of the North East Atlantic in the Mapping European Seabed Habitats (MESH) project (Joint Nature Conservation Committee, 2007).

'Marine landscapes' or 'seascapes' also use sediment type in combination with oceanographic data to distinguish broadscale habitats. This system was pioneered by Roff & Taylor (2000) in Canada to make benthic marine landscape maps of the Canadian marine environment. The marine landscape approach has been used in the UK by the UKSeaMap project (Connor et al., 2006) and the Irish Sea project (Vincent et al., 2004), in the north east Atlantic by European partners in the MESH project (Joint Nature Conservation Committee, 2007), in the Baltic by the Balance project (Leth, 2008), in Australia (Bax and Williams, 2001, Jordan et al., 2005, Stevens and Connolly, 2005, Harris, 2007), New Zealand (Snelder et al., 2007) and in East Antarctica (Beaman and Harris, 2005).

The landscape maps are seen as the first step in characterising the benthic marine environment by providing a platform which can be used to identify areas which may contain important habitats (e.g. Annex 1 habitats which must be protected under the European Habitats Directive) and species. They can also be used to identify areas to be protected such as marine protected areas which are required under the OSPAR convention and the EU Marine Strategy Directive. As conservation moves more towards the protection of representative habitats, rather than distinctive habitats, benthic habitat maps provide the best indication of the probable locations and types of differents habitats.

It is important to collate biological, physical and hydrographical information on mapping surveys in order to learn more about the range of conditions in which species and habitats can be found. This information can be used to further refine classification systems such as MNCR and EUNIS by improving habitat and biotope descriptions and by supplying information which can lead to the

designation of new habitats and biotopes. It is generally recognised that both the MNCR and EUNIS classification systems suffer from a lack of data in offshore and deep-sea areas. This means that biotopes in the easily accessible littoral zone are well described while biotopes in more remote offshore areas remain unknown due to lack of survey information.

3.1.3 Benthic habitats in the Irish & Celtic Seas

Jones (1950) divided the benthic environment into zoogeographic regions containing macrofaunal associations. The Atlantic boreal region, in which the Irish Sea is located, was defined as the area from the southern coasts of Britain to the southern limit of the Arctic with a temperature range of 3 - 16 °C and a salinity range of 7 - 34‰ (Jones, 1950). This area was divided into ten different associations based on depth, sediment type and important species ranging from the 'boreal shallow sand association' to the 'boreal deep coral association' (Jones, 1950).

The Irish Sea was subsequently divided into nine different types of macrobenthic communities by Mackie (1990). These communities were again related to substrate and depth (see Table 3.1). Boelens et al. (1999) presented a provisional comprehensive map of the benthic assemblages in the Celtic Sea based on a unpublished map by Cabioch (in prep) who separated the Celtic Sea into seven different benthic assemblages, based on sediment type (see Table 3.2). The only one of the Celtic Sea habitats to appear similar to one of Mackie's Irish Sea assemblages is the '*Venus fasciata*' assemblage associated with coarse sands and gravels in the Celtic Sea which has similar characterising species to Mackie's 'Deep *Venus*' gravel communities (Mackie, 1990, Boelens et al., 1999).

Mackie et al. (1995a) discovered three main macrofaunal assemblages on the Welsh side of the southern Irish Sea and associated these with sediment type. Assemblage A occurred in the soft sediments of the Celtic Deep, with assemblage A being further subdivided into A1 and A2 which were respectively associated with muds and sands. Assemblage B occurred in inshore stations associated with sands and muddy sands. Assemblage C accounted for any gravelly stations.

Table 3.1: Mackie (1990) biological communities with associated depth, typical species and boreal association (Jones, 1950, Holme, 1966, Keegan et al., 1987, Mackie, 1990).

Mackie Community	Boreal Associations	Depth	Typical species
Amphiura	Boreal Offshore Muddy Sand (Jones, 1950)	15-100m	*Amphiura filiformis* *Echinocardium cordatum* *Turritella communis*
Brissopsis	Boreal Offshore Mud (Jones, 1950)	15-100m	*Brissopsis lyrifera* *Amphiura chiajei*
Abra	Boreal Offshore Muddy Sand (Jones, 1950)	5-30m	*Abra alba* *Pectinaria koreni*
Shallow *Venus* (*Tellina* sub community)	Boreal Offshore Sand (Jones, 1950)	5-40m	*Tellina fabulina* *Magelona mirabilis*
Shallow *Venus* B (*Spisula* sub-community)	Boreal Offshore Sand (Jones, 1950)	5-40m	*Spisula elliptica* *Nephtys cirrosa*
Deep *Venus*	Boreal Offshore Gravel (Jones, 1950)	40-100m	*Spatangus purpureus* *Glycimeris glycimeris* *Astarte sulcata* *Venus* sp.
Muddy-gravel	Boreal Offshore Muddy-gravel (Holme, 1966)	Not specified	*Upogebia deltaura* *Upogebia stellata* *Nucula nucleus* *Venus verrucosa* *Turritella communis* *Gibbula magus* *Golfingia elongate* *Golfiniga vulgaris*
Modiolus	Boreal offshore gravel (Jones, 1950)	Moderate	*Modiolus* *Ophiothrix fragilis*
Hard substrate	Keegan et al. (1987)	Not specified	*Balanus crenatus* *Bicellariella ciliate* *Cellaria fistulosa* *Eucrata loricata* *Flustra foliacea*

Mackie et al. (1995b) examined polychaete species and distribution in the southern Irish Sea from the BIOMÔR sites. They identified polychaetes as the major group in the Irish Sea both in terms of abundance (52.8%) and species (48.5%) and found that particle size and depth were the best indicators of polychaete species distribution in the southern Irish Sea, with offshore gravelly sediments having the highest species diversity (Mackie et al., 1995b).

Table 3.2: Provisional Celtic Sea macrobenthic habitats as provisionally produced in Boelens et al. (1999) from Cabioch et al. (Cabioch et al., in prep).

Habitat	Sediment type	Species
Epifauna	Rock	*Ophiothrix fragilis* *Psammechinus milaris*
Amphiura/ Chammelea	Muddy/fine sand	*Amphiura* *Chamelea* *Cultellus pellucidus* *Ditrupa arietina* *Astropecten irregularis* *Nucula nitidosa* *Turritella communis*
Abra	Not specified	*Abra prismatica*
Venus fasciata	Coarse sand/ gravels	*Venus fasciata* *Amphioxus lancelolatus* *Spatangus purpureus* *Astarte* sp. *Chamelea casina*
Nephrops	Sandy mud	*Nephrops norvegicus* *Notomastus latericeus* *Amphiura chiajei* *Goneplax rhomboids*
Deep water sand 1	Medium/ fine clean sands	*Similipecten similes*
Deep water sand 2	Medium/ fine clean sands	*Luidia cilaris*

The most extensive classification of sediments in the Irish Sea is the BGS modified Folk map DigiSBS which covers UK waters (Tappin, 1994, Jackson et al., 1995). The map splits the southern Irish Sea area into fifteen Folk sediment categories based on percentages of gravel, sand and mud. The map does not extend to the littoral zone but only covers sublittoral sediments. The Folk classification is a geological sediment classification system and therefore its sediment boundaries do not always directly correspond to the boundaries of the biological communities. UKSeaMap attempted to make these sediment classes more biologically relevant by using aggregated sediment classes to classify UK waters into EUNIS Level 3 sedimentary habitats; rock, coarse sediments, mixed sediments, 'sand and muddy sands' and 'mud and muddy sands'(Connor et al., 2006).

3.1.4 Study sites

There were five sites from the southern Irish Sea in this study: Arklow, the Celtic Deep transect, Caernarfon Bay, St. George's Channel North transect and St. George's Channel South transect. The Arklow site (see Figure 3.1) is located on the Irish shelf which is an area characterised by

ridges, channels and sand banks, such as the Arklow Bank and Codling Bank, and influenced by tidal currents which run parallel to the shore (Dobson et al., 1971). The Arklow Bank which occurrs to the east of the sample area is approximately 33m in height and flat-topped and varies between 2 and 25m in depth (Dobson et al., 1971, Anonymous, 2001). The tidal range is about 2m (Tappin, 1994).

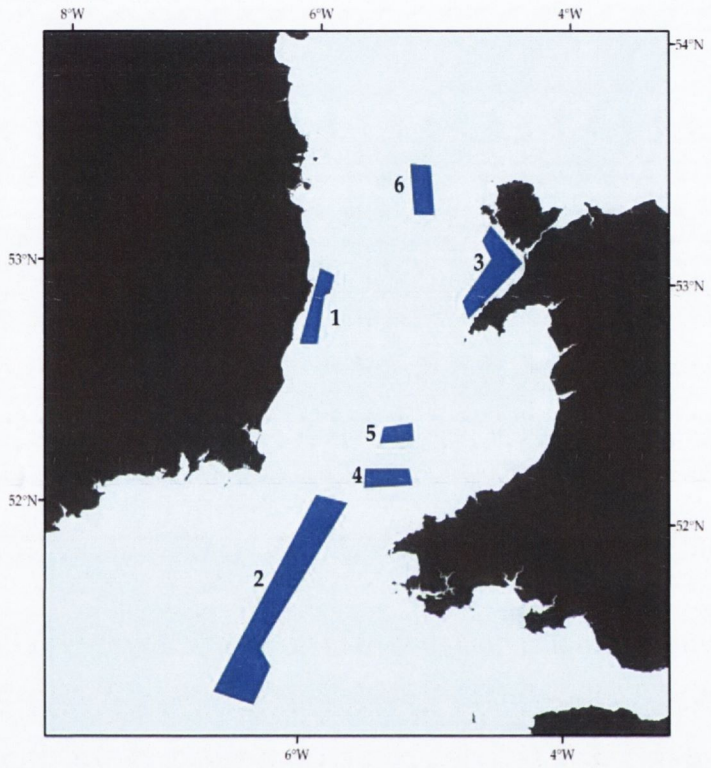


Figure 3.1: HABMAP sampling areas, 1 = Arklow, 2 = the Celtic Deep transect, 3 = Caernarfon Bay, 4 = St. George's Channel South Transect, 5 = St. George's Channel North Transect, 6 = West of Anglesey.

The Celtic Deep transect is located in the Celtic Deep trough, which runs south to south-west through St. George's Channel to the Celtic Deep and has an average depth of 110m (Tappin, 1994). The trough traverses the Celtic Front, the frontal boundary between the Celtic and Irish Seas. The area consists of mud, muddy sands and sandy muds in the south, which grade into sands and gravelly sands in the north (Tappin, 1994).

Caernarfon Bay is located on the Welsh platform (see Figure 3.1). It stretches out to the 35m deep isobath (Dobson et al., 1971). The bay's dominant feature is a central broad sand patch of medium sand, however exposed cobble zones also exist (Dobson et al., 1971). Jackson et al. (1995) showed that Caernarfon Bay sediments consist mainly of sand, sandy gravel and gravelly sand. The

bedforms in the area consist of sand ribbons and sand wave fields with patches of rock outcrop (Jackson et al., 1995).

St. George's Channel North transect and St. George's Channel South transect are both located in the northern section of St. George's Channel, west of Cardigan Bay (Figure 3.1). Tidal streams in St. George's Channel create a bed-load parting zone (Tappin, 1994). St. George's Channel consists of a series of channels and low ridges with sediments mainly made up of sandy gravel with patches of sand and gravelly sand (Dobson et al., 1971, Tappin, 1994).

Macrofaunal biotopes were identified by the Natural Museum of Wales for these areas during the HABMAP project (Robinson et al., 2007) using the MNCR 04.05 classification system (see Table 3.3) (Connor et al., 2004). The quantitative stations from the Arklow site consisted of the SS.SCS.ICS.MoeVen, a biotope dominated by *Goodalia triangularis, Mytilus edulis, Spisula solida, Hesionura elongata* and *Spisula elliptica*. The Caernarfon Bay area and the Celtic Deep transect were more diverse; both comprising 5 biotopes while the St. George's Channel transects only consisted of three. A list of the biotopes found during the HABMAP project along with the areas in which they were found and the quality of the biotope fit with known MNCR 04.05 biotopes is shown in Table 3.4. Mackie also noted that macrofaunal changes had occurred at stations previously sampled during the BIOMÔR project.

Table 3.3: Breakdown of MNCR 04.05 classification system, using S.SCS.ICS.MoeVen as an example (Connor et al., 2004).

MNCR 04.05 Levels		Example, S.SCS.ICS.MoeVen	
		Code	**Explanation**
Level 1	Environment	SS	Sublittoral sediment
Level 2	Broad Habitat Types	SCS	Sublittoral coarse sediment (unstable cobbles and pebbles, gravels and coarse sands)
Level 3	Habitat complexes	ICS	Infralittoral coarse sediment
Level 4	Biotope complexes	MoeVen	*Moerella* spp. with venerid bivalves in infralittoral gravelly sand
Level 5 & 6	Biotopes & sub-biotopes		

Table 3.4: Table of biotope designations for HABMAP sites in the southern Irish Sea (Robinson et al., 2007).

Group number	Biotope	Area	Biotope Match	No. of Sites
1	SS.SCS.OCS.HeloPkef	St. George's Channel	Fairly good	8
2	SS.SCS.ICS.MoeVen	Arklow	Fairly good	7
3a	SS.SMu.OMu.LevHet	Celtic Deep	Fair	5
3b	SS.SMu.CSaMu.AfilMysAnit	Celtic Deep	Fair	3
3c	SS,SSA,CfiSa.ApriBatPo	Celtic Deep	Fairly good	2
4a	SS,SMu.CSaMu.LkorPpel	Caernarfon Bay	Poor	5
4b	SS.SSa.CFiSa.EpusOborApri	St. George's Channel Celtic Deep Caernarfon Bay	Fairly good	5
5a	SS.SCS.CCS.MedLumVen & Including SS.SBR.SMus.ModMx	St. George's Channel Celtic Deep Caernarfon Bay	Good	8
5b	SS.SCS.CCS. MedLumVen	Caernarfon Bay	Good	2
5c	SS.SBR.SMus.ModT	Caernarfon Bay	Good	2
5d	SS.SMx.OMx/ SBR.SMus.ModCvar	West of Anglesey		2
6	New biotope	West of Anglesey		1

3.1.5 Aims

More information is needed on the relationship between species and chemical sediment characteristics such as organic content, organic carbon and calcium carbonate in the southern Irish Sea. The overall aim of this chapter is to investigate the physical and chemical sediment characteristics of the HABMAP sampling stations to enable the comparison of physical habitats with biological assemblages. This inclusion of chemical characteristics of sediments as input data layers in seabed habitat mapping could lead to improved habitat maps which could better predict the presence of macrofaunal communities. The specific aims of this chapter are outlined below.

- Investigate the physical and chemical properties of the sediments at the HABMAP stations in the southern Irish Sea.
- Explore the relationship between particle size and the chemical characteristics of the sediment at these stations.
- Test the relationship between sediment characteristics and biological assemblages in the southern Irish Sea.
- Compare HABMAP particle size data with British Geological Survey (BGS) modified Folk maps for the southern Irish Sea.

3.2 *Methods*

As part of the HABMAP project, two surveys were conducted on board the *RV Celtic Voyager* in the summer of 2005, an acoustic survey and a sampling survey. The sampling sites were located in 5 main areas; the Arklow Bank, the Celtic Deep transect, Caernarfon Bay, St. George's Channel North Transect and St. George's Channel South Transect (see Figure 3.1). Samples were taken at an additional area referred to as 'West of Anglesey' on the last day of the second cruise (see Figure 3.1). The acoustic multibeam and backscatter data from the initial survey (processed by Katrien Van Landeghem from UCC) were used to identify areas which were likely to differ from each other in each survey area and was therefore used to designate priority sampling locations in areas which appeared to contain different sediment types, geological features or were possibly biologically interesting (van Landeghem and Mitchell, 2005).

On the HABMAP cruises, sediment samples were taken in the field using a $0.1m^2$ long-armed continuous warp Van Veen grab. Quantitative sediment samples were taken at 70 out of a total of 97 stations surveyed during the two HABMAP cruises. Stations 1 - 85 were sampled from 25th July to the 08th August 2005 during the Sampling Survey. Stations 86 - 97 were sampled during the acoustic survey between from the 14th - 28th June 2005. Six locations were sampled on the acoustic survey. Two grabs were taken at each station. The sediment samples were taken from the top of the grab and were placed in polythene bags, labelled and frozen.

3.2.1 Laboratory work

Sediment analysis in the laboratory was completed with the help of technical assistant Katie Reeves-Arnold in Trinity College Dublin. Sediment samples were dried at 105^0C in the oven. Sediment samples were analysed for organic content, total organic carbon, total organic nitrogen, calcium carbonate and particle size. Sediment analysis was carried out using the same methods outlined in Chapter 2.

Total organic nitrogen content was also examined. The results for total organic nitrogen were generally below detection limits so the results are not discussed in this chapter.

3.2.2 Particle size analysis (PSA)

Using percentage of gravel, sand and mud, each of the 70 stations were characterised using the BGS modified Folk classification system (see Figure 3.2 and Table 3.5) (Folk, 1954, Jackson et al., 1995). As with the previous BIOMÔR and SWISS projects, gravel, sand, silt and clay were expressed as a percentage of the organic-free sediment (Mackie et al., 1995a, Wilson et al., 2001).

The median grain size, mean grain size, modal class, degree of sorting, skewness and kurtosis were calculated for each station using the logarithmic Folk and Ward method (Folk and Ward, 1957, McManus, 1988). Grain size statistics were calculated using the GRADISTAT excel macro (Blott and Pye, 2001). The GRADISTAT programme classifies sediments using the Folk (1954) classification as opposed to the BGS modified Folk classification (Jackson et al., 1995). The main difference between these systems is the fact that the Folk classification uses 0.1% gravel as the boundary between slightly gravelly sediments and sediments containing practically no gravel, whereas the BGS modified Folk classification uses 1% gravel as the boundary (see Figure 3.2). The sediment descriptions were adjusted to fit the BGS modified Folk descriptions to enable comparisons with BGS Folk sediment map covering the southern Irish Sea area (Jackson et al., 1995).

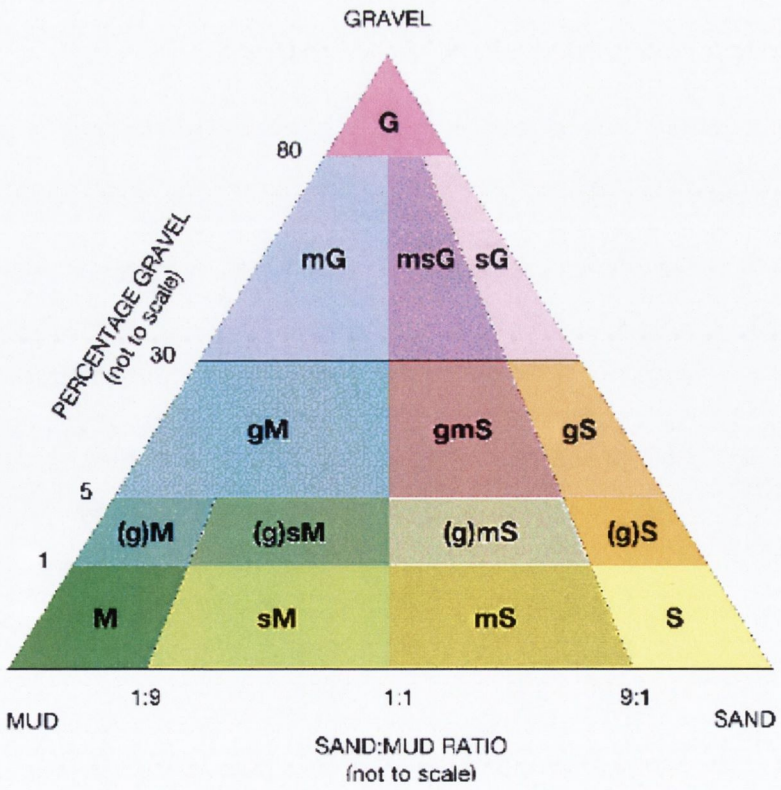


Figure 3.2: BGS Modified Folk sediment classification system where m = mud, g = gravel, s = sand (Jackson et al., 1995).

Table 3.5: List of BGS Modified Folk classifications.

Code	Folk classification	Code	Folk classification
M	Mud	**(g)mS**	Slightly gravelly muddy sand
sM	Sandy Mud	**gmS**	Gravelly muddy sand
(g)M	Slightly gravelly mud	**gS**	Gravelly sand
(g)sM	Slightly gravelly sandy mud	**G**	Gravel
gM	Gravelly mud	**mG**	Muddy gravel
S	Sand	**msG**	Muddy sandy gravel
mS	Muddy Sand	**sG**	Sandy gravel
(g)S	Slightly gravelly Sand		

3.2.3 Multivariate statistics

Non-metric Multi-Dimensional Scaling (MDS) plots were constructed in PRIMER v6 (Clarke, 1993) using physical and chemical sediment characteristics. The data were normalised before being assembled into a Euclidian similarity matrix which was used to produce MDS ordination graphs. MDS produces a map which clusters sites together based on the similarity of the variables in the matrix. The adequacy of the MDS representation shown is indicated by the stress levels (Clarke, 1993):

- stress < 0.05 indicates representation without the possibility of misinterpretation
- stress < 0.1, indicates a good ordination with no real prospect of a misleading interpretation
- stresses > 0.1 could not be easily relied on

3.2.4 Abiotic and biotic patterns

BIO-ENV matches biotic patterns to environmental patterns by considering which single variable or groups of variables best explain the biotic patterns (Clarke and Ainsworth, 1993). This procedure can be tested with a permutation test that tests the null hypothesis that there is no relationship between the biotic patterns (communities) and the abiotic patterns (physical and chemical sediment characteristics) (Clarke and Warwick, 2001).

The biological data consisted of macrofaunal abundance data for 53 sites (Robinson et al., 2007). These data were log transformed using the log(x+1) transformation in PRIMER v6 (Clarke and Ainsworth, 1993). The data were then converted into a Bray-Curtis similarity matrix. The sediment data were log transformed and normalised before using the BIO-ENV procedure in PRIMER v6 to compare the biotic patterns with the abiotic patterns.

The use of binary logistic regression to examine the power of the environmental variables to predict membership of a biotope or macrofauna cluster group was considered, however it was decided that it would be more advantageous to use this procedure in a later chapter where BIOMÔR and HABMAP sites could be examined together, thus increasing the overall sample size for the procedure.

3.3 *Results*

Van Veen grab sampling was attempted at every station; however at several stations the grab was unsuccessful due mainly to the coarseness of sediments at these sites; as a result there are no sediment samples for these stations. In total, there was sediment information for 71 out of a possible 86 stations from the HABMAP project; 16 from Arklow (1 - 21), 20 from Caernarfon Bay (22 - 36 and 73 - 81) , 17 from the Celtic Deep transect (38 - 51 and 55 - 57), 5 from St. George's Channel North transect (65 - 70), 8 from St. George's Channel South transect (52, 53 and 58-63) and 2 from the area west of Anglesey (82 and 83). The samples from the area west of Anglesey were supplementary to the HABMAP project and were taken on the last day after the main sampling had been completed; however they were included in the overall analysis.

The sampling stations at Arklow ranged from 15 – 60 m water depth. The sites mainly consisted of gravelly sands and sandy gravels in the north and gravelly sands and slightly gravelly sands in the south. The more northerly stations occur in gravel banks, boulder fields and biotic reefs (Jackson et al., 1995). The more southerly stations occur in sandy features such as sand banks and flat sheet rippled sand (Jackson et al., 1995). The sites at Caernarfon Bay ranged from 17 – 41 m water depth and contained a wide range of sediment types. The sites at the Celtic Deep transect ranged from 95 – 129 m water depth. St. George's Channel North and South transects are located west of Cardigan Bay in depths of 75 – 105m. The southern and northern transects occur over a mixture of gravels and sands. Of the two sites West of Anglesey, station 83 stood out as the sample consisted of boulder clay.

The results for particle size, organic content, organic carbon and calcium carbonate content for each station are displayed in Table 3.6. The sediment data for station 87 only includes particle size data as the sample did not contain enough fine sediment to conduct chemical analysis. Overall the stations were dominated by gravelly sands and sandy gravels. Any station which did not have information for all physical and chemical sediment categories was excluded from the overall analysis (station 87 & 90). Stations which had only one sediment sample were also excluded from any multivariate analyses (stations 30 & 89). This resulted in the overall analysis of 68 stations in total.

Sample stations that had been originally surveyed during either the BIOMÔR (Mackie et al., 1995a) or SWISS (Wilson et al., 2001) projects, were re-surveyed during the HABMAP project and changes in the sediment composition of these sites over time were examined.

3.3.1 Particle size analysis (PSA)

The results for the PSA are displayed in Table 3.6 and show the percentages of gravel, sand and mud and the BGS modified Folk sediment category for each station. The BGS modified Folk category was determined from the BGS modified Folk trigon as shown in Figure 3.2. Figure 3.3 shows the proportion of Folk sediment types recorded in all sample areas, which again illustrates the fact that sites throughout the study area were dominated by gravelly sands, followed by sandy gravels and sands.

Figures 3.5 – 3.9 show the Folk classification overlaid on underlying backscatter images for the HABMAP stations in Arklow, Caernarfon Bay, the Celtic Deep transect, St. George's Channel North and St. George's Channel South transects. Backscatter shows the reflectivity of the seabed. In general, areas of higher backscatter indicate coarser sediments. Backscatter images for the HABMAP areas were interpreted by Katrien van Landeghem from UCC (van Landeghem and Mitchell, 2005, Robinson et al., 2007). The Arklow area was dominated by gravelly sands and slightly gravelly sands. The muddiest samples were found in the southern part of the Celtic Deep transect. The Celtic Deep transect graded from sandy muds in the South through to gravelly sands in the North. Caernarfon Bay had a range of sediment types notably sandy gravels, slightly gravelly muddy sands and slightly gravelly sands. St. George's Channel North and South transects comprised mainly gravelly sands and sandy gravels.

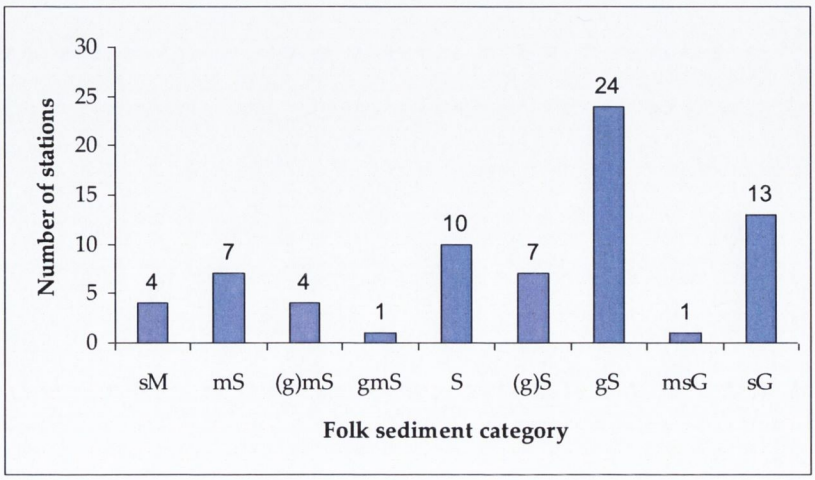


Figure 3.3: Barchart of Folk sediment types for HABMAP samples

Table 3.6: Detailed sediment information for each HABMAP station. Long = longitude, Lat = latitude, $CaCO_3$ = calcium carbonate, Org = total organic matter, and OC = total organic carbon.

Stn	Long (°N)	Lat (°W)	Depth m	Folk	Gravel (%)	Sand (%)	Mud (%)	$CaCO_3$ (%)	Org (%)	O.C. (%)
H2	52.97	5.91	60	gS	5.1	93.5	1.4	16.24	0.84	0.12
H3	52.95	5.91	54	gS	12.0	87.3	0.7	35.02	1.2	0.20
H11	52.86	5.97	27	gS	22.7	77.2	0.1	24.14	1.06	0.21
H13	52.83	5.98	29	(g)S	4.7	94.9	0.5	16.44	0.59	0.06
H14	52.83	5.98	30	gS	6.7	92.2	1.0	10.07	0.77	0.03
H15	52.82	5.98	30	(g)S	3.1	96.2	0.6	13.9	0.83	0.10
H17	52.81	6.00	15	S	0.2	99.0	0.8	6.46	0.65	0.02
H18	52.77	5.99	35	gS	9.7	89.3	1.0	17.7	0.99	0.03
H19	52.79	5.99	25	S	0.0	98.4	1.6	8.08	0.55	0.02
H20	52.76	6.00	35	gS	5.7	93.3	1.0	44.92	1.62	0.24
H22	53.15	4.60	37	(g)mS	1.5	82.1	16.3	15.57	2.22	0.29
H23	53.14	4.59	30	(g)mS	2.0	87.6	10.3	13.01	1.19	0.10
H24	53.14	4.59	30	S	0.1	98.5	1.4	11.42	0.98	0.08
H25	53.07	4.52	18	sG	49.0	50.9	0.1	17.98	1.25	0.30
H26	53.05	4.56	26	S	0.0	98.6	1.4	11.35	0.83	0.14
H27	53.03	4.59	32	sG	30.1	68.9	1.0	21.67	1.24	0.15
H29	53.01	4.62	37	gS	23.4	74.4	2.3	19.88	1.4	0.34
H30	52.97	4.67	37	gS	24.6	74.5	1.0	22.52	1.87	0.24
H32	52.97	4.62	34	gmS	6.9	78.3	14.8	28.96	3.63	0.82
H33	52.94	4.70	39	gS	14.5	81.9	3.7	66.88	2.42	2.41
H34	52.94	4.69	38	sG	38.6	60.6	0.8	30.74	1.7	0.30
H35	52.92	4.68	38	(g)mS	3.2	84.7	12.1	35.68	3.68	1.18
H36	52.91	4.67	38	msG	41.1	52.5	6.4	50.87	1.94	0.51
H38	51.27	6.50	116	(g)mS	2.8	83.9	13.3	31.47	4.67	0.84
H39	51.33	6.42	129	mS	0.0	68.5	31.5	39.5	10.8	1.59
H40	51.35	6.40	127	sM	0.0	26.7	73.3	36.87	9.46	1.53
H41	51.36	6.40	127	sM	0.0	20.8	79.2	37.74	9.78	2.37
H42	51.37	6.28	118	sM	0.0	19.9	80.1	37.67	7.64	1.49
H43	51.40	6.41	115	mS	0.2	65.4	34.5	33.66	5.63	1.23
H44	51.43	6.38	108	mS	0.0	88.6	11.4	18.03	2.18	0.30
H45	51.50	6.31	105	mS	0.9	86.6	12.5	21.75	2.58	0.32
H46	51.59	6.30	95	S	0.0	94.8	5.2	14.41	1.52	0.45
H47	51.69	6.16	114	S	0.1	95.9	4.0	13.01	1.21	0.36
H48	51.75	6.12	115	(g)S	2.5	94.0	3.5	14.93	1.18	0.33
H49	51.75	6.12	112	gS	5.2	93.6	1.1	16.04	0.73	0.10
H50	51.80	6.07	115	S	1.0	94.9	4.2	21.83	1.42	0.72
H51	51.85	6.02	110	gS	15.0	82.9	2.0	40.53	1.43	0.84
H52	52.17	5.30	75	gS	27.0	70.3	2.7	13.04	1.72	0.25

Table 3.6 (continued): Detailed sediment information for each HABMAP station. Long = longitude, Lat = latitude, $CaCO_3$ = calcium carbonate, Org = total organic matter, and OC = total organic carbon.

Stn	Long. (°N)	Lat. (°W)	Depth (m)	Folk	Gravel (%)	Sand (%)	Mud (%)	$CaCO_3$ (%)	Org (%)	Org.C (%)
H53	52.16	5.36	84	sG	35.2	62.3	2.5	16.88	1.49	0.15
H55	51.94	5.92	106	sG	30.2	68.4	1.3	44.17	2.21	0.59
H56	51.95	5.93	104	sG	38.7	58.4	2.8	43.3	2.66	0.52
H57	51.95	5.92	103	gS	24.2	74.1	1.8	52.55	2.21	0.28
H58	52.03	5.75	104	gS	21.5	74.8	3.7	44.47	1.96	1.52
H59	52.16	5.51	94	sG	46.6	52.9	0.5	36.14	1.8	0.75
H60	52.16	5.48	99	gS	7.8	91.7	0.6	25.67	1.13	0.32
H61	52.16	5.45	101	gS	20.6	79.0	0.4	18.44	0.91	0.13
H62	52.16	5.43	105	gS	12.7	86.8	0.5	15.93	1.12	0.13
H63	52.16	5.43	103	sG	44.1	54.9	1.0	45.01	1.04	0.09
H65	52.36	5.27	91	gS	19.2	80.1	0.8	16.99	0.98	0.14
H66	52.36	5.27	91	sG	48.8	50.9	0.3	19.24	0.94	0.10
H68	52.36	5.27	80	gS	20.1	79.8	0.1	19.86	1.07	0.12
H69	52.36	5.27	80	(g)S	4.9	94.9	0.2	17.83	0.83	0.44
H70	52.36	5.27	86	(g)S	2.7	97.0	0.3	13.75	1.27	0.08
H73	53.09	4.56	34	S	0.3	91.7	8.0	13.01	1.36	0.11
H74	53.11	4.54	28	mS	0.4	89.4	10.1	12.44	1.46	0.15
H76	53.09	4.41	17	mS	0.3	88.2	11.5	11.21	1.42	0.18
H77	53.11	4.43	17	(g)S	1.9	96.0	2.1	10.12	1.1	0.09
H78	53.12	4.45	17	sG	43.1	53.8	3.2	16.77	1.24	0.14
H79	53.15	4.51	19	S	0.4	98.7	0.9	7.23	0.75	0.03
H80	53.17	4.54	22	(g)S	1.4	97.0	1.6	8.6	1.16	0.08
H81	53.19	4.58	26	mS	0.5	86.2	13.3	10.07	1.59	0.16
H82	53.31	5.09	171	sG	46.6	49.6	3.8	28.78	1.26	0.33
H83	53.31	5.16	129	sM	0.4	29.7	69.9	27.67	10.72	1.02
H87	52.99	5.90	21	gS	7.6	89.1	3.3	-	-	-
H89	52.97	5.90	17	sG	77.8	21.5	0.6	20.81	1.87	0.50
H92	52.84	5.98	26	gS	13.7	86.1	0.2	26.62	1.19	0.03
H93	52.78	5.99	29	S	0.1	98.1	1.9	7.91	0.64	0.11
H94	52.75	6.00	35	gS	19.0	79.9	1.1	23.28	1.19	0.50
H95	52.92	4.72	41	sG	30.8	65.5	3.8	25.84	1.81	0.05
H96	53.19	4.57	26	gS	8.8	89.4	1.8	9.57	0.91	0.42
H97	52.92	4.69	37	gS	13.3	85.2	1.5	31.78	1.57	0.25

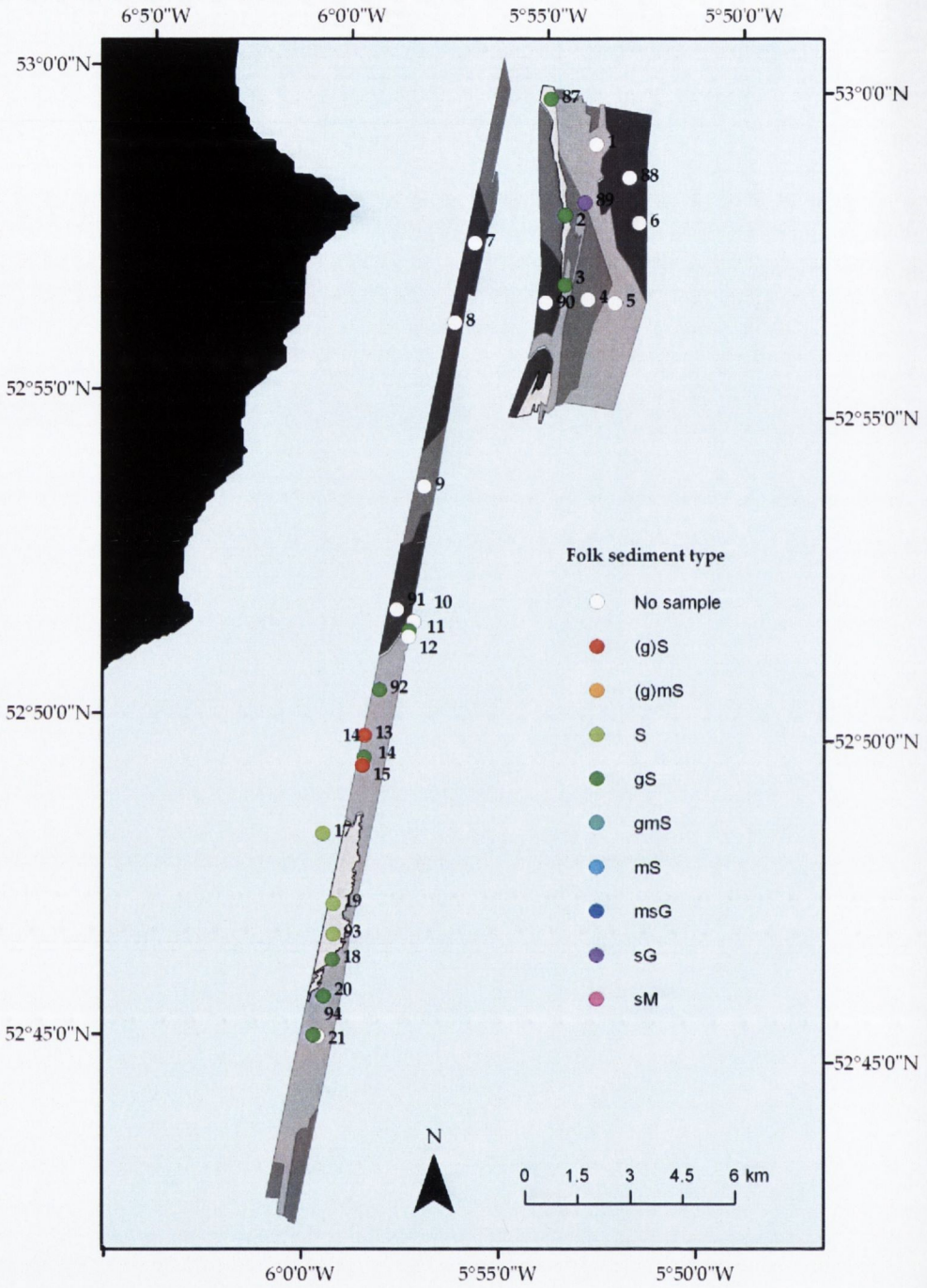


Figure 3.4: Folk sediment categories at stations from Arklow (for detailed sediment station information see Table 3.6). The sample stations are overlaid on the backscatter images produced by Katrien van Landeghem of UCC. 'No sample' indicates that a Van Veen sediment sample was not available for analysis at this station.

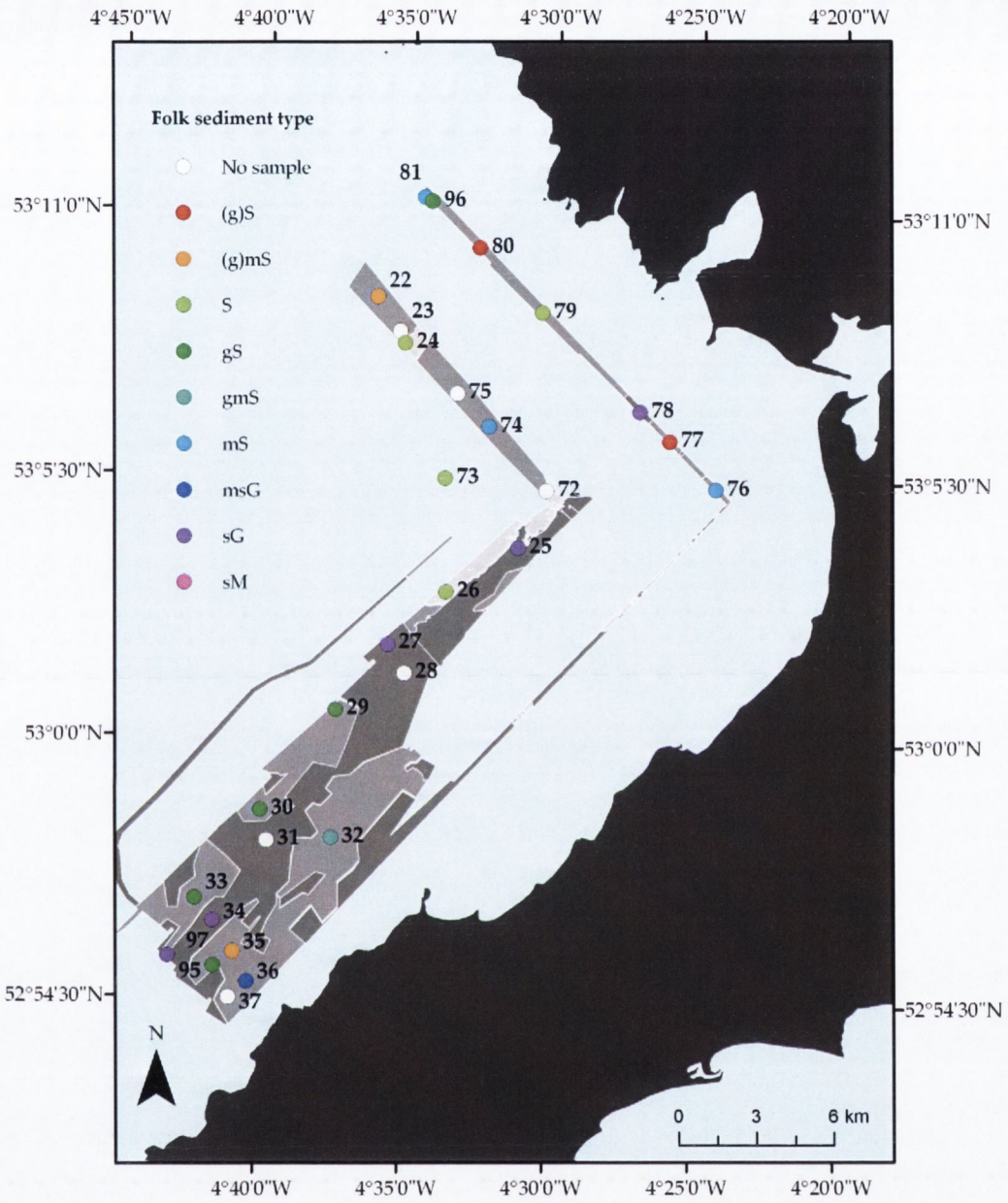


Figure 3.5: Folk sediment categories at stations from Caernarfon Bay (for detailed sediment station information see Table 3.6).

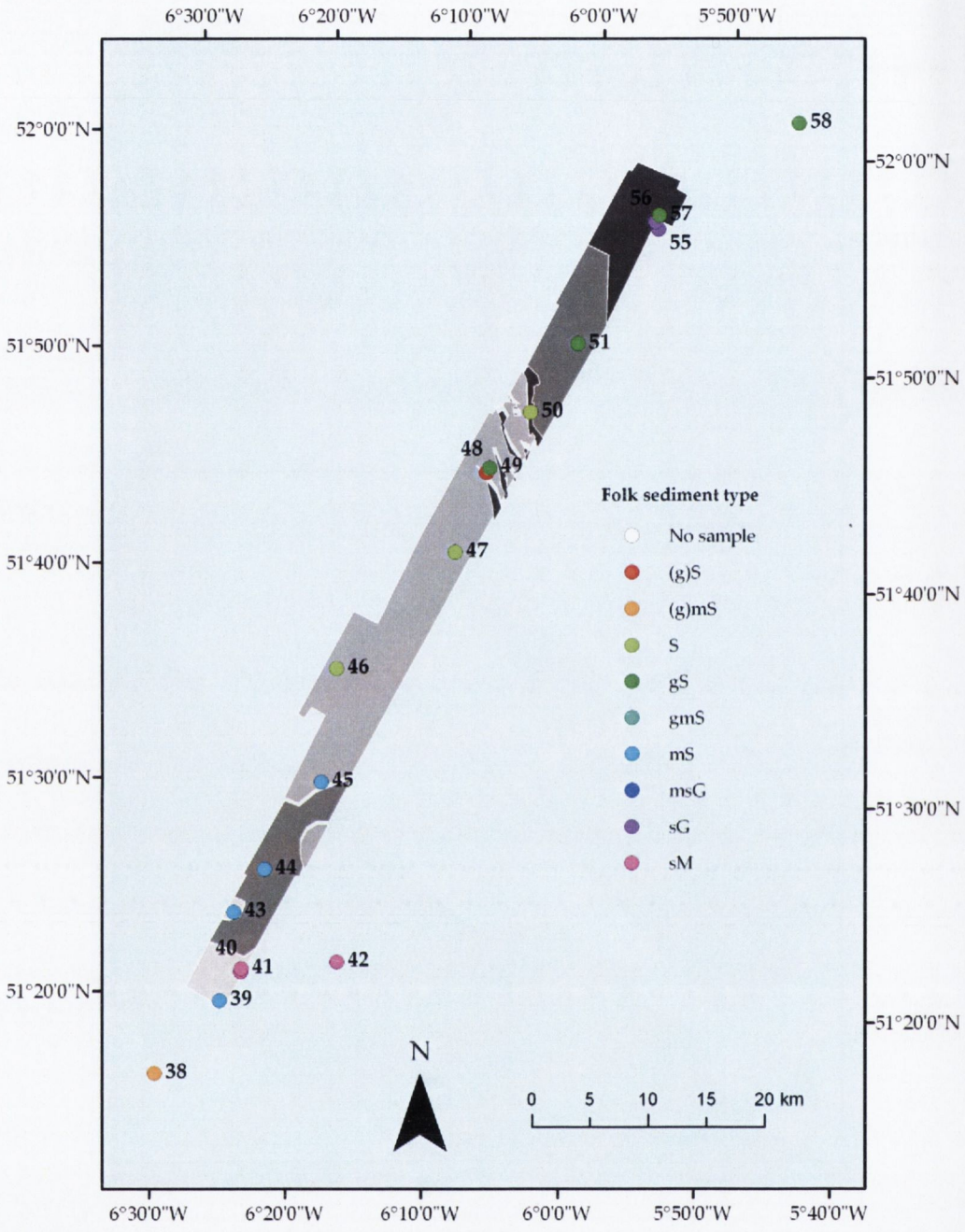


Figure 3.6: Folk sediment categories at stations from the Celtic Deep transect (for detailed sediment station information see Table 3.6).

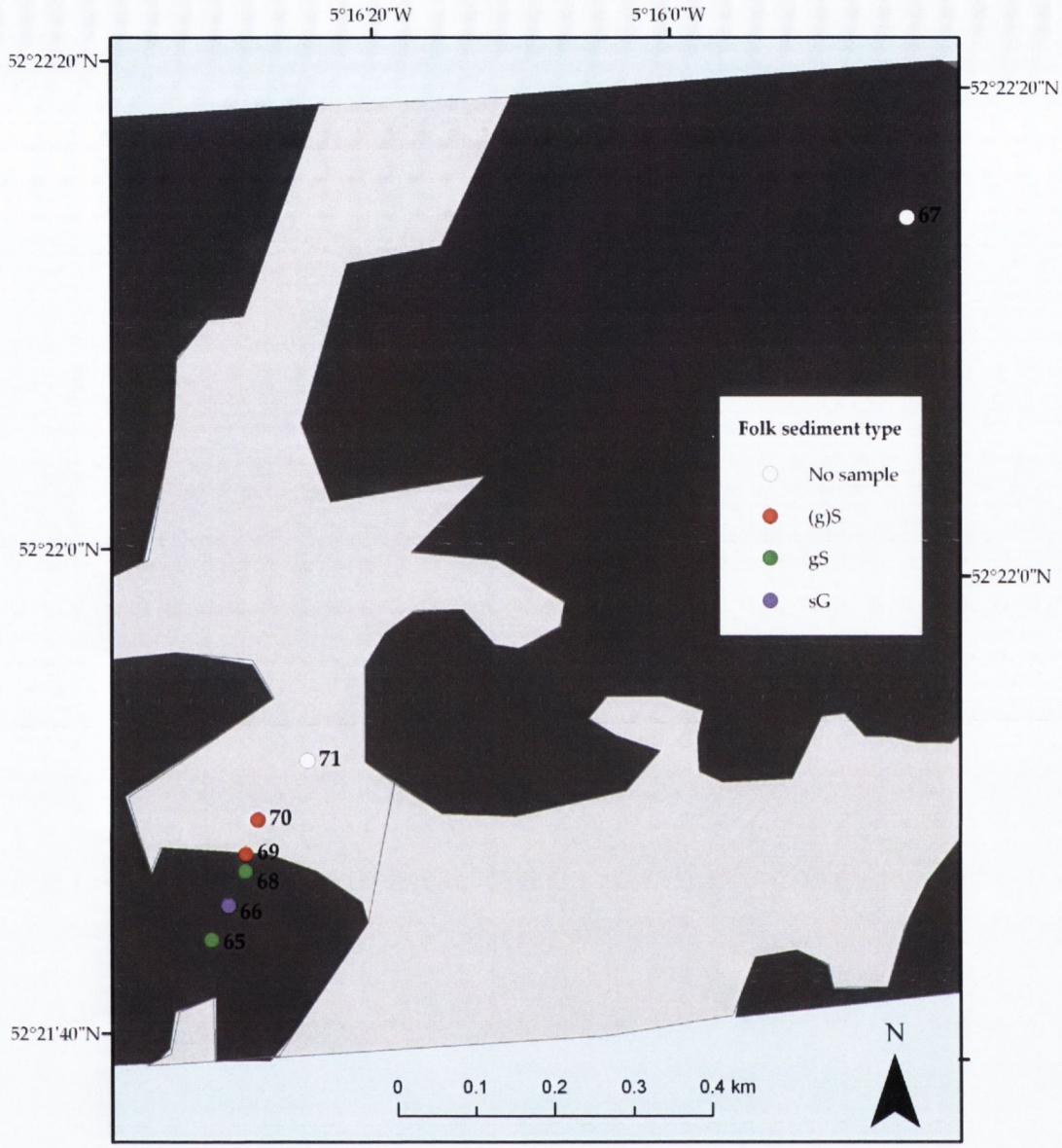


Figure 3.7: Folk sediment categories at stations from the St. George's Channel North transect (for detailed sediment station information see Table 3.6).

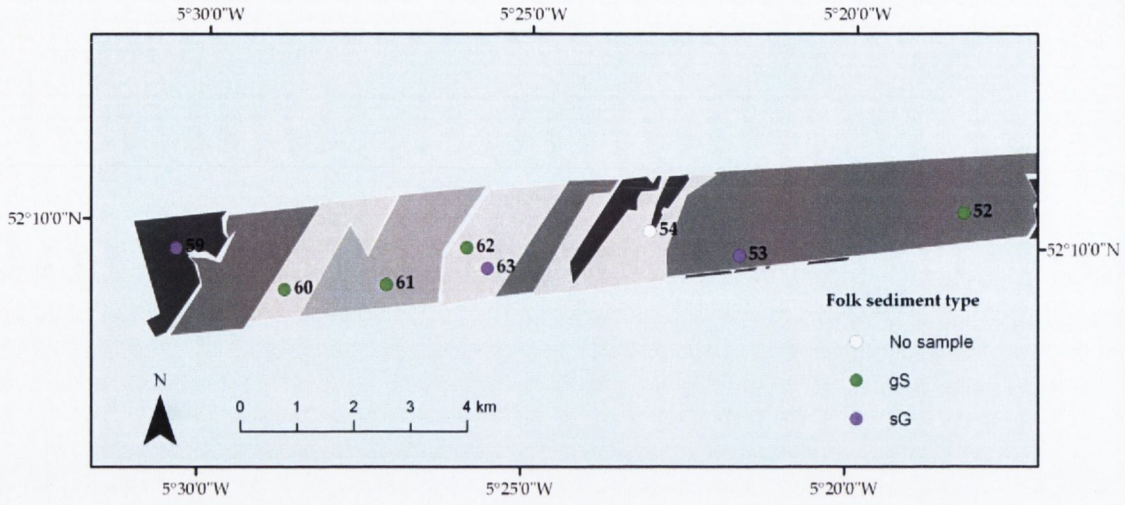


Figure 3.8: Folk sediment categories at stations from the St. George's Channel South transect (for detailed sediment station information see Table 3.6).

Table 3.7: Summary statistics (ϕ sizes) for sedimentological data collected from HABMAP stations.

Stn.	FOLK AND WARD						
	Folk	Mean Grain Size	Sorting	Skewness	Kurtosis	Mode	Median Grain Size
H2	gS	1.16	0.96	-0.24	1.38	1.50	1.28
H3	gS	0.77	1.21	-0.28	1.42	1.50	0.87
H11	gS	-0.11	1.22	-0.35	1.04	0.50	0.21
H13	(g)S	1.13	0.87	-0.14	1.13	1.50	1.20
H14	gS	1.16	1.14	-0.30	1.64	1.50	1.28
H15	(g)S	1.18	0.80	-0.03	0.97	1.50	1.26
H17	S	1.30	0.68	-0.09	1.23	1.50	1.38
H18	gS	1.10	1.23	-0.33	1.77	1.50	1.22
H19	S	1.80	0.64	0.22	0.91	1.50	1.70
H20	gS	1.14	0.97	-0.28	1.39	1.50	1.28
H22	(g)mS	2.36	1.83	0.52	2.01	1.50	1.87
H23	(g)mS	1.93	1.40	0.39	2.02	1.50	1.78
H24	S	1.40	0.69	-0.04	1.37	1.50	1.45
H25	sG	-0.75	0.79	0.91	0.21	0.50	-0.96
H26	S	1.24	0.75	-0.03	1.06	1.50	1.32
H27	sG	0.00	1.48	-0.05	0.61	1.50	0.27
H29	gS	0.24	1.69	-0.34	0.83	1.50	0.89
H32	gmS	1.84	2.25	0.25	2.47	1.50	1.52
H33	gS	0.12	1.16	-0.13	1.41	0.50	0.29
H34	sG	-0.25	1.42	-0.09	0.30	0.50	0.28
H35	(g)mS	1.63	1.64	0.37	2.00	1.50	1.48
H36	msG	-0.24	2.13	0.21	0.62	1.50	0.16
H38	(g)mS	1.40	1.71	0.51	2.19	0.50	1.12
H39	mS	3.05	2.56	0.66	0.78	1.50	1.74
H40	sM	5.05	2.65	-0.40	0.70	6.50	5.85
H41	sM	5.68	2.19	-0.30	0.95	6.50	5.97
H42	sM	5.70	2.07	-0.23	0.97	6.50	5.83
H43	mS	3.23	2.73	0.59	0.69	1.50	1.93
H44	mS	1.63	1.52	0.41	2.95	1.50	1.49
H45	mS	1.80	1.74	0.43	1.73	1.50	1.56
H46	S	1.58	1.10	0.22	1.54	1.50	1.52
H47	S	1.77	0.87	0.18	1.20	1.50	1.67
H48	(g)S	1.41	0.86	0.01	1.33	1.50	1.44
H49	gS	1.07	0.95	-0.19	1.28	1.50	1.14
H50	S	1.53	0.97	0.12	1.35	1.50	1.50
H51	gS	0.45	1.39	-0.21	1.51	0.50	0.60
H52	gS	0.06	1.73	-0.27	0.69	1.50	0.68
H53	sG	0.37	1.49	-0.26	0.30	1.50	1.09
H55	sG	-0.26	1.45	-0.20	0.61	0.50	0.21
H56	sG	-0.07	1.39	0.14	0.33	0.50	0.18
H57	gS	0.00	1.43	-0.26	0.76	0.50	0.41
H58	gS	0.23	1.71	-0.25	1.15	0.50	0.56
H59	sG	-0.32	0.93	0.59	0.31	0.50	-0.46
H60	gS	0.83	0.98	-0.13	1.52	0.50	0.76
H61	gS	0.28	1.61	-0.54	1.36	1.50	0.91
H62	gS	0.70	1.08	-0.15	1.79	0.50	0.63
H63	sG	0.05	1.24	0.22	0.29	1.50	0.14

Table 3.7 (continued): Summary statistics (ϕ sizes) for sedimentological data collected from HABMAP stations.

Stn.	FOLK AND WARD						
	Folk	Mean Grain Size	Sorting	Skewness	Kurtosis	Mode	Median Grain Size
H65	gS	-0.01	1.38	-0.32	1.35	0.50	0.54
H66	sG	-0.83	1.27	0.23	0.59	0.50	-0.90
H68	gS	0.07	1.26	-0.41	1.96	0.50	0.44
H69	(g)S	0.65	0.72	0.02	1.58	0.50	0.59
H70	(g)S	0.89	0.65	0.16	0.77	0.50	0.82
H73	S	1.70	1.34	0.33	1.95	1.50	1.60
H74	mS	1.82	1.43	0.39	2.07	1.50	1.68
H76	mS	2.43	1.50	0.25	2.01	2.50	2.38
H77	(g)S	2.04	0.90	-0.17	1.11	2.50	2.12
H78	sG	-0.23	1.60	0.12	0.38	1.50	0.12
H79	S	1.52	0.68	0.03	1.35	1.50	1.51
H80	(g)S	1.78	0.76	0.07	1.06	1.50	1.69
H81	mS	1.99	1.47	0.46	2.09	1.50	1.80
H82	sG	0.02	1.21	0.53	0.45	0.50	-0.17
H83	sM	5.01	2.68	-0.35	0.71	6.51	5.66
H87	gS	0.91	1.09	0.00	1.40	0.50	0.86
H89	sG	-1.07	0.56	3.88	-39.90	-2.50	-2.61
H92	gS	0.15	1.03	-0.26	1.24	0.50	0.34
H93	S	1.72	0.74	0.12	1.16	1.50	1.63
H94	gS	0.59	1.78	-0.45	1.43	1.50	1.17
H95	sG	-0.02	1.75	-0.27	0.45	1.50	0.93
H96	gS	1.28	1.27	-0.29	1.87	1.50	1.38
H97	gS	0.75	1.22	-0.25	1.32	1.50	0.90

3.3.1.1 Mean grain size

Mean grain size values ranged from -1.073 ϕ (very fine gravel at station H89) to 5.702 ϕ (coarse silt at station H42) (see Table 3.7). The most common mean grain size was medium sand, followed by coarse sand and very coarse sand (see Figure 3.9). Very few of the sites had mean grain sizes in the gravel (site H89) or silt categories (sites H40, H41, H42 and H83). The sites which had coarse silt as their mean grain size were the muddiest sites from the Celtic Deep transect (H40, H41 and H42) and site H83 (some of whose samples contained boulder clay).

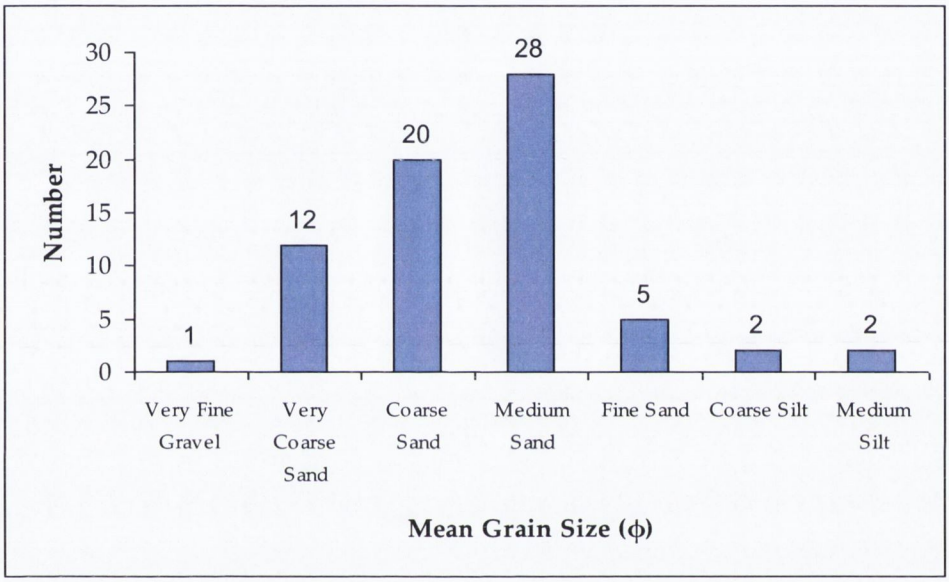


Figure 3.9: Barchart of mean grain size (Mz) for HABMAP samples (SPSS 15.0.10).

3.3.1.2 Median grain size

Median grain size values ranged from -2.611 (very fine gravel) to 5.970 (coarse silt) (see Table 3.7). As with mean grain size, sites H40, H41, H42 and H83 were the only sites to have coarse silt as their median grain size and site H89 from Arklow was the only site to have very fine gravel as its median grain size (see Figure 3.10). The majority of stations had median grain sizes in the sand categories. The low number of sites with median or mean grain sizes in the gravel category may be due to the fact that the Van Veen grab tends not to operate in gravelly sediments. Stations with more gravelly sediment than station H89 would not have been quantitatively sampled.

3.3.1.3 Sorting

The sediments ranged from moderately well sorted sediments to very poorly sorted sediments (see Table 3.7 and Figure 3.11). Sediments from Arklow and St. George's Channel North transect

range from moderately well sorted to poorly sorted sediments. Caernarfon Bay's sands were mainly poorly sorted. 'Slightly gravelly sands' were moderately sorted except for H70 which was moderately well sorted. All of the 'Slightly gravelly muddy sands' sites and the majority of 'muddy sands' sites were classified as poorly sorted. 'Gravelly sands', 'sandy gravels' and 'sands' ranged from poorly sorted to moderately well sorted. The four 'sandy mud' stations were all very poorly sorted.

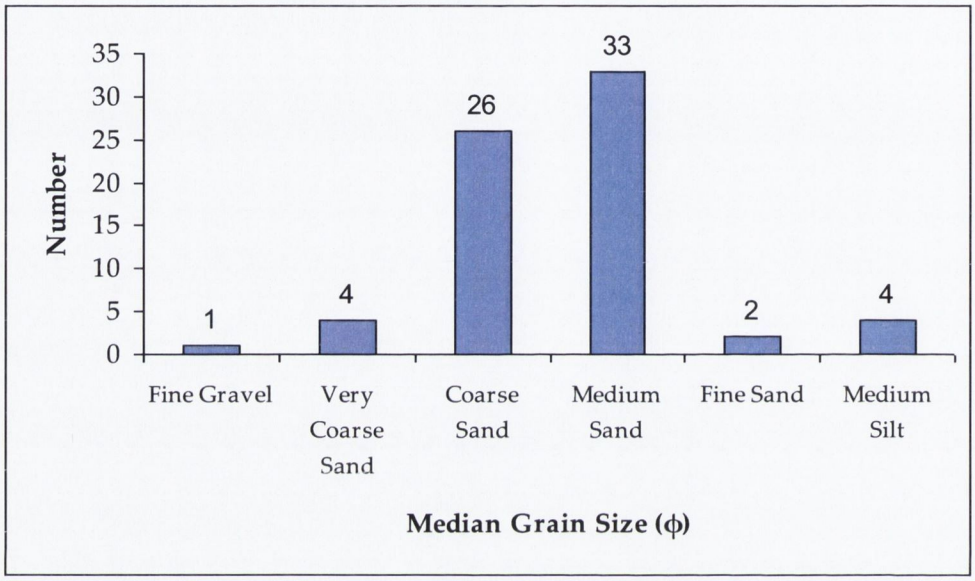


Figure 3.10: Barchart of Median grain size (Md) for HABMAP samples (SPSS 15.0.10).

3.3.1.4 Skewness

Skewness values ranged from -0.542 (very negatively skewed) at station H61 to 0.909 (very positively skewed) at station H25 (see Table 3.7). 'Slightly gravelly muddy sands' were all very positively skewed. 'Gravelly sands' were all very negatively or negatively skewed except for station H87 which was symmetrical. All the 'muddy sand' stations (except station H76) were very positively skewed. The 'sandy mud' stations had a tendency to be very negatively skewed. The 'sands' and 'sandy gravels' showed no real trends. Figure 3.12 examines skewness versus mean grain size. No strong relationship is evident apart from the tendency for the muddiest stations to be positively skewed. The symmetrical sediment categories consisted of 'sandy gravels', 'slightly gravelly sands' and 'sands'.

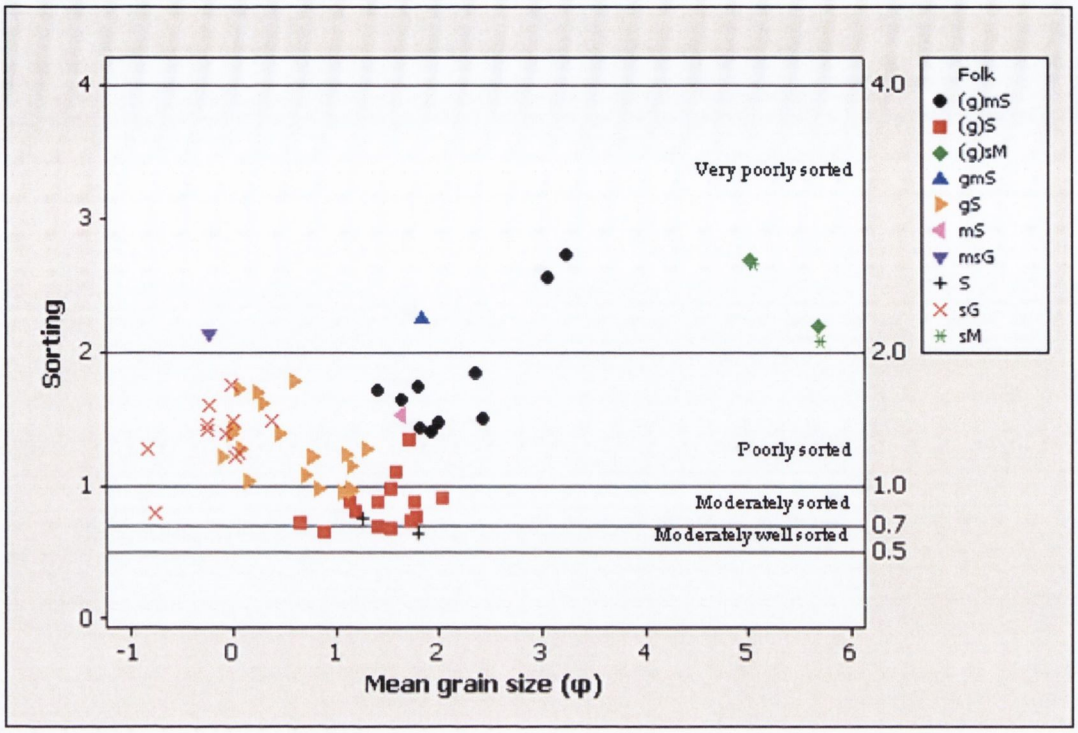


Figure 3.11: Sorting versus mean grain size (Minitab 15.1.1.0).

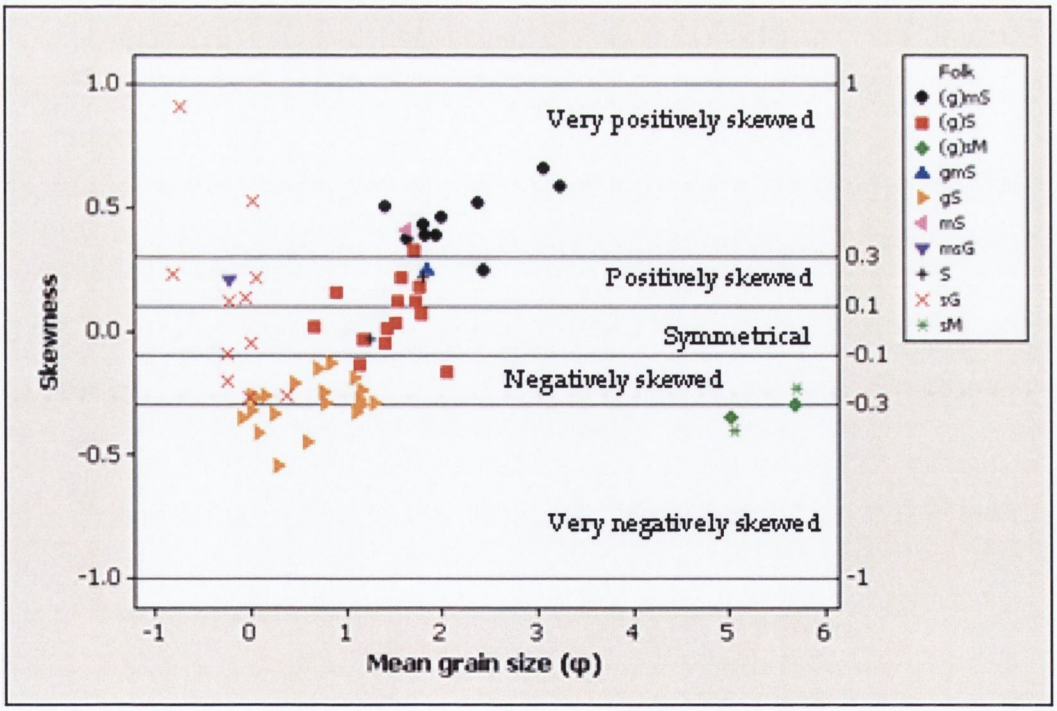


Figure 3.12: Skewness versus mean grain size (Minitab 15.1.1.0).

3.3.1.5 Kurtosis

Kurtosis values ranged from 0.213 (very platykurtic) at station H25 to 2.950 (very leptokurtic) at station H44 (see Table 3.7). All the 'sandy gravels' and the one 'muddy sandy gravel' station were very platykurtic. 'Slightly gravelly sands' ranged from one very leptokurtic sediment to one platykurtic sediment. 'Muddy sands' were either platykurtic or very leptokurtic. 'Sandy muds' were either platykurtic or mesokurtic.

Table 3.8: BIOMÔR (Mackie et al., 1995a) and SWISS (Wilson et al., 2001) stations classified using the BGS modified Folk classification system.

Stations	Survey	Lat.	Long.	Folk	Stations	Survey	Lat.	Long.	Folk
B1	BIOMÔR	53.44	-4.85	gmS	S74	SWISS	53.35	-4.23	mS
B2	BIOMÔR	53.38	-5.00	sG	S75	SWISS	53.44	-6.07	(g)S
B6	BIOMÔR	53.05	-5.17	gmS	S76	SWISS	53.62	-6.05	mS
B7	BIOMÔR	51.36	-6.40	sM	S77	SWISS	53.62	-5.95	mS
B8	BIOMÔR	51.37	-6.28	sM	S78	SWISS	53.44	-5.80	mS
B9	BIOMÔR	51.38	-6.15	sM	S79	SWISS	53.44	-5.88	(g)S
B10	BIOMÔR	51.39	-6.00	mS	S80	SWISS	53.35	-5.90	gmS
B11	BIOMÔR	51.40	-5.87	S	S81	SWISS	53.32	-5.83	S
B12	BIOMÔR	51.42	-5.65	S	S82	SWISS	53.22	-5.87	gS
B13	BIOMÔR	51.43	-5.35	S	S83	SWISS	53.20	-5.75	(g)S
B14	BIOMÔR	51.95	-5.93	msG	S84	SWISS	53.19	-5.95	sG
B15	BIOMÔR	52.03	-5.75	sG	S85	SWISS	53.20	-6.07	(g)mS
B16	BIOMÔR	52.10	-5.56	sG	S87	SWISS	53.32	-5.98	gS
B17	BIOMÔR	52.17	-5.39	gS	S88	SWISS	53.32	-6.08	S
B18	BIOMÔR	52.24	-4.40	(g)mS	S89	SWISS	53.22	-5.55	sG
B19	BIOMÔR	52.27	-4.29	gmS	S90	SWISS	53.32	-5.52	(g)S
B20	BIOMÔR	52.36	-4.18	mS	S91	SWISS	53.44	-5.62	S
B21	BIOMÔR	52.35	-4.24	S	S92	SWISS	53.52	-5.66	mS
B22	BIOMÔR	52.35	-4.30	S	S93	SWISS	53.51	-5.69	mS
B23	BIOMÔR	52.34	-4.35	S	S95	SWISS	53.56	-5.71	mS
B24	BIOMÔR	52.71	-4.51	mS	S96	SWISS	53.62	-5.75	mS
B25	BIOMÔR	52.71	-4.41	S	S97	SWISS	53.62	-5.52	mS
B26	BIOMÔR	52.74	-4.44	mS	S98	SWISS	53.62	-5.33	S
B27	BIOMÔR	52.77	-4.38	mS	S99	SWISS	53.62	-4.93	Gs
B28	BIOMÔR	52.81	-4.30	S	S100	SWISS	52.92	-4.67	mS

Table 3.8 (continued): BIOMÔR (Mackie et al., 1995a) and SWISS (Wilson et al., 2001) stations classified using the BGS modified Folk classification system.

Stations	Survey	Lat.	Long.	Folk	Stations	Survey	Lat.	Long.	Folk
B29	BIOMÔR	52.86	-4.19	sM	S101	SWISS	52.62	-5.31	gS
B32	BIOMÔR	53.15	-4.49	S	S103	SWISS	51.40	-5.87	mS
B33	BIOMÔR	53.12	-4.73	sG	S104	SWISS	51.35	-6.40	sM
B34	BIOMÔR	53.33	-4.15	(g)mS	S105	SWISS	51.50	-6.52	S
B38	BIOMÔR	52.73	-4.69	msG	S106	SWISS	51.75	-6.75	(g)S
B39	BIOMÔR	52.66	-4.61	sG	S107	SWISS	51.98	-6.75	S
B42	BIOMÔR	52.62	-4.23	S	S108	SWISS	52.08	-6.75	S
B43	BIOMÔR	52.52	-4.22	S	S110	SWISS	52.03	-6.45	(g)S
B45	BIOMÔR	52.40	-4.24	S	S111	SWISS	52.16	-6.49	S
B46	BIOMÔR	52.32	-4.62	sG	S112	SWISS	52.27	-6.24	S
B47	BIOMÔR	52.16	-4.54	mS	S113	SWISS	52.29	-6.32	gmS
B48	BIOMÔR	52.11	-4.92	sG	S114	SWISS	52.44	-6.25	gS
B49	BIOMÔR	52.29	-5.00	gmS	S116	SWISS	52.64	-6.15	S
B50	BIOMÔR	52.51	-4.77	gS	S118	SWISS	52.80	-5.62	sG
B51	BIOMÔR	52.44	-5.02	gS	S120	SWISS	52.80	-6.00	S
B52	BIOMÔR	52.37	-5.24	S	S121	SWISS	52.97	-5.64	(g)S
B54	BIOMÔR	52.16	-5.43	mS	S122	SWISS	53.02	-5.54	S
B55	BIOMÔR	52.03	-5.52	gS	S126	SWISS	52.52	-4.22	S
B57	BIOMÔR	51.81	-5.71	sG	S127	SWISS	52.35	-4.17	sM
B58	BIOMÔR	51.71	-5.76	gmS	S128	SWISS	52.32	-4.62	gS
B59	BIOMÔR	51.53	-5.94	mS	S129	SWISS	51.84	-5.22	S
B60	BIOMÔR	51.26	-6.00	mS	S130	SWISS	51.78	-5.20	mS
B61	BIOMÔR	51.27	-6.27	sM	S131	SWISS	51.79	-6.31	sG
B62	BIOMÔR	51.27	6.50	(g)mS	S132	SWISS	51.94	-5.92	S
B63	BIOMÔR	51.59	6.30	S	S133	SWISS	52.19	-5.80	sG
					S135	SWISS	52.27	-5.98	S
					S137	SWISS	52.44	-6.05	sG
					S140	SWISS	53.10	-5.84	sG

3.3.2 Comparison of BIOMÔR, SWISS & HABMAP sites

As the BIOMOR and SWISS projects used the Buchanan sediment classification system (Buchanan, 1984) all stations were firstly reclassified using the BGS modified system of sediment classification (Folk, 1954, Jackson et al., 1995) (see Table 3.8). Comparisons were made of BIOMÔR and SWISS sites re-sampled during the HABMAP project (see Tables 3.9 - 3.12).

Results showed that station H63 (station B54) was the only station at which the sediment sampled substantially differed from the BIOMÔR stations (see Table 3.9). Station H63 was classed as 'Sandy Gravel'; however the B54 was classed as 'muddy sand'. A further difference was observed at station H58 (station B15) which was classed as 'sandy gravel' in BIOMÔR, however there was a decrease in the gravel component and a corresponding increase in the sand component for HABMAP leading to it be classed as 'gravelly sand'.

Table 3.9: Comparison between particle size and calcium carbonate concentrations at stations originally sampled during the BIOMÔR survey (Mackie et al., 1995a) which were re-sampled during the HABMAP survey. G = gravel, S = sand, M = mud.

HABMAP						BIOMÔR					
Stn.	Folk	G (%)	S (%)	M (%)	$CaCO_3$ %	Station	Folk	G (%)	S (%)	M (%)	$CaCO_3$ %
H38	(g)mS	2.8	83.9	13.3	31.5	B62	(g)mS	4.6	59.1	35.9	32.9
H41	sM	0.0	20.8	79.2	37.7	B7	sM	0.0	11.1	88.3	34.6
H42	sM	0.0	19.9	80.1	37.7	B8	sM	0.0	33.6	66.4	36.7
H46	S	0.0	94.8	5.2	14.4	B63	S	0.0	91.4	8.6	18.9
H56	sG	38.7	58.4	2.8	43.3	B14	msG	34.7	57.1	8.0	46.4
H58	gS	21.5	74.8	3.7	44.5	B15	sG	37.1	58.5	4.1	40.1
H63	sG	44.1	54.9	1.0	45.0	B54	mS	0.0	62.9	37.4	7.5

When HABMAP stations were compared with re-sampled SWISS stations, 2 out of 4 of the stations were assigned to different Folk categories (see Table 3.10). Station H36 (S100) was classified as 'muddy sandy gravel' compared to 'muddy sand' in the SWISS survey and station H55 (S132) was classified as 'sandy gravel' compared to ' gravelly sand' in the SWISS survey.

Results of further comparisons between HABMAP, BIOMÔR and SWISS are summarised in the following sections, along with results of further analysis of the HABMAP sediments.

Table 3.10: Comparison between particle size and calcium carbonate concentrations at stations originally sampled during the SWISS survey (Wilson et al., 2001) which were re-sampled during the HABMAP survey.

HABMAP						SWISS					
Stn.	Folk	G (%)	S (%)	M (%)	$CaCO_3$ %	Station	Folk	G (%)	S (%)	M (%)	$CaCO_3$ %
H17	S	0.2	99.0	0.8	6.5	S120	S	0.0	99.2	1.0	6.4
H36	msG	41.1	52.5	6.4	50.9	S100	mS	0.5	67.3	32.2	21.5
H40	sM	0.0	26.7	73.3	36.9	S104	sM	0.0	11.2	88.8	28.1
H55	sG	30.2	68.4	1.3	44.2	S132	gS	32.0	66.4	1.6	49.8

3.3.3 Calcium carbonate

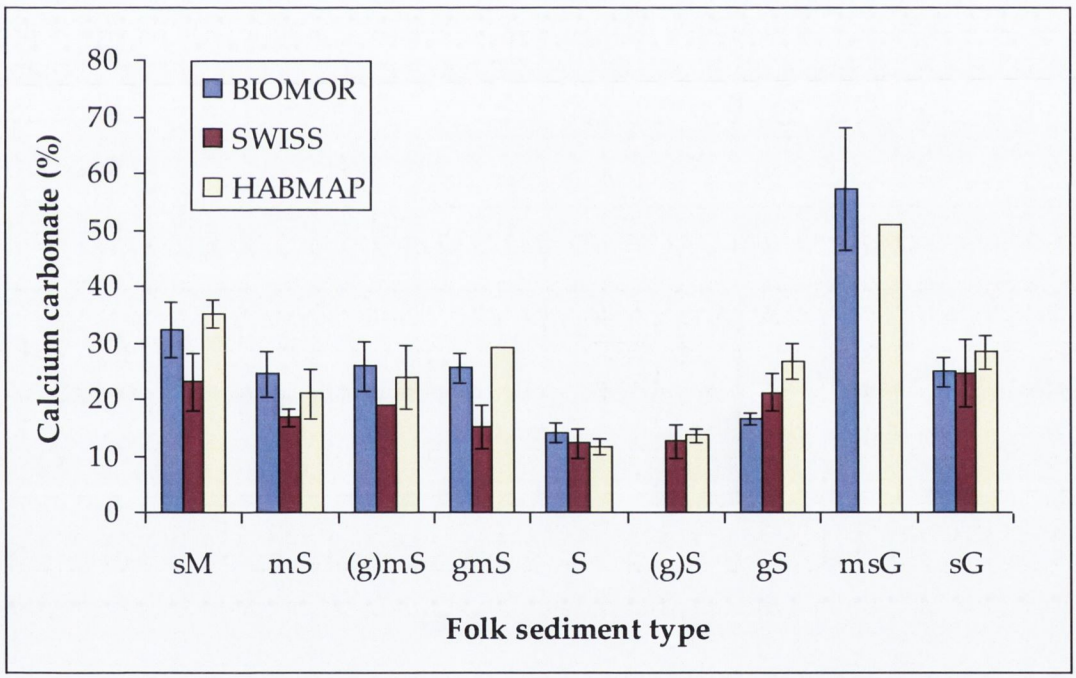


Figure 3.13: Mean calcium carbonate content of sediment in the southern Irish Sea, as found during the HABMAP, BIOMÔR (Mackie et al., 1995a) and SWISS (Wilson et al., 2001) projects. Error bars represent the standard error (SE) of the mean. An absence of error bars indicates a single data point.

The calcium carbonate content of the HABMAP stations ranged from 6.46% to 66.88% (see Table 3.6). The lowest concentrations of calcium carbonate were found in the sandier sediments (see Figure 3.13). Mean calcium carbonate levels occurring within the different sediment categories were compared with those from the BIOMÔR and SWISS surveys (see Figure 3.13, Table 3.9 and Table 3.10). Calcium carbonate levels for the different Folk categories showed generally similar

levels for all surveys (see Figure 3.13). 'Muddy sandy gravels' showed substantially higher levels of calcium carbonate than other sediments (~ 50 - 57%), compared to the next highest category 'sandy mud' which had levels ranging from approximately 23 - 32%. This can probably be attributed to the presence of shell as part of the gravel component for the 'muddy sandy gravel' category. When compared with BIOMÔR sediments found at each station, the results from HAMAP station 63 seemed to differ substantially in terms of calcium carbonate compared with those observed previously, probably due to differences in gravel content found between the two studies (as shown in Table 3.9). Results at all other stations were comparable with those found during the BIOMÔR study.

Calcium carbonate results from the HABMAP project show a similar trend to those found by the SWISS project, though a much higher level of calcium carbonate was found for station H36 (S100), which was composed of 'muddy sandy gravel' as opposed to 'muddy sand' during SWISS (see Table 3.10). *Modiolus modiolus* shells were present at the HABMAP station which may have contributed to the elevated calcium carbonate levels. Maps of calcium carbonate distribution for all the areas are displayed in Appendix 2.

3.3.4 Organic matter content

The organic matter content of the HABMAP stations ranged from 0.55% (station H19) to 10.80% (station H39) (see Table 3.6). This appeared to be related to the muddiness of sediments, as organic matter content shows a significant correlation with the silt/clay content (see Figure 3.14).

Results of regression analysis are shown in Figure 3.14 which shows that in the HABMAP sediment sampled, organic matter content was highly correlated with the silt/clay fraction (r^2 (adjusted) = 81.7%, p = <0.001, n= 64). The regression relationship between the two variables was described as:

$$\text{Organic Matter} = 1.09 + 0.12\ (\text{Silt/clay}),\ r^2 = 0.817$$

The removal of outlier stations H38, H39 and H42 improved the regression analysis (r^2 (adjusted) = 93.3%, p = <0.001, n= 61). The regression relationship between the two variables was described as:

$$\text{Organic Matter} = 0.98 + 0.12\ (\text{Silt/clay}),\ r^2 = 0.993$$

Maps of organic matter distribution for Arklow, Caernarfon Bay and the Celtic Deep transect are displayed in Appendix 2.

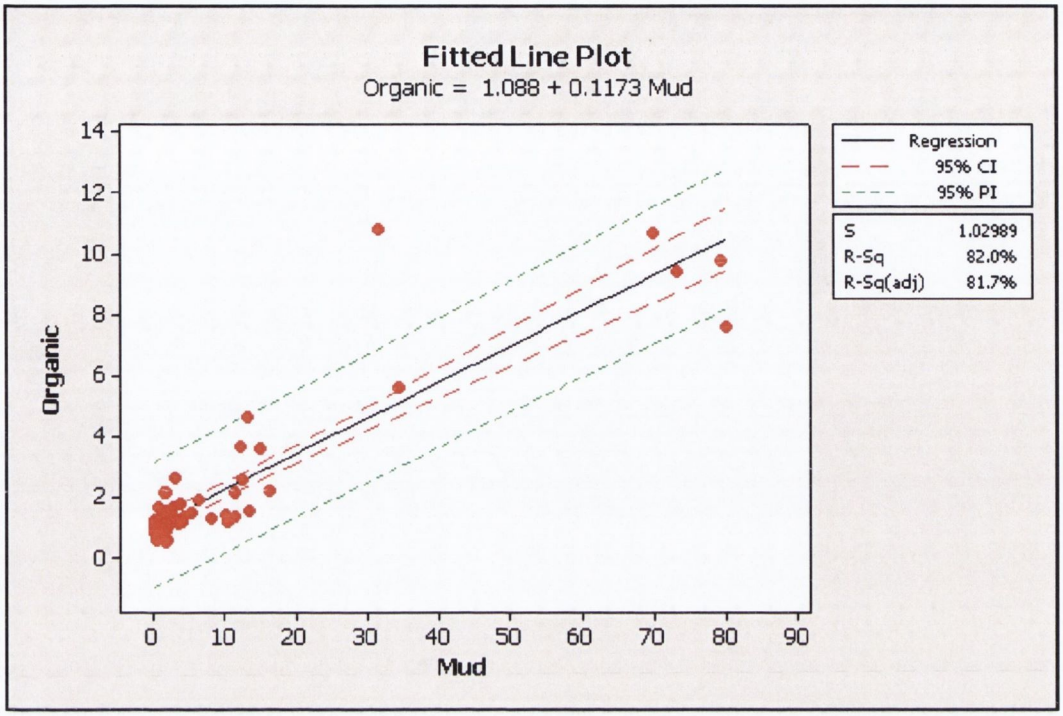


Figure 3.14: Relationship between organic content (%) and silt/clay fraction (%) of HABMAP stations (Minitab 15.1.1.0).

When the levels of organic matter of the HABMAP sediments were compared with those found during BIOMÔR and SWISS, 'sandy muds' were found to have substantially higher levels of organic matter (4.3 – 9.4%) than all other sediment types, particularly for the SWISS and HABMAP sediments. Organic content levels from other Folk types ranged from approximately 0.9% - 1.1% for 'sand' to 2.3% - 3.7% for 'muddy sand' (see Figure 3.15). Organic matter levels for the different Folk categories showed similar levels over all the projects.

HABMAP stations show generally higher levels of organic content than the BIOMÔR stations (see Figure 3.15). The largest differences were found at stations H41 and H42 where the organic content concentrations almost doubled.

The HABMAP and SWISS stations show no particular trends for organic content. Station H40 was very similar to station S104. Stations H17 and H55 both had higher levels of organic matter than the SWISS stations. The reverse occurred for station H36; this may be due to the presence of a high amount of *Modiolus modiolus* faecal matter observed. Some of these differences may be due to

the different methods of analysis used in the projects. The SWISS and HABMAP projects tended to use more similar methods of analysis.

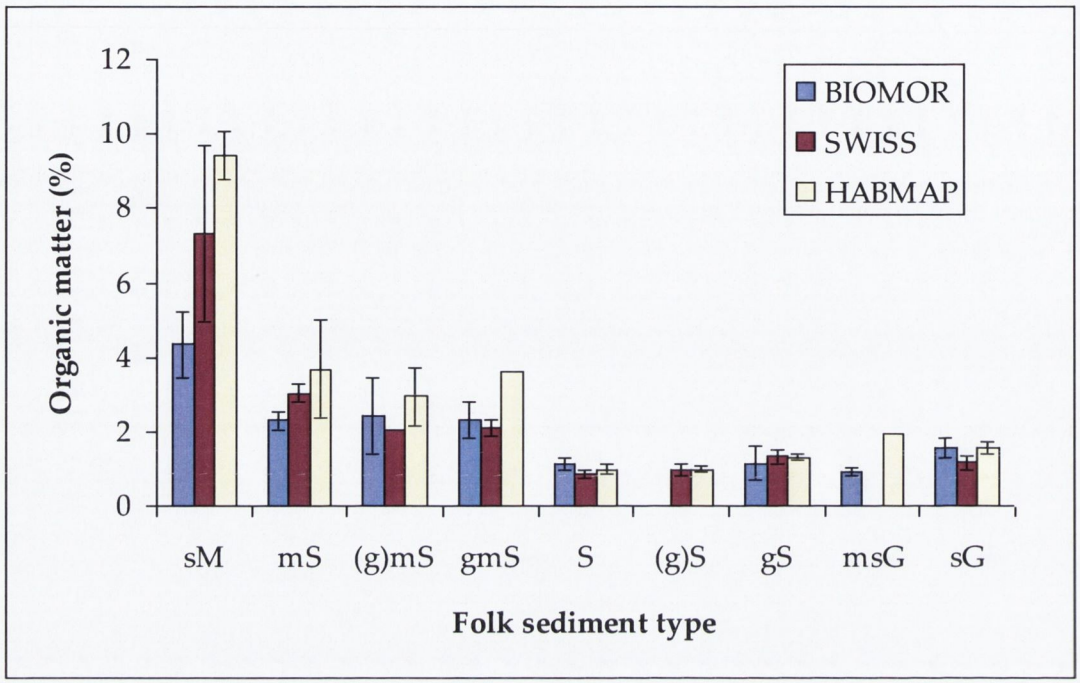


Figure 3.15: Mean organic content of sediment in the Southern Irish Sea. Legend as Figure 3.13.

Table 3.11: Comparison between organic content and organic carbon concentrations at stations originally sampled during the BIOMÔR survey (Mackie et al., 1995a) which were re-sampled during the HABMAP survey.

HABMAP			BIOMÔR		
Stations	**Organic content (%)**	**Organic Carbon (%)**	**Stations**	**Organic content (%)**	**Organic Carbon (%)**
H38	4.67	0.87	B62	4.31	0.66
H41	9.78	2.37	B7	4.85	1.39
H42	7.64	1.49	B8	3.40	0.93
H46	1.52	0.45	B63	1.23	0.15
H56	2.24	2.20	B14	1.01	0.29
H58	1.96	1.94	B15	1.19	0.14
H63	1.04	0.16	B54	0.68	0.04

Table 3.12 : Comparison between organic content and organic carbon concentrations at stations originally sampled during the SWISS survey (Wilson et al., 2001) which were re-sampled during the HABMAP survey.

HABMAP			SWISS		
Stations	**Organic content (%)**	**Organic Carbon (%)**	**Stations**	**Organic content (%)**	**Organic Carbon (%)**
H17	0.65	0.02	S120	0.48	0.20
H36	1.94	0.86	S100	4.64	1.79
H40	9.46	1.53	S104	9.67	1.45
H55	2.21	1.90	S132	1.37	0.52

3.3.5 Total organic carbon

Total organic carbon values of the HABMAP stations ranged from 0.02 (station H17) to 2.41% (station H33) (see Table 3.6). Muddier sediments appeared to contain the most organic carbon, followed by gravel and then sand.

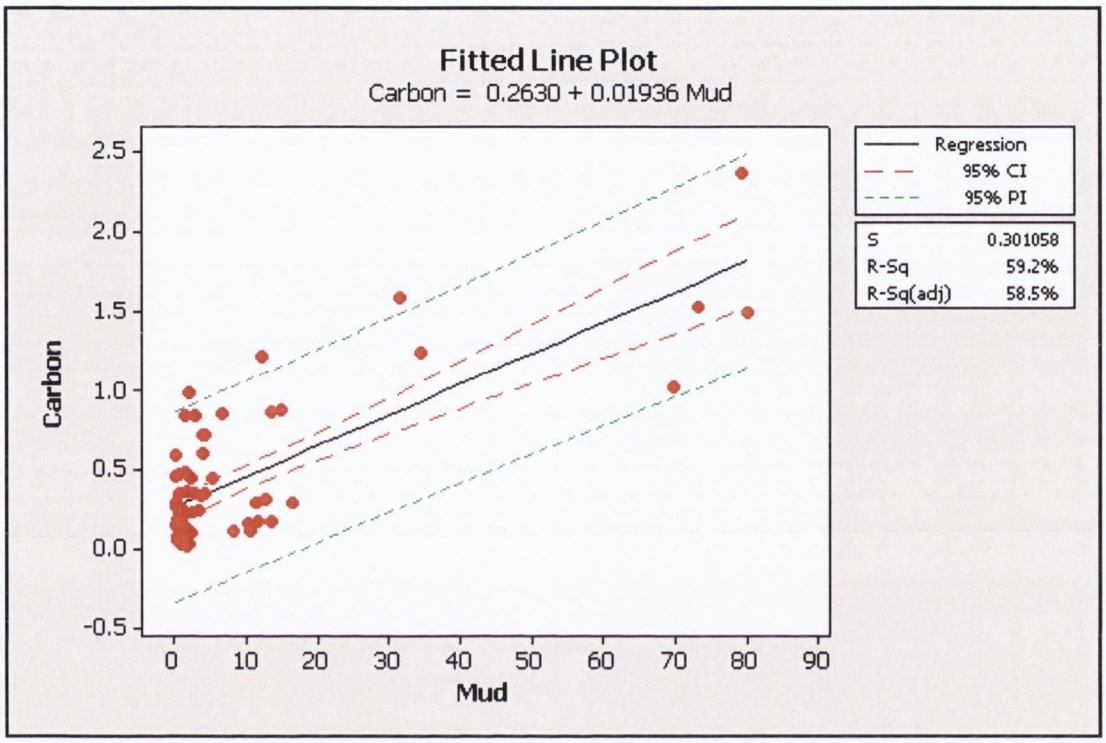


Figure 3.16: Regression relationship between total organic carbon (%) and the silt/clay(%) fraction for all HABMAP stations (Minitab 15.1.1.0).

The result of regression analysis (see Figure 3.16) shows that organic carbon was positively correlated with the silt/clayfraction (r^2 (adjusted) = 58.5%, p = <0.001, n = 64). The regression relationship between the two variables was described as:

Organic Carbon = 0.23 + 0.019 (silt/clay), r^2 = 0.59.

The removal of outlier stations H35, H39 and H51 improved the regression analysis (r^2 (adjusted) = 64.2%, p = <0.001, n = 61).

The overall relationship between organic content and organic carbon at the stations was also examined. The regression relationship between organic content and organic carbon at all the sites was relatively high (r^2 (adjusted) = 72%, p <0.001, n = 64) (see Figure 3.17). The removal of outlier

stations H83, H39, H40, H42 and H51 improved the regression analysis (r^2 (adjusted) = 80%, p <0.001, n = 59).

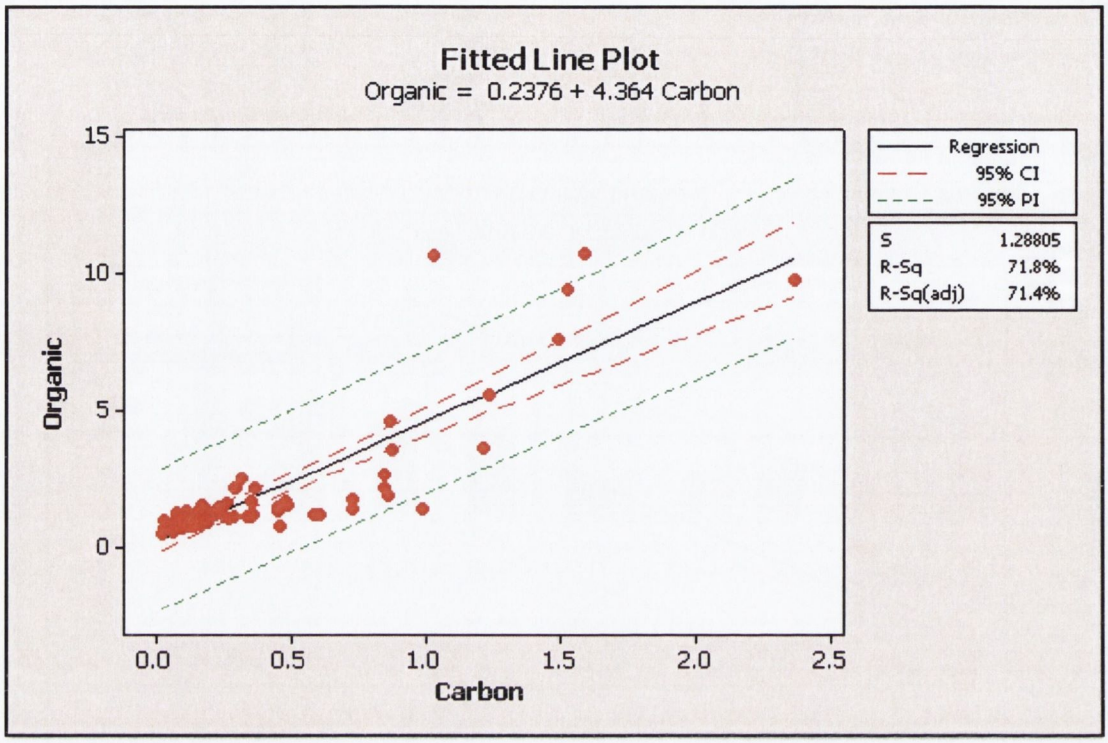


Figure 3.17: Regression relationship between organic carbon and organic content for all HABMAP stations (Minitab 15.1.1.0).

A comparison between Folk sediment types and organic carbon content from the three surveys showed a substantially higher average organic carbon level for the 'gravelly muddy sand' category from the HABMAP project compared with the earlier surveys (see Figure 3.18). However, it must be noted that the HABMAP survey only contained one 'gravelly muddy sand' site (site 32); this site had a high level of the bivalve *M. modiolus* present. The high level of organic carbon at this site is probably due to the presence of *M. Modiolus* faeces. Similar to organic matter content, high levels of organic carbon were found in all surveys for the 'sandy mud' category, ranging from approximately 0.9 – 1.6%.

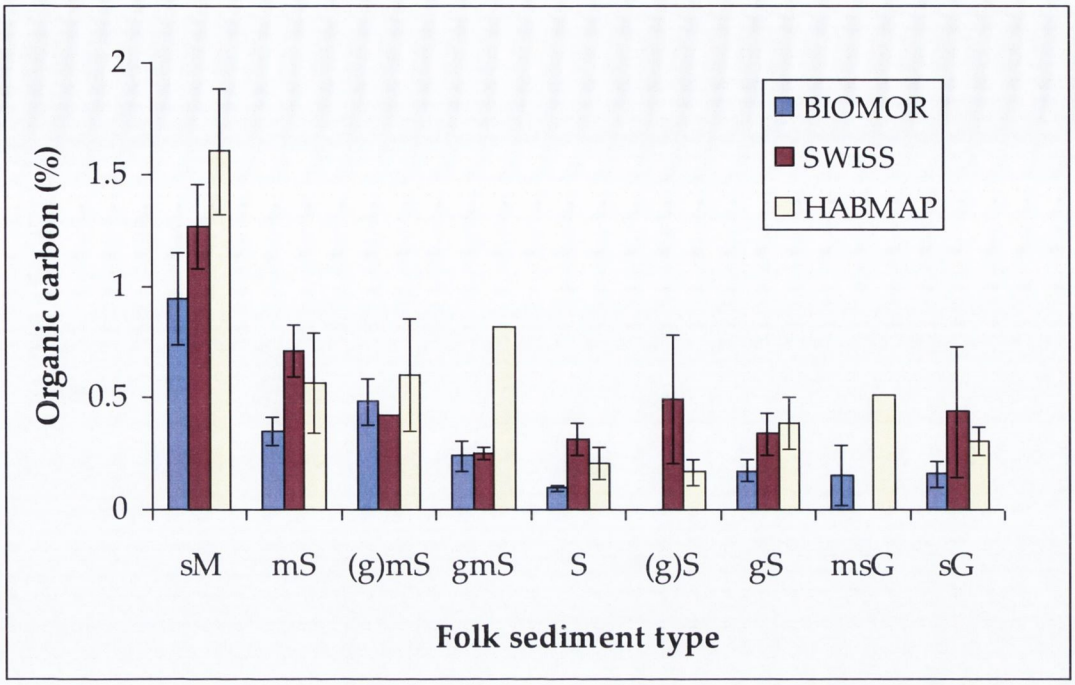


Figure 3.18: Mean organic carbon content of sediment in the southern Irish Sea. Legend as Figure 3.13.

3.3.6 Spearman rank correlation

Table 3.13: Spearman Rank Correlation table, n=64. Significant correlations are highlighted in grey. * Correlation is significant at the 0.01 level (2-tailed). ** Correlation is significant at the 0.05 level (2-tailed).

	BS	MGS	Folk	Depth	G	S	M	$CaCO_3$	OM	TOC
BS	1									
MGS	-0.323**	1								
Folk	-0.224	0.430**	1							
Depth	-0.318*	0.057	-0.036	1						
G	0.394**	-0.900**	-0.394**	-0.049	1					
S	-0.114	0.305*	0.072	-0.402**	-0.487**	1				
M	-0.086	0.663**	0.260*	0.320**	-0.497**	-0.254*	1			
$CaCO_3$	-0.027	-0.287*	-0.005	0.574**	0.363**	-0.685**	0.123	1		
OM	0.067	0.238	0.233	0.473**	-0.089	-0.597**	0.705**	0.603**	1	
TOC	0.011	0.005	0.152	0.615**	0.078	-0.657**	0.492**	0.755**	0.815**	1

Table 3.13 shows the results of a Spearman rank correlation showing the correlations between the environmental variables. Significant correlations ($p < 0.05$) have been highlighted. The highest positive correlations were observed between organic carbon and organic content (+0.815 p= <0.001) and organic carbon and calcium carbonate (+0.755, p= <0.001), indicating that as organic carbon increased, both organic content and calcium carbonate concentrations increased. The most significant negative correlations were observed between sand and calcium carbonate (-0.685, p =

<0.001) and between sand and organic carbon (-0.657, p = <0.001), indicating that as the sand component increased the calcium carbonate and organic carbon concentrations decreased. The backscatter categories of high, medium high, medium low and low had the least number of significant correlations as they were only found to correlate with the gravel component. This correlation would be expected as backscatter shows the reflectivity of the seabed, which is expected to be higher in coarser sediments.

3.3.7 Comparison with BGS modified Folk map

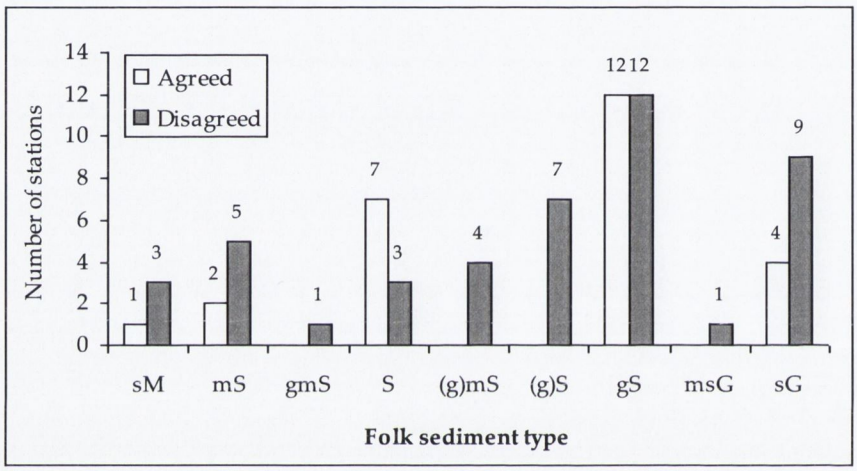


Figure 3.19: Number of HABMAP stations per sediment Folk category which agree with their BGS sediment classification.

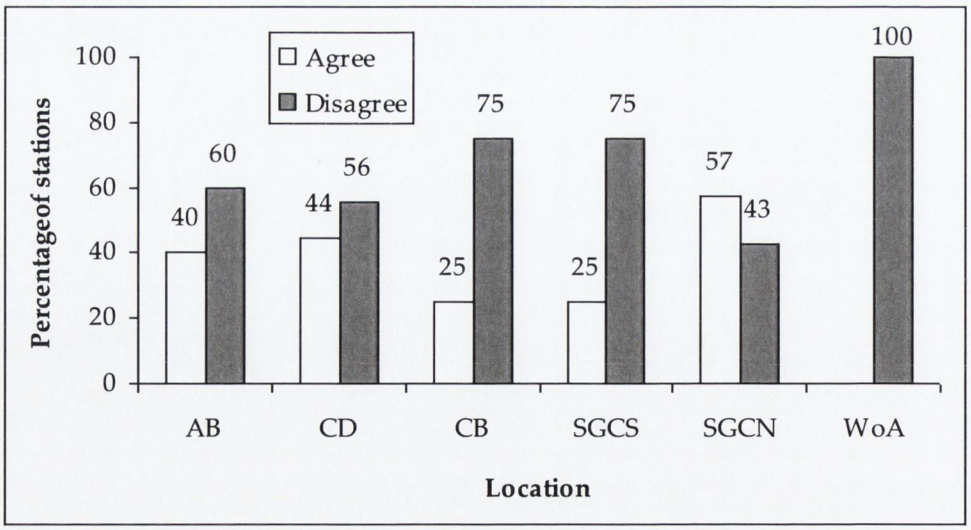


Figure 3.20: Breakdown of the agreement of HABMAP Folk sediment stations with the BGS Folk sediment classification. AB = Arklow Bank, CD = Celtic Deep, CB = Caernarfon Bay, SGCS = St. George's Channel South, SGCN = St. George's Channel North & WoA = West of Anglesey.

As shown in Figure 3.19, there was huge disagreement between the BGS modified Folk classification for HABMAP stations and the values achieved for this project. The Folk categories of 'gravelly muddy sand', 'slightly gravelly muddy sand', 'gravelly sand' and 'muddy sandy gravel' all showed 100% disagreement with the BGS sediment maps. The 'sand' category had the most agreements, agreeing with BGS sediments 70% of the time.

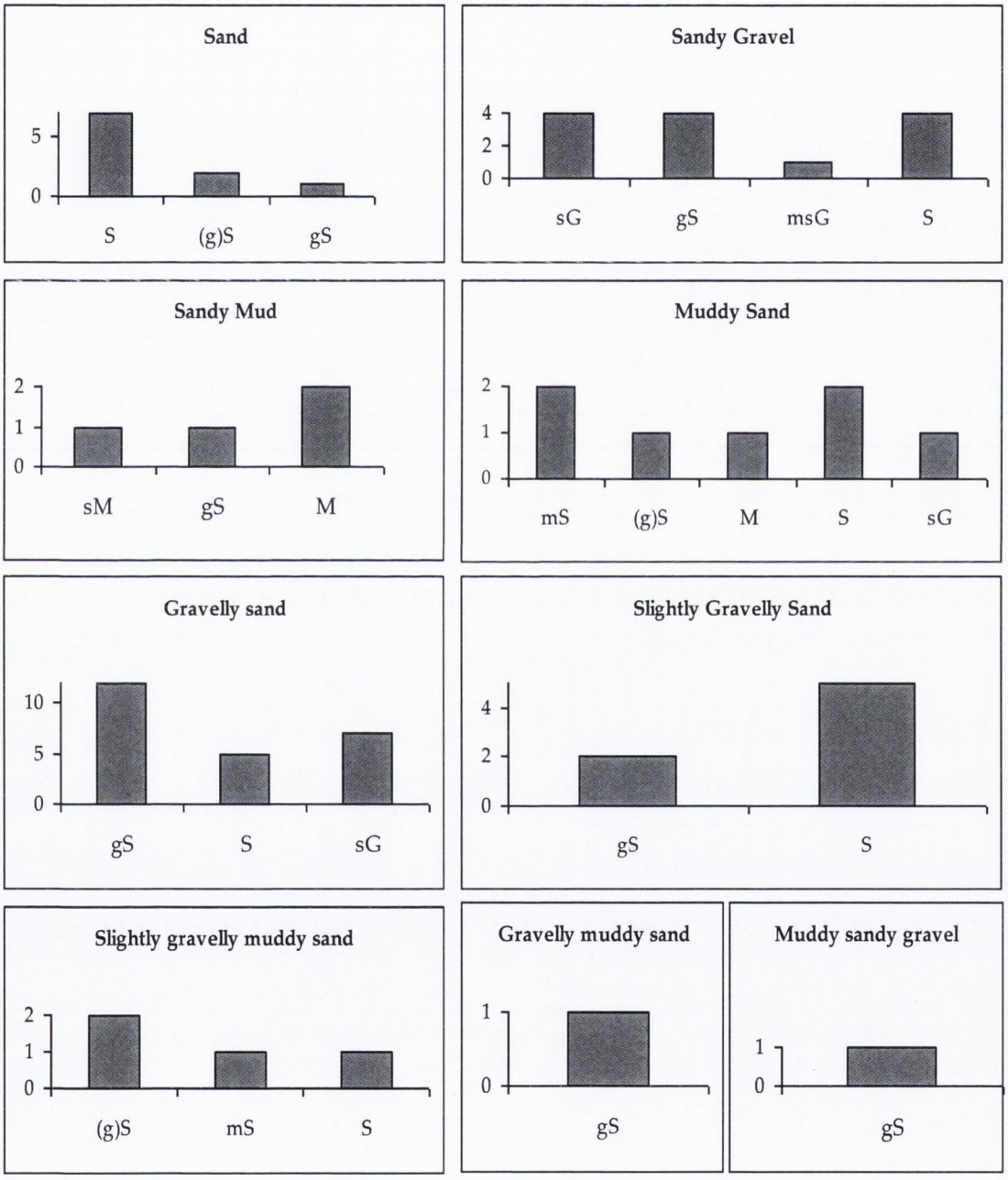


Figure 3.21: Breakdown of the BGS modified Folk sediment classes found in this project into the sediment classes found on the BGS modified Folk map DigiSBS,

Figure 3.20 shows the breakdown of how the HABMAP Folk categories from the individual survey areas matched the BGS Folk categories. Figure 3.20 shows that there is a high level of

disagreement between the HABMAP and BGS data at all survey locations with only St. George's Channel North area showing greater than 50% agreement.

Figure 3.21 shows the breakdown of the sediment classes found in this project into the classes found on the BGS modified Folk map. It shows that often the point sample data differs hugely from the mapped polygon data.

3.3.8 Multivariate statistics

PRIMER v.6 was used to construct Multi-dimensional Scaling (MDS) plots for 68 sites in the Irish Sea. Both plots had stress levels between 0.05 and 0.1, indicating that they were good ordinations with no real possibility of misinterpretation (Clarke, 1993). In Figure 3.22 the MDS plot examined depth, sand, gravel and mud concentrations at these sites. The plot shows a clear separation between the sandy mud stations (H40, H41, H42 and H83) and the rest of the stations. The muddy sand stations H39 and H43 and station H82 also appear to be different from the rest of the sites. There also appears to be a tendency for 'Sandy gravels' and 'Gravelly sands' to group together.

Figure 3.23 examines the similarity of sites using depth, gravel, sand, mud, organic content, organic carbon and calcium carbonate content. Here again, sites 40, 41, 42 and 83 cluster together away from the rest of the sites, indicating a different type of habitat. Site 33 stands out on its own, site 33 has previously been shown to have unusual proportions of organic carbon to organic content and this probably explains its dissimilarity from the rest of the sites. There again appears to be a tendency for the 'sandy gravels' to cluster together. This shows that sites group together differently when both physical and chemical sediment characteristics are considered as opposed to solely physical characteristics.

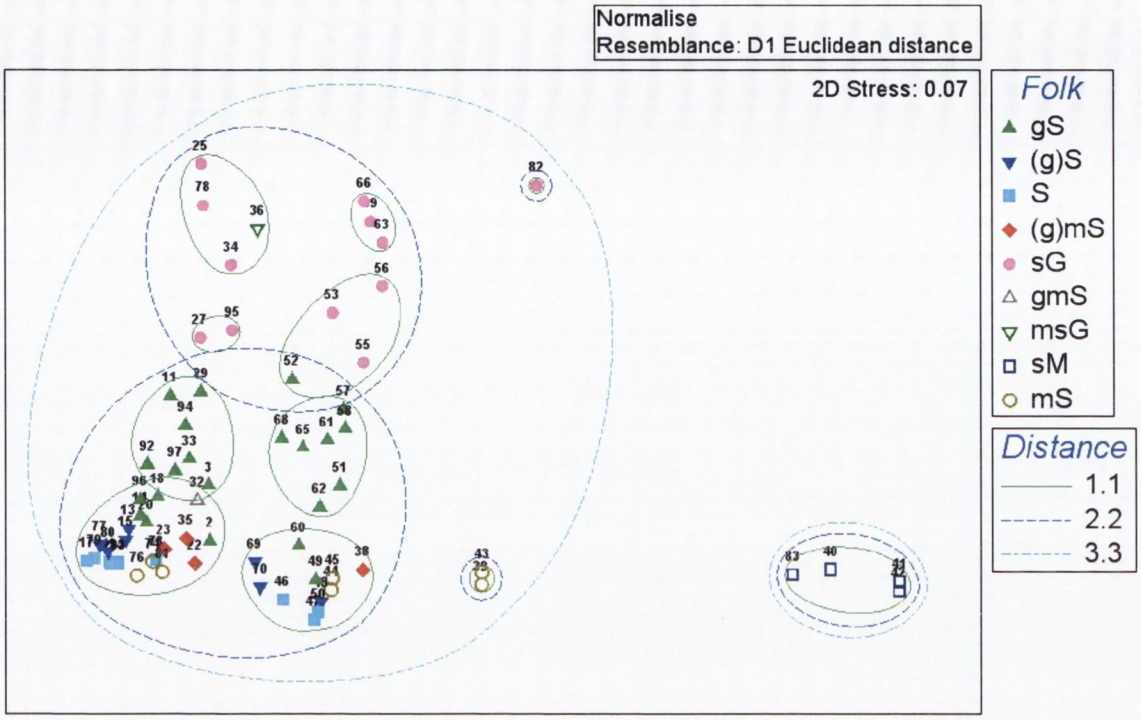


Figure 3.22: MDS plot of normalised environmental variables (depth, gravel, sand, silt\clay) for all sites in the southern Irish Sea. Symbols represent the Folk sediment classification for the station (PRIMER v6).

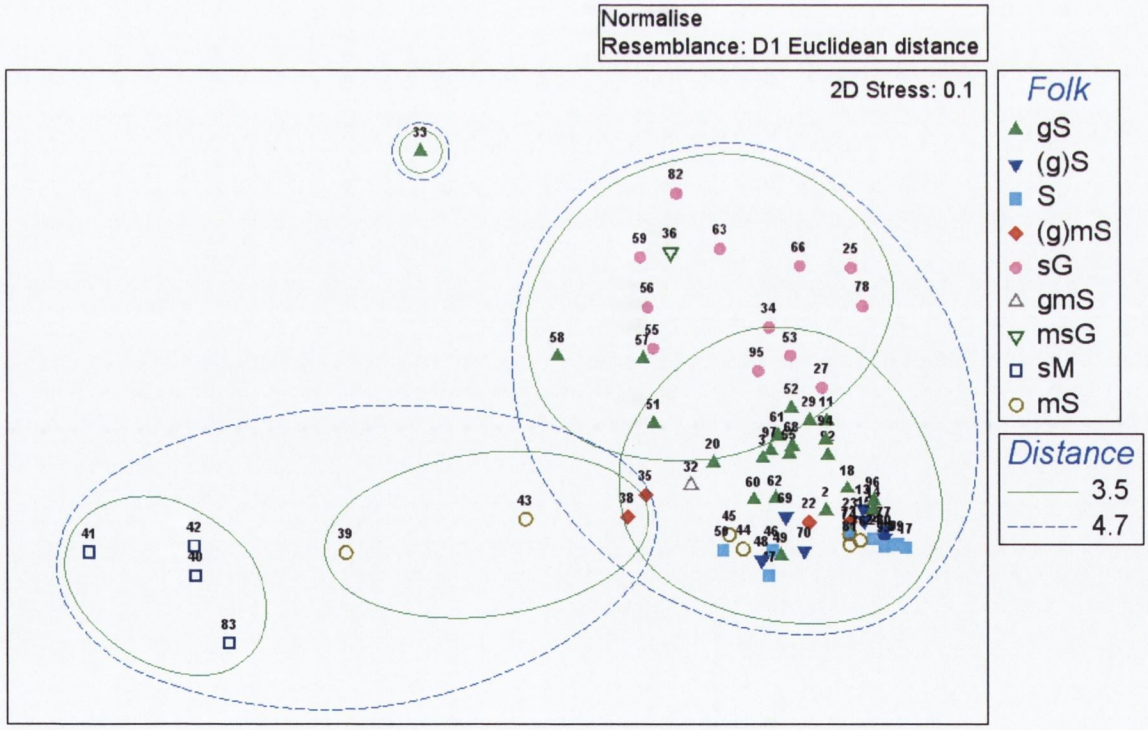


Figure 3.23: MDS plot of normalised environmental variables (depth, gravel, sand, silt\clay, organic content, calcium carbonate and organic carbon) for all sites in the southern Irish Sea. Symbols represent the Folk sediment classification for the station (PRIMER v6).

3.3.9 Abiotic and biotic patterns

BIO-ENV results revealed that a combination of depth, gravel, mud and organic content produced the best match with the biotic patterns resulting from the log transformation of macrofaunal abundance data (see Table 3.14). Depth, gravel and mud all featured in the top four combinations and gravel and mud both featured in the top 9 combinations. Sand was notable in its absence from all the top combinations; however this is understandable as it is closely linked to the gravel component (see Table 3.13). These results indicate that sediment type is indeed an important factor in the location of macrofaunal communities; however it alone is not responsible for the presence or absence of macrofaunal communities. A permutation test rejected the null hypothesis that the biotic patterns had no relationship with the environmental variables.

Table 3.14: Summary of BIO-ENV results showing the highest correlations of groups of abiotic factors with biotic patterns.

No. Variables	Correlation	Selections
4	0.546	depth, gravel, mud, organic matter
5	0.535	depth, gravel, mud, calcium carbonate, organic matter
3	0.533	depth, gravel, mud
5	0.532	depth, gravel, mud, organic matter, organic carbon
3	0.531	gravel, mud, organic matter
2	0.525	gravel, mud
4	0.521	depth, gravel, mud, organic carbon
4	0.519	depth, gravel, mud, calcium carbonate
4	0.518	gravel, mud, calcium carbonate, organic matter
4	0.516	depth, mud, calcium carbonate, organic matter

3.4 *Discussion*

This chapter facilitates the exploration, in Chapter 4, of the relationship between the HABMAP chemical and physical sediment characteristics and the foraminiferal assemblages in the Celtic Deep. It also facilitates the exploration, in Chapters 5 and 6, of the relationships between sediment characteristics and depth with abundance, biomass or productivity-based macrofaunal assemblages from the BIOMÔR, SWISS and HABMAP projects in the southern Irish Sea in more detail.

Figures 3.4 – 3.8 show the HABMAP stations in their categorised Folk classifications overlaid on interpreted backscatter for the areas. A wide range of Folk categories occur over the same backscatter categories perhaps indicating that either a more detailed backscatter interpretation is needed or that the categorical Folk descriptions are perhaps not the best way to present the data and that mean grain size, which correlated with the backscatter categories (-0.323, $p < 0.05$) may be more appropriate. It also indicates changes in substrate over small spatial scales; this further highlights the problem of identifying the boundaries of habitats and the loss of information which can result when broad scale habitat designations are applied.

Mackie et al. (1995a) found in the BIOMÔR study that the environmental variables gravel, silt/clayand depth (correlation = 0.78) best explained the separation of macrofaunal assemblages in the southern Irish Sea. This study found that depth, gravel, silt/clayand organic content (correlation = 0.546) best explained the separation of macrofaunal assemblages in the southern Irish Sea. This may indicate that more diverse habitats were surveyed in the later study resulting in a lower correlation than that found in the previous study. HABMAP looked at areas on both sides of the Irish Sea, whereas BIOMÔR focused solely on the Welsh side.

This study found a strong positive correlation of organic matter and silt/clay ($r^2 = 9.33\%$, $p < 0.001$, $n = 61$). The correlation was further improved by the removal of three outlier stations which all had very high levels of silt/clayand organic matter ($r^2 = 93.3\%$, $p < 0.001$, $n = 61$). This result from the HABMAP sediments compares well with results for the southern Irish Sea from the SWISS project ($r^2 = 87.3\%$, $p < 0.001$, $n = 63$).

Mackie et al. (1995a) found a positive correlation between organic carbon and silt/clay in the southern Irish Sea ($r^2 = 70.8\%$, $p < 0.0001$). Omission of three stations with very high organic carbon resulted in an improved regression analysis ($r^2 = 88.9\%$, $p < 0.0001$) (Mackie et al., 1995a). Wilson et al. (2001) reported that organic carbon and silt/clayhad an unusually low positive

correlation in the southern Irish Sea (r^2 = 17.3%, p = 0.0006, n = 63), even after the omission of seven stations where organic carbon levels were higher than organic matter levels. The correlation although higher was still very low (r^2= 27.2%, p<0.0001, n= 56). This study showed an initial positive correlation (r^2 = 58.5%, P < 0.001, n= 64) being increased with the removal of three stations (which had higher organic carbon levels than organic matter levels), (r^2 = 64.2%, p < 0.001, n = 61). These results indicate that there may have been a problem with the LECO elemental analyser machine which was used in both the SWISS and HABMAP studies (but not in the BIOMÔR study), as organic carbon levels should not be higher than organic matter levels. The HABMAP organic matter and organic carbon results for the outlier stations were thoroughly checked and re-analysed but the same results were obtained. The HABMAP positive correlation values between organic carbon and silt/clay fell between those of the BIOMÔR and SWISS projects.

Both the muddy and gravelly sediments contained high levels of calcium carbonate (e.g. see the 'muddy sandy gravel', 'sandy gravel' and 'sandy mud' categories in Figure 3.13). This could be due to foraminifera in the muddy sediments and shell in the gravelly sediments. The high levels of organic carbon and calcium carbonate content for the 'muddy sandy gravel' Folk category could be explained by the presence of the bivalve *Modiolus modiolus* (Robinson et al., 2007). This resulted in a large amount of shell which contributed to the gravel component and a large amount of faeces which contributed to the mud component.

The differences between trends from this study and those from the BIOMÔR and SWISS projects over time may be due to various reasons such as changes in the type of habitats over time or to the presence of different types of habitats in a small area. The Van Veen grab sampler may not have sampled exactly the same location every time; while the position of the research vessel may be known, the positions of sampling equipment are affected by wind, waves, tides and currents and unless a Geographical Positioning System (GPS) is fitted to the sampler, its exact location cannot be determined. These issues highlight the difficulty in obtaining reliable time series benthic data in the marine environment, without the use of samplers fitted with GPS.

The comparisons of data from this project with the British Geological Survey maps show that there is room for improvement in the most widely used broadscale sediment map for the southern Irish Sea. A loss of data is normal when broadscale maps are used instead of finescale maps. Finescale data are more accurate but can not realistically be used to cover large regions. However, broadscale habitat maps of the southern Irish Sea would be improved with the addition of multibeam maps for the area and large scale groundtruthing efforts to fill in the gaps where

they exist. Data from the HABMAP project showed huge areas where no sediment samples to groundtruth broadscale sediment maps for the region were available (Robinson et al., 2007)

Many authors have recognised that there is a link between the substrate and benthic macrofauna both in the Irish Sea and in the wider northeast Atlantic area (Jones, 1950, Warwick and Davies, 1977, Mackie et al., 1995a, Seiderer and Newell, 1999, Newell et al., 2001). Sediment type should be defined not only by its physical grain size but by a combination of its physical and chemical properties. While many previous studies have factored hydrographical factors into their studies, factors such as seabed temperature vary throughout the year so that a mean value is of more relevance than a temperature taken on a lone sampling trip. Chemical sediment characteristics from the marine environment may provide a better real time view of the type of habitat than hydrographical factors which are often derived from either modelled data or from a single sample of a variable which is known to constantly change throughout the year.

Grain size may act as a proxy for other hydrographic conditions such as currents and waves which affect the transport and deposition of sediments (Gray and Elliott, 2009). While grain size, gravel, sand or mud content may appear to be related to patterns in macrofaunal assemblages, one cannot be sure whether this is directly related to the sedimentary environment or to the hydrographical conditions which affect the distribution of sediments. Grain size could also be acting as a proxy for sediment related properties such as porosity, permeability and redox potential. Percentages of gravel, sand and mud will co-vary as they must add up to 100%.

Particle grain size statistics such as mean grain size, sorting, skewness and kurtosis were calculated for each site in this study. However, due to the often bi-modal or poly-modal nature of marine sediments these may not be the best statistics to use as they do not account for the non-normal distribution of the sediments. Today there is a move towards entropy analysis which can account for this bimodal\polymodal nature (Woolfe, 1995, Woolfe and Michibayashi, 1995, Orpin and Kostylev, 2006, Stewart et al., 2009). Traditional particle size classifications such as Wentworth (Wentworth, 1922), Folk (Folk, 1954) and BGS modified Folk (Jackson et al., 1995) do account for the bi- or poly-modal nature of sediments. It was necessary in this study to use the BGS modified Folk classification system in order to compare the results of this study to the BGS modified Folk map for the southern Irish Sea area. This study showed that broadscale maps, while necessary can often differ substantially to the actual sediment types.

There are currently no clear guidelines for biologists in relation to the collection and processing of sediment samples. The National Marine Biological Analytical Quality Control Scheme in the UK

is currently trying to address this issue (NMBAQCS, 2009). Geologists prefer to remove the organic matter from sediments as they are more interested in the particles. Biologists on the other hand, tend to believe the organic matter is inherent to the structure of the sediment and thus should not be removed. These problems are just one example of how geologists and biologist differ in the information they require from sediments. Different methods of sampling, analysis and geological sediment classification systems which generally have not been biologically tested all add to the complexity of integrating sedimentary data with biological information. Standards for sediment sampling and analysis, biologically relevant sediment classifications and more information on the chemical nature of the sediment are just some ways in which this process can be moved forward in order to produce more reliable benthic habitat and biotope maps.

Traditionally, benthic habitat maps, such as the marine landscape approach, focus solely on grain size and do not incorporate chemical characteristics. The availability of food to the different trophic levels, for example, is particularly important as this is crucial to the ability of the fauna to survive. Grain size, while it can act as a proxy for porosity, permeability and habitat type should not be looked at in isolation when considering benthic habitats but in combination with its structure and chemical composition.

Chapter 4

4 Foraminifera of the Celtic Deep

4.1 Introduction

4.1.1 General Overview

In contrast to macrofaunal communities, foraminiferal communities are more often studied from a geological perspective than from a biological perspective. Foraminifera first appeared in the Cambrian period and can be either epifaunal or infaunal (Goldstein, 1999, Murray, 2006). Their tests are preserved in the sediment and can be used as useful indicators of climate change (Murray, 2006). The tests of foraminifera can however make studying of the cytoplasmic parts of foraminifera difficult, as they obscure the view of the cytoplasm (Murray, 2006). Little is known about the individual life cycles of species and it was estimated by Murray (2006) that the life cycle of only 30 of an estimated 10,000 species have been studied so far. Foraminiferal life cycles are believed to be characterized by alternating asexual and sexual reproductive cycles (Goldstein, 1999). Murray (2006) highlights the fact that there is very little knowledge about the physiological response of foraminifera to environmental conditions, in contrast to the more widely studied responses of macrofauna.

Foraminifera are either planktonic or benthic single-celled amoeboid protists (Murray, 2006). Loeblich and Tappan (1987) have defined a foraminifer as a 'cytoplasmic body enclosed in a test or shell of one or more interconnected chambers'. However this traditional definition of a foraminifer has recently been challenged by Palowski and Holzmann (2002) who have suggested that foraminifera can be marine, freshwater or terrestrial and can include both species with or without 'tests'. Their conclusions are based on molecular phylogenetic studies (Pawlowski and Holzmann, 2002).

Although foraminifera are unicellular specimens, they can be up to several centimetres in length (Murray, 2006). Foraminifera consist of two different types of cytoplasm; cell body cytoplasm and reticulopodia (Murray, 2006). The main difference between foraminifera and other protozoans is the presence of granules in the cytoplasm and the fact that pseudopodia form a net, which becomes the reticulopodia (Murray, 2006). The pseudopodia are important in gathering food, digestion, motility, attachment, building and structuring tests, protection and also in some parts of respiration and reproduction (Goldstein, 1999, Murray, 2006).

Foraminifera have several different methods of feeding; herbivory, bactivory, passive suspension feeding, detritivory, carnivory, omnivory, parasitism, resource partitioning and uptake of dissolved organic material (Murray, 2006). They are known to feed on algae, bacteria, yeast, fungi and sometimes small animals (Goldstein, 1999).

Unlike macrofauna, benthic foraminifera do not have swimming abilities and thus they cannot actively enter the water column of their own accord (Alve, 1999). Motile benthic foraminifera can be dispersed actively by self-locomotion along the sea floor (Alve, 1999), although this only occurs over short distances (Murray, 2006). Motile benthic foraminifera can be dispersed passively when they get into suspension in the water column (Murray, 2006), through release to the water column following asexual or sexual reproduction, through adaptation to a temporary planktonic stage or through entrainment into the water column and subsequent transport of the different growth stages (Alve, 1999). Thus foraminifera cannot actively select preferred habitats over wide distances.

Foraminiferal taxonomy is complicated and constantly evolving. Identification to species level can be difficult. There is no complete guide or key to foraminifera. Loeblich and Tappan (1987) published 'Foraminiferal genera and their classification' in 1987. However this contains descriptions for genera rather than for individual species (Loeblich and Tappan, 1987). The foraminiferal classification diagram of Goldstein (1999) splits the class into 16 orders. However even this classification system changes regularly and differs from the Systema Naturae classification system (http://taxonomicon.taxonomy.nl/), which only contains 13 orders.

4.1.2 Reconstructing past environments

Foraminifera can be used to monitor both natural and anthropogenic environmental change over decades or millennia by monitoring changes in salinity, temperature, dissolved oxygen, food supply, eutrophication, pollution and changes in sea level (Murray and Alve, 2002). While modern and past foraminifera cannot be considered to be exactly the same, interpretations of the fossil record usually depend on modern comparisons (Murray, 2006). As species evolve and habitats change over time, differences in the species niche will occur (Murray, 2006). A past environment may not have a comparable modern analogue, as the environmental conditions may no longer exist or species my not have been able to survive and adapt during periods such as the ice age (Murray, 2006). Paleoecological interpretations of foraminiferal assemblages are used both in the fossil record and in archaeological investigations (Murray and Alve, 2002, Murray, 2006).

Although caution would be advised, it may be possible to use foraminiferal assemblages as proxies to produce habitat maps for both past and modern day habitats due to their close associations with the hydrographic and sedimentary conditions of their environment. Foraminifera are present in sediment samples routinely collected for groundtruthing accoustuc data. If strong correlations between macrofaunal and formainiferal assemeblages exist, foraminifera taken from these acoustic groundtruthing sediment samples may provide suffiecient data on the biology of the area, thus removing the need for additional biological sampling and analysis.

Changes in foraminiferal assemblages over time due to environmental change would indicate by association that macrofaunal assemblages would also change with new conditions. Little work has been done comparing foraminiferal assemblages to macrofaunal assemblages. Klitgaard-Kristensen and Buhl-Mortensen (1999) examined total benthic foraminifera (live and dead assemblages) along with amphipods and molluscs along an offshore-fjord gradient in Norway. The groups were found to respond differently, with more abundant foraminifera in the outer fjord and more abundant molluscs and amphipods in the inner fjord (Klitgaard-Kristensen and Buhl-Mortensen, 1999). Dead foraminifera are a component of the sediments in which the macrofauna live, reflecting the hydrographic conditions of the area. If relationships between foraminifera and macrofauna were well understood it may be possible to use foraminiferal data to reconstruct past macrofaunal assemblages.

4.1.3 The Celtic Deep

The Celtic Deep area crosses the Celtic Front which represents the boundary between Boreal and Lusitanian species. The Celtic Front occurs at the boundary between the well mixed waters of the southern Irish Sea and the highly stratified waters of the Celtic Sea (Boelens et al., 1999). The Celtic Front is generally established by mid-June and the greatest gradient in sea temperatures between the southern Irish and Celtic Seas occurs in mid-August (Boelens et al., 1999). The samples for this study were taken from 30th July 2005 to 3rd August 2005 when the front should have been in existence. In Chapter 3 it was found that the sediments of the Celtic Deep graded from gravelly sands and sandy gravels in the north through sands, slightly gravelly sands to muddy sands and sandy muds in a north-east to south-west direction (see Figure 3.6).

4.1.4 Celtic Deep macrofaunal biotopes

Robinson et al. (2007) classified the sites of the Celtic Deep transect into five separate macrofaunal biotopes (see Figure 4.1 and Figure 4.2). Stations 39, 40, 41, 42 and 43 were classified as biotope 3a, an area with 'sandy muds' and 'muddy sands' dominated by species such as the polychaetes *Mediomastus fragilis* and *Magelona minuta* and the mollusc *Abra nitda* (see Table 4.1 and Figure 4.1) (Robinson et al., 2007). Biotope 3b comprised the 'muddy sands' and 'gravelly muddy sand' stations 38, 44 and 45 (Robinson et al., 2007). These stations were dominated by the molluscs *Abra nitda* and *Corbula gibba* and the polychaete *Mediomastus fragilis.* Biotope 3c contained the 'sandy' stations 46 and 47, which were dominated by the polychaete *Galathowenia* sp., the mollusc *Corbula gibba* and juvenile polychaete Opheliidae species.

The northerly stations of the Celtic Deep were divided into two biotopes 4b (stations 48-50) and 5a (stations 51, 55 - 57). Biotope 4b's sediments ranged from sand to gravelly sand and were dominated by species such as the mollusc *Abra prismatica,* the echinoderm *Echinocyamus pusillus* and the polychaete *Aonides paucibranchiata.* Biotope 5a included 'sand' and 'sandy gravel' stations, which were dominated by the polychaetes *Aonides paucibranchiata* and *Pomatoceros lamarckii* and the mollusc *Timoclea ovata.*

Table 4.1: Table of macrofaunal biotopes and dominant species from the Celtic Deep transect. Table adapted from Table 4.17, pg 170-172 (Robinson et al., 2007).

Biotope	**3a**	**3b**	**3c**
Stations	39, 40, 41, 42, 43	38, 44, 45	46, 47
Location	Celtic Deep	Celtic Deep	Celtic Sea transect (mid)
Sediments	sM (3) & mS (2)	mS (2) & gmS (1)	S
Depth	115-129m	105-116m	95-114m
Dominant Species	*Mediomastus fragilis* *Magelona minuta* *Abra nitda* Tubificidae sp. *Levinsenia gracilis*	*Abra nitda* *Corbula gibba* *Mediomastus fragilis* *Galathowenia sp.* *Alvania abyssicola*	*Galathowenia* sp. *Corbula gibba* *Opheliidae* juv *Abra pismatica* *Amphiura filiformis*

Table 4.1 (continued): Table of macrofaunal biotopes and dominant species from the Celtic Deep transect. Table adapted from Table 4.17, pg 170-172 (Robinson et al., 2007).

Biotope	4b	5a
Stations	48, 49, 50	51, 55, 56, 57
Location	N part of Celtic Deep transect	Northernmost part of Celtic Deep transect
Sediments	Sand to Gravelly Sand	Sand to Sandy Gravel
Depth	101-115m	75-172m
Dominant Species	*Abra prismatica* *Echinocyamus pusillus* *Aonides paucibranchiata* *Timoclea ovata* *Paradoneis* cf. *ilvana*	*Aonides paucibranchiata* *Pomatoceros lamarckii* *Timoclea ovata* *Harmothoinae* juv *Laonice bahusiensis*

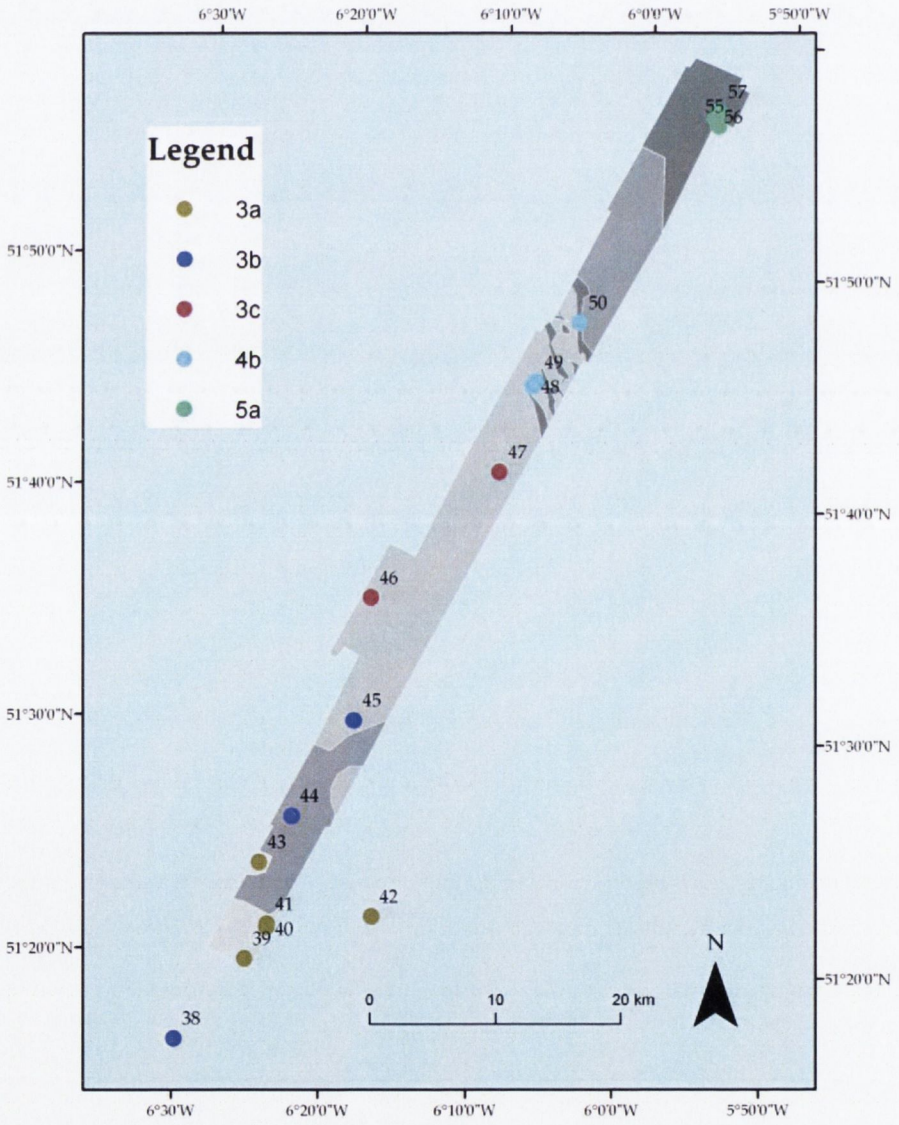


Figure 4.1: Macrofaunal biotopes for Celtic Deep HABMAP stations (Robinson et al., 2007). See Table 4.1 for details.

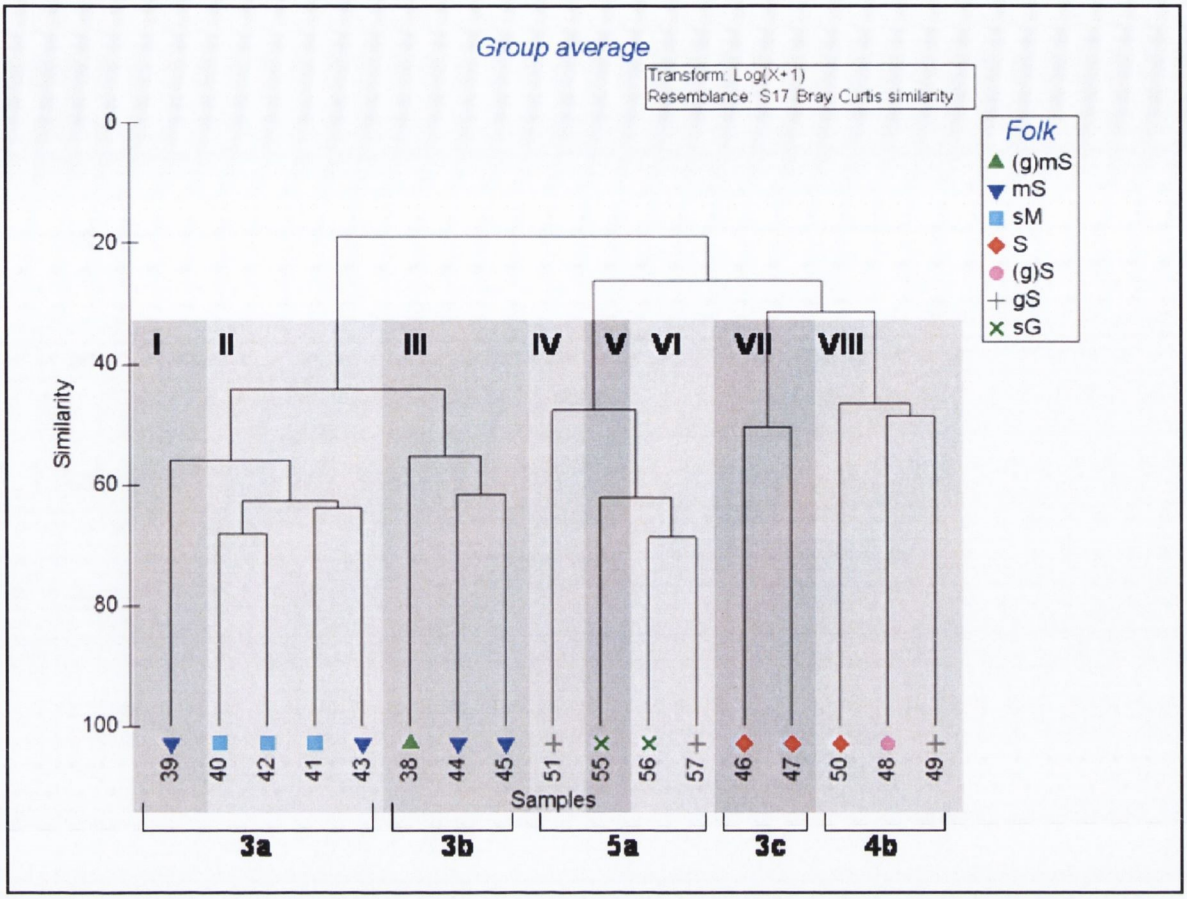


Figure 4.2: Hierarchical agglomerative cluster analysis of macrofaunal species data (Mackie et al., 1995a) for the Celtic Deep. Biotopes designated by Robinson et al. (Robinson et al., 2007).

4.1.5 Previous research in the Celtic Sea

Le Calvez (1958), Murray (1970, 1979) and Scott *et al.* (2003) have studied the distribution of foraminifera in the Celtic Sea. Le Calvez's (1958) sites were located to the west of France and were further south than those covered by this and previous studies (Murray, 1979, Scott et al., 2003) (see Figure 4.3).

Le Calvez found two distinct communities; 'Les Fonds détritiques' and 'Les Fonds sablo-vaseux'. 'Les Fonds détritiques' consisted of detrital sediments abundant in species from the Verneuilinidae, Textulariidae, Milioildae, Rotaliidae and Anomalinidae families. Species from other families were either not represented or only represented by some individuals (Le Calvez, 1958). 'Les fonds sablo-vaseux' consisted of two groups; one sandy (sableux) group which ranged from 120-210m in depth and one muddy (vaseux) group which ranged from 90-105m in depth. The 'sandy' group was comprised mainly of Buliminidae, Cassidulinidae and *Anomalina balthica*. The muddy group differs from the sandy group, although Buliminidae and *Anomalina balthica* species are again abundant, the Cassidulinidae species are less so and are at this point replaced by

the Nonion species which do not exist at the sandy stations (Le Calvez, 1958). Both Le Calvez (1958) and Murray (2003) refer to the species *Nautilus balthicus* identified by Schröter (1783). Le Calvez (1958) refers to this species as *Anomalina balthica*, however Murray refers to it as *Hyalinea balthica*. Three stations did not belong to any of the main groups.

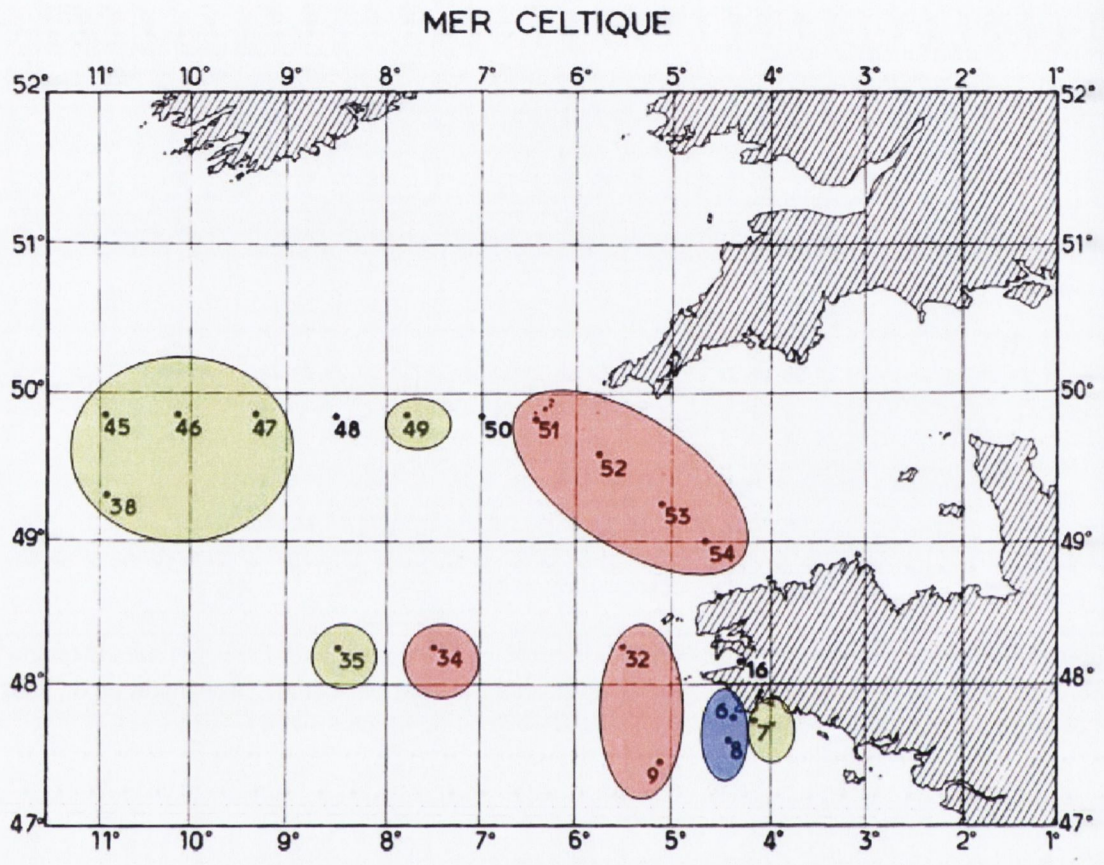


Figure 4.3: Map of sites surveyed by Le Calvez (1958) in 1948. The three main groups are classified by colour. 'The detrital group' is shown in red, the 'muddy' group is shown in blue and the 'sandy' group is shown in green.

Murray (1970) examined dead and living foraminifera from the western approaches of the English Channel and the Bristol Channel. At the four sites which were surveyed in the Celtic Sea, the sediment ranged from 'muddy fine to coarse quartz sand with shell debris' (Murray, 1970). The dominant living species were *Nonionella turgida, H. balthica* and *Bulimina marginata,* while *Cassidulina carinata* and *Cassidulina crassa* were locally abundant (see Table 4.2) (Murray, 1970). *Martinottinella communis* and *Melonis pompiloides* were only found alive at the Celtic Sea sites (Murray, 1970). *B. marginata, C. carinata, C. crassa, Fursenkoina fusiformis, H. balthica, N. turgida* and the *Textularia sagittula* group were found to be the dominant species among the dead assemblages at the Great Sole Bank in the Celtic Sea (see Table 4.3) (Murray, 1970). *Trifarina angulosa* was locally common. The main differences between the living and dead assemblages at the Great Sole Bank in the Celtic Sea were the high dominance of *N. turgida* in the living assemblages and the

abundance of the *T. sagittula* group in the dead assemblages (Murray, 1970). Haynes (1973) revised the taxonomy of *F. fusiformis* to *Stainforthia fusiformis* as first identified by Williamson (1858) as *Bulimina pupoides* var. *fusiformis*.

Murray (1979) examined recent benthic foraminifera in the Celtic Sea. He found the diversity for dead assemblages to be greater than that for living assemblages. The size of the dead foraminifera indicated that specimens smaller than 200μm in size move from areas of higher energy to those of lower energy (Murray, 1979). Slow sedimentation rates combined with rising sea level, bioturbation and storms leading to the mixing of assemblages, were thought to have been responsible for the differences in living and dead assemblages (Murray, 1979). Only one of the six main species found in dead assemblages was common in the live assemblages (see Table 4.2 and Table 4.3). Table 4.2 and Table 4.3 show the difference between the dominant species for living and dead species found by Murray (1970, 1979) in the western and eastern North Celtic Sea.

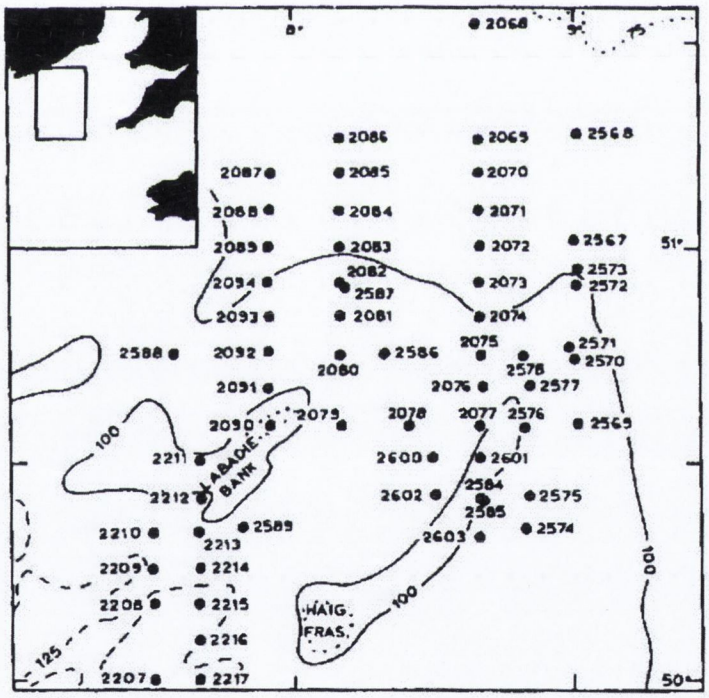


Figure 4.4: Map of sites surveyed by Murray (1979) from 1970-197.

Table 4.2: Summary of dominant live foraminifera species in the Celtic Sea (Murray, 1970, Murray, 1979) , taken from Table 5 in Murray (1979).

	North Celtic Sea	
	West	East
Dominant Species	*Nonionella turgida* *Hyalinea balthica* *Bulimina marginata*	*Nonionella turgida* *Fursenkonia fusiformis* *Cancris auricula* *Textularia sagittula* group
Depth	128-138m	75-132m

Table 4.3: Summary of dominant dead foraminifera species in the Celtic Sea (Murray, 1970, Murray, 1979) , taken from Table 5 in Murray (1979).

	Celtic Sea	
	West	East
Dominant species	*Bulimina marginata* *Cassidulina carinata* *Fursenkonia fusiformis* *Hyalinea balthica* *Noniionella turgida* *Textularia sagittula* group	*Textularia sagittula* group *Cibicides lobatulus* *Fursekonia fusiformis* *Gavellinopsis prageri* *Epistomella vitrea* *Cassidulina obtusa*
Depth	128-138m	75-132m

Scott et al. (2003) in their study of the distribution of foraminifera in the Celtic Sea identified four main living assemblages characterised by tidal stratification. Figure 4.5 shows the sites surveyed by Scott et al. (2003) in 1995. The frontal assemblage was dominated by *S. fusiformis* species, the mixed assemblage by *C. lobatulus, Textularia bockii, Spiroplectammina wrightii, Ammonia batavus* and *Quinqueloculina seminulum,* the stratified assemblage was dominated by *B. marginata, H. balthica, Adercotryma wrightii* and *N. turgida* while the final eastern assemblage was dominated by *Bulimina gibba, Elphidium excavatum* and *Eggerelloides scaber* (Scott et al., 2003). The frontal assemblage was the only assemblage not found in the analysis of the dead assemblages (Scott et al., 2003). The highest densities of living foraminifera were found in the region of the Celtic Front which was attributed to high organic flux associated with the front (Altenbach, 1987, Scott et al., 2003). Scott et al. (2003) concluded through Canonical Correspondence Analysis (CCA) that mean grain size, percentage gravel, temperature and depth were important factors in the distribution of living foraminiferal species, while depth, temperature, longitude and latitude were important factors in the distribution of dead foraminiferal species.

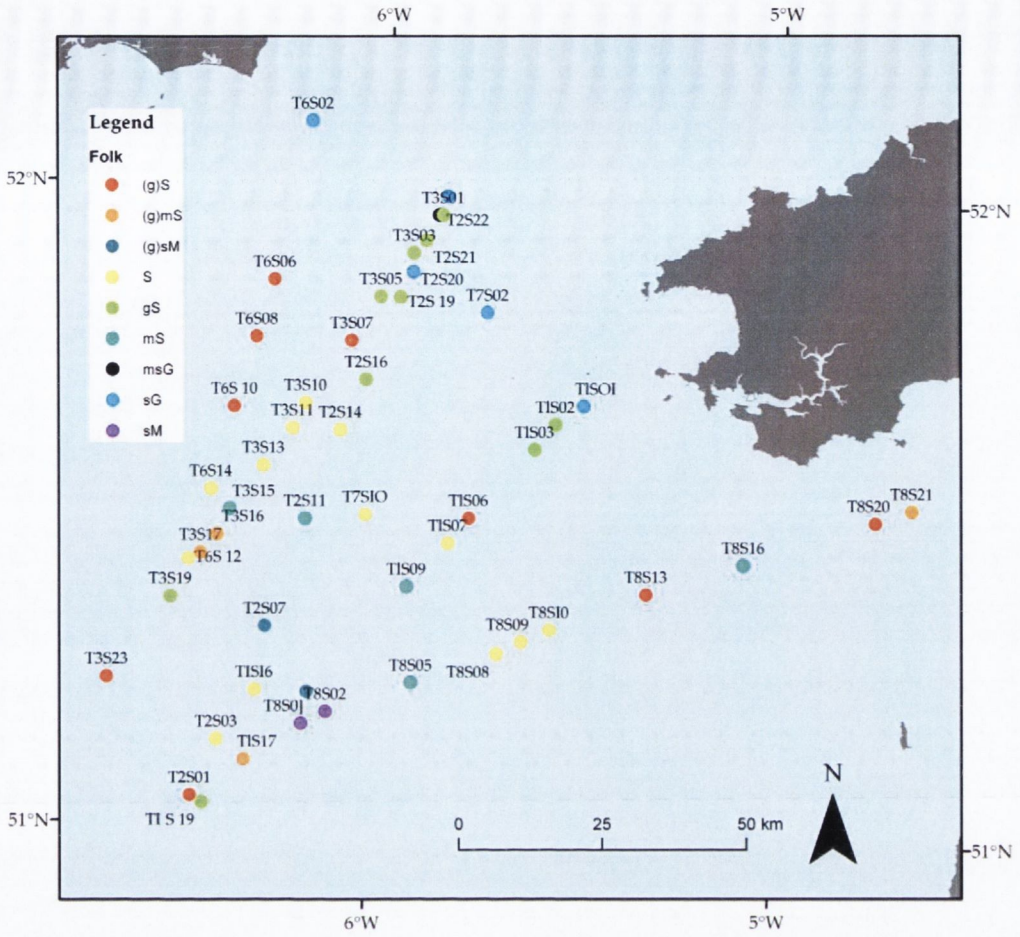


Figure 4.5: Location of stations sampled by Scott et al. (2003) in 1995.

4.1.6 Aims

This chapter will identify the main foraminiferal assemblages in the Celtic Deep. Total foraminiferal assemblages (live & dead) will be identified. Comparisons will be made with previous studies by Le Calvez (1958), Murray (1970, 1979) and Scott et al. (2003). Issues associated with the difficulties in identifying formainifera and their identification to different levels of the taxanomy will be discussed. The relationships between the assemblages, sediment characteristics and live macrofaunal assemblages will be explored.

4.2 *Methods*

4.2.1 Field work

Foraminiferal samples were taken by hand from the surface of Van Veen grab samples at each station. Foraminiferal samples were taken from the same grabs as the sediment samples analysed in Chapter 3. Samples were preserved on board in alcohol and Rose Bengal in 120ml tubs. Rose Bengal was used to stain the living foraminifera.

4.2.2 Laboratory work

The foraminiferal samples were wet sieved in the laboratory through a 500μm and 63μm sieve and the fractions between 500μm and 63μm were dried in the oven at 40 °C. Foraminifera were separated from the sediment using trichloroethylene following the method outlined in Murray (2006). The process was carried out in the fume cupboard as trichloroethylene is highly toxic. The floated sediment fractions were gently shaken onto a Petri dish divided into $1cm^2$ squares on a black background. Foraminifera were methodically picked out from each $1cm^2$ square and mounted on Chapman slides. The process was repeated until approximately 300 specimens were obtained. It is estimated that counts of 300 specimens are sufficient to find any species that make up 10 percent of the samples (Patterson and Fishbein, 1989). Live and dead foraminifera were combined together to examine total foraminiferal assemblages, as so few live foraminifera were found in each sample identified. They were identified under the dissection microscope in the lab (up to magnifications of 100x).

Species were identified where possible using drawings and Scanning Electron Microscope (SEM) photographs from previous literature. Further identification of some species was enabled by using a Hitachi S-4300 Field Emission SEM located in the Centre for Microscopy and Analysis (CMA) in Trinity College Dublin to take photographs of certain foraminiferal species. The specimens were placed on carbon stubs and gold plated before being placed in the SEM. SEM photos were taken of the most common species and of species which proved difficult to identify.

4.2.3 Data analysis

Data were analysed using Canonical Correspondence Analysis (CCA), hierarchical agglomerative cluster analysis and non-metric Multi-Dimensional Scaling (MDS) plots (ter Braak, 1986, Clarke

and Warwick, 2001). Hierarchical agglomerative cluster analysis with group average linking uses a similarity matrix to group samples based on their similarity to each other. It was carried out using the programme PRIMER v6 (Clarke and Warwick, 2001). For biological data, the cluster analysis uses a Bray-Curtis similarity matrix. This analysis produces a dendrogram, where similarity is represented on the y-axis and is used to differentiate between groups which have distinct community structures (Clarke and Warwick, 2001). SIMPROF tests were used in conjunction with cluster analysis to test which groups could be significantly differentiated from others (Clarke and Gorley, 2006). SIMPER tests were used in PRIMER v6 to distinguish the characterising species in each assemblage identified (Clarke and Warwick, 2001).

BEST matches biotic patterns to environmental patterns by considering which single variable or groups of variables best explain the biotic patterns (Clarke and Ainsworth, 1993). This procedure can be tested with a permutation test in PRIMER v6 that tests the null hypothesis that there is no relationship between the biotic patterns (communities) and the abiotic patterns (Clarke and Warwick, 2001). The biological data consisted of foraminiferal or macrofaunal abundance, log transformed using the log(x+1) transformation in PRIMER v6 (Clarke and Ainsworth, 1993). The macrofaunal data were analysed by the National Museum of Wales and published in Robinson et al. (2007). The macrofaunal data were used to compare macrofaunal assemblages to foraminiferal assemblages. The macrofaunal samples were taken separately by the National Museum of Wales at the same sites and at the same time as the foraminiferal samples. The data were then converted into a Bray-Curtis similarity matrix. The sediment data were normalised before using the BEST procedure in PRIMER v6 to compare the biotic and abiotic patterns.

The RELATE procedure in PRIMER v6 allows comparison of two similarity matrices (Clarke and Gorley, 2006). This function was used to compare the similarity matrices for foraminiferal and macrofaunal species using a Spearman correlation. The RELATE test matches the among-sample correlations, where rank correlations range from 0 to 1 (Clarke and Gorley, 2006). The test is based on Mantel coefficients although the original test used Pearson correlations (parametric) instead of Spearman correlations (nonparametric) (Clarke and Gorley, 2006). The RELATE function can be used to compare abiotic or biotic patterns.

Canonical Correspondence Analysis (CCA) is an ordination technique which shows the relationship between species and environmental gradients, by producing an ordination diagram where species or sites are represented by points and environmental gradients are represented by vectors (ter Braak, 1986). It was used to plot foraminiferal species and environmental data.

4.3 *Results*

Identification of species proved to be difficult, however where an exact identification could not be made, species were dealt with in one of three ways:

1. Grouped together where taxonomy of the species was generally recognised to be difficult (e.g. *Bulimina* species)
2. Differentiated by number where the genera had been identified (e.g. *Textularia* sp. 1 and *Textularia* sp. 2.).
3. Identified as a different species where the genus was unknown (e.g. Species C)

Species from the latter of these options had to be eliminated from the analysis when considering foraminiferal superfamilies or orders or data from other surveys.

4.3.1 Foraminiferal assemblages of the Celtic Deep

Hierarchical cluster analysis of the log transformed foraminiferal species abundance Bray-Curtis similarity matrix with SIMPROF tests recognised 8 distinct groups with the sites; Ia, Ib, Ic, Id, IIa, IIb, IIc and IId (see Figure 4.6 and Table 4.4). These sites were delineated from each other at 63% similarity. As some of these groups only contained a single assemblage, it was felt that it would be more valid to look at the assemblages I and II. A SIMPER test was run in PRIMER v6 to distinguish the species which contributed to assemblages I and II (see Table 4.4).

Assemblage I was clearly associated with the more muddy sites comprising sites of 'sandy muds', 'slightly gravelly muddy sands' and 'muddy sands'. The assemblage was dominated by calcareous foraminifera species associated with muddier sediments such as *Bulimina* sp., *Stainforthia fusiformis*, and *Hyalinea balthica*. Assemblage II was associated with coarser sediment such as 'sands', 'slightly gravelly sands', 'gravelly sands' and 'sandy gravels'. Assemblage II was dominated by *Cibicides* sp and agglutinated *Textularia* species. Scanning Electron Microscope (SEM) photos of some of the most common species or the most characterisic species are shown in Figures 4.7 – 4.14.

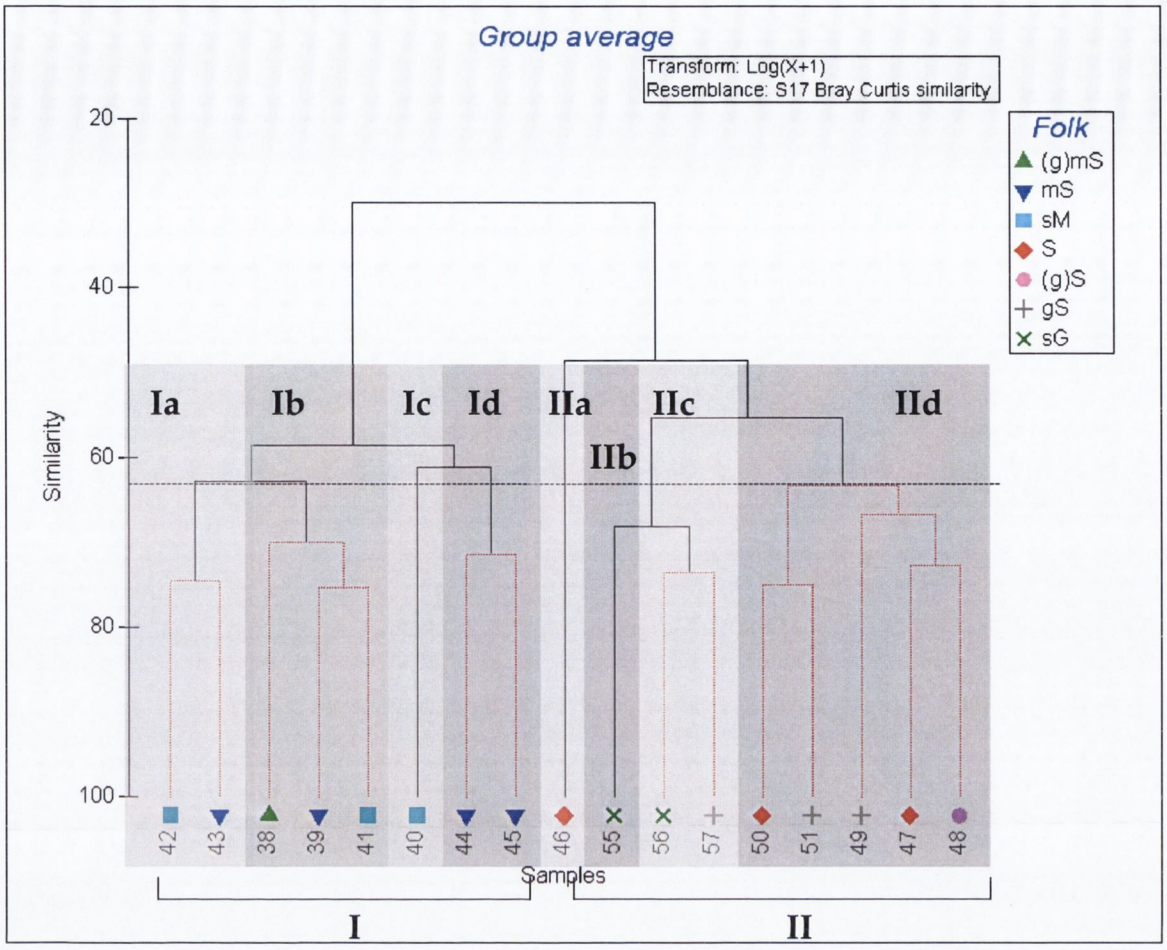


Figure 4.6: Hierarchical agglomerative cluster analysis (PRIMER v6) using abundance of foraminiferal species data showing groups Ia to IId delineated from each other at 63% similarity. Clusters highlighted in red show groups which were found to be significant using SIMPROF tests.

Table 4.4: Foraminiferal biotopes found in the Celtic Deep. Dominant species and their percentage contribution are shown, (SIMPER, PRIMER v6).

BIOTOPE	I		II	
Stations	42, 43, 38, 39, 41, 40, 44, 45		46, 55, 56, 57	
Sediments	sM (3), (g)mS (1), mS (4)		S (3), (g)S (1), gS (3), sG (2)	
Depth (m)	105 - 188		95 - 115	
Average similarity (%)	62.08		57.96	
	Dominant species	**% contribution**	**Dominant species**	**% contribution**
	Bulimina sp.	20.98	*Cibicides* sp.	14.38
	Stainforthia fusiformis	11.89	*Textularia* sp. 2	10.11
	Hyalinea balthica	8.33	*Ammonia batavus*	7.47
	Rosalina sp. 15	7.67	*Textularia sagittula*	7.15
	Nonionella turgida	7.43	Textularia sp. 1	4.86
	Cibicides sp.	6.42	*Asterigerinata mamilla*	4.60
	Bolivina sp.	4.81	*Ammonia* sp. 2	4.03

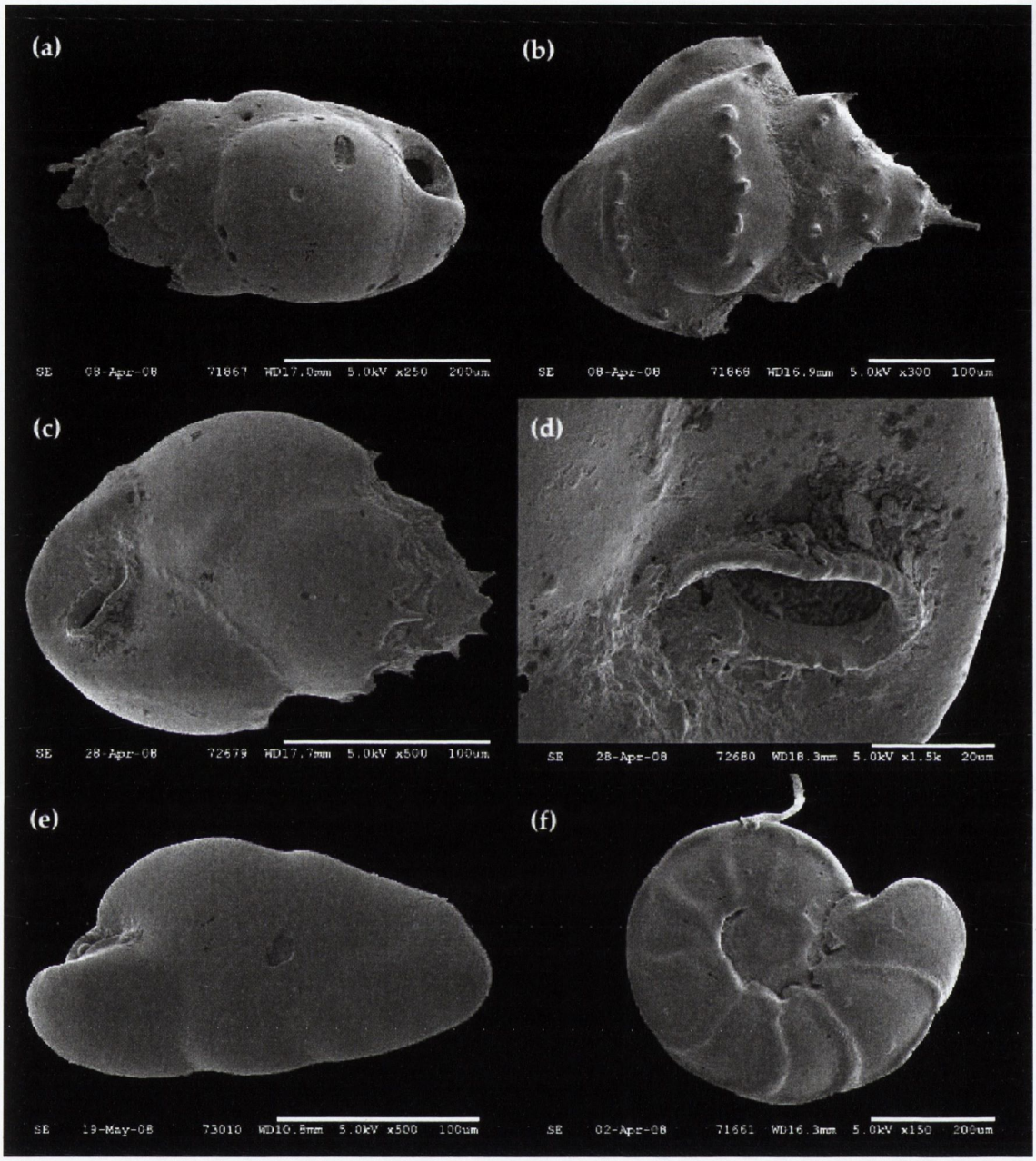


Figure 4.7: (a) *Bulimina* species A; (b) *Bulimina* sp. B; (c) *Bulimina* sp. C; (d): *Bulimina* sp. C – aperture; (e): *Bolivina* sp.; (f): *Hyalinea balthica*.

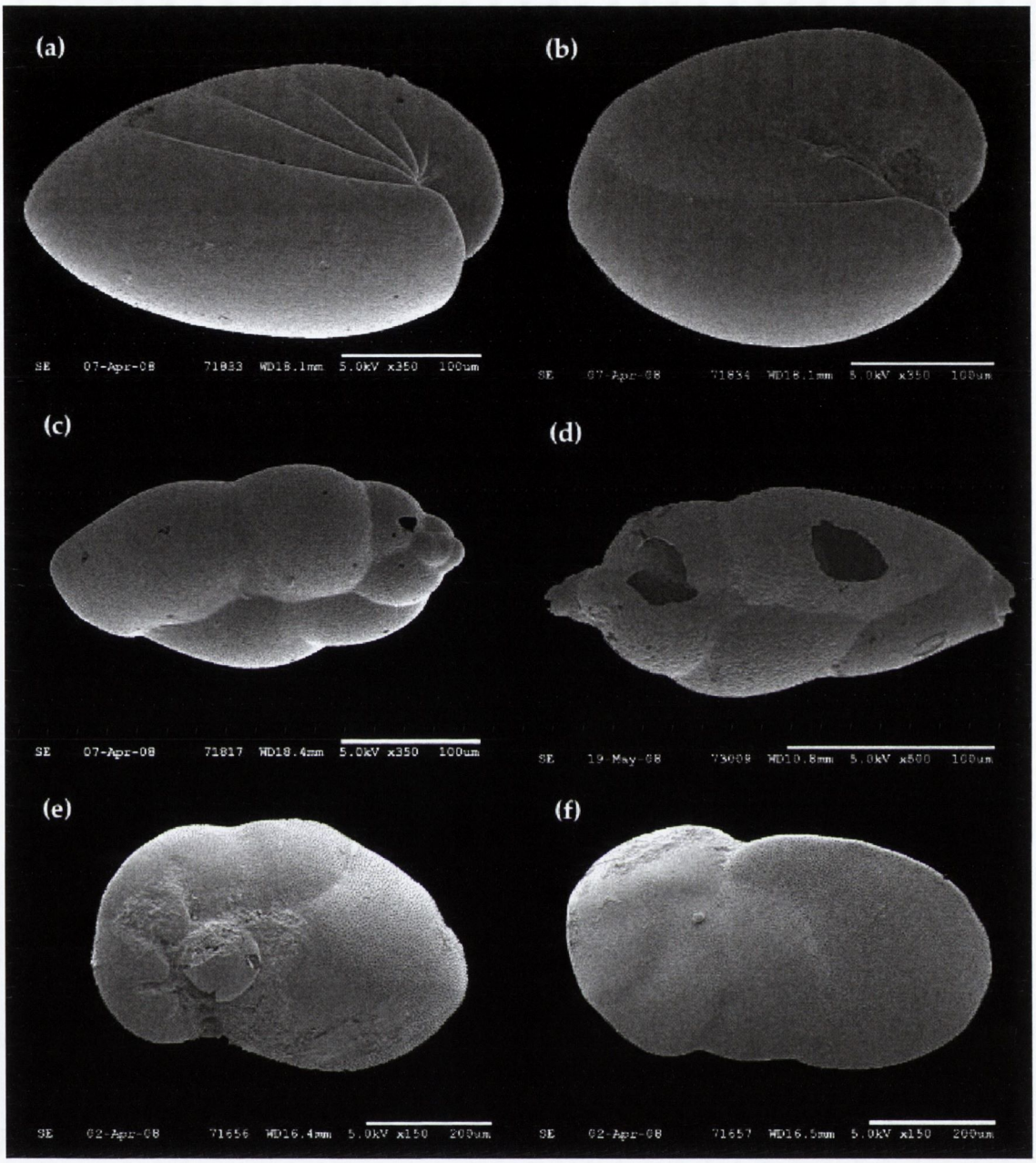


Figure 4.8: (a) *Nonionella turgida*; (b) *Nonionella turgida*; (c) *Stainforthia fusiformis*; (d) *Stainforthia fusiformis*; (e) *Cancris auriculus*; (f) *Cancris auriculus*.

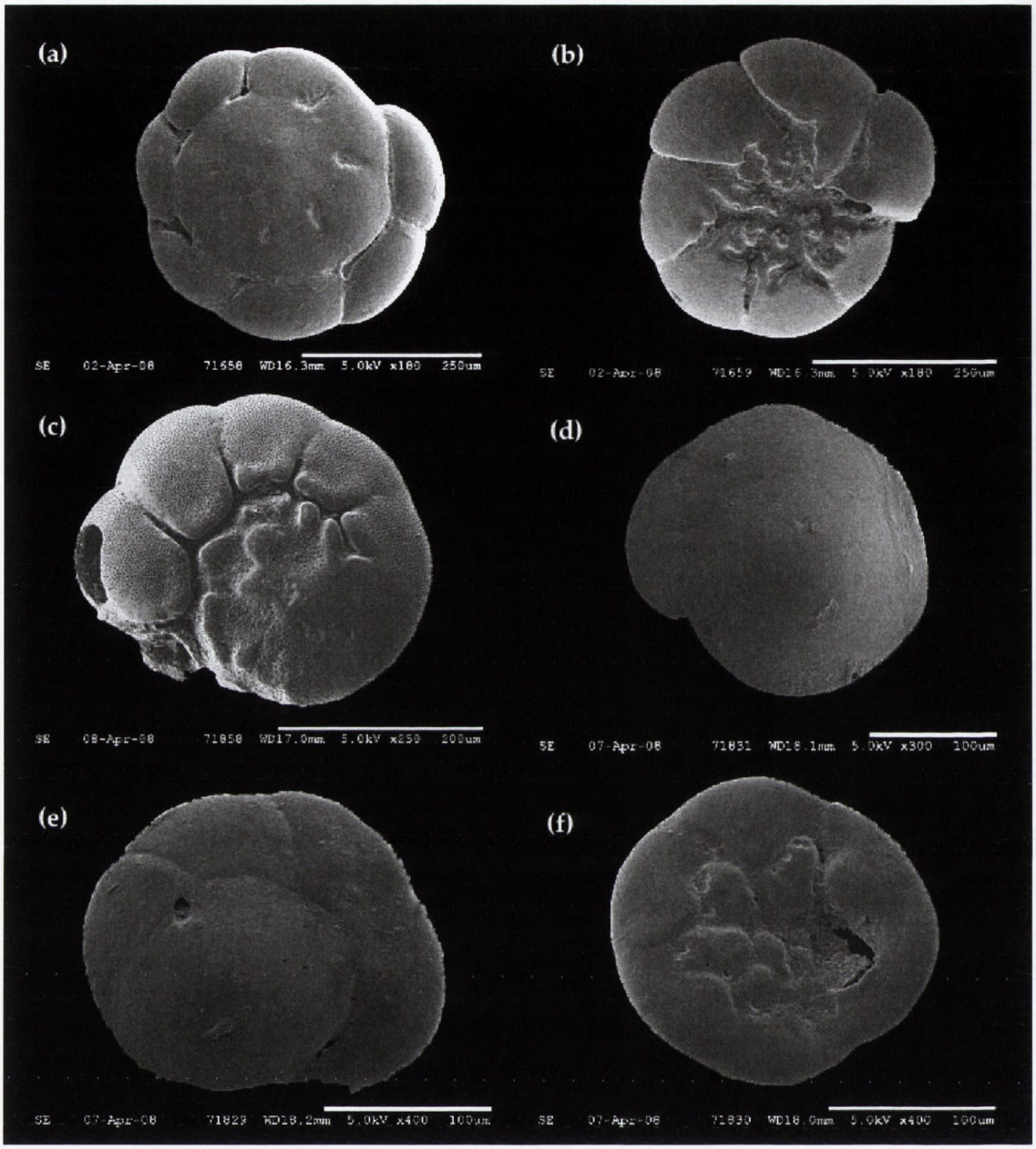


Figure 4.9: (a) *Ammonia batavus;* (b) *Ammonia batavus;* (c) *Ammonia sp.;* (d) *Rosalina sp. 7-Gavelinopsis praegeri;,* (e) *Rosalina sp. 15;* (f) *Rosalina sp. 15.*

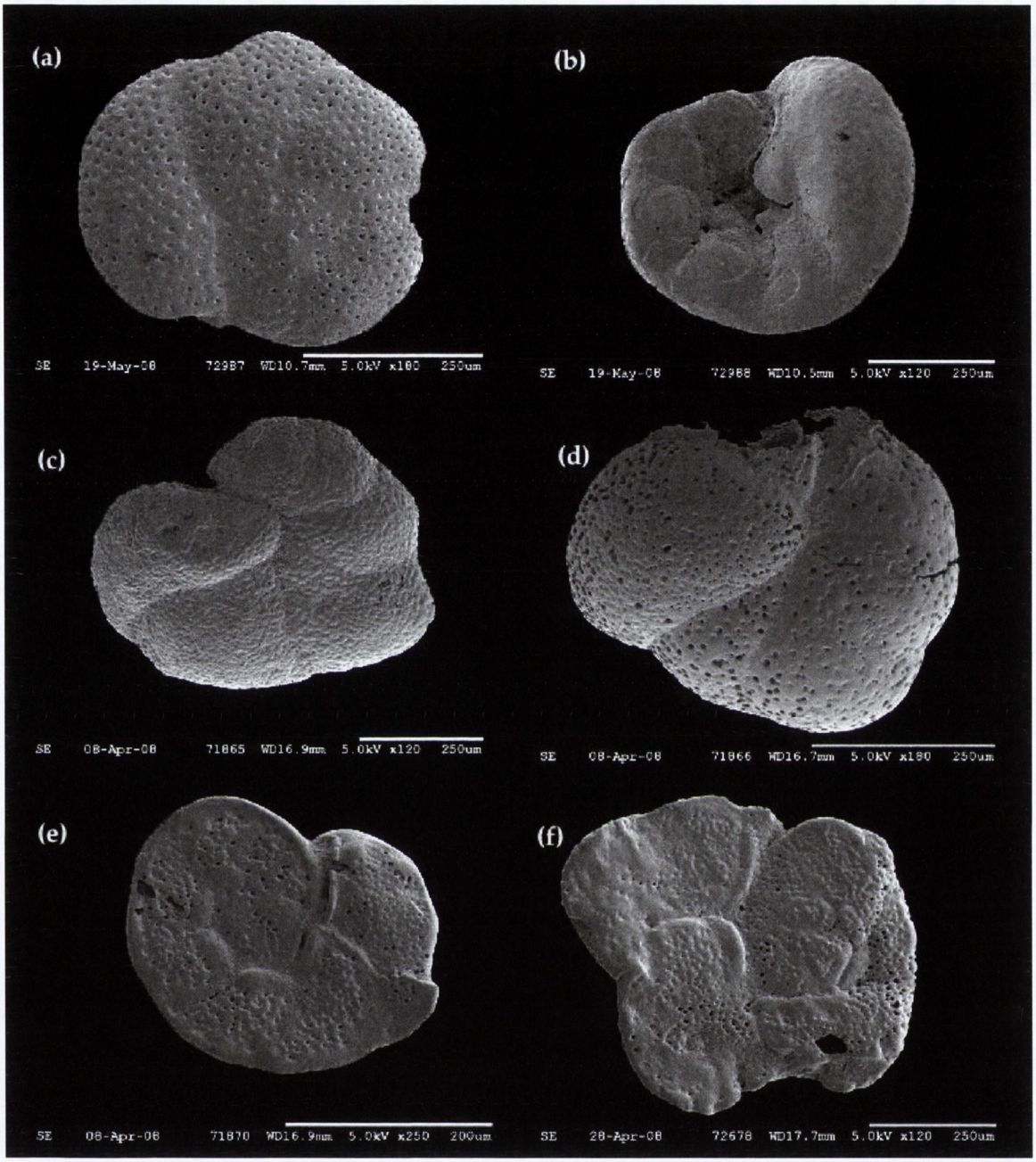


Figure 4.10: (a) *Rosalina globularis* – Rosalina sp. 10; (b) *Rosalina globularis* – Rosalina sp. 10; (c) *Cibicides* sp.; (d) *Cibicides* sp.; (e) *Cibicides* sp.; (f) *Cibicides* sp.

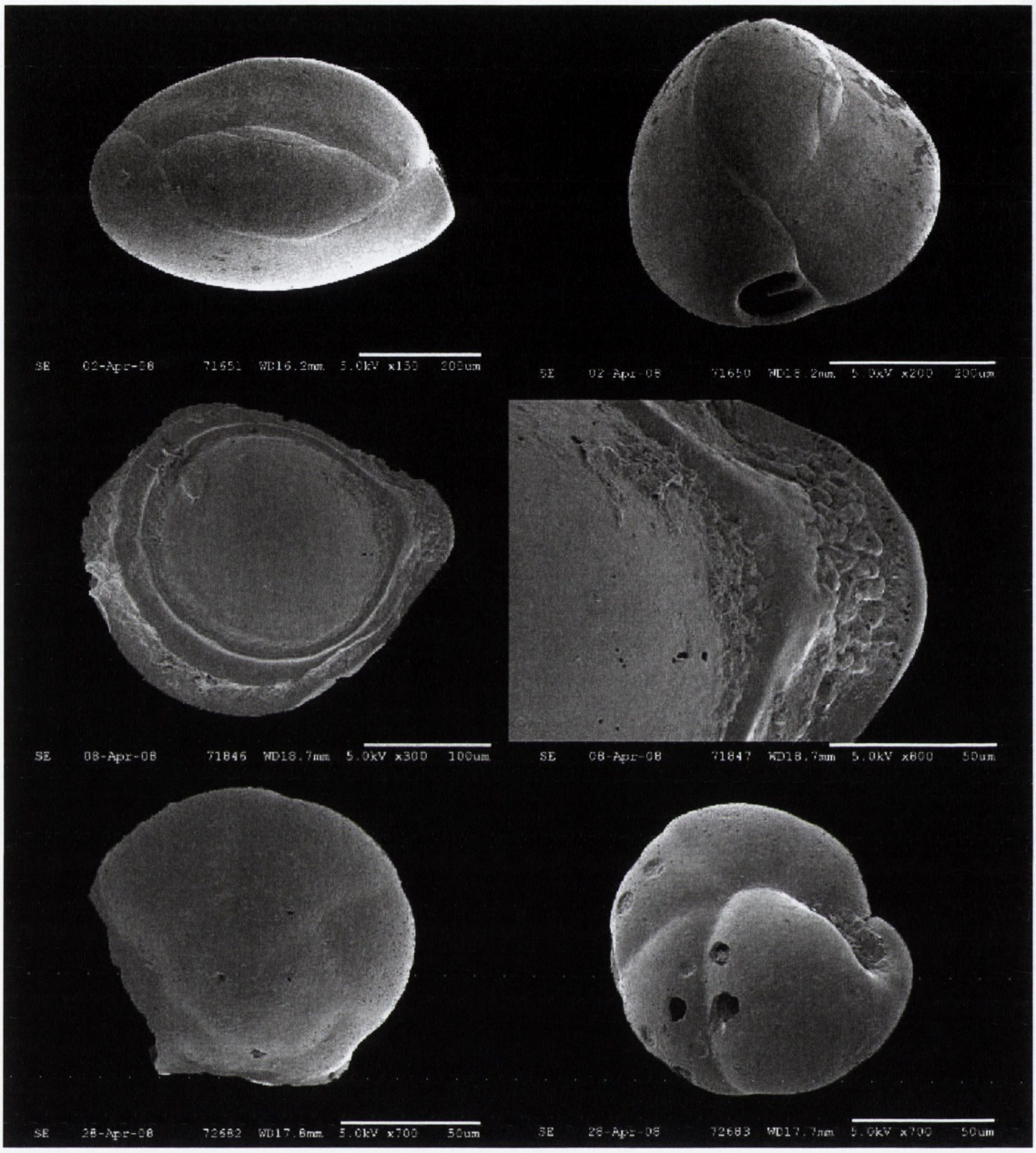


Figure 4.11: a) ***Quinqueloculina seminula;*** **(b)** ***Quinqueloculina seminula;*** **(c)** ***Fissurina orbignyana;*** **(d)** ***Fissurina orbignyana;*** **(e) Unidentified sp. C; (f) Unidentified sp. C.**

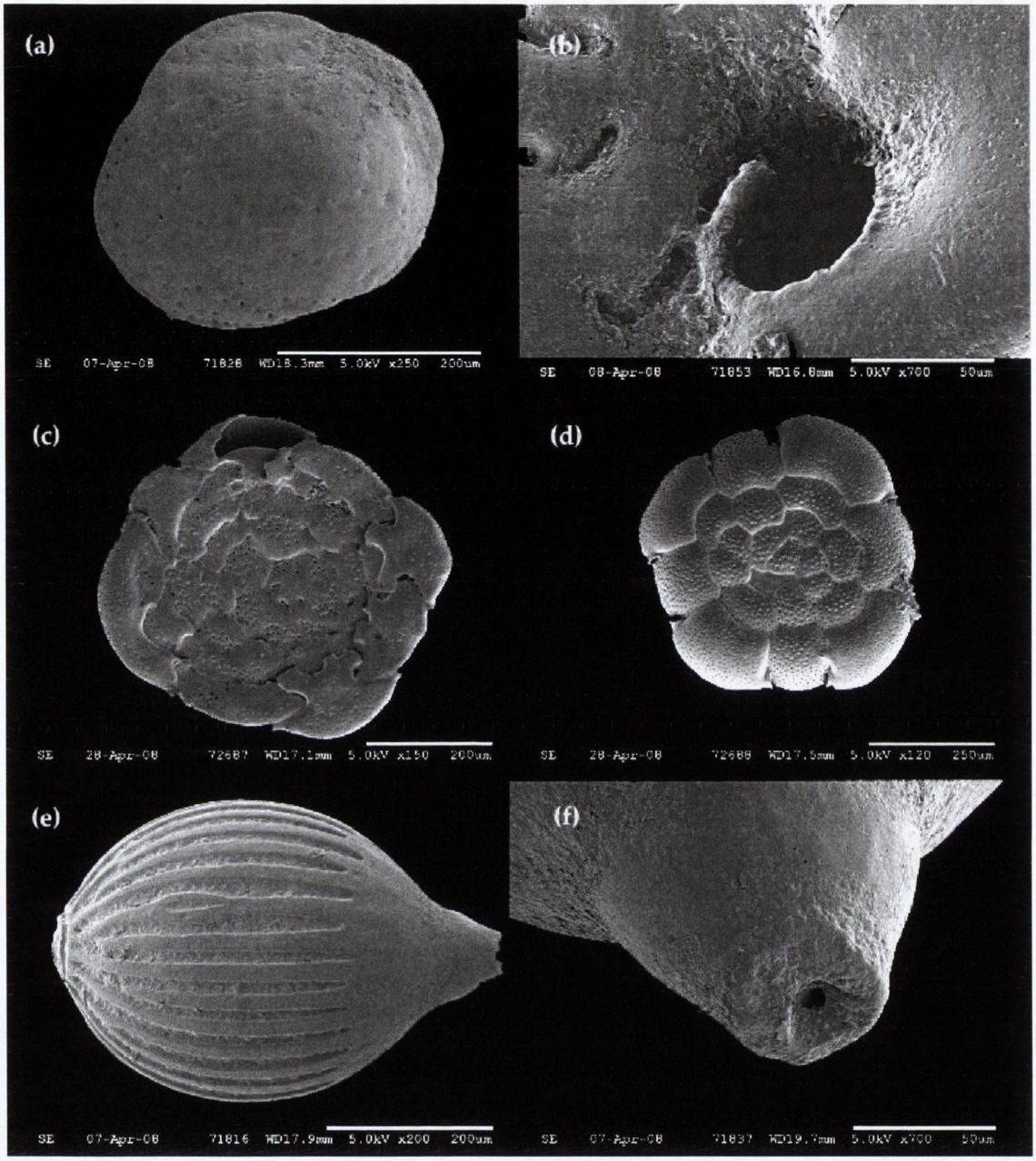


Figure 4.12: (a) ***Asterigerinata mamilla;*** **(b)** ***Asterigerinata mamilla*** **– aperture; (c)** ***Planorbulina mediterannias;*** **(d)** ***Planorbulina mediterannias;*** **(e)** ***Oolina sp. 4 ;*** **(f)** ***Oolina sp. 4*****- aperture.**

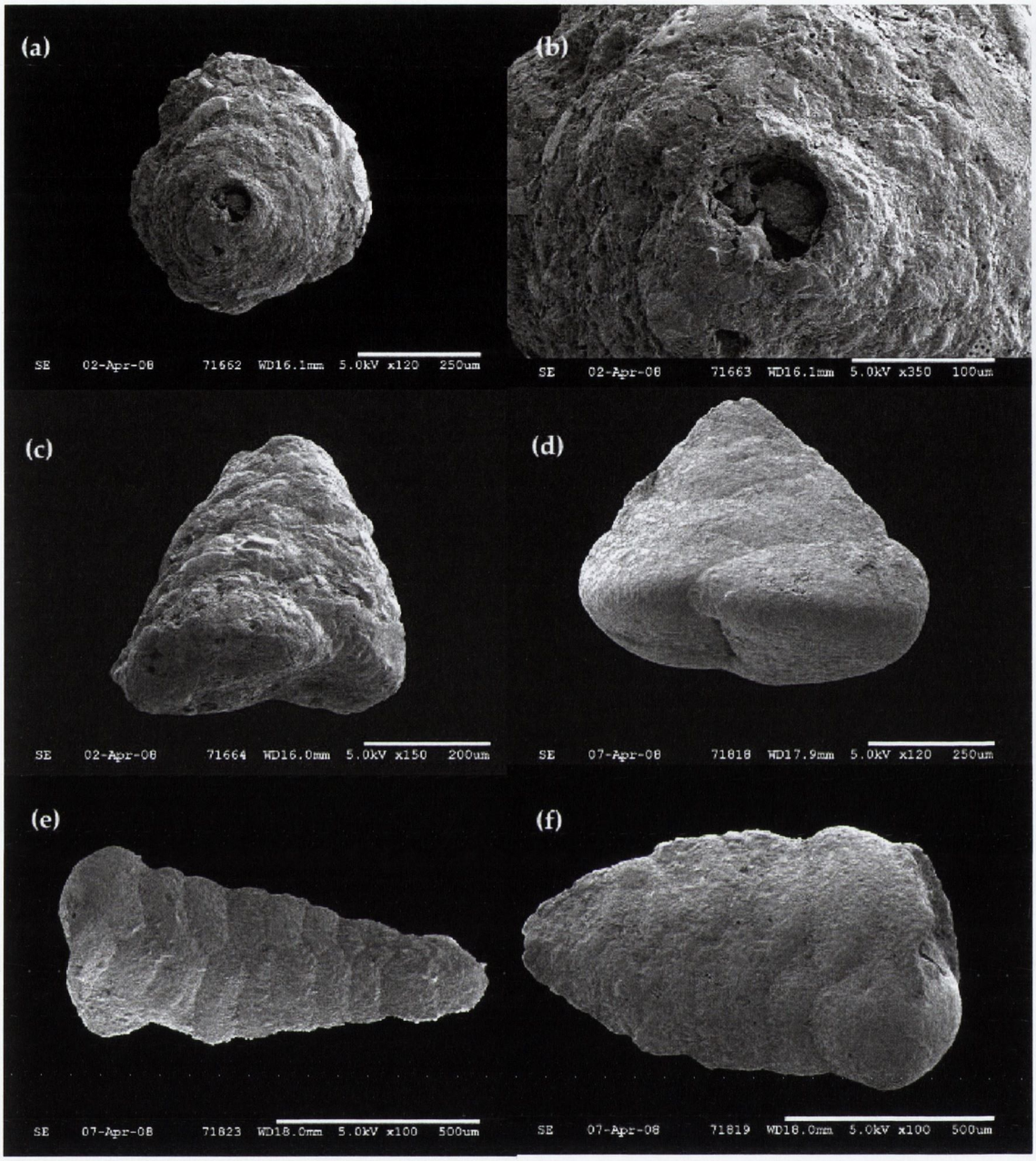


Figure 4.13: (a) ***Gaudryina rudis;*** **(b)** ***Gaudryina rudis*** **– aperture; (c)** ***Gaudryina rudis;*** **(d)** ***Textularia truncata;*** **(e)** ***Textularia saggitula;*** **(f)** ***Textularia*** **sp. 1.**

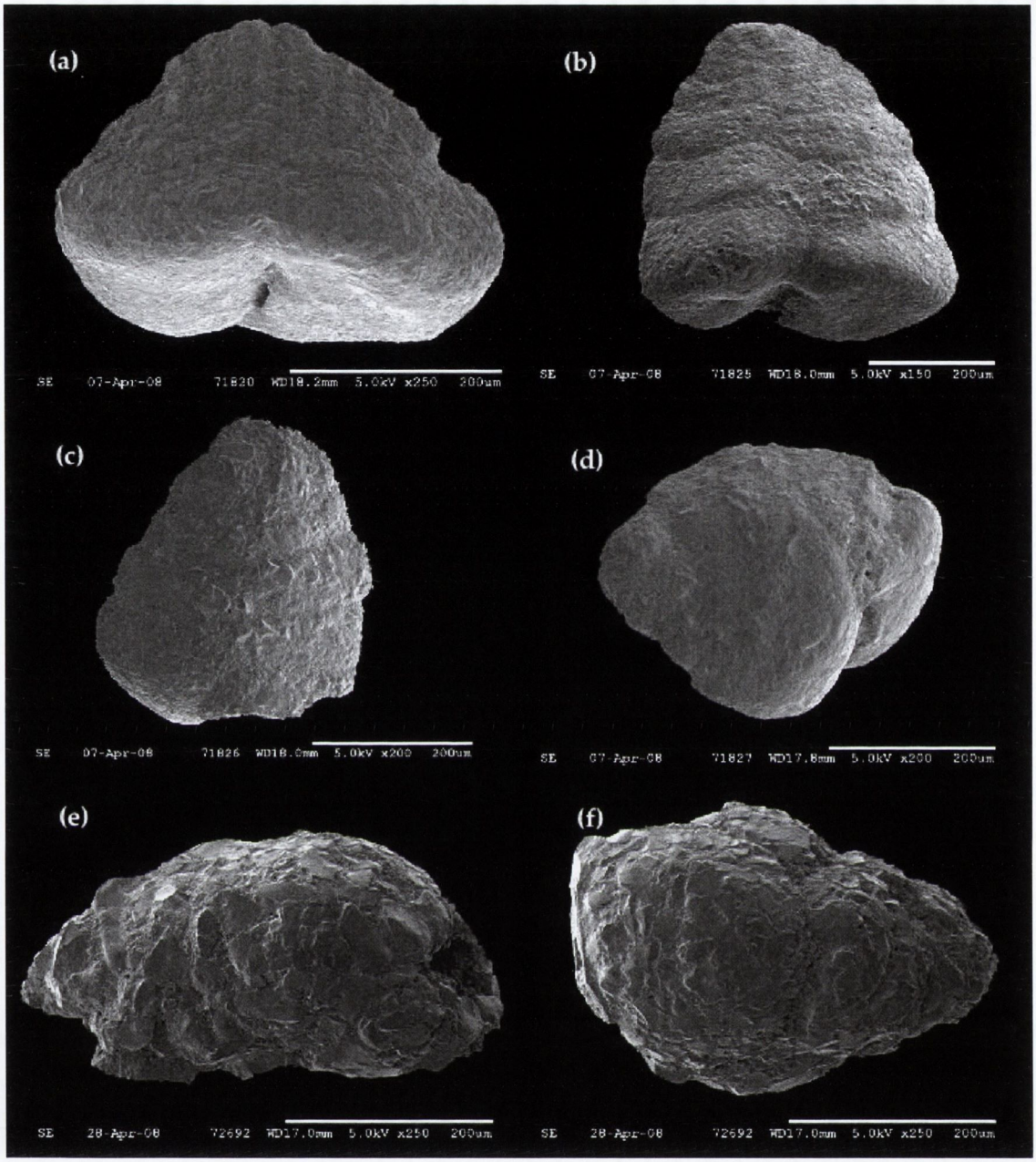


Figure 4.14: (a) ***Textularia sp. 3;*** **(b)** ***Textularia sp. 4;*** **(c)** ***Textularia sp. 6;*** **(d)** ***Textularia sp. 7;*** **(e) Agglutinated sp.; (f) Agglutinated sp.**

4.3.2 Foraminiferal taxonomic levels

Hierarchical agglomerative cluster analysis with SIMPER tests were carried out for species (Figure 4.6), orders (Figure 4.15) and superfamilies (Figure 4.16) for the foraminifera at the Celtic Deep sites using Bray-Curtis similarity matrices of abundance data. Both the superfamily and order cluster analysis only showed two significantly different groups, showing a loss in resolution of the data from the species cluster analysis which had shown 8 distinct groups. Groups are distinguished at higher levels of similarity for the superfamilies and orders as there is a loss in the resolution of the data as the data are aggregated to superfamilies or orders making sites more similar. An examination of the cluster analysis of the abundance of different foraminiferal orders at each site shows the sandy site 46 moving from the group containing sites in coarser sediments (47 – 57) to the group containing muddier sites (38 – 45) (see Figure 4.15 and Figure 4.16). More information is lost as species are aggregated into orders.

The RELATE function in PRIMER v6 was used to compare the similarity of the species Bray-Curtis similarity matrix with the similarity matrices for superfamily and order to see how well the matrices compare. As would be expected, there was a higher correlation of the species similarity matrix with the superfamily matrix (0.935) than with the order matrix (0.906) as more information is retained in the superfamily matrix (with 17 superfamilies) than in the order matrix (with six orders).

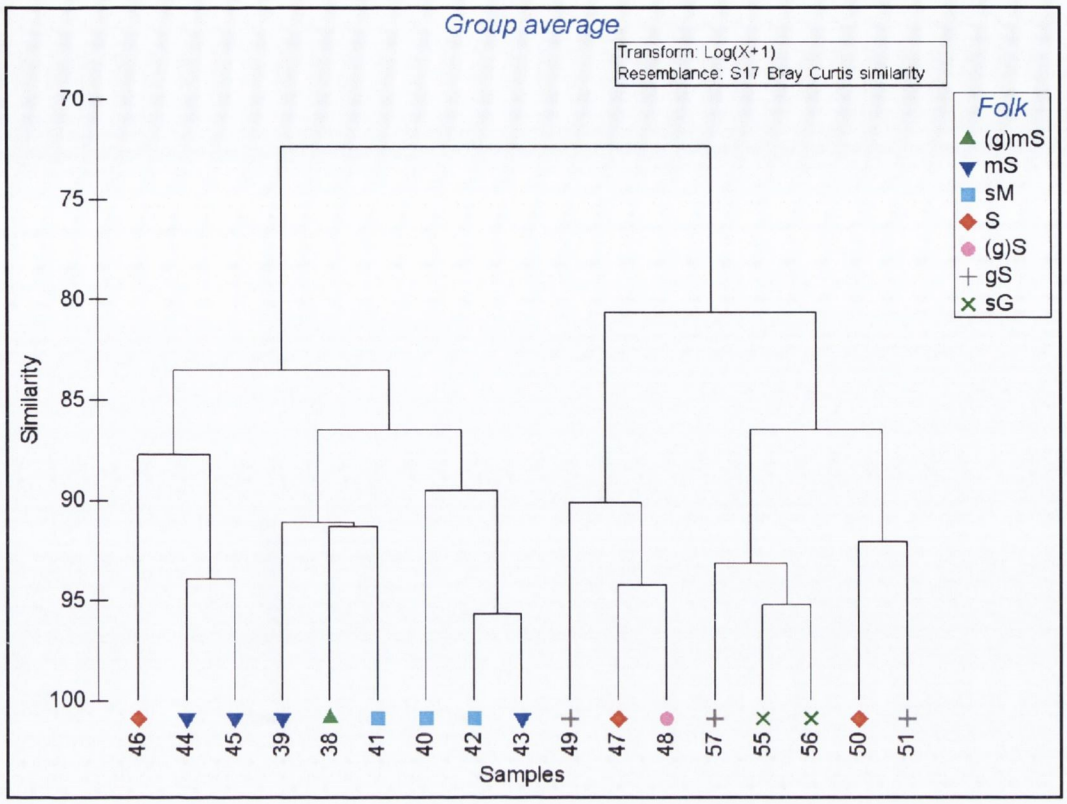


Figure 4.15: Hierarchical agglomerative cluster analysis (PRIMER v6) of sites using abundance of foraminiferal orders at each site, showing only two groups delineated from each other at 80% similarity.

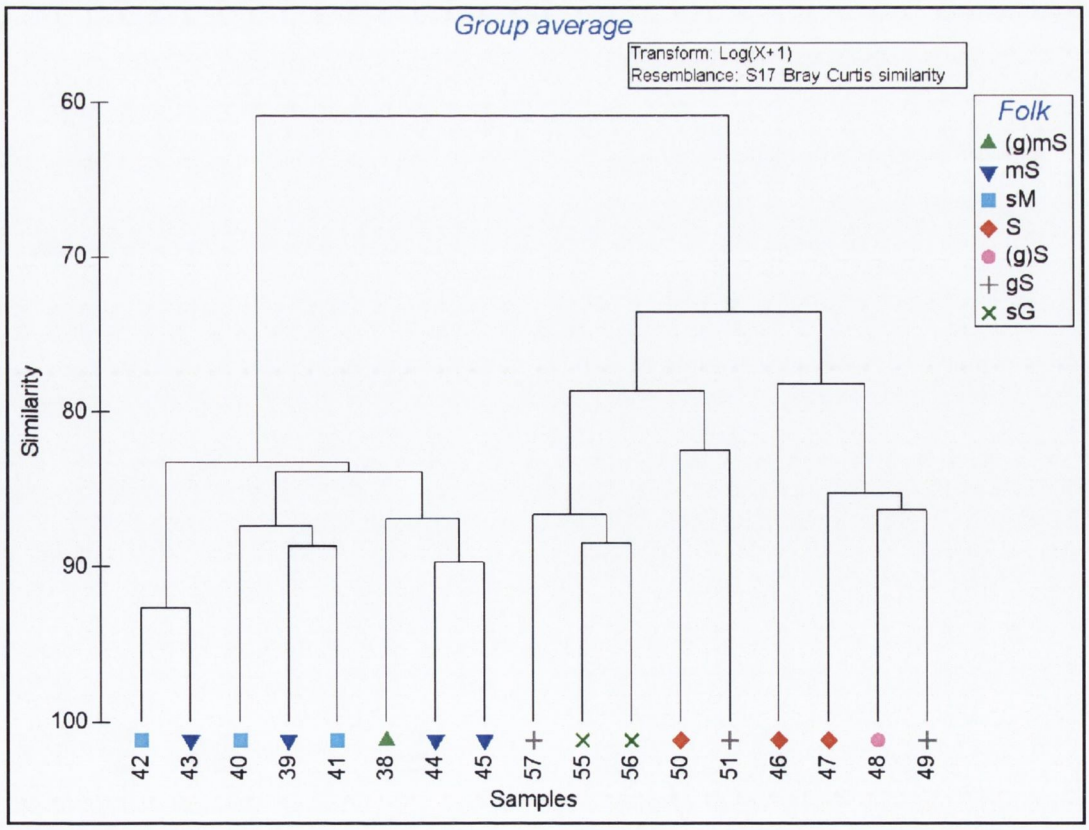


Figure 4.16: Hierarchical agglomerative cluster analysis (PRIMER v6) of sites using abundance of foraminiferal superfamilies at each site, showing only two groups delineated from each other at 75% similarity.

4.3.3 Physical and chemical characteristics of biotopes

4.3.3.1 Spearman rank correlation

A Spearman rank correlation of the environmental variables is shown in Table 4.5. There were strong correlations between gravel, sand and mud and many of the other variables and thus it was decided to use mean grain size as a proxy for gravel, sand and mud (see Table 4.5). Median grain size correlated highly with mean grain size (0.98) and was also removed from the analysis. Sorting correlated highly with organic matter and organic carbon and was also removed. As organic matter and organic carbon also correlated highly, it was decide to remove organic carbon from the analysis as it also correlated with depth. This resulted in six of the original fourteen environmental variables being considered in any further analysis; depth, calcium carbonate, organic matter, mean grain size, skewness and kurtosis.

4.3.3.2 BEST analysis

The BEST procedure (PRIMER v6) using all the environmental variables found that sorting (σ =0.632, $p<0.01$) best explained the biotic patterns. The same analysis was performed with the macrofaunal species Bray-Curtis similarity matrix. Using the six environmental variables mentioned above, gravel, mean grain size and sorting ($\sigma = 0.694$, $p<0.01$) are found to best explain the biotic patterns.

Table 4.5: Spearman rank correlation of environmental variables from the Celtic Deep. Significant correlations are highlighted in grey. * Correlation significant at $p \leq 0.01$ level (2-tailed). ** Correlation significant at $p \leq 0.05$ level (2-tailed).

	Depth	Gravel	Sand	Mud	$CaCO_3$	OM	OC	Mean	Sorting	Skew.	Kurt.	Median
Depth	1											
Gravel	-.53*	1										
Sand	-0.35	0.15	1									
Mud	.66**	-.81**	-0.47	1								
Calcium	0.02	0.36	-.73**	-0.06	1							
OM	.50*	-0.41	-.82**	.75**	.53*	1						
OC	.64**	-0.29	-.74**	.62**	.56*	.80*	1					
Mean	.64**	-.90**	-0.30	.90**	-0.26	.54*	0.44	1				
Sorting	0.47	-0.47	-.76**	.75**	0.43	.92**	.68**	.60*	1			
Skewness	-0.06	-0.04	0.37	0.12	-0.36	0.02	-0.19	0.04	0.08	1		
Kurtosis	-0.12	-0.21	.63**	0.04	-.61**	-0.40	-0.46	0.04	-0.30	0.32	1	
Median	.65**	-.88**	-0.25	.84**	-0.28	.49(*)	0.46	.98**	.54*	-0.02	-0.02	1

4.3.3.4 Canonical Correspondence Analysis (CCA)

Canonical Correspondence Analysis (CCA) was carried out using the foraminiferal species and the environmental variables, depth, calcium carbonate, organic matter, mean grain size, skewness and kurtosis. Species data were log-transformed and rare species were down weighted. Inter-sample distances were examined rather than inter-species distances, as the aim was to look at the effect of environmental variables on species distribution at sites. Automatic forward selection was used as the selection procedure. From Table 4.6 it is clear that axis 1 and axis 2 contribute to most of the variation with 49% and 69% of the variation in species data and species-environment relations respectively.

Table 4.6: Summary of CCA data for foraminiferal species and environmental variables in the Celtic Deep.

Axes	1	2	3	4	Total inertia
Eigenvalues :	0.426	0.176	0.083	0.076	1.442
Species-environment correlations :	0.974	0.983	0.982	0.929	
Cumulative percentage variance					
of species data :	29.6	41.8	47.5	52.8	
of species-environment relation:	48.6	68.6	78.1	86.8	
Sum of all eigenvalues					1.442
Sum of all canonical eigenvalues					0.877

Table 4.7 and Table 4.8 show both the marginal and conditional effects of the CCA respectively. Marginal effects explain the amount of variance which the environmental variables contribute when only that environmental variable is considered ($\lambda 1$). The marginal effects show organic matter (0.32), followed by mean grain size (0.28) account for the most variance if considered singly (Table 4.7). The conditional effects show the order in which the variables were included in the model and the additional variance that each variable explained (λA). A Bonferroni correction was applied to the data which found that variables were significant if $\alpha^1 \leq 0.0083$ (as $\alpha^1 = \alpha/h$, if h is the number of variables in the analysis). The p-values show that organic matter ($p = 0.002$), calcium carbonate ($p = 0.002$) and depth ($p = 0.006$) were significant (see Table 4.8).

The relationship between sites and the significant environmental variables is graphically displayed in Figure 4.17 which clearly shows two distinct groups comprising stations 51, 55, 56 and 57 and stations 47-50, both groups containing less organic matter than the other stations but with the groups comprising stations 51, 55, 56 and 57 containing more calcium carbonate than

stations 47-50. The rest of the stations, containing the highest amounts of organic matter, group together on the right hand side of the graph. Organic matter is clearly shown to have the greatest influence in the clustering of the stations, followed by calcium carbonate and depth to a lesser extent.

Table 4.7: Summary of the marginal effects showing the variance contributed by the environmental variables in the CCA.

Variable	λ1
Organic matter	0.32
Mean grain size	0.28
Calcium carbonate	0.17
Depth	0.16
Skewness	0.12
Kurtosis	0.09

Table 4.8: Summary of the conditional effects showing the variance contributed by the environmental variables in the CCA.

Variable	λA	P	F
Organic matter	0.32	0.002	4.32
Calcium carbonate	0.18	0.002	2.7
Depth	0.12	0.006	1.92
Kurtosis	0.11	0.016	1.69
Skewness	0.07	0.250	1.2
Mean grain size	0.08	0.090	1.44

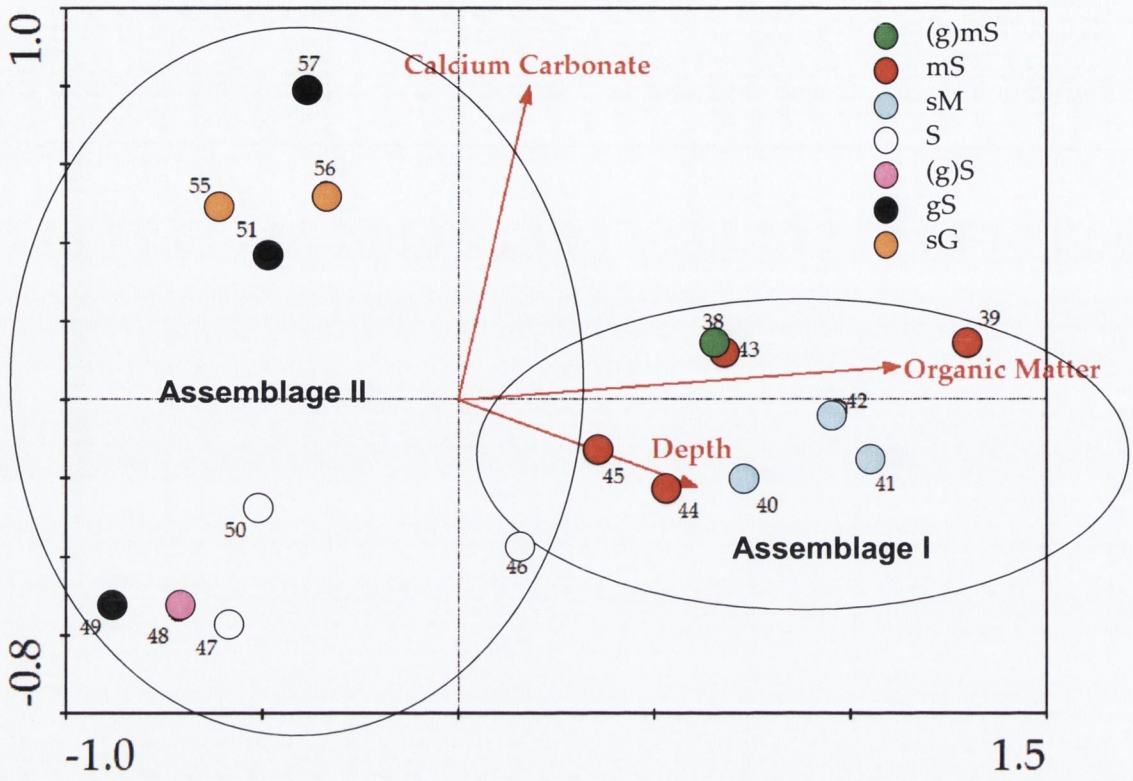


Figure 4.17: CCA biplot of sites and selected environmental variables. Foraminiferal assemblages I and II are overlaid on the plot. Folk sediment types are represented by circles.

4.3.4 Foraminiferal and macrofaunal assemblages

The RELATE function in PRIMER v6 was used to show how well the Bray-Curtis similarity matrices based on macrofaunal and foraminiferal species related to each other. The procedure was based on a Spearman rank correlation, and a value of 0.81 ($P < 0.1\%$) was obtained indicating that the matrices were highly related.

4.4 *Discussion*

Two distinct groups of foraminiferal assemblages were recognised in both the species and superfamily based cluster analyses. Group 1 contained the stations 38 - 45 and Group 2 contained the stations 46 - 57. Site 46 switched from Group 2 to Group 1 in the foraminiferal order-based cluster analysis.

Foraminiferal species-based assemblage I resembled the living western assemblage found by Murray (1970) in the North Celtic Sea, the western Celtic assemblage identified by Murray (1979) and the stratified assemblage found by Scott et al. (2003) which was dominated by *Nonionella turgida, Hyalinea balthica* and *Bulimina marginata* where the sediments ranged from 'muddy fine to coarse quartz sand with shell debris' (Murray, 1970). Assemblage I also bears a resemblance to Le Calvez's (1958) 'muddy' group comprising Buliminidae, *Hyalinea balthica* and *Nonionella* species.

Foraminiferal assemblage II compared favourably with the dead eastern assemblage, dominated by *Textularia sagittula* group and *Cibicides lobatulus* found by Murray (1979) in the Celtic Sea. These assemblages are also closest to Scott et al.'s (2003) mixed assemblage which was dominated by *Cibicides lobatulus, Textularia bockii, Spiroplectammina wrightii, Ammonia batavus* and *Quinqueloculina seminulum*. Assemblage II also compared favourably with Le Calvez's (1958) 'Les fonds détritiques' assemblages which have an abundance of Verneuilinidae, Textulariidae, Milioildae, Rotaliidae and Anomalinidae (see Table 2, Appendix 1 for an outline of species, genera, superfamilies and orders).

Environmental variables in the Celtic Deep were found to be highly correlated, thus it was difficult to distinguish which if any of the environmental variables were responsible for the patterns in foraminiferal or macrofaunal distribution in the Celtic Deep. The analysis could only examine variables which had been taken on board during the survey or which were analysed in the laboratory. Unfortunately many physical variables such as temperature and bed shear stress were not analysed during the survey and therefore could not be included in the analysis, thus the CCA analysis cannot be directly compared to that of Scott et al.'s (2003) as different parameters were measured in both studies. Scott et al. (2003) did note that longitude and latitude seemed to be acting as proxies for environmental variables. This is most likely to be explained by the north – south gradient in both depth and sediment type occurring in the Cetic Sea and the transition from Boreal to Lusitain waters experienced at the Celtic Front..

Sites from the Celtic Deep were analysed both in terms of foraminiferal and macrofaunal species abundance through hierarchical agglomerative cluster analysis using PRIMER v6 (see Figure 4.6 and Figure 4.2). Both cluster analyses used SIMPER tests to discover which groups of sites were significantly different from each other. Both the foraminiferal species and macrofaunal species cluster analyses discovered eight groups of sites; Ia, Ib, Ic, Id, IIa, IIb , IIc an IId for the foraminifera and I, II, III, IV, V, VI, VII and VIII for the macrofauna. Two of the macrofaunal groups (I and V) consisted of one site only, sites 39 and 55 respectively. These sites were incorporated into their closest clusters to produce the biotopes recognised by Robinson et al. (2007). However, these eight groups are not directly compared as it was felt that at this level there were too many issues in regard to foraminiferal identification to accept the eight foraminferal groupings distinguished by the SIMPROF tests. At the lower similarity of 40% for the foraminifera and 20% for the macrofauna, both faunal groups formed two distinct assemblages: sites 38 - 45 and sites 46 - 57.

The potential exists for foraminifera to be used as a tool for constructing past and modern benthic habitat maps. There is not currently enough data to prove a link between formainiferal and macrofaunal assemblage patterns. Further studies would be required. Based on the limited information available from this study in the southern Irish Sea, it may be possible to limit the taxonomic resolution of the foraminiferal data to the superfamily level in order to construct benthic habitat maps. Even if no definitive link between foraminiferal and macrofaunal assemblages can be made due to the limited sample size, live foraminifera could still be incorporated into modern day benthic habitat mapping. An ecosystem based approach to benthic habitat mapping including not only physical particle size and macrofaunal abundance data, but also including information on the structure and chemical composition of the sediments, data on fauna less than 1mm or 0.5mm in size (the usual size of sieves used in sampling) and information on ecosystem function could lead to a better understanding of benthic habitats. These approaches could be particularly useful in reconstructing both past benthic environments and in learning more about the properties and functions of today's benthic ecosystems. Foraminifera are useful indicators of changes in environmental conditions, e.g. climate change and pollution and their incorporation into marine surveillance and monitoring programmes could prove beneficial.

The use of foraminifera to learn more about modern macrofaunal assemblages has the potential to save time, money and resources. Only one specialist would be needed to identify the foraminifera rather than the many specialists used to identify species in the different orders of macrofauna, and the cost of re-surveying an area already surveyed by geologists could be reduced. Ideally,

both geologists and biologists would work together in planning new surveys but information could be gathered from historical surveys where only sediment data exits.

This study was limited by the difficulties in identifying formainifera to species level. Scanning electron microscope pictures did improve identification. The main problem with foraminiferal identification is the lack of a thorough comprehensive up-to–date identification guide. Due to the huge numbers of foraminiferal species in existence, the most useful tool would be an internet database including all synonyoms and officially recognised names. This tool could contain both modern day SEMs pictures and historical drawings of species, making it easier for scientists to ensure that they have the correct species and providing scientists with the ability to submit their own records and pictures (subject to verification by experts). While SEM pictures are useful, original drawings are more useful if students are unable to take their own SEM pictures for comparison.

Chapter 5

5 Seabed mapping in the southern Irish Sea: predicting benthic biological communities based on sediment characteristics

This chapter was originally published as 'McBreen, F., et al., 2008. Seabed mapping in the southern Irish Sea: predicting benthic biological communities based on sediment characteristics. Hydrobiologia 606, 93-103', however changes have been made to the method of binary logistic regression analysis in this chapter.

5.1 Introduction

The importance of sediment characteristics (particularly particle size) to the distribution of macrobenthic species and communities has been recognized by many authors (Petersen, 1924, Jones, 1950, Jones, 1951, Holme, 1966, Mackie, 1990). The idea of using a characteristic species dominant in either numbers or biomass to define sublittoral community assemblages was first put into practice by Petersen (1913). Petersen (1913) was also the first to separate macrofaunal communities into epifaunal and infaunal communities, distinguishing on the basis of the bottom type animals living in the sediment and animals living on substrates such as rocks and cobbles. Jones (1950) in his review of the literature concluded that communities were more dependent on the physical factors of temperature, salinity, bottom type and depth than on biological factors. His community classification system was based mainly on temperature, salinity, bottom type and depth. Jones also recognized the fact that communities did not have distinct boundaries, but graded into one another. Thorson (1957), expanded on these ideas by applying the community theory globally. Thorson's (1957) global parallel communities were characterized not only by taxonomic affinities but also by functional (particularly feeding) characteristics, thus emphasizing the biological aspects of the ecological niche.

Snelgrove & Butman (1994) have reviewed the relationship between sediments and infauna and have concluded that particle size alone was not sufficient to explain community structure, but that particle size may be correlated with other factors. Gray (1974) concluded that the structure and contours of the surface, sediment particle size, the presence of organic and inorganic compounds, bio-films and populations of the same species were important factors in the settlement of macrobenthic larvae (Gray, 1974).

Much work has been conducted on habitats and communities in the Irish Sea. The Irish Sea Study Group (1990) conducted an environmental review of the Irish Sea focusing on four main areas: nature conservation, waste inputs and pollution, exploitation of living marine resources and planning, development and management. Within this, Mackie (1990) produced a benthic faunal map derived from earlier studies in the Irish Sea and delimited 9 communities. In 2002, the Irish Sea Pilot project was set up by the Joint Nature Conservation Committee (JNCC) (Vincent et al., 2004). This project recommended using the marine landscapes to identify habitats for conservation. Geophysical and hydrographical data were used to define 18 different types of coastal and marine landscapes. Despite their different approaches, in practice both assessments of the Irish Sea benthic environment rely heavily on the distributions of the surficial sediments.

Mackie et al. (1995a) found that gravel and silt content were the two main sediment variables which, together with depth, 'best explained' the benthic macrofaunal distributions in the southeast Irish Sea. A subsequent Canonical Correspondence Analysis (CCA) similarly found that the sediment composition (gravel, silt and sand) and depth were the main environmental variables influencing the polychaete worms (Mackie et al., 1995b). A cluster analysis of benthic variability (Mackie (2004); corrected in Mackie et al., (2006): p 209) showed that both macrofaunal replicates at 49 quantitative stations were paired. Despite the lack of high precision in station positioning, the replicates of only 2 stations were separated in the dendrogram of 102 samples.

There have been a number of approaches using logistic regression technique to predict the presence or absence of biotic data from abiotic variables (Ysebaert et al., 2002, Thrush et al., 2003, Ellis et al., 2006). Ysebaert et al. (2002) used the abiotic variables of depth, salinity, current velocities and particle grain size to predict the presence or absence of macrobenthic species in the Schelde estuary while Thrush et al. (2003) looked at the species-specific model for 13 macrobenthic species to examine their relationship to sediment mud content in the intertidal areas of the North Island in New Zealand. Ellis et al. (2006) examined the relationship between individual species and variable environmental conditions such as depth, silt/clay content, tidal currents and wind/wave disturbance in five estuaries in New Zealand. Ysebaert et al. (2002) and Ellis et al. (2006) found they could predict some species better than others, with correct predictions for the presence of species ranging from 59 to 97% in the 2006 study (Ellis et al., 2006). Ysebaert et al. (2002), Thrush et al. (2003) and Ellis et al. (2006) found that specificity (the absence of a species) was better predicted than sensitivity (the presence of a species). Estuaries normally have strong environmental gradients (e.g. salinity) which may show stronger correlations with the presence of species than in marine environments.

The aim of this chapter is to test the validity of using physical and sediment characteristics to predict benthic macrofaunal assemblages in the southern Irish Sea. The chapter will use sediment and biological data from three EU funded projects in the southern Irish Sea, BIOMÔR (1989-91) (Mackie et al., 1995a), the South West Irish Sea Survey (SWISS) (Wilson et al., 2001) and HABMAP (2005 – 2007).

5.2 *Materials and methods*

The study area was located in the southern Irish Sea (see Figure 1.13). This chapter examines sediment and biological data from three surveys, 51 stations from BIOMÔR (Mackie et al., 1995a), 55 from SWISS (Wilson et al., 2001) and 77 stations from HABMAP (Robinson et al., 2007). During each survey sediment and replicate biological samples were taken at each station with a $0.1m^2$ Van Veen grab.

5.2.1 Sediment samples

Sediment samples for all three surveys were taken from the surface sediment in a $0.1m^2$ Van Veen grab. Samples were taken by hand from the surface of the sediment. The samples were frozen initially and subsequently dried in the oven at 105°C before chemical analysis for organic content, total organic carbon (TOC), calcium carbonate and particle size. Only the HABMAP samples were processed during this study (see Chapter 3). BIOMÔR and HABAMP sediment data was provided by the National Museum of Wales (Mackie et al., 1995a) and Trinity College Dublin respectively (Nic Aonghusa, 1999). The sampling surveys all took place in the summer with BIOMÔR sampling taking place in 1989 and 1991, SWISS in 1997 and 1998 and HABMAP in 2005.

Organic content of the sediment was determined through loss-on-ignition at 550 °C in a muffle furnace (SWISS & HABMAP) or from sediment pre-digested in concentrated hydrochloric acid (to remove calcium carbonate) at 600 °C for two hours (BIOMÔR) (Buchanan, 1984, Mackie et al., 1995a, Wilson et al., 2001). As carbonate minerals tend to breakdown at temperatures over 650 °C, calcium carbonate should not have been combusted during the loss-on-ignition procedure at 550 °C (Boyle, 2004); thus results from both procedures have been examined. Sediment samples used to estimate total organic carbon content were digested in sulphurous acid (SWISS & HABMAP) or hydrochloric acid (BIOMÔR) to remove any inorganic carbon (Bale and Kenny, 2005). The samples were then analysed in a LECO elemental analyser (Verardo et al., 1990, Mackie et al., 1995a, Wilson et al., 2001, Bale and Kenny, 2005). The calcium carbonate content of the sediment was determined through digestion with hydrochloric acid (Buchanan, 1984, Wilson et al., 2001).

Particle size analysis was used to classify the sediment using the BGS modified Folk classification system (Folk, 1954, Jackson et al., 1995). Sediment samples were pre-treated with hydrogen peroxide to remove organic matter before analysis (Buchanan, 1984, Mackie et al., 1995a). Sediment was dry sieved through 8mm, 4mm, 2mm, 1mm, and 500μm sieves. Fractions less than 500μm in size were analysed in the Malvern Mastersizer laser particle size machine (HABMAP) (Bale and Kenny, 2005). BIOMÔR and SWISS sediment samples were also dry sieved through 250μm, 125μm and 63μm sieves. The silt/clayfraction for the BIOMÔR and SWISS sediments were analysed using pipette analysis (Buchanan, 1984; Mackie et al., 1995a; Wilson et al., 2001).

5.2.2 Macrofaunal data

Macrofaunal data from the three projects were processed by the National Museum of Wales (Mackie et al., 1995a, Wilson et al., 2001, Robinson et al., 2007). Biological samples were taken with a 0.1m² Van Veen grab with two grabs at each quantitative station and were sieved through a 500μm sieve (Mackie et al., 1995a, Wilson et al., 2001, Robinson et al., 2007). All macrofauna were identified and counted at each station (Mackie et al., 1995a, Wilson et al., 2001, Robinson et al., 2007). As some polychaete records form the SWISS project were still incomplete they were excluded from some of the overall biological community analysis (Wilson et al., 2001). The molluscs, arthropods and other animals included are estimated to comprise about 55% of the species and 45% of the total abundance with polychaetes making up the remainder (see Mackie et al., (1995a)).

5.2.3 Statistical analysis

The data were analysed using two different approaches, one method examining categorised data by exploring a combination of Folk sediment types and organic matter and the second method using continuous abiotic data to predict biological communities through the use of binary logistic regression. The biological data were analysed using cluster analysis and the SIMPER routine in PRIMER v.6 (Clarke, 1993). Species abundance data were log (x+1) transformed before constructing a Bray-Curtis similarity matrix. A dendrogram, which grouped individual sites based on their similarities and group average clustering, was created from the similarity matrix. Biological assemblages were then identified from groupings of sites at two different levels of similarity (e.g. 15% and 23%). Level 1 was determined by the similarity at which major groupings in the hierarchical classification system were identified (e.g. A – E). Level 2 was determined by the

similarity at which these larger classes subdivided into smaller groups. Assemblages at greater similarities were not examined as the number of sites per assemblage was deemed to be too low. The levels of similarity used were determined by the cluster analysis (Figure 5.1) A one-way SIMPER test in PRIMER v.6 was used to distinguish the species which had the greatest effect on the assemblages identified in the dendrogram.

Binary logistic regression (SPSS 14.0) was used to predict the presence or absence of a categorical biological variable from a number of continuous environmental variables. Two different groups of data were analysed, quantitative environmental and macrofaunal data (excluding polychaetes) from the BIOMÔR and SWISS projects and quantitative environmental and total macrofaunal data from the HABMAP and BIOMÔR projects. The environmental variables to be used in the analysis were selected after examining the multicollinearity of the following variables; depth, longitude, latitude, mean grain size, median grain size, sorting, skewness, kurtosis, gravel, sand, mud, organic content, organic carbon and calcium carbonate concentrations. Any outliers were eliminated from the analysis after examining Mahalanobis and Cook's distance (Pallant, 2007). Mahalanobis distance measures the distance of the case from the centroid of the remaining cases (Tabachnick and Fidell, 2007). Most cases lie in a swarm around the centroid, multivariate outliers lie outside the swarm some distance from the other cases (Tabachnick and Fidell, 2007). Cook's distance measures influences of variation by assessing changes in regression coefficients when a case is deleted, cases with values larger than 1.00 are suspected outliers (Tabachnick and Fidell, 2007). The biological assemblages designated from the cluster analysis were used as the categorical variables.

Forced entry binary logistic regression was adopted in the analysis as opposed to the stepwise backward elimination method used by McBreen et al. (2008) to analyse the BIOMÔR and SWISS data. Forced entry was chosen as Tabachnick & Fidell (2007) recommend using it instead of sequential logistic regression if there is no hypothesis regarding the order or importance of the predictors.

The Hosmer and Lemeshow Test was used to test the goodness of fit of the model., in which significance levels for the Hosmer and Lemeshow Test > 0.05 indicate that the model is valid (Pallant, 2007). The Cox & Snell R Square and Nagelkerke R Square values indicate the amount of variance explained by the model (Pallant, 2007). Environmental variables are considered to significantly contribute to the model if the significance level for the Wald statistic is > 0.05.

Multiple regression was attempted in order to test the validity of using continuous independent environmental variables to predict the continuous dependent variable of total benthic macrofaunal abundance, using data from BIOMÔR and HABMAP, but the environmental variables did not correlate highly enough with total abundance for the analysis to be performed.

5.3 *Results*

5.3.1 Categorical analysis

The physical and chemical sediment characteristics of 183 quantitative stations from the three projects were analysed. Firstly, the sites were divided by categorising data (using the BGS modified Folk sediment classification) to give 11 different types of Folk habitat from a possible 15 (see Table 5.1). These habitats were further subdivided by organic matter concentration (Table 5.1). Organic matter was divided into three categories low (< 1%), medium (1 – 7.5%) and high (> 7.5%). In the absence of a marine model, these categories were derived from the estuarine Pollution Load Index (PLI) (Jeffrey and Wilson, 1985), where the baseline level for organic matter as a pollutant is 1% and the threshold is 7.5%. The addition of a second categorised environmental variable increased the number of habitats from 11 to 23 (Table 5.1 and Table 5.2). It should be noted that 12 of these categories had 5 or fewer stations within them (i.e. ~ 50%).

Table 5.1: Quantitative samples classified using the BGS modified Folk sediment classification and subdivided by organic matter level, where low = <1%, medium = 1 - 7.5% and high = >7.5%.

	Sediment type	Number of sites	Organic Matter		
			Low	Medium	High
1	Sand	57	29	28	
2	Sandy gravel	35	4	31	
3	Gravelly sand	32	12	20	
4	Muddy Sand	24	1	1	22
5	Sandy Mud	10		5	5
6	Slightly gravelly sand	9	3	6	
7	Slightly gravelly muddy sand	6	1	5	
8	Gravelly muddy sand	5		5	
9	Gravel	2		2	
10	Muddy sandy gravel	2		2	
11	Mud	1			1
	Total	**183**			

Through this inclusion of chemical sediment characteristics, the physical sediment habitats could be further subdivided into categories more highly linked to biological assemblages (Table 5.2) (complete species abundance data, BIOMÔR project) (Mackie et al., 1995a). In Table 5.2 differences can be seen between physical sediment habitat types and biological assemblages where levels of organic matter differ, e.g. the slightly gravelly muddy sand category divides into low and medium organic matter associated with biological assemblages B1 and B3 respectively. It should also be noted that the same biological assemblages occur over different physical sediment

types, e.g., B1 occurs in slightly gravelly muddy sand, gravelly muddy sand and muddy sand. This shows that categorical physical sediment classifications alone cannot predict biological assemblages. Also different biological assemblages such as A2, B2, B3, B4 and C1 were found in the same physical sediment category (Table 5.3).

Table 5.2: BIOMÔR sites, divided by the BGS modified Folk classification system and subdivided by organic matter. Biological assemblages from Mackie et al. (1995a: p 80).

	Sediment type	Organic matter level	Biological Assemblage	No. of sites
1	**Sand**	low	B2	2
2			B4	2
3			C1	1
4		medium	A2	2
5			B3	1
6			B4	4
7	**Sandy gravel**	low	C1	2
8		medium	C1	5
9			C2	3
10	**Gravelly sand**	low	C1	3
11		medium	C1	1
12			B3	1
13	**Muddy sand**	medium	A1	2
14			A2	2
15			B1	5
16	**Sandy mud**	medium	B1	1
17			A1	3
18		high	A1	1
19	**Slightly gravelly sand**	low	B4	1
20	**Slightly gravelly muddy sand**	low	B1	1
21		medium	B3	1
22	**Gravelly muddy sand**	medium	C1	3
23			B1	1

5.3.2 Binary logistic regression & cluster analysis

In view of the limitations of categorized sediment data, a second approach was taken to test whether biological assemblages in the southern Irish Sea could be predicted from the continuous environmental variables. Using species abundance data, dendrograms were constructed from a Bray-Curtis similarity matrix of the log(x+1) transformed data using PRIMER v6 (see Figure 5.1).

Forced entry binary logistic regression (BLR) was used to examine to what extent biological assemblages (Figure 5.1) could be correctly predicted from the environmental variables; depth (m), organic content (%), organic carbon (%), calcium carbonate (%), median grain size, sorting and kurtosis. These variables were chosen as they showed no multicollinearity with each other and they all had Pearson product correlations of less than 0.7 for both data sets. Outliers were also eliminated where Mahalanobis values were greater than the critical value of 26.125 ($p<0.001$) and Cook's distances were less than 1.0 (Pallant, 2007, Tabachnick and Fidell, 2007). This resulted in the deletion of BIOMÔR station 38 and HABMAP stations 25, 33 and 83C from the BIOMÔR and HABMAP data and the deletion of BIOMÔR station 38 and SWISS stations 104, 106 and 133 from the BIOMÔR and SWISS data.

5.3.2.1 BIOMÔR and SWISS projects

From the dendrogram, different assemblages were identified according to the level of similarity; four (I, II, III and IV) at level 1 (15% similarity), and four (II.1, II.2, II.3 and II.4) at level 2 (23% similarity) (Figure 5.1). Predictions for assemblages at Levels 1 could only be made for two of the four assemblages and at level 2 for three of the four assemblages (see Table 5.3). Assemblage I did not show any variables contributing significantly and this may be due to the low number of stations (5) included in assemblage I (see Table 5.3). Assemblages II and II.3 had a Hosmer & Lemeshow significance < 0.05 and therefore the models were deemed not to be significant (Pallant, 2007). In the case of assemblage II.3, this again may due to be the small sample size and this is probably why assemblage II.3 is not significant as it only contained 5 stations. Assemblage II was not significant even though it contained a high number of stations (63) although at Level 2 predictions could be made regarding assemblages II.1 and II.2, indicating that a higher level of discrimination was required for assemblage II (see Table 5.3).

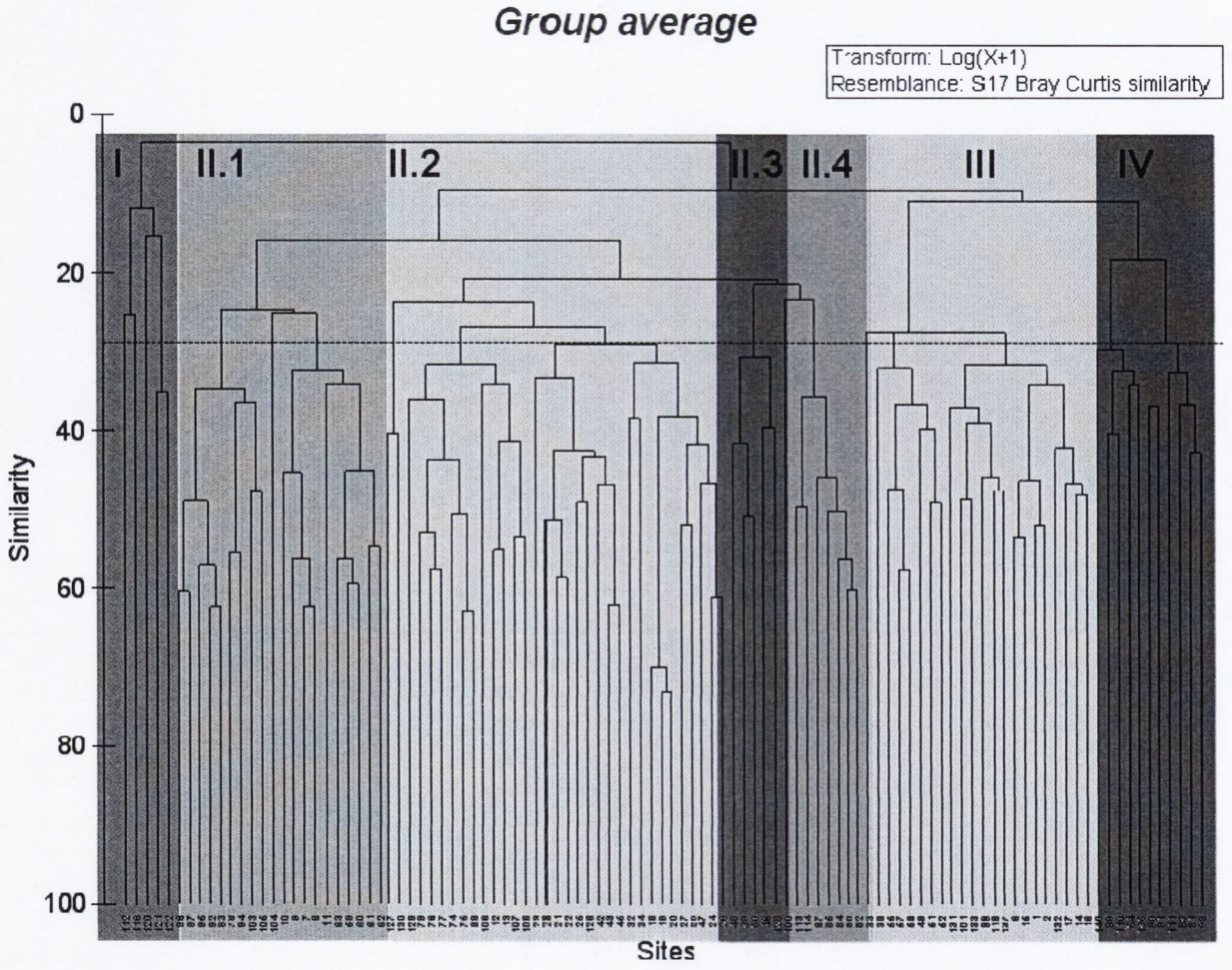


Figure 5.1: Dendrogram (Bray-Curtis similarity matrix, PRIMER v6) of log (x+1) transformed species abundance data from the BIOMÔR and SWISS projects (excluding polychaetes).

Table 5.3: Presence and absence of biological assemblages predicted correctly from the environmental variables; depth (m), % organic matter, % organic carbon and % calcium carbonate, median grain size, kurtosis and sorting. Percentage presence and absence calculated using direct entry binary logistic regression (SPSS 14.0).

Level	No. of sites	Biological Assemblage	Cox & Snell R square	Nagelkerke R square	Hosmer & Lemeshow test sig.	Percentage predicted correctly (Model)		Contributing variables
						Presence	Absence	
1	5	I	.197	.597	.997	60.0	98.9	None
	63	II	.516	.706	0.00	n/a	n/a	n/a
	20	III	.495	.780	.845	80.0	97.5	Kurtosis Depth
	11	IV	.381	.759	.918	72.7	97.7	Organic Carbon
2	18	II.1	.613	1.000	1.000	100.0	100.0	Median grain size Organic carbon Depth
	32	II.2	.529	.739	.700	81.3	92.5	Median grain size Organic carbon Depth
	5	II.3	.197	.597	.000			n\a
	8	II.4	.182	.424	.999	25.0	100.0	Latitude

Assemblages III, IV, II.1 and II.2 all show significant models (see Table 5.3). They also show high sensitivity (presence of assemblages predicted correctly (%)) and specificity (absence of assemblages predicted correctly (%)). Assemblage II.4 shows a very high specificity (100%) but a low sensitivity (25%) and it is also the model with the least number of stations (8) and the lowest percentage of variance explained by the environmental variables (see Table 5.3). The percentage of variance explained ranges from 18.2% - 42.4% for Assemblage II.4 to 61.3% – 100% for Assemblage II.1, which showed the highest possible scores for sensitivity (100%) and specificity (100%) (see Table 5.3).

5.3.2.2. BIOMÔR and HABMAP

From the dendrogram (Figure 5.2) a number of assemblages were identified at different levels of similarity; five assemblages (A, B, C, D and E) were identified at Level 1 (15% similarity) and seven assemblages (C1, C2, D1, D2, E1, E2 and E3) are examined at Level 2 (29% similarity) (see Figure 5.2 and Table 5.4). Assemblages A, B and E3 were excluded from the analysis as they each contained only one station. From the forced entry binary logistic regression, predictions of which environmental variables contributed significantly to assemblages C and E1 could not be made, as the Hosmer & Lemeshow tests had significance levels < 0.05. However, unlike the BIOMÔR and SWISS data, this cannot necessarily be attributed to low numbers of stations as assemblage C contained 19 stations.

At level 1, assemblages D and E showed high sensitivity and specificity levels. Assemblages C1 had a very low sensitivity (9.1%) (see Table 5.4). Assemblage C2 had the second lowest sensitivity at 50% (see Table 5.4). In both the case of both C1 and C2, small samples sizes of 11 and 8 stations respectively could have contributed to lower sensitivities than for other stations. Assemblages D1, D2, E2 and E4 have higher sensitivity and specificity values indicating that the environmental variables included in the analysis were greater predictors of these macrofaunal assemblages (see Table 5.4). As already shown with the BIOMÔR and SWISS data, there were no consistent predictors for all of the assemblages, indicating that predictors are assemblage specific (see Table 5.4).

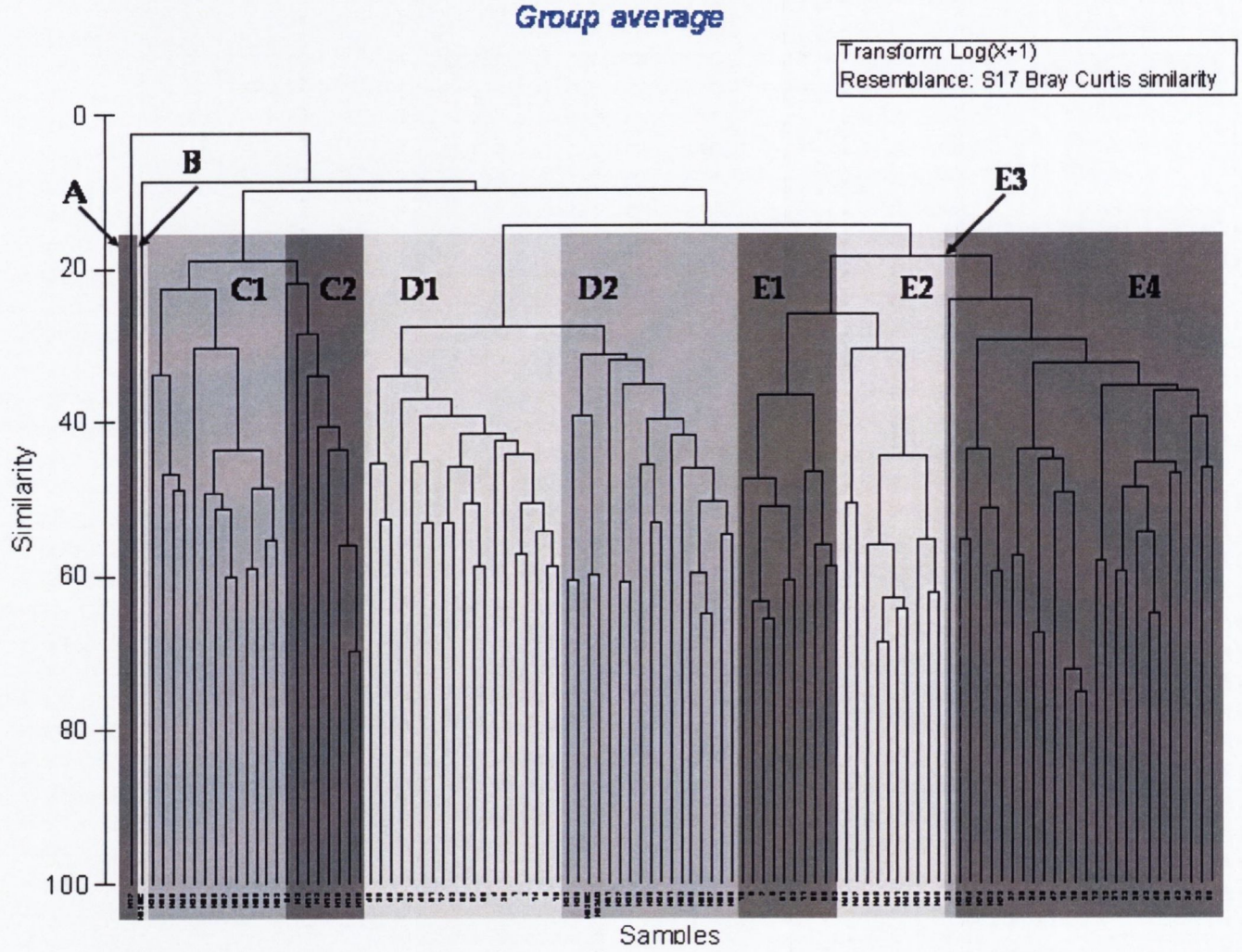


Figure 5.2: Dendrogram (Bray-Curtis similarity matrix, PRIMER v6) of log (x+1) transformed species abundance data from the BIOMÔR and SWISS projects (excluding polychaetes).

Table 5.4: Presence and absence of biological assemblages predicted correctly from the environmental variables; depth (m), % organic matter, % organic carbon and % calcium carbonate, median grain size, kurtosis and sorting. Percentage presence and absence calculated using direct entry binary logistic regression (SPSS 14.0).

Level	No. of sites	Biological Assemblage	Cox & Snell R square	Nagelkerke R square	Hosmer & Lemeshow test sig.	Percentage predicted correctly (Model)		Contributing variables
						Presence	Absence	
1	19	C	0.199	0.318	0.947	5.3	96.3	**None**
	33	D	0.563	0.782	0.554	87.9	90.9	Latitude Depth Sorting Kurtosis Median grain size
	46	E	0.700	0.935	1.000	93.5	98.1	Depth
2	11	C1	0.219	0.435	0.238	9.1	98.9	Depth
	8	C2	0.249	0.579	0.995	50.0	97.8	Organic matter
	17	D1	0.407	0.678	0.962	64.7	97.6	Depth Organic carbon Sorting Kurtosis Median grain size
	16	D2	0.513	0.874	0.988	87.5	98.8	Latitude Organic carbon Kurtosis
	10	E1	0.480	1.000	1.000	100.0	100.0	**None**
	10	E2	0.347	0.762	1.000	77.8	97.8	Latitude Calcium carbonate
	26	E4	0.558	0.816	0.988	80.8	94.5	Depth

Table 5.5 and Table 5.6 show the top five contributing species for each of the group assemblages. The results show that communities cannot be defined by one characterizing species as Petersen (1913) suggested but are a combination of species more similar to the associations of Jones (1950). The main contributing species change as similarity increases at lower levels (e.g. from II through to II.1, II.2, II.3 and II.4 and from E to E1, E2 and E4). Depending on the level of discrimination, a different number of communities can be said to exist in the southern Irish Sea.

Table 5.5: Top five contributing species for each biological assemblage in group II. Contributing species identified using SIMPER (PRIMER v6).

Biological Assemblage	Average % Similarity within assemblage	Top five contributing species	% Contribution of each species
II	22.29	*Abra alba* (Wood, 1802)	9.20
		Phaxas pellucidus (Pennant, 1777)	8.27
		Mysella bidentata (Montagu, 1803)	8.06
		Nemertea sp.	4.44
		Pariambus typicus (Kröyer, 1845)	3.75
II.1	31.66	*Abra nitida* (Müller, 1776)	10.99
		Nuculoma tenuis (Montagu, 1808)	6.66
		Harpinia antennaria (Meinert, 1890)	5.11
		Nucula sulcata (Bronn, 1831)	5.03
		Corbula gibba (Olivi, 1792)	4.79
II.2	30.50	*Mysella bidentata*	11.03
		Phaxas pellucidus	10.83
		Abra alba	7.37
		Nucula nitidosa (Winckworth, 1930)	5.44
		Pseudocuma longicornis (Bate, 1858)	5.03
II.3	35.83	*Abra alba*	6.67
		Nemertea sp.	6.53
		Goodallia triangularis (Montagu, 1803)	4.86
		Megamphopus cornutus (Norman, 1869)	4.76
		Nucula hanleyi (Winckworth, 1931)	4.15
II.4	38.52	*Abra alba*	10.07
		Pariambus typicus	6.45
		Mysella bidentata	5.60
		Mya truncata (Linnaeus, 1758)	4.95
		Amphipoda indet.	4.40

Table 5.6: Top four contributing species for each biological assemblage for the BIOMÔR & HABMAP data. Contributing species identified using SIMPER (PRIMER v6).

Biological Assemblage	Average % Similarity within assemblage	Top five contributing species	% Contribution of each species
C	26.40	*Goodallia triangularis*	13.55
		Spisula elliptica	9.28
		Hesionura elongate	8.66
		Mytilus edulis	4.10
D	33.22	*Aonides paucibranchiata*	3.63
		Mediomastus fragilis	3.14
		Laonice bahusiensis	2.73
		Lumbrineris gracilis	2.71
E	26.19	*Mediomastus fragilis*	5.46
		Ophiuroidea juv.	4.32
		Lagis koreni	3.49
		Spiophanes bombyx	3.03
C1	33.52	*Spisula elliptica*	7.00
		Hesionura elongate	6.86
		Aonides paucibranchiata	6.58
		Glycera lapidum	5.71
C2	34.65	*Goodallia triangularis*	28.08
		Mytilus edulis	13.09
		Spisula solida	11.76
		Spisula elliptica	8.09
D1	39.99	*Aonides paucibranchiata*	3.30
		Mediomastus fragilis	2.57
		Polycirrus sp.	2.43
		Laonice bahusiensis	2.35
D2	37.06	*Aonides paucibranchiata*	2.91
		Mediomastus fragilis	2.87
		Lumbrineris gracilis	2.43
		Ampharete lindstroem	2.33
E1	44.02	*Ophiuroidea juv.*	5.56
		Nemertea sp.	5.33
		Praxillella affinis	4.89
		Spiophanes kroyeri	4.84
E2	44.17	*Abra nitida*	5.76
		Magelona minuta	5.55
		Mediomastus fragilis	4.35
		Tubificidae sp	3.68
E4	35.52	*Spiophanes bombyx*	5.68
		Lagis koreni	5.51
		Phaxas pellucidus	4.27
		Mediomastus fragilis	3.89

5.3 *Discussion*

It is clear that biological assemblages based on abundance are not only linked to particle size but also to the chemical properties of the sediments. Median grain size only featured as a predictor in two assemblages in each dataset indicating that particle size alone is not sufficient to predict biological assemblages based on total abundance. Assemblages where environmental variables were not shown to be significant predictors of the assemblage may suffer from the fact that the forced entry method does not consider a combination of predictors.

The forced entry binary logistic procedure shows that environmental variables can be used to predict the presence and absence of macrofaunal assemblages; however, a minimum number of stations may need to be set before an assemblage can be included in the analysis. Problems can also occur if there are too many variables relative to too few outcomes for a case (Tabachnick and Fidell, 2007). There were no consistent predictors from assemblage to assemblage in either logistic regression analysis. This indicates that different sets of environmental variables are better predictors for different assemblages; therefore the set of variables cannot be reduced to one or two predictors for all assemblages.

McBreen et al. (2008) showed higher sensitivity and specificity values (using step-wise backward elimination binary logistic regression) than those found in this chapter (using forced entry binary logistic regression) (see Table 5.3, Table 5.4 and Table 5.7). More environmental variables were needed in the stepwise backward elimination binary logistic method than in the forced entry model, with often all the variables being used in the former as opposed to one or two variables in the latter (McBreen et al., 2008) (see Table 5.3, Table 5.4 and Table 5.7). Both methods have issues associated with them. Tabachnick and Fidell (2007) state that stepwise logistic regression is based only on statistical criteria, which can lead to the exclusion of predictors, which may be highly correlated with the categorical variable but can be ousted by another predictor or combination of predictors. A difficulty with forced entry binary logistic regression is that while predictors may themselves be highly correlated with the outcome they may not be great predictors in the presence of other variables (Tabachnick and Fidell, 2007).

Table 5.7: Presence and absence of biological assemblages predicted correctly from the environmental variables: depth (m), % gravel, % sand, % mud, % organic matter, % organic carbon and % calcium carbonate ($CaCo_3$), (stepwise backward elimination binary logistic regression, SPSS 12.0).

Level	No. of sites	Biological Assemblage	No. of sites	Percentage predicted correctly		Optimum variables needed
				Presence	Absence	
1	103	I	5	40.0	100.0	Depth, Sand, Organic matter, Organic carbon
		II	65	95.4.	77.8	All
		III	22	77.3	96.3	Depth, Sand, Mud
		IV	11	54.5	96.7	All
2	76	II.1	19	100.0	100.0	All
		II.2	33	75.8	91.4	Depth, Sand, Mud, $CaCo_3$, Organic matter
		II.3	5	60.0	100.0	All except mud
		II.4	8	0.0	100.0	Depth
		IV.1	5	100.0	100.0	All
		IV.2	6	100.0	33.3	Mud, $CaCo_3$
3	33	II.2.1	2	100.0	100.0	All except sand
		II.2.2	12	8.3	100.0	Depth, Sand, Mud, $CaCo_3$, Organic carbon
		II.2.3	9	100.0	100.0	All except $CaCo_3$
		II.2.4	10	50.0	100.0	All except mud

Thrush et al. (2003) used logistic regression of presence/absence data to predict the presence of species in the Schelde estuary. The ability to predict the presence of one of the species ranged from 59.4 – 81.7%. These results are more similar to the results obtained in this chapter using the forced entry method of binary logistic regression than those of McBreen et al. (2008). Unfortunately, Thrush et al. (2003) do not specify which method they use. The ability to correctly predict species in five estuaries in New Zealand ranged from 59 to 97%, with a combination of 1 to 6 variables environmental variables required (Ellis et al., 2006). Ysebaert et al. (2002) used stepwise multiple logistic regression in their analysis of species in the Schelde estuary, where sensitivities ranged from 33.3% to 85.4% and specifities ranged from 80.0% to 95.6%. Although different methods of regression analysis were used in these studies, the lowest values predicted correctly are higher than those found either in this study or in McBreen et al. (2008). This could indicate either that logistic regression is better at predicting species than biological assemblages or simply that more sites are needed in some of the biological categories before assumptions could be made as to the significance of this.

As with all analyses, the accuracy of the prediction is a function of the data available. More rigorous testing becomes possible as more information becomes available, such as the inclusion of SWISS polychaete data enabling a study of complete quantitative macrofaunal and environmental data from the BIOMÔR, SWISS and HABMAP data projects. The inclusion of hydrographical variables (e.g. seabed temperature, salinity and bed shear stress) and of macrofaunal and sediment data from similar surveys (e.g., The Outer Bristol Channel Marine Habitat Study: Mackie et al. (2006)) would increase both the sample size and the number of environmental variables of the study, enabling a better overview of the usefulness of binary logistic regression method as a tool for predicting macrofaunal assemblages. Hydrographical variables could be better predictors than sediment characteristics. However, logistic regression has the potential to be used to distinguish the presence of biotopes which may need protection as Marine Protected Areas in the southern Irish Sea. It is recommended that this approach be tested in other marine areas to see whether the general principles can apply to different zoogeographic zones. Different levels of discrimination may need to be applied to different biological assemblages depending on the number of sites, e.g. assemblage I at Level 1 and assemblage II at Level 3. This approach is similar to the EUNIS classification system where different levels from 1 to 7 are deemed appropriate for marine habitats based on the available information. It is also recommended that an attempt be made to integrate chemical variables into existing classification systems such as EUNIS.

This study is limited by the fact that the predictive model presented here could not be validated with an independent data set. Predictive models can be overestimated if they only look at the sample used to construct the model (Steyerberg et al., 2001). Methods of improving predictive analysis include data splitting, cross-validation and bootstrapping (Harrell, 2001, Steyerberg et al., 2001).

Data splitting involves randomly splitting data into a 'training' model (development) and 'testing' model (validation) (Harrell, 2001). The 'testing' data is used to validate the model's calibration and discrimination (Harrell, 2001). R^2 is compared between the training sample and the test sample and over-fitting of the model is indicated by a drop in R^2 (Harrell, 2001). The test sample should usually be at least equal to or greater than 100 in number (Harrell, 2001). In binary outcomes, there should be at east 100 occurrences of the least frequent outcome (Harrell, 2001). Once the size of the test sample is decided, the remaining portion of the original sample can be assigned to the training sample (Harrell, 2001). Data splitting reduces sample sizes for both the model development and model testing (Harrell, 2001). It requires larger sample sizes than either

cross validation or bootstrapping (Harrell, 2001). The final model is not validated as the training and test datasets are combined to produce the final model (Harrell, 2001). Data splitting need to be done initially before analysing the data (Harrell, 2001). Steyerberg et al. (2001) in their study of internal validation of predictive models found data splitting led to over pessimistic results and large variability.

Split-half cross validation is an extension of the data splitting approach (Steyerberg et al., 2001). Split-half cross validation randomly splits the data and tests one half of the data on the other half (Steyerberg et al., 2001). Other cross validation methods involve using 10% of the data to test the other 90% (Harrell, 2001). The processes are then repeated ten times (Harrell, 2001, Steyerberg et al., 2001). This process can be repeated many times to improve the stability of the cross validation, using different subsamples (Steyerberg et al., 2001). The jack-knife version of cross validation involves leaving out one of the samples (Steyerberg et al., 2001). A jack-knife removes bias of the order of 1/n from a sample population size of n (Manly, 1997).

Bootstrapping is said to be the most effective model testing procedure. It is a computer intensive technique (Harrell, 2001, Steyerberg et al., 2001). Bootstrapping is based on the idea that the distribution of values found in a random sample of a population is the best guide to the distribution of the population (Manly, 1997). The best way to resample is to resample the actual population. Resampling is done by replacement (Manly, 1997). An original object is constructed from a 'list of data'. A new list is constructed with the same number of elements from the original list by randomly picking elements from the list (any one element can be picked any number of times). A new object is computed. The process is typically repeated 100 – 1000 times (Manly, 1997). Steyerberg et al. (2001) found that bootstrapping was the best method of internal validation as split-samples were overly pessimistic, cross validation had low bias and low variability but was not always appropriate, while bootstrapping had low bias and provided stable estimates.

It is recommended that future studies which use binary logistic regression to predict habitats should adopt a model validation technique. This chapter explores the technique of using logistic regression to predict marine benthic habitats and has shown that while the method can be used with some success, further study using larger datasets is recommended to test the method further. One example of a large dataset which could be used to explore the method further would be the Marine Recorder database in the U.K. which holds thousands of biological survey records from around the U.K

Marine conservation has traditionally focused on two areas: the conservation of species and the conservation of spaces, such as marine reserves (Zacharias and Roff, 2000). Both approaches lead to the conservation of the traditional biological communities recognized by Petersen (1913), Jones (1950) and Thorson (1957). However, it is now being widely recognized that an ecosystem-based conservation approach incorporating the structure and function of habitats is needed (Olenin and Ducrotoy, 2006). Both distinctive and representative habitats need to be conserved (Roff and Evans, 2002). In order to conserve both species and spaces through enforcement and legislation, habitats and biotopes need to be mapped and identified in detail.

Little weight, if any, has traditionally been given to the structure and function of the sediment in the production of habitat and biotope maps and the designation of Marine Protected Areas (MPAs). Roff & Evans (2002) point out the need to focus on 'the relationships between the structure and function of marine entities for all levels of the ecological hierarchy from genes to ecosystems'. More weight should be given to the functional characteristics of biological assemblages such as those suggested by Thorson (1957). If biological habitat mapping uses particle size as a proxy for biological assemblages, distinct and representative habitats may be overlooked in areas designated for MPAs, especially if the MPAs are small in size. Biological marine habitat mapping can benefit from the examination of the links between biological structuring and system functioning. An ecosystem approach to marine habitat classifications incorporating physical, chemical and biological data could be used to produce more detailed habitat and biotope maps for the southern Irish Sea.

Chapter 6

6 Sediment characteristics and benthic macrofaunal biomass and productivity of the southern Irish Sea

6.1 Introduction

This chapter will test the validity of using sediment characteristics to predict benthic macrofaunal assemblages based on biomass or production, as opposed to the abundance-based macrofaunal assemblages examined in Chapter 5. As in Chapter 5, forced entry binary logistic regression will be utilized to predict the biomass and production-based benthic macrofaunal assemblages (categorical variables). However, this chapter will also explore the use of multiple regressions to test the ability of sediment characteristics to predict benthic macrofaunal biomass and production (continuous variables). Predictive maps of total benthic macrofaunal biomass and productivity maps were produced for the southern Irish Sea.

6.1.1 Energy cycles

An idealised energy flow of an ecosystem involves energy being recycled through different trophic levels (Gray and Elliott, 2009). Primary producers occur at the first trophic level where they utilise a combination of sunlight and nutrients to produce organic matter (Gray and Elliott, 2009). These are then consumed by herbivores and detritivores at the second trophic level (Gray and Elliott, 2009). The third trophic level involves the consumption of herbivores and detritivores by primary carnivores (Gray and Elliott, 2009). Decomposers will consume the remains of any animals at the previous trophic levels, recycling their nutrients back into the system (Gray and Elliott, 2009).

The energy budgets of species have been standardized by the International Biological Programme and can be divided into separate processes (Crisp, 1984, van der Meer et al., 2005, Gray and Elliott, 2009).

$C = P + R + G + U + F$

$Ab = C - F = P + R + G + U$

$A = P + R + G$

Where C = consumption, R = respiration, Ab = Absorption, G = gonad input, A = assimilation, U = urinary excretion, P = production and F = faeces. Energy budgets of organic matter, carbon or nitrogen can be constructed for individual species (Gray and Elliott, 2009).

6.1.2 Biomass & Secondary Production

Biomass has been defined as the 'amount of living substance constituting the organism under study'. Biomass is generally measured in three ways: wet weight (WW), dry weight (DW) and ash-free dry weight (AFDW) (van der Meer et al., 2005). Estimating biomass from ash-free dry weights is the preferred method (Crisp, 1984, van der Meer et al., 2005). This involves drying specimens to a constant weight at 105°C and subsequently ashing the specimens in a muffle furnace at 550°C for 2 - 3 hours (Crisp, 1984). The difference between the dry weight and the ash weight is the ash-free dry weight. Ash-free dry weights are less variable than wet and dry weights both within and between species (van der Meer et al., 2005). Measuring ash-free dry weights is the most destructive method as the specimen is completely destroyed but it is also the most accurate method for energetic and trophic studies as the weight of the organic content of a specimen can be measured as opposed to the total weight of the specimen including inorganic skeletons and shells.

Gray and Elliott (2009) define ecological functioning as 'rate processes that either affect or are inside the organisms that live in the sediment', thus primary and secondary productivity are ecological functions as they are produced by organisms living in the sediment. Primary production is defined as the production of organic matter by plants through photosynthesis (Gray and Elliott, 2009). Productivity is the rate at which the organism grows. Secondary production has been defined by McLusky and Elliott (2004) as 'that part of assimilated energy that is retained and incorporated in the biomass of the organism' (e.g. in growth). The growth refers to somatic production only and not to reproduction. As the biomass of an organism is not a sufficient indicator for the amount of food available in an ecosystem, the production of organic matter by an organism is used instead (McLusky and Elliott, 2004)

The production to biomass (P:B) ratio is often used to compare different organisms, as it gives a comparable value for the ratio of the production of an organism to its biomass over a year (Brey, 2001, McLusky and Elliott, 2004, Eleftheriou and Moore, 2005, Gray and Elliott, 2009). The P:B ratio can vary for communities of the same biomass, as smaller animals tend to have higher P:B ratios than larger animals (McLusky and Elliott, 2004). Juvenile animals tend to have higher P:B

ratios than adults which is why it is important to use mean biomass values for species which incorporate several life stages or to compare P:B ratios for animals at similar life stages (McLusky and Elliott, 2004).

There are several different methods for measuring production, these include:

- Cohort methods
- Size based methods
- Empirical methods

6.1.2.1 Cohort Methods

Cohort methods use cohorts (age classes) within populations to calculate production (Brey, 2001). There may be several cohorts within a year depending on the reproductive cycles of the animals (Brey, 2001). Cohort methods can only be used if populations have synchronised reproductive cycles and if the individual ages of all the individuals can be determined (Brey, 2001). Changes in the numbers and mass of cohorts are tracked for a period of time to calculate the production for that time (Brey, 2001).

Allen curves are used to calculate somatic production, where the integration of the area under an abundance versus mean weight curve gives the value for somatic production (Brey, 2001, Gray and Elliott, 2009). For any cohort or year class the decrease in abundance of organisms is matched by an increase in the biomass of the individuals in the year class (Gray and Elliott, 2009). The increment summation method is equivalent to the Allen curves method (Brey, 2001). Cohort methods usually over-estimate production and productivity as they use linear interpolation of the non-linear processes of growth and mortality between sampling times (Brey, 2001).

This study could not use any of the cohort methods as it was not possible to measure the age of individuals.

6.1.2.2 Size based methods

Body size is often used in energy budget studies (van der Meer et al., 2005). Body size is calculated using the length and width of individuals (van der Meer et al., 2005). Size class methods require size frequency data, average body mass per size class data and individual information on growth (Brey, 2001). Size-mass relationships are calculated either by linear regression of log(mass) versus the log(size) or by a non linear fit of the exponential function of the

original data (Brey, 2001). Average body mass is calculated using a size mass relationship (see below from Brey (2001)), where a and b are known constants.

Body Mass $M = a * \text{Body Size } S^b$

$\log(\text{Body Mass } M) = \log(a) + b * \log(\text{Body Size } S)$

Size class methods include the size frequency method and the mass specific growth rate method. The main assumption of the size frequency method is that there is linear growth in the individuals, e.g. specimens grow at the same rate in each size class (Brey, 2001). The bigger the discrepancy between the assumed linear growth and the actual growth, the larger the errors in the production calculation will be (Brey, 2001). Production based on size frequency data is calculated through elimination. The mass specific growth rate method requires representative size-frequency samples of the population, the average body mass per size class and a mass specific growth rate per size class (Brey, 2001).

This study could not use body-size methods due to unforeseen circumstances where samples were no longer available to measure the size of the specimens.

6.1.2.3 Empirical models

Empirical models are based on linear regression models related either to one or several parameters (see Table 6.1) (Brey, 2001). Initially, empirical models showed relationships between P:B and individual body mass only (Banse and Mosher, 1980, Schwinghamer et al., 1986, Edgar, 1990). Over time regression equations became more complicated and calculated the P:B using more parameters such as temperature and depth (Brey, 1990, Tumbiolo and Downing, 1994, Brey, 2001).

Seabed temperature data was not available in this study, and therefore a single parameter empirical model had to be used to calculate secondary production. The Schwinghamer (1986) model was therefore selected. Sprung (1993) criticises the methods of Banse and Mosher (1980), Schwinghamer (1986) and Brey (1990) as they use extrapolations to produce results which are not matched by reality. It is recognised by the author that these methods may have been superseded by more comprehensive models such as Brey (2001) however due to a lack of temperature data for each site, it was felt that it was not possible to use the most modern models.

Table 6.1: Productivity as a functions of biomass (B), body mass (M, kcal equivalents), temperature (T, °C) and water depth (Z, m), Subt = subtidal (yes or no), In-Epi = infauna or epifauna, MoEpi = Motile epifaunal (yes or no), Taxon 1 = annelida or crustacea, Taxon 2 = echinodermata, Taoxn 3 = Insecta, Habiata1 = Lake (yes or no).

Group	Relationship	
Bacteria	$P:B = 0.696*M^{-0.208}$	Schwinghamer et al. (1986)
Meiofauna	$P:B = 0.73 * M^{-0.337}$	Schwinghamer et al. (1986)
Macrofauna	$P:B = 0.525*M^{-0.304}$	Schwinghamer et al. (1986)
Benthic invertebrates	$P:B = 0.65*M^{-0.37}$	Banse & Mosher (1980)
Benthic invertebrates	$Log10P = -0.473 + 1.007*\log_{10}B - 0.274*\log_{10}M$	Brey (1990)
Benthic invertebrates	$P = 0.0049 * B^{0.80} T^{0.89}$	Edgar (1990)
Benthic invertebrates	$\log P = 0.24 + 0.96*\log(B) - 0.21 \log(M_{max}) + 0.03* T - 0.161og (Z+1)$	Tumbiolo & Downing (1994)
Benthic invertebrates	$LogP = 7.947 + logB - 2.294 \log(M) - 2409.856 (1/T + 273) + 0.168 (1/Z) + 0.194*Subt + 0.180$ In-Epi + 0.277 MoEpi + 0.174 Taxon1 – 0.188 Taxon2 + 0.330 Taxon 3 - 0.062*Habitat1 582.851 log(M)*(1/T + 273)	Brey (2001)

6.1.3 Ecopath

Ecopath with Ecoism models have been used to model food webs for several environments. (Bradford-Grieve et al., 2003, Harvey et al., 2003, Araújo et al., 2005, Essington, 2007, Lees and Mackinson, 2007). These require production data to model interactions between different trophic levels (UBC Fisheries Center, 2009). As this project was only assessing data at a single trophic level, it was not possible to use Ecopath with Ecoism. However outputs from this project could possibly be used in future Ecopath models of the Irish Sea.

6.1.4 Global macrofaunal benthic biomass and production

Cusson and Bourget (2005) examined global patterns of marine benthic macro-invertebrate production, using data from published studies. Higher P:B ratio values were generally found in the Northern Hemisphere, in mid-latitudinal zones and on algae (Cusson and Bourget, 2005), while higher production values were found for filter feeders and molluscs on hard substrates. Cusson and Bourget (2005) also found that while production and P:B ratios were negatively

related to water depth and positively related to water temperature, biotic variables were better at explaining variations in production and P:B ratios than environmental variables. Both life span and body mass had a negative affect on production and P:B values (Cusson and Bourget, 2005), indicating that both older and bigger individuals invest more in reproduction while smaller and younger individuals invest more in growth.

Table 6.2: Summary of P:B values for previous studies . Table adapted from Table 4 in Nilsen et al. (2006) through the addition of studies not mentioned in Nilsen et al. (2006).

Reference	Latitude	Location	P:B
Aller et al. (2002)	35°N	Cape Hatteras, USA	1.3
Wildish et al. (1986)	45°N	Bay of Fundy, Canada	0.48
Rybarczyk et al. (2003)	50°N	Bay of Somme, France	0.5 – 2.8
Warwick & Price(1975)	~50°N	Lynher estuary, GB	1.0
Warwick et al. (1979)	~50°N	Cornwall, GB	1.0
Warwick & George (1980)	~51°N	Swansea Bay, GB	1.28
Duineveld et al. (1991)	51 - 57°N	North Sea	1.9
Wolff & de Wolf, (1977)	~52°N	Grevelingen, Netherlands	2.6
Steele (1974)	52 - 62°N	North Sea	5
Asmus (1987)	~55°N	Wadden Sea	0.36
Buchanan & Warwick (1974)	~55°N	Northumberland, GB	0.44
Wilson & Parkes (1998)	53°N	Dublin Bay	0.83
Harvey et al. (2003)	55 - 60°N	Baltic Sea	0.32
Christensen (1995)	57°N	North Sea	2.0 – 3.0
McLusky & McIntyre (1988)	57°N	North Sea	0.1 – 5.0
Salvanes et al. (2003)	60°N	Masfjord, West Norway	2.6
Denisenko & Titov (2002)	68 - 78°N	Barents Sea	0.3
Denisenko (2001)	69°N	Southwestern Barents Sea	0.25
Edgar & Barrett (2002)	69°N	Tasmania	1.5 – 11
Nilsen et al. (2006)	69°N	North Norway	0.29
Warwick et al. (1978)	~ 52 °N	Carmarthen Bay, S. Wales	0.56
Thatje & Mutschke (1999)	48-56°S	Chile	0.2
Bradford-Grieve et al. (2003)	50°S	Southern Plateau, New Zealand	1.0
Brey & Gerdes (1999)	~75°S	Magellan	0.7
Brey & Gerdes (1999)	~75°S	Weddell Sea	0.3
Lees & Mackinson (2007)	51-54 °N	Irish Sea	0.70

Biomass, secondary production and P:B values have been calculated for many areas around the world. A selection of these is shown in Table 6.2. The table adapted from Nilsen et al. (2006) presents a range of global P:B values. These will be compared to the value obtained for this study. Limited food is suggested as a reason for low P:B values in high latitude areas such as North Norway and the Weddell Sea (Brey and Gerdes, 1998, Nilsen et al., 2006). Nilsen et al. (2006) points out that using P:B estimates from the North Sea for the North Norway area could severely overestimate secondary production, indicating there is no substitute for actual survey data.

6.1.5 Benthic biomass and secondary production in the North Sea

Several studies in the North Sea have examined the diversity, abundance and biomass of benthic fauna (Eleftheriou and Basford, 1989, Heip et al., 1992, Huys et al., 1992, Kuenitzer et al., 1992, Daan and Mulder, 2005). Eleftheriou & Basford (1989) found the biomass of 76 stations in the offshore northern North Sea to range from 0.13 to 18.8 g dry weight m^{-2}. Using conversion factors from McLusky & Elliott (2004), this equates to approximately 0.11 - 16.1 g AFDW m^{-2}. High biomass values were usually due to high abundances of polychaetes or bivalves (Eleftheriou and Basford, 1989), while the biomass of crustaceans was generally found to be low. The highest biomass figures were found in areas with strong currents and coarse sediments, such as the south-east of Shetland and the west of the Norwegian Trench, and in areas of fine sand, while areas of low biomass were generally found in coarser sediments off the north east of Shetland and in the shallower stations (<100m) (Eleftheriou and Basford, 1989).

Heip et al. (1992) concluded that earlier studies of biomass in the North Sea had underestimated the biomass as they had used limited data. Heip et al. (1992) sampled 175 stations in the North Sea and their results estimated the biomass of the North Sea as being twice that of previous estimates, with a total average biomass of 7g AFDW g m^{-2}. The relationship between log transformed total macrofaunal biomass and environmental variables (latitude, longitude, depth, median grain size, silt, chlorophyll a content of the sediment and particulate organic carbon content of the sediment) was explored using multiple linear regression (Heip et al., 1992). A combination of latitude, chlorophyll a content of the sediment and silt content (logged) explained the greatest amount of the variation in total biomass (Heip et al., 1992).

Clark and Frid (2001b) reviewed long term benthic datatsets for the North Sea and found major changes in the benthos. Marofaunal biomass and abundance at both littoral and sublittoral stations were higher in the 1970s than the 1980s. The change in macrofaunal biomass and abundance occurred at Northumberland between 1980 and 1981 and at Skaggerak and Balzgand stations between 1979 and 1980. Three out of five communities in the Central and southern North Sea showed definite change between the 1920s and 1980s and benthos in the Dogger Bank showed a decrease in long-lived taxa, and an increase in opportunistic species and an increase in total biomass between the 1950s and 1980s (Clark and Frid, 2001b). These changes were attributed to either increased nutrients or climate change, leading to increased amounts of plankton aggregating on the seabed and increasing food supply (Clark and Frid, 2001b). Unfortunately, similar long term dataset reviews are not available for the Irish Sea. Frid et al. (2009) studied data

from a central North Sea site of the Northumberland coast over 33 years. They concluded that while the site showed long term changes in macrofaunal abundance, it was not always linked to one factor such as climate change, temperature or food availability but that at different times, one of these factors would usually dominate (Frid et al., 2009). These studies emphasize how examining ecosystems over time can further increase our understanding of the systems. It is important to collect physical, chemical and biological data over time to better understand the dynamics of marine benthos.

6.1.6 Benthic biomass and secondary production in the Irish Sea

Hiddink (2006) used a size-based model previously designed for the North Sea (Duplisea et al., 2002, Hiddink et al., 2006) to model the benthic macrofaunal biomass, production and species richness in the Welsh Coastal zone, both with and without bottom trawling (see Figure 6.1). Hiddink (2006) used remote-sensed chlorophyll-a data to calculate an average biomass per $\log_3$ size class for areas in the study area unfished by bottom trawling. It was found that biomass, production and species richness were highest in the coastal areas, in particular in Carmarthen Bay, Cardigan Bay and Liverpool Bay (Hiddink, 2006). Hiddink (2006) states that due to the nature of the model, biomass, production and species richness were likely to correlate. Bottom trawling was found to strongly reduce benthic biomass and species richness, and to reduce benthic production to a lesser extent (Hiddink, 2006). In contrast to the North Sea model (Duplisea et al., 2002), there were no available data to validate the Irish Sea model so caution is advised in relation to the results (Hiddink, 2006). The model assumed that correlations between sediment type and benthic community biomass could be explained by the correlation of sediment type with shear stress, remote-sensed chlorophyll-a data and erosion rates (Hiddink, 2006). Limitations in the model were noted for areas with coarser sediments such as gravel (Hiddink, 2006). It is unlikely that the Hiddink model based on cholorphyll-a would be successful in subtidal areas of the southern Irish Sea, a model based on benthic organic matter concentrations and sediment type would perhaps be more logical as they reflect the amount of food and habitat actually existing at the seabed. Models will predict the highest biomass values in coastal areas if linked to chlorophyll-a concentrations as these chlorophyll-a concentrations will be naturally higher in coastal areas due to the high levels of nutrients present compared to offshore areas, the model will not necessarily reflect the reality.

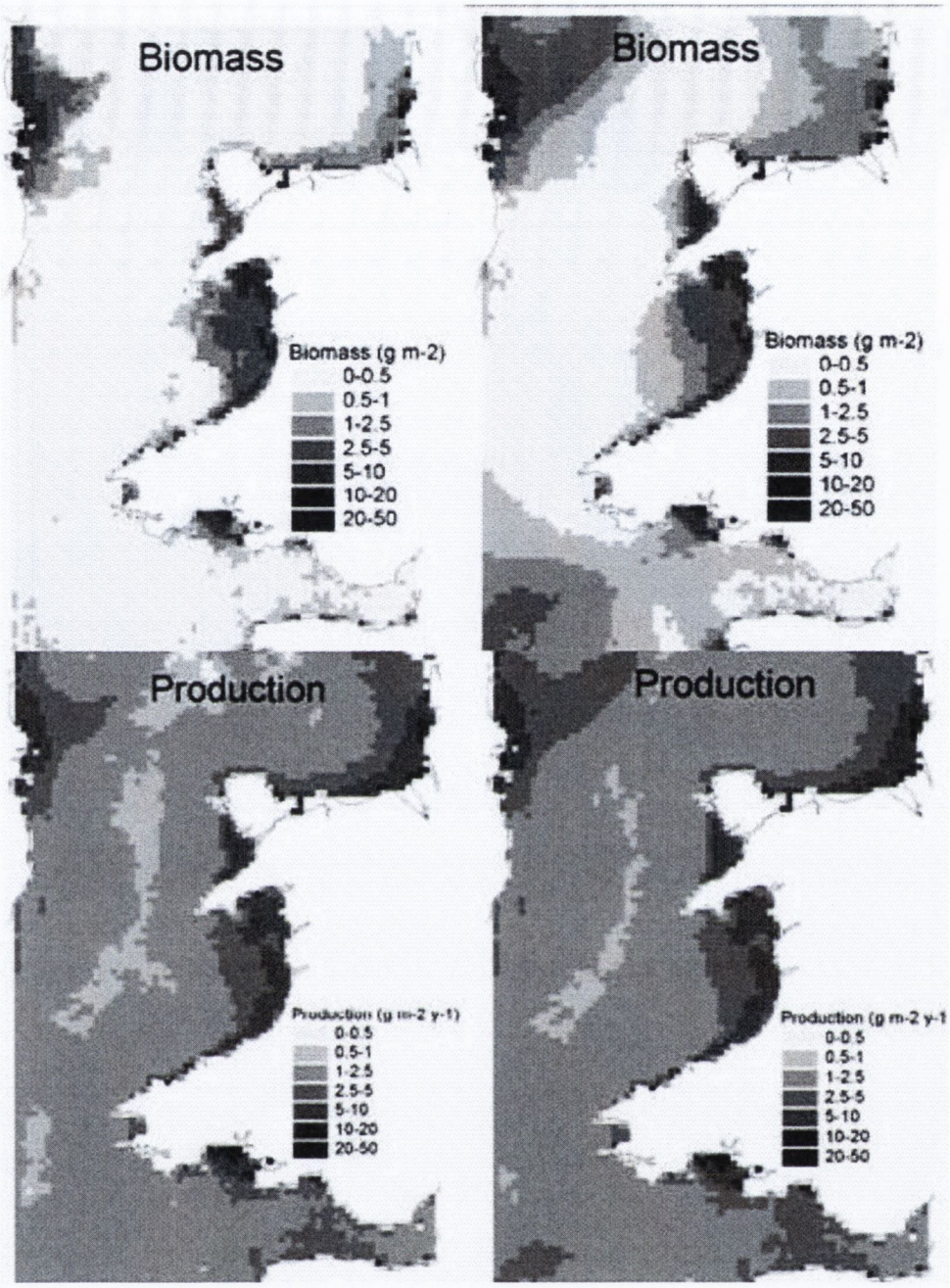


Figure 6.1: Modelled benthic macrofaunal biomass and production from remote-sensed chlorophyll-a data for the Irish Sea (Hiddink, 2006). Images on the left are modelled at current levels of bottom trawling; images on the right are modelled with no bottom trawling.

Lees & Mackinson (2007) used an Ecopath model to estimate the total biomass and food consumption in the Irish Sea in 1973. The Irish Sea Ecopath model used fifty-three functional groups, which were assigned to five groups: marine mammals and seabirds, fish, invertebrates, primary producers, bacteria and detritus (Lees and Mackinson, 2007). Ecopath models use data from literature, stock assessments and ecological studies (Lees and Mackinson, 2007). The model requires several parameters: diet composition, fishery landings and discards (categorized by gear type), and three of the following four parameters for each group in the model: biomass,

production to biomass ratio (P:B) or mortality rate, consumption to biomass ratio and ecotrophic efficiency (Lees and Mackinson, 2007). An emphasis was placed on commercially valuable species. Epifaunal and infaunal macro and mesobenthic data were calculated using data from CEFAS 2003 beam trawl survey (Kaiser et al., 1994, Lees and Mackinson, 2007) (see Table 6.3). Infaunal macrobenthos were found to have a P:B of 0.695 and an average biomass of 0.111 g wet weight m^{-2} (Lees and Mackinson, 2007). Wet weights (WW) from Lees and Mackinson (2007) were converted into dry weights (DW) using a conversions factor of 0.2. (Thorson, 1957, Wilson and Parkes, 1998), and from DW to ash-free dry weights (AFDW) using conversion factors from McLusky and Elliot (2004). This led to an average value of 0.019 AFDW g m^{-2} for infaunal macrobenthos in the southern Irish Sea.

Table 6.3: Biomass and P:B estimates for invertebrate groups for the 1973 Ecopath model of the Irish Sea (Lees and Mackinson, 2007). Wet Weights were converted to Ash-Free-Dry Weights using conversion factors from McLusky & Elliott (2004).

Functional Group	P:B yr^{-1}	Average Biomass Wet weight (g m^{-2})	Average Biomass AFDW (g m^{-2})
Epifaunal macrobenthos	0.561	9.8103	1.682
Epifauna mesobenthos	1.062	0.6918	0.119
Infauna (polychaetes)	1.683	0.000006	0.0000010
Infaunal macrobenthos	0.695	0.111	0.0190
Infaunal mesobenthos	1.552	0.0605	0.0104
Lobster & large crab	0.783	0.0943	0.0161
Nephrops	No value	0.203	0.0348
Cephalopods	No value	0.1666	0.0286
Prawn & shrimp	0.959	0.0335	0.0057
Sessile epifaunal	0.066	13.944	2.390

The Ecopath model calculated a net system productivity of 6,945 tonnes km^{-2} and a total primary production to biomass ratio (PP:B) of 33.71 for the Irish Sea (Lees and Mackinson, 2007). The total PP:B was slightly higher than that of the English Channel (31.11) (Stanford and Pitcher, 2000) and substantially higher than that of the Western Channel (15.02) (Araújo et al., 2005) and the North Sea (3.82) (Mackinson and Daskalov, 2007). The Lees and Mackinson (2007) report notes however that caution is advised when comparing models as the ecosystems are sensitive to differences in how the models were specified. Quantitative grab sampling would more accurately calculate infaunal biomass values than qualitative beam trawling methods.

It has been found that fishing reduces both benthic macrofaunal abundance and biomass in the Irish Sea (Kaiser and Spencer, 1996, Hiddink et al., 2006). Kaiser et al. (2000) found that the structure of two soft-sediment biological assemblages and habitats were significantly changed by

chronic bottom fishing (towed nets and dredges). Biomass abundance curves indicated that repeated bottom fishing removed larger bodied fauna, leading over-fished areas to be dominated by smaller fauna which may be less vulnerable to disturbance (Kaiser et al., 2000). The Irish Sea supports less fishing than the North Sea as fish yields are lower, thus leading to fewer disturbances by fishing vessels in the Irish Sea (Brander and Dickson, 1984, Kaiser et al., 1996). Many of the areas fished heavily in the Irish Sea are in areas adapted to regular natural disturbances; therefore these habitats are less disturbed by over-fishing (Kaiser et al., 1996).

6.1.7 Aims

The aim of this chapter is to test the relationship between the ecosystem functions of benthic macrofaunal biomass, productivity, depth and sediment characteristics. This will be tested using binary logistic regression and multiple regressions. Total benthic biomass and production maps for the southern Irish Sea are produced using BIOMÔR, SWISS and HABMAP biological data provided by the National Museum of Wales (Mackie et al., 1995a, Wilson et al., 2001, Robinson et al., 2007) An overall benthic macrofaunal P:B value for the southern Irish Sea is calculated and compared to those from other areas.

6.2 *Methods*

Macrofaunal data from the BIOMÔR (Mackie et al., 1995a), SWISS (Wilson et al., 2001) and HABMAP (Robinson et al., 2007) projects were used to produce both total biomass and production maps for the southern Irish Sea. Southern Irish Sea macrofaunal samples for biomass analysis were taken on board the second HABMAP cruise (25th July to the 08th August 2005) and the inaugural 'Bright Sparks' cruise awarded to postgraduate students by the Marine Institute (9th -13th September 2006) (van Landeghem and Wheeler, 2006). Due to unforeseen circumstances, it was only possible to obtain ash-free dry weight values for two species (*Modiolus modiolus* and *Glycymeris glycymeris)* from the samples taken from the Irish Sea for the final dataset. Biomass values for other species were obtained from the literature (see Table 6.5). If biomass data could not be obtained for a species, an average value for the phylum was used instead. No conversion factors or ash-free dry weight values were available for the phylum Chelicerata (one species: *Achelia echinata*) or the phylum Chordata (one species: *Dendrodoa grossularia*), therefore these two species were eliminated from the analysis.

6.2.1 Field work

Van Veen grab sampling procedures in the southern Irish Sea used by the BIOMOR, SWISS and HABMAP projects to estimate macrofaunal abundance are outlined in Chapter 3. Samples taken solely for biomass on the HABMAP cruise were taken with a Van Veen grab sampler. They were preserved in 10% formaldehyde and Rose Bengal. Calcium carbonate chips were added to the samples as a buffering agent.

6.2.2 Laboratory work

Modiolus modiolus and *Glycymeris glycymeris* individuals were identified, blotted and then weighed in pre-weighed crucibles to obtain the wet weight (WW). The specimens were dried overnight at 105°C to obtain the dry weight (DW). Once the DW was obtained the macrofauna was combusted at 550°C in a muffle furnace for three hours. The ash-free dry weight (AFDW) was obtained by subtracting the ash weight from the DW and biomass was expressed in g AFDW m^2.

6.2.3 Data analysis

All data obtained from the literature, both WW and DW, were converted into AFDW using the conversion factors for the appropriate classes from Ricciardi & Bourget (1998) (see Table 6.4 and Table 6.5). Conversion factors for individual species were not available. Riccardi and Bourget (1998) studied unpublished and published data to produce general conversion factors (e.g. WW to DW or shell-free dry weight (SFDW) to AFDW) for twenty-eight taxonomic groups for marine benthic invertebrates (see Table 6.4 for conversions used). Dry weight data for molluscs and echinoderms were only used if the shell had been first removed from the specimens before combustion. AFDWs were used to produce biomass values in AFDW g m^2 for individual sites.

Table 6.4: Conversion factors (mean %) applied to literature data. Table adapted from Table 1, Riccardi & Bourget (1998) to show conversion factors for the relevant classes only. WW = wet weight, DW = dry weight, AFDW = ash-free dry weight and SFDW = shell-free dry weight.

	AFDW/WW	AFDW/DW	AFDW/SFDW
Annelid			
• Oligochaetea		32.3	
• Polychaeta	16.0	75.7	
Mollusca			
• Gastropoda			
Prosobranchia	7.5		82.6
• Bivalvia	5.8		82.7
Crustacea			
• Amphipoda	16.0	72.9	
• Isopoda	14.2	63.0	
• Decapoda	16.5	66.9	
• Mysidacea	15.5	82.4	
• Cumacea	7.6	61.1	
• Cirripedia	3.9	78.4	
Echinodermata			
• Ophiuroidea	7.4		22.9
• Echinoidea	3.5		
• Holothuroidea	10.9	49.6	

Before the calculation of biomass values, species which represented more than 4% of the abundance at any individual site were kept in the analyses while those that did not represent more than 4% abundance at any site were eliminated from the dataset using PRIMER v.6 (Clarke and Warwick, 2001). This reduced the overall number of species at the 160 stations from 1170 to 229 (see Table 6.6 for breakdown). No conversion factors or ash-free dry weight values were available for the phylum Chelicerata (one species: *Achelia echinata*) or the phylum Chordata (one species: *Dendrodoa grossularia*), and thus these species were also eliminated from the analysis.

Table 6.5: Sources of biomass data for conversion into Ash-Free Dry weight values (g).

Reference	No. of taxa	Original type of data	Location
Collie et al. (1997)	8	Wet weight	NW Atlantic
Rosenberg (1995)	5	Wet weight	Skagerrak. Sweden
Kröncke (1998)	3	Wet weight	Amundsen Basin
Bech et al. (2004)	21	Wet weight	North Sea
Kamp & Witte (2005)	3	Wet weight	North Sea
Sanders (1960)	3	Dry weight	Buzzards Bay, US
Martínez et al. (unknown date)	105	Dry weight	Guipuzcoa, Spain
Martínez et al. (2006)	84	Dry weight	Basque region, Spain
Ibanez & Dauvin (1988)	7	Dry weight	Western English Channel
Kaiser & Spence (2002)	5	Dry weight	English Channel
Sømod (2001)	16	Dry weight	Mariager Fjord, Denmark
Buchanan & Warwick (1974)	15	AFDW	Northumberland Coast
Warwick et al. (1978)	13	AFDW	Carmarthen Bay, S. Wales
Brey (1990)	5	AFDW	
Daan & Mulder (2005)	60	AFDW	North Sea
Dauwe et al. (1998)	11	AFDW	North Sea
Zettler (2000)	18	AFDW	Western Baltic Sea
Herrmann (2004)	4	AFDW	Spitsbergen

Table 6.6: Breakdown of taxa with abundance greater than 4% broken down by phylum.

Phylum	Total no. of taxa	No. of taxa using data from literature	No. of taxa using average values	Average values used (g AFDW)
Annelida	91	61	30	0.0028
Chelicerata	1	Omitted	-	-
Chordata	1	Omitted	-	-
Crustacea	63	44	19	0.0097
Echinodermata	15	8	7	0.0059
Mollusca	56	34	22	0.0304
Nemertea	1	1	-	-
Phoronis sp.	1	1	-	-

The P:B ratio was calculated using the following formula from Schwinghammer et al. (1986):

$$P:B = aW^{b}$$

where W is the mean individual body mass in kcal, a is 0.525, b is -0.304, P is productivity and B is biomass. Conversion factors to convert from g AFDW to kilocalories were taken from McLusky and Elliot (2004). Data were derived from species counts. The individual P:B value was calculated for each individual species before factoring in abundance values for each species at each site.

6.2.3.1 Mapping

Maps were produced using point data from the BIOMÔR, SWISS and HABMAP projects to produce contour maps of total benthic macrofaunal biomass and productivity for the study area (ArcView 3.2 and ArcMap 9.1) using the inverse distance weighting (IDW) and nearest neighbour options. In all of the maps, the values were classified into eight categories of equal size, as artificially changing the classifications on the maps into different categories could lead to changes in patterns observed.

6.2.3.2 Total benthic macrofaunal P:B

A total benthic macrofaunal P:B value was calculated for the southern Irish Sea. The areas of Folk sediment categories for the Irish Sea were calculated in ArcGIS using the map of Irish Sea sediments shown in Figure 1.12. The map was projected in the WGS84 UTM 30N coordinate system to enable areas to be calculated in m^2. Figure 1.12 provides more detailed sediment categories than the Folk sediment classification, so sediment categories were converted into Folk categories where possible, e.g. mixtures such as Mimsg became msG and categories such as cobbles (C) and pebbles (P) were reclassified into the gravel category.

The total biomass (B) in AFDW g m^{-2} and productivity (P) in AFDW g m^{-2} yr^{-1} values for the Folk sediment categories in the Irish Sea were calculated using the following formula:

$$\textbf{Average B or P per Folk Category} \times \frac{\textbf{Total area of Folk category}}{\textbf{Total area of the southern Irish Sea}}$$

6.2.4 Statistical analysis

6.2.4.1 Multiple regression

Standard multiple logistic regression (SPSS 15.0.1) was used to predict both total benthic macrofaunal biomass and total benthic macrofaunal productivity from environmental variables. Data were checked for outliers, multicolinearity, normality, linearity, homoscedasticity, independence and singularity. The environmental variables were selected if they had a correlation greater than 0.3 with the dependent variable, and a correlation of less than 0.7 with the other variables chosen (Pallant, 2007).

6.2.4.2 Logistic regression

The benthic macrofaunal biomass and productivity data for all sites were analyzed using cluster analysis and the SIMPER routine in PRIMER v.6 (Clarke, 1993). Species biomass and production data were log (x+1) transformed before constructing a Bray-Curtis similarity matrix. A dendrogram, which grouped individual sites based on their similarities and group average clustering, was created from the similarity matrix. Biological assemblages were then identified from groupings of sites at three different levels of similarity, the first level depicting the main groups and the second level showing the breakdown of these main groups into smaller clusters. Assemblages at greater similarities were not examined as the number of sites per assemblage was deemed to be too low. The levels of similarity used were determined from the cluster analysis (Clarke and Warwick, 2001). A one-way SIMPER test in PRIMER v.6 was used to distinguish the species which had the greatest effect on the assemblages identified in the dendrogram.

Forced-entry binary logistic regression (SPSS 15.0.1) was used to predict the presence or absence of a categorical biological variable from a number of continuous environmental variables. The same procedures as used in Chapter 5 were followed. Quantitative environmental, biomass and productivity data from the HABMAP and BIOMÔR projects were analyzed. SWISS data could not be included as individual species biomass and productivity values were not available for annelids. The environmental variables to be used in the analysis were selected after examining the multicolinearity of the following variables: depth, longitude, latitude, mean grain size, median grain size, sorting, skewness, kurtosis, gravel, sand, mud, organic content, organic carbon and calcium carbonate concentrations (McBreen et al., 2008). Any outliers were eliminated from the analysis after examining Mahalanobis and Cook's distance (Pallant, 2007). The biomass-based biological assemblages designated from the cluster analysis were used as the categorical variables.

As with Chapter 5, forced entry binary logistic regression was adopted in the analysis to test the ability of the sediment characteristics to predict benthic macrofaunal total biomass and production in the southern Irish Sea. Data from the BIOMÔR, SWISS and HABMAP were used (Mackie et al., 1995a, Wilson et al., 2001, Robinson et al., 2007). Forced-entry was chosen as Tabachnick & Fidell (2007) recommend using it instead of sequential logistic regression if there is no hypothesis regarding the order or importance of the predictors.

The Omnibus Tests of Model Coefficients give an overall indication of how the binary logistic model performs (Pallant, 2007). These coefficients were firstly examined to ensure that the significance levels were < 0.05. The Hosmer and Lemeshow Test was then used to test the

goodness of fit of the model. Significance levels for the Hosmer and Lemeshow Test > 0.05 indicate that the model is worthwhile (Pallant, 2007). The Cox and Snell R Square and Nagelkerke R Square values indicate the amount of variance explained by the model (Pallant, 2007). Environmental variables are considered to contribute significantly to the model if the significance level for the Wald statistic is 0.05.

6.3 *Results*

As there were no annelid data available for the SWISS project, annelid data were thus extrapolated for the SWISS project using the geometric means of annelid data per Folk category from the BIOMÔR and HABMAP data. The geometric means are shown in Table 6.7.

Table 6.7: Mean values for annelid biomass (AFDW g m^{-2}) and productivity (g m^{-2} yr^{-1}) per Folk category (BIOMÔR and HABMAP projects). N = the number of sample stations.

Folk		Biomass AFDWg m^{-2}	Production AFDW g m^{-2} yr^{-1}
(g)mS	N	5	5
	Mean	15.84	12.59
(g)S	N	7	6
	Mean	4.58	3.03
gmS	N	4	4
	Mean	7.67	6.14
gS	N	16	17
	Mean	4.72	3.15
mS	N	14	14
	Mean	5.31	1.00
msG	N	2	2
	Mean	18.87	18.46
S	N	19	19
	Mean	8.02	6.33
sG	N	26	26
	Mean	7.85	5.97
sM	N	8	8
	Mean	5.39	3.88

6.3.1 Mapping

6.3.1.1 Biomass

The ash-free dry weight values (AFDW g m^{-2}) used for each species are shown in Appendix 4, Table 1 and total biomass values for each station are shown in Appendix 4, Table 2. Data was derived from species counts at each site.

Table 6.8: Geometric mean values for total biomass (g m^{-2}) and productivity (g m^{-2} yr^{-1}) per Folk category (BIOMÔR, SWISS & HABMAP). N = the number of sample stations.

Folk		Biomass AFDWg m^{-2}	Production AFDW g m^{-2} yr^{-1}
(g)S	Mean	69.61	22.66
	N	7	7
	Minimum	11.88	6.60
	Maximum	258.56	81.36
	Std. Error of Mean	32.61	9.95
(g)mS	Mean	105.81	55.95
	N	5	5
	Minimum	50.63	32.87
	Maximum	179.43	102.56
	Std. Error of Mean	21.48	12.32
S	Mean	110.80	37.55
	N	51	51
	Minimum	1.94	1.47
	Maximum	1016.95	198.81
	Std. Error of Mean	24.32	5.09
gS	Mean	498.09	73.35
	N	24	24
	Minimum	9.17	5.40
	Maximum	3064.57	372.18
	Std. Error of Mean	150.02	17.61
gmS	Mean	335.97	53.48
	N	5	5
	Minimum	10.60	7.39
	Maximum	908.11	116.67
	Std. Error of Mean	189.90	21.93
mS	Mean	80.11	29.60
	N	22	22
	Minimum	7.57	5.27
	Maximum	583.56	159.68
	Std. Error of Mean	29.65	7.26
msG	Mean	1818.34	243.63
	N	2	2
	Minimum	614.88	107.29
	Maximum	3021.80	379.96
	Std. Error of Mean	1203.46	136.33
sG	Mean	773.79	109.03
	N	29	29
	Minimum	27.77	7.90
	Maximum	5220.75	622.78
	Std. Error of Mean	233.57	27.50
sM	Mean	20.81	12.16
	N	9	9
	Minimum	6.99	4.75
	Maximum	61.09	29.76
	Std. Error of Mean	7.05	3.43

A total benthic macrofaunal biomass (including the extrapolated annelid values) map for the southern Irish Sea is shown in Figure 6.2, while Figure 6.3 shows a similar map showing the total macrofaunal biomass, excluding annelids, for the southern Irish Sea. Figure 6.2 and Figure 6.3 are almost identical, thus indicating that the inclusion of the extrapolated SWISS annelid data did not affect the pattern of biomass values.

Biomass values for Folk categories ranged from 20.81 AFDW g m^{-2} for 'slightly gravelly muddy sand' to 1818.34 AFDW g m^{-2} for 'muddy sandy gravels'. 'Sandy gravels' had the second highest biomass (773.79 AFDW g m^{-2}) (see Table 6.8). 'Slightly gravelly sands' and 'muddy sand' also had low biomass values with 69.61 AFDW g m^{-2} and 80.11 AFDW g m^{-2} respectively (see Table 6.8).

6.3.1.2 Productivity

The productivity values (AFDW g m^{-2} yr^{-1}) used for each species are shown in Appendix 4, Table 1 and total productivity values for each station are shown in Appendix 4, Table 2.

A total benthic macrofaunal productivity map is shown in Figure 6.4. This map was also compared to a total productivity map which excluded annelids (see Figure 6.5). As with the biomass maps, the same general patterns could be observed within both productivity maps indicating that the inclusion of the extrapolated SWISS annelid data did not substantially affect the total productivity patterns.

Productivity values per Folk category ranged from 12.16 AFDW g m^{-2} yr^{-1} for 'sandy muds' to 243.63 AFDW g m^{-2} yr^{-1} for 'muddy sandy gravels'. 'Sandy gravels' were the second most productive sediment type (109.03 AFDW g m^{-2} yr^{-1}) (see Table 6.8). 'Slightly gravelly sands' and 'muddy sand' also had low productivity values with 22.66 AFDWg m^{-2} yr^{-1} and 29.60 AFDWg m^{-2} yr^{-1} respectively (see Table 6.8).

Both the biomass and productivity maps show the same patterns, with two areas of high productivity, one to the northwest of the coast of Anglesey and Caernarfon Bay, on the Welsh coast, and one to the southeast between Carnsore Point on the Irish coast and St. David's Head in Pembrokeshire, on the Welsh coast.

The 'muddy sandy gravel' category contains only two stations, H32 and H35, both of which were in Caernarfon Bay and had high abundances of *Modiolus modiolus* with 320 m^{-2} and 1760 m^{-2} and high biomasses *M. modiolus* of 537.95 g AFDW m^{-2} and 2958.72 g AFDW m^{-2} respectively. *M.*

modiolus, was found in this study to have the lowest P:B ratios (0.1150) of all species (see Appendix 1, Table 1), leading to high biomass values but relatively low production values for the 'muddy sandy gravels'. A low P:B would be expected for *M. modiolus* as it is a large animal, and smaller animals tend to have higher P:B ratios (McLusky and Elliott, 2004).

The 'sandy gravels' had the second highest total benthic macrofaunal biomass and productivity values and also included many stations with high *M. modiolus* biomass values, eg. B2 (5076.89 g AFDW m^{-2}), B15 (4774.30 g AFDW m^{-2}), H36 (1395.51 g AFDW m^{-2}), B17 (1260.82 g AFDW m^{-2}) and S133 (1244.01 g AFDW m^{-2}). The species with the second lowest P:B (0.1430), *Glycymeris glycymeris*, also had the majority of its highest biomass values at 'sandy gravel' stations. The highest was at station H59 (639.64 g AFDW m^{-2}), followed by stations H33 (221.41 g AFDW m^{-2}), B15 (172.21 g AFDW m^{-2}), and H58 (139.41 g AFDW m^{-2}).

Table 6.9: Biomass, productivity and P:Bs for selected species in the study.

Species	Phylum	Biomass G AFDW m^2	Productivity g AFDW m^2 yr^{-1}	P:B
Modiolus modiolus	Mollusca	0.0006	0.0001	0.115
Glycymeris glycymeris	Mollusca	0.0002	0.00004	0.143
Mytilus edulis	Mollusca	0.1749	0.0629	0.3593
Mya truncata	Mollusca	0.0015	0.0005	0.3622
Turritella communis	Mollusca	0.0004	0.0001	0.3885
Amphiura filiformis	Echinodermata	0.0097	0.004	0.4146
Lumbrineris scopa	Annelida	0.0097	0.0043	0.4445
Nephtys incisa	Annelida	0.0003	0.0002	0.498
Abra alba	Mollusca	0.0002	0.0001	0.6981
Abra nitida	Mollusca	0.0023	0.0017	0.7444
Levinsenia sp.	Annelida	0.0304	0.0244	0.8048

In contrast, the 'sandy mud' sediment category had the lowest total benthic macrofaunal biomass. The biomass of stations H40, H41 and H42 in the Celtic Deep were all dominated by *Abra nitida* (1.59 g AFDW m^{-2}, 2.27 g AFDW m^{-2} and 1.41 g AFDW m^{-2}) and *Nephtys incisa* (1.08 g AFDW m^{-2}, 3.52 g AFDW m^{-2} and 2.03 g AFDW m^{-2}). Stations B7 and B8 were dominated by *Lumbrineris scopa* (2.36 g AFDW m^{-2} and 2.76 g AFDW m^{-2}), B10 by *Abra alba* (11.19 g AFDW m^{-2}) and *Lumbrineris scopa* (2.17 g AFDW m^{-2}), B29 by *Mytilus edulis* (16.65 g AFDW m^{-2}) and *Mya truncata* (11.58 g AFDW m^{-2}), B61 by *Levinsenia* sp. (2.57 g AFDW m^{-2}) and *Lumbrineris scopa* (2.36 g AFDW m^{-2}) and S127 by *Turritella communis* (34.32 g AFDW m^{-2}) and *Amphiura filiformis* (13.86 g AFDW m^{-2}). Clearly the species which dominated the biomass of these 'sandy mud' stations had a much lower

overall biomass than those dominated by *M. modiolus* and *G. glycyermis*. All these species had, however, much higher P:B values than *Modiolus modiolus* and *G. glycymeris* (see Table 6.9), resulting in the 'sandy mud' category having the highest P:B value of 0.58.

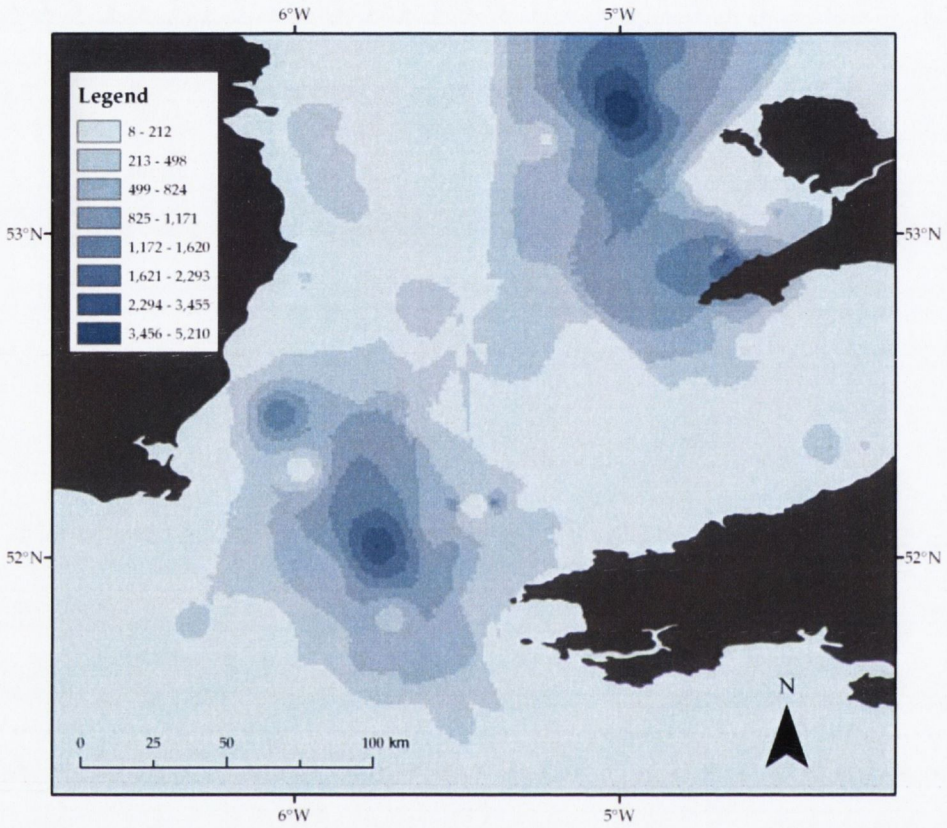


Figure 6.2: Total benthic macrofaunal biomass (g AFDW m^{-2}) for the Southern Irish Sea, based on BIOMÔR, SWISS and HABMAP data.

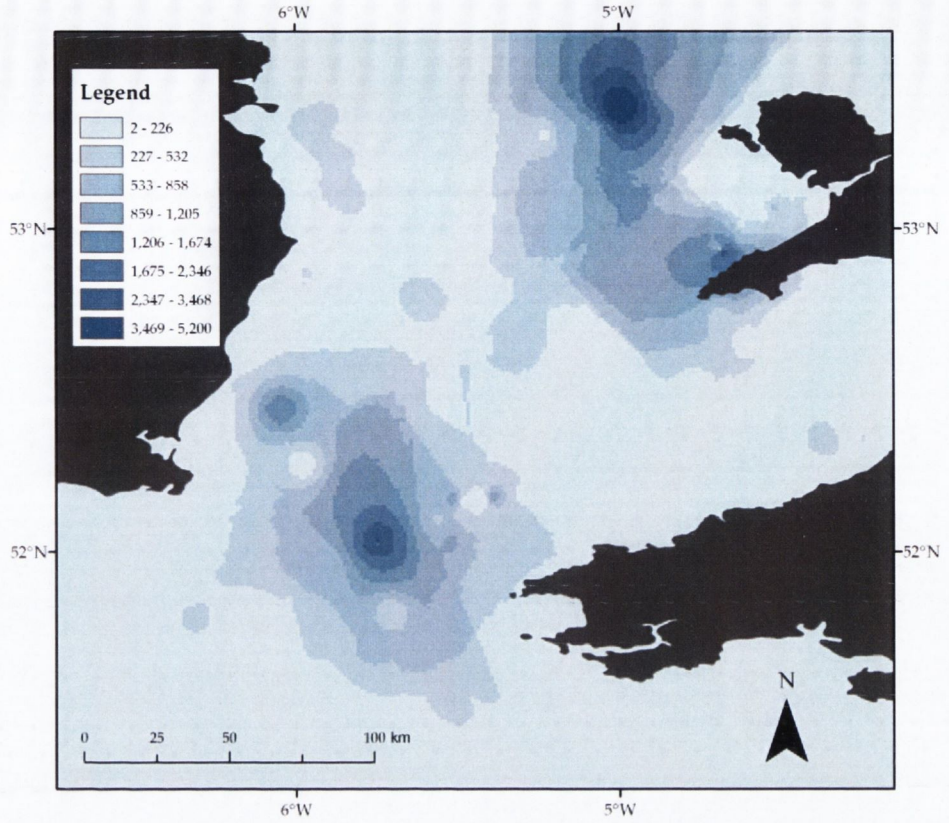


Figure 6.3: Total benthic macrofaunal biomass (minus annelid data (g AFDW m^{-2}) for the Southern Irish Sea, based on BIOMÔR, SWISS and HABMAP data.

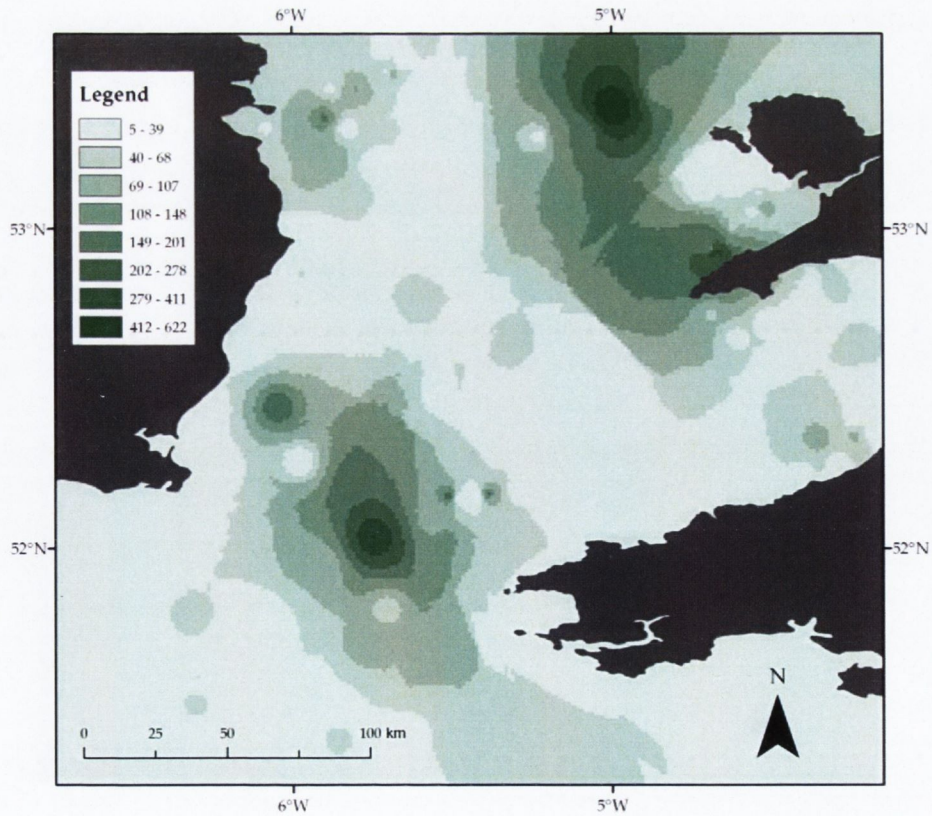


Figure 6.4: Total benthic macrofaunal productivity (g AFDW m^{-2} yr^{-1}) for the Southern Irish Sea, based on BIOMÔR, SWISS and HABMAP data.

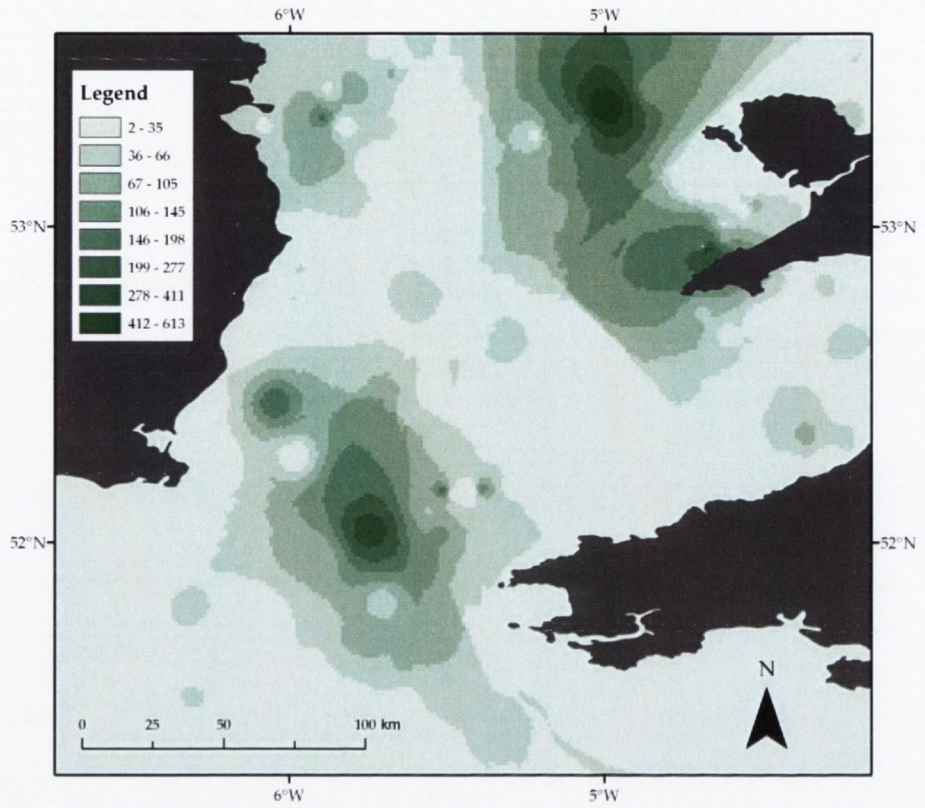


Figure 6.5: Total benthic macrofaunal productivity (minus annelid data) (g AFDW $m^{-2} yr^{-1}$) for the Southern Irish Sea, based on BIOMÔR, SWISS and HABMAP data.

6.3.2 Benthic macrofaunal P:B

Table 6.10 shows the nine Folk categories for which biomass and production data were available. These made up 89.4% of the total sediments in the southern Irish Sea. Categories for which biomass and production data were not available (or those that could not be converted into Folk categories) made up the remaining 6.2% of the total area of sediments in the Irish Sea (see Table 6.11). The remainder of the area was comprised three categories; 'intertidal', 'island' and 'rock'. The most substantial of these unavailable categories for which there was no biomass or production data were the gravel (G) and mixture (Mi) categories at 3.0% and 2.4% of the total area respectively. The rest of the categories each constituted less than 1% of the total sediments of the southern Irish Sea.

Table 6.10: Area (km²) of sediment Folk categories available for biomass and productivity analysis

Folk	Area (km²)	Area (% of total)
(g)mS	230	0.54
(g)S	3,712	8.71
gmS	378	0.89
gS	6,739	15.81
mS	2,145	5.03
msG	563	1.32
S	11,247	26.38
sG	12,005	28.16
sM	1,105	2.59
Total	**38,124**	**89.4**

Table 6.11: Area (km²) of sediment Folk categories unavailable for biomass and productivity analysis. Mi = mixture, Mimshell = mixture of mud & shell. Mishell = mixture of shell.

Folk	Area (km²)	Area (% of total)
(g)sM	27	0.063
G	1,257	3.004
gM	8	0.020
M	259	0.619
mG	26	0.063
mgS	2	0.004
Mi	1,005	2.402
Mimshell	2	0.004
Mishell	8	0.018
(g)M	5	0.001
Total	**2,599**	**6.2**

Table 6.12 shows the P:B value for each Folk category used in the analysis. Total biomass and productivity values for the Irish Sea of 370.89 AFDW g m^{-2} and 61.10 AFDW g m^{-2} yr^{-1} respectively were obtained. P:B values ranged from 0.13 for 'muddy sandy gravel' to 0.58 for 'sandy mud' for the various Folk categories. An overall benthic macrofaunal P:B of 0.165 was obtained for the southern Irish Sea as a whole.

As with biomass and productivity, P:B values for individual species are shown in Appendix 4, Table 1.

Table 6.12: Mean Irish Sea biomass, productivity and P:B values per Folk category

Folk	Biomass AFDWg m^{-2}	Productivity AFDW g m^{-2} yr^{-1}	Irish Sea P:B
(g)mS	0.58	0.31	0.53
(g)S	6.18	2.01	0.33
gmS	3.04	0.48	0.16
gS	80.22	11.81	0.15
mS	4.11	1.52	0.37
msG	24.45	3.28	0.13
S	29.78	10.09	0.34
sG	221.99	31.28	0.14
sM	0.55	0.32	0.58
Total	**370.89**	**61.10**	**0.165**

6.3.3 Multiple regression

For both biomass and secondary production analyses, percentage gravel, mean grain size and sorting were the only independent variables that had a correlation greater than 0.3 with the dependent variable. Percentage gravel correlated too highly with both mean grain size (0.904) and sorting (0.772) and was therefore eliminated from the analysis. Both dependent variables were log transformed before analysis.

6.3.3.1 Biomass

The biomass model incorporated data from 156 stations in the southern Irish Sea. Mean grain size and sorting together explained 29.5% of the variance in the biomass model ($p < 0.005$). Mean grain size and sorting both made a unique statistically significant contribution to the model (-0.419, $p < 0.005$; 0.180, $p = 0.031$ respectively). Mean grain size was found to decrease while total biomass increased and sorting increased when total biomass increased. Mean grain size was uniquely responsible for 11.77% of the variance in the model, while sorting was only uniquely responsible for 2.16% of the variance.

6.3.3.2 Production

The productivity model incorporated data from 156 stations in the southern Irish Sea. Mean grain size and sorting together explained 32.6% of the variance in the productivity model ($p < 0.005$). In this case, only mean grain size made a unique statistically significant contribution to the model (-

0.525, p <0.005) while sorting did not uniquely contribute to the model (0.075, p = 0.359). As with the biomass multiple regression, mean grain size was found to decrease while total productivity increased. Mean grain size was uniquely responsible for 18.49% of the variance in the model, while sorting was only uniquely responsible for 0.37% of the variance.

6.3.4 Binary logistic regression analysis

Forced-entry binary logistic regression (BLR) was used to test to what extent biological assemblages could be correctly predicted from the environmental variables: depth (m), organic content (%), organic carbon (%), calcium carbonate (%), median grain size, sorting and kurtosis. These variables were chosen as they showed no multicollinearity with each other, as they all had Pearson product correlations of less than 0.7 for both data sets. Outliers were also eliminated where Mahalanobis values were greater than the critical value of 26.125 ($p<0.001$) and Cook's distances were less than 1.0 (Pallant, 2007, Tabachnick and Fidell, 2007). This resulted in the deletion of stations B38, H25, H33 and H83C from the BIOMÔR and HABMAP datasets.

6.3.4.1 Biomass

From the dendrogram (see Figure 6.6) assemblages were identified at different levels of similarity: level 1 at 12% similarity (A, B, and C), level 2 at 18% similarity (e.g. A1, A2, B1 and B2), level 3 at 22% (e.g. A1.1, A1.2, B1.1, B1.2, B2.1 and B2.2) and level 4 at 30% (e.g. A1.1.1 and A1.1.2) (see Figure 6.6).

Predictions could not be made for assemblages A and B1.2 as the Homer and Lemeshow significance was less than 0.05 (see Table 6.13). Although assemblage B appeared to meet the requirements for the model, no variables were found to be significant. At level 2, all the binary logistic regression models were significant. Sensitivity was lowest for assemblage A2 at 50%, however this was probably due to the low number of sites (8). Specificity was high for each assemblage ranging from 87.7% at assemblage A1 to 98.9% at assemblage B1.1. From the Cox & Snell R Square and Nagelkerke R Square values we can see that predictions for assemblages A2 (20.4% - 47.4%) and B1.1 (13.7% - 27.3%) explained the lowest ranges of variation in the dependent variables. Predictions for assemblage B2 explained the most amount of variation in the dependent variable (50.9% - 80.3%). Depth, organic matter, and sorting were the most common variables in the prediction of assemblages.

The environmental variables appeared to poorly predict assemblages at level 3 and while 2 assemblages were explained well at level 4. Only assemblage A1.1 was predicted well at level 3, most likely due to the high number of sites (40). The decision on which level to stop at depends on the data and expert judgement. In this case, stopping at level two would be recommended until more stations could be incorporated into the analysis.

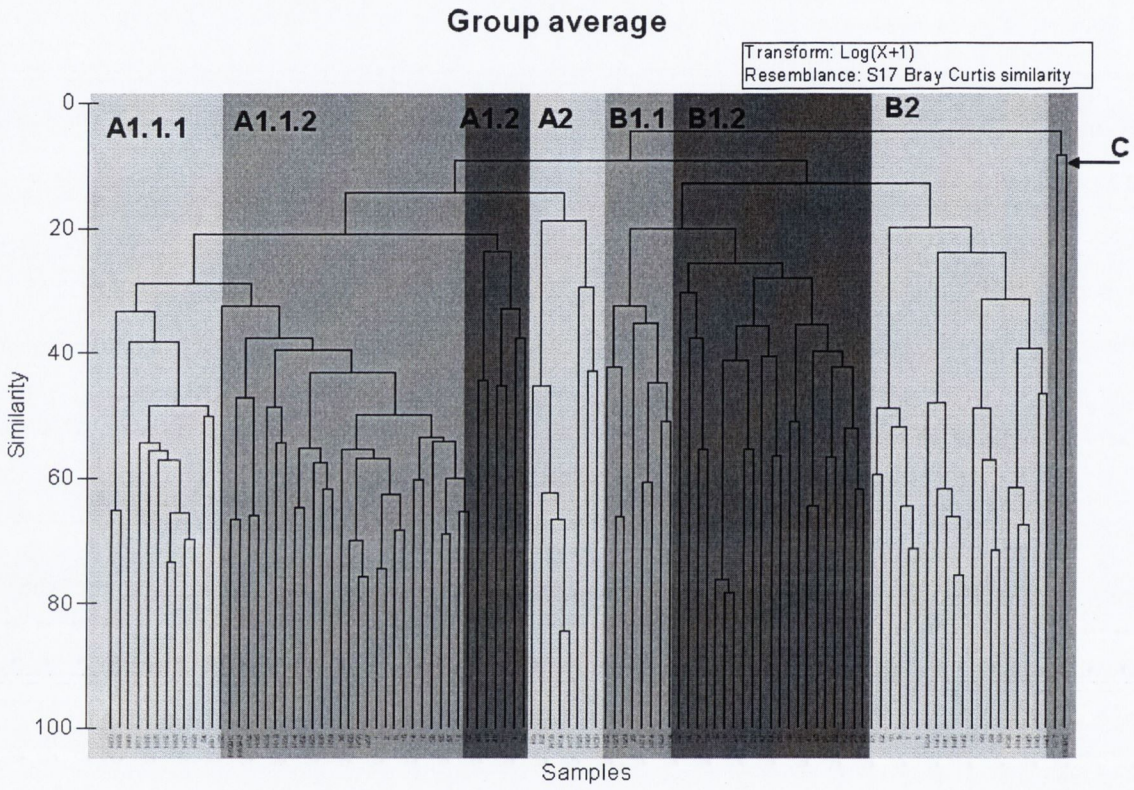


Figure 6.6: Sites clustering by total benthic macrofaunal biomass (Bray-Cutis similarity, PRIMER v6). Data from the BIOMOR & HABMAP projects.

Table 6.13: Presence and absence of biological assemblages (based on biomass) predicted correctly from the environmental variables: depth (m), % organic matter, % organic carbon and % calcium carbonate, median grain size, kurtosis and sorting. Percentage presence and absence calculated using direct entry binary logistic regression (SPSS 15.0.1).

Level	No. of sites	Biological Assemblage	Hosmer & Lemeshow test sig.	Cox & Snell R square	Nagelkerke R square	Percentage predicted correctly (Model)		Contributing variables
						Presence	Absence	
1	54	A	0.021	0.451	0.602	n/a	n/a	n/a
	48	B	0.054	0.424	0.566	n/a	n/a	n/a
2	46	A1	0.111	0.496	0.666	85.7	87.7	Organic matter, Depth, Sorting
	8	A2	0.977	0.204	0.474	50.0	97.8	Organic matter, Kurtosis, Sorting
	28	B1	0.837	0.473	0.680	71.4	95.8	Depth
	20	B2	0.911	0.509	0.803	75.0	93.7	Calcium carbonate, Depth, Sorting
3	40	A1.1	0.384	0.404	0.539	82.6	88.7	Organic matter, Depth, Sorting
	6	A1.2						
	8	B1.1	0.398	0.137	0.273	0	98.9	Depth
	21	B1.2	0.001	0.400	0.580	n/a	n/a	n/a
4	6	A1.1.1	1.000	0.262	0.713	66.7	100	Median
	14	A1.1.2	0.915	0.371	0.666	64.3	96.5	Sorting

6.3.4.2. Production

From the dendrogram different assemblages were identified at different levels of similarity; level 1 at 14% similarity (X, Y, and Z), level 2 at 22% similarity (e.g. X1, X2, Y1 and Y2) and level 3 at 26% (e.g. X2.1, X2.2) (see Figure 6.6). Homer and Lemeshow significance was greater than 0.05 for any assemblage that achieved results, indicating that they could be analysed using logistic regression (see Table 6.14). Environmental variables proved to be poor predictors at all levels for assemblages grouped by productivity (see Table 6.14). Where environmental variables did predict assemblages (for 5 of the 9 assemblages), the percentage of variance explained was generally a lot less than where assemblages were grouped by biomass, e.g. assemblage Y had the highest amount of variance explained with 21.4 – 28.6%.

6.3.4.3. SIMPER tests

Table 6.15 and Table 6.16 show the top five species contributing to assemblages based on biomass and production respectively. Clear parallels can be made between the assemblages at Level 1, where assemblages A and X contain the same top five contributing species, although the order is slightly different. The same is true for assemblages B and Y. Assemblages A and X were both dominated by *M. modiolus* (with contributions of 39.24% and 36.90% respectively), followed by a combination of *Spisula elliptica, Leptochiton asellus, Hesionura elongate* and *G. glycymeris* (see Table 6.15 and Table 6.16). Assemblages B and Y, both have *Ophiuroidea* sp. as the highest contributing species, followed by the second highest contributing species *Phaxas pellucidus* and a combination of *Amphiua filiformis, Abra Alba* and *Nemertea* sp. Assemblages B and Y do not have any species which contributes as highly as *M. modiolus* in assemblages A and X, with contributions ranging from 5.5% - 8.7%.

At level 2, only one of the assemblages from each table, A1 and X2, contained all the same top five contributing species (although again in a different order). Assemblage B1 is close to assemblage Y1, with four of the same species. Assemblages A2 and B2 both contain three of the same species as assemblages X1 and Y2 respectively. At level 3, assemblages X2.1 and X2.2 both have three species in assemblage A1.1. Strongly characterizing species are evident in assemblages at level 2, with *M. modiolus* for A1 (44.17%) and X2 (39.14%), *S. elliptica* and *Mytilus edulis* for A2 (43.58% and 21.15%), *Phaxas pellucidus* for B1 (12.92%) and Y1 (9.33%) and *Abra nitida, Corbula gibba* and *Ophiuroidea* sp. for assemblages B2 and Y2.

At level 3, again certain species are shown to characterize assemblages with their high contributions, e.g. *M. modiolus* (50.14%) at assemblage A1.1. Similarities between species characterizing biomass and production assemblages are less obvious at level 3, with assemblage A1.1 appearing to be a mix of X2.1 and X2.2.

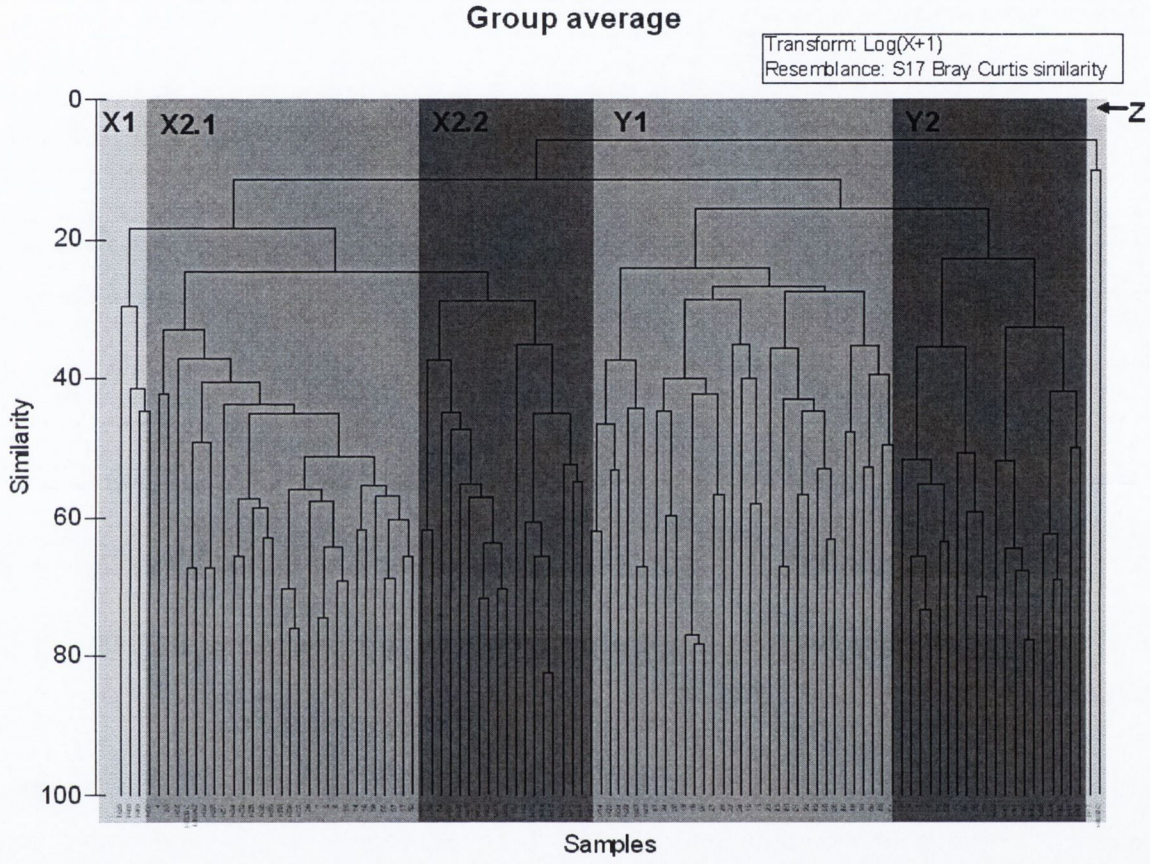


Figure 6.7: Sites clustering by total benthic macrofaunal productivity (Bray-curtis similarity, PRIMER v6). Data from the BIOMOR & HABMAP projects.

Table 6.14: Presence and absence of biological assemblages (based on production) predicted correctly from the environmental variables: depth (m), % organic matter, % organic carbon and % calcium carbonate, median grain size, kurtosis and sorting. Percentage presence and absence calculated using direct entry binary logistic regression (SPSS 15.0.1).

Level	No. of sites	Biological Assemblage	Hosmer & Lemeshow test sig.	Cox & Snell R square	Nagelkerke R square	Percentage predicted correctly (Model)		Contributing variables
						Presence	Absence	
1	46	X	0.464	0.194	0.259	60.9	81.1	Organic Carbon
	54	Y	0.537	0.214	0.286	80.8	66.0	Organic Carbon
2	4	X1	n/a	n/a	n/a	n/a	n/a	n/a
	47	X2	0.021	0.366	0.492	n/a	n/a	n/a
	34	Y1	0.507	0.194	0.271	43.8	92.5	Kurtosis
	20	Y2	0.166	0.122	0.192	10.0	94.9	Organic carbon
3	25	X2.1	0.077	0.134	0.199	24.0	98.6	Organic Carbon
	17	X2.2	n/a	n/a	n/a	n/a	n/a	n/a

Table 6.15: Top five contributing species for biomass assemblages. Contributing species identified using SIMPER (PRIMER v6).

Biological Assemblage	Average % Similarity within assemblage	Top five contributing species	% Contribution of each species
A	28.20	*Modiolus modiolus* (Linnaeus, 1758)	39.24
		Spisula elliptica (Brown, 1827)	6.92
		Leptochiton asellus (Gmelin, 1791)	5.62
		Hesionura elongate (Southern, 1914)	5.60
		Glycymeris glycymeris (Linnaeus, 1758)	4.29
B	23.12	*Ophiuroidea* sp.	8.70
		Phaxas pellucidus	8.65
		Amphiura filiformis (Müller, 1776)	7.27
		Abra alba	6.31
		Nemertea sp.	5.97
A1	33.75	*Modiolus modiolus*	44.17
		Leptochiton asellus	6.63
		Spisula elliptica	5.84
		Glycymeris glycymeris	5.06
		Hesionura elongata	4.04
A2	34.72	*Spisula solida* (Linnaeus, 1758)	43.58
		Mytilus edulis (Linnaeus, 1758)	21.15
		Hesionura elongata	10.21
		Spisula elliptica	6.91
		Abra prismatica (Montagu, 1808)	3.80
B1	27.39	*Phaxas pellucidus*	12.92
		Ensis ensis(Linnaeus, 1758)	8.39
		Lagis koreni (Malmgren, 1866)	8.01
		Abra alba	7.64
		Lanice conchilega (Pallas, 1766)	5.56
B2	29.36	*Abra nitida*(Müller, 1776)	15.15
		Corbula gibba(Olivi, 1792)	12.52
		Ophiuroidea sp.	10.44
		Lumbrineris scopa (Fauchald, 1974)	6.36
		Amphiura filiformis	4.83
A1.1	37.72	*Modiolus modiolus*	50.14
		Spisula elliptica	5.84
		Leptochiton asellus	5.21
		Glycymeris glycymeris	4.72
		Hesionura elongata	4.29
B1.1	38.25	*Ensis ensis*	26.78
		Modiolus modiolus	10.89
		Scalibregma inflatum	7.13
		Ophiuroidea sp. juv.	5.03
		Lumbrineris gracilis	4.63
B1.2	31.85	*Phaxas pellucidus*	19.03
		Lagis koreni	9.20
		Nemertea sp.	8.43
		Abra alba	7.26
		Amphiura filiformis	6.05

Table 6.16: Top five contributing species for productivity assemblages. Contributing species identified using SIMPER (PRIMER v6).

Biological Assemblage	Average % Similarity within assemblage	Top five contributing species	% Contribution of each species
X	31.73	*Modiolus modiolus*	36.90
		Spisula elliptica	6.60
		Hesionura elongate	5.17
		Leptochiton asellus	4.33
		Glycymeris glycymeris	3.65
Y	23.12	*Ophiuroidea* sp.	8.22
		Phaxas pellucidus	6.80
		Nemertea sp.	5.98
		Abra alba	5.83
		Amphiura filiformis	5.48
X1	36.07	*Abra prismatica*	16.37
		Hesionura elongate	9.55
		Spisula elliptica	8.36
		Amphiura filiformis	8.06
		Ophelia sp.	5.70
X2	34.04	*Modiolus modiolus*	39.14
		Spisula elliptica	5.98
		Leptochiton asellus	4.78
		Hesionura elongate	4.42
		Glycymeris glycymeris	4.03
Y1	29.09	*Phaxas pellucidus*	9.33
		Lagis koreni	7.34
		Abra alba	7.10
		Ensis ensis	6.33
		Nemertea sp.	5.79
Y2	32.92	*Abra nitida*	11.75
		Corbula gibba	11.02
		Ophiuroidea sp.	9.82
		Spiophanes kroyeri (Grube, 1860)	5.49
		Praxillella affinis	5.09
X2.1	45.06	*Modiolus modiolus*	37.85
		Leptochiton asellus	9.25
		Glycymeris glycymeris	5.60
		Polycirrus sp.	3.02
		Guernea coalita (Norman, 1868)	2.39
X2.2	37.91	*Modiolus modiolus*	26.94
		Hesionura elongate	14.87
		Spisula elliptica	12.70
		Mytilus edulis	11.04
		Spisula solida	8.50

6.4 *Discussion*

Maps of total benthic macrofaunal biomass and productivity were produced for the whole of the southern Irish Sea. It must be noted that these maps may suffer from a lack of data in areas with rock or gravel substrates as the Van Veen grab sampler which was used in sampling does not perform on well in hard substrates. The maps also suffer from a lack of biomass and production data for muddy sediments, as the muddy stations were only found in the SWISS dataset and could not be included in the overall analysis as annelid data could not be extrapolated for this category. The inclusion of data from other data sources, such as the Outer Bristol Channel Marine Habitat Survey (Mackie et al., 2006) or the IMAGIN project (O'Mahony et al., 2008), would improve the resolution of the maps by increasing the number of stations and possibly the number of Folk categories. There was a clear link between 'slightly gravelly sands' and 'muddy sands' and low total benthic macrofaunal biomass and production, and between 'muddy sandy gravels' and 'sandy gravels' and high total benthic macrofaunal biomass and production. Heip et al. (1992) conversely found higher benthic biomass in the fine sediments of the North Sea where a high chlorophyll a content of the sediment was also found to be associated with increased biomass. This discrepancy is most likely due to the fact that many of the stations in the finer sediment categories studied in this chapter would have been at depths too deep (e.g. >100m in the Celtic Deep) for chlorophyll a to be a factor.

Additional data may be used to further refine the maps in the future. The use of underlying layers such as depth and habitat type would improve the map. However, it was felt that there was too little data for some habitat types to use average values for each habitat type to create a map. A larger number of sample stations in several habitat types would be needed. This is something that should be explored further in the future.

The use of literature derived values was not ideal, however due to unforeseen circumstances, actual samples were not available. It must be acknowledged that the literature data used are from species from a range of environments and therefore they may not exactly match those in the southern Irish Sea. There is no substitute for actual sample data, but in its absence the best attempt was made to learn more about the possible patterns in benthic macrofaunal biomass and production in the southern Irish Sea. While there are extensive long-term datasets for benthic macrofaunal abundance, biomass and production in the North Sea (Clark and Frid, 2001a, Clark and Frid, 2001b, Frid et al., 2009), there are no comparable datasets for the Irish Sea and thus we

changes in communities over time cannot be distinguished. It is recommended that long term monitoring sites are established in the Irish Sea.

It is recognised that the Schwinghamer (1986) method used here to estimate secondary production, may not have been the most ideal method. Due to the lack of seabed temperature and age class data, it was felt that it was the most suitable model. This chapter aims to give an indication of macrofaunal biomass and production for the southern Irish Sea, where no data currently exists. It may not be the best method, but it provides the platform for future studies. The inclusion of other available datasets and modelled seabed temperature data from the HABMAP report (Robinson et al., 2007) could enable the data to be refined using the more comprehensive Brey (2001) model.

Multiple regressions were found to be more effective for the biomass and production models than for abundance models. The environmental variables did not correlate highly enough with total abundance to perform a multiple regression analysis (see Section 5.2.3). Mean grain size and sorting were important for both biomass and production, with the variables accounting for slightly more of the variance in the production model (32.6%). This indicates that particle size is more important in predicting the continuous variables of total benthic biomass and total benthic production, than the chemical sediment characteristics.

Binary logistic regression analysis worked well for dendrograms grouped both by abundance (see Chapter 5) and by biomass. It was unsuccessful, in this study, in using environmental variables to predict production. The abundance model worked better at lower levels of similarity (Level 1 in both the biomass and production models). The abundance model would therefore be preferred to the biomass model. The biomass binary logistic regression model was able to explain more of the variance in assemblages than mean grain size and sorting could explain in the multiple regression biomass and production models. The binary logistic regression model would therefore be preferred. However, it is unsuccessful when the number of sites in an assemblage is low. In both types of regression analysis, the inclusion of physical parameters such as seabed temperature and shear bed stress could improve the analysis. The binary logistic regression analysis in this chapter, like chapter 5, also suffers from a lack of model testing. The dataset would not be big enough for data splitting but re-running the data using bootstrapping techniques would be recommended.

Hiddink (2006), in his biomass model of the Irish Sea predicted the highest biomass to be concentrated in coastal areas (see Figure 6.1). The same result is not observed in this study (see

Figure 6.2). This is most likely due to the different methods employed in modelling biomass data. This study used benthic macrofaunal abundance data, a more accurate dataset than that used by Hiddink (2006), who used remote-sensed chlorophyll-a data to estimate benthic biomass data values. Remote-sensed chlorophyll a data would not be accurate in modelling deep water areas such as the Celtic Deep (>100m). Both studies were limited in coarser sediment areas.

Cusson and Bourget (2005) found that biotic variables were better at explaining variations in production and P:B ratios than environmental variables were for benthic and suprabenthic crustaceans. The environmental variables used in this study were not effective at explaining variations in benthic macrofaunal production.

The P:B values found during this and previous studies are summarized in Table 6.2 (adapted from Nilsen et al. (2006)). The total benthic macrofaunal P:B value obtained for this study in the southern Irish Sea was 0.165, lower than any values shown for other studies. McLusky and McIntyre (1988), however did state that the P:B values in the North Sea ranged from 0.1 to 5.0. The results from this study would fall at the lower end of that range. This study also achieves a lower P:B value than the value of 0.695 used for infaunal macrobenthos by Lees & Mackinson (2007) in their Ecopath model of the Irish Sea. This discrepancy is due to the fact that Lees and Mackinson (2007) used qualitative epifaunal beam trawl data to calculate infaunal macrobenthos P:B values, whereas this study used quantitative grab sampling data. The P:B value obtained in this study is closest to values found in Chile (0.2), the southwest Barents Sea (0.25), North Norway (0.29), the Barents Sea (0.3) the Weddell Sea (0.3) and the Baltic Sea (0.32) (see Table 6.2). These studies showed the lowest P:B values of all the studies in Table 6.2. Conversely areas such as the Grevelingen, Netherlands (2.6), Masfjord, West Norway (2.6), the North Sea (1.9, 5 and 0.1 – 5.0) and Tasmania (1.5 -11) had much higher P:B values (see Table 6.2).

Table 6.17 also shows a breakdown of the productivity, biomass and P:B values for the studies in Table 6.2. The values were not available for every study, which is why they are only shown for a selection. From Table 6.17 we can see that the highest P:B values found for sediment categories in the Irish Sea, 'slightly gravelly muddy sand' (0.53) and 'sandy mud' (0.58) are closest to the values for the Central North Sea (0.6), Northern North Sea (0.7) and Carmarthen Bay (0.56). These southern Irish Sea areas were dominated by smaller fauna with high P:B values. The North Sea and Carmarthen Bay P:B values had substantially higher biomass and productivity values than those for the 'slightly gravelly muddy sand' and 'sandy mud' (see Table 6.17). The P:B values for the other Irish Sea Folk sediment categories were very close to the values for the Wadden Sea (0.36), North Norway (0.29), Chile (0.2) and Brey and the Weddell Sea (0.3) (see Table 6.17). The

fact that individual Folk sediment categories tally more closely with values from other studies than the total value for the Irish Sea, indicate that sediment Folk categories in the Irish Sea would be a more appropriate unit to look at than the total value.

Table 6.17: Biomass, productivity and P:B for selected studies from Table 6.2. Studies were omitted if biomass, productivity and P:B values were not available.

Reference	Location	P:B	B g AFDW m^{-2}	P g AFDW m^{-2} yr^{-1}
Warwick & Price (1975)	Lynher estuary	1	13.2	13.3
Asmus (1987)	Wadden Sea	0.36	1,243	468
Buchanan & Warwick (1974)	Northumberland, GB	0.44	4.5	1.7
Salvanes et al. (1992)	Masfjord, West Norway	2.6	3.8	9.9
Nilsen et al. (2006)	North Norway	0.29	52.6	15.3
Warwick et al. (1978)	Carmarthen Bay, S. Wales	0.56	45.8	25.8
Thatje & Mutschke (1999)	Chile	0.2	6.4	1.2
Bradford-Grieve et al. (2003)	Southern Plateau, New Zealand	1	0.6	0.6
Brey & Gerdes (1999)	Magellan	0.7	14.6	10.2
Brey & Gerdes (1999)	Weddell Sea	0.3	24.0	7.2
Duineveld et al. (1991)	**North Sea**			
	• Southern	2.5	8	20
	• Central	0.6	8	5
	• Northern	0.7	2	1.4
	• **Total**	**1.9**	**5.3**	**10.1**
Present study	**southern Irish Sea**			
	• (g)mS	0.53	0.58	0.31
	• (g)S	0.33	6.18	2.01
	• gmS	0.16	3.04	0.48
	• gS	0.15	80.22	11.81
	• mS	0.37	4.11	1.52
	• msG	0.13	24.45	3.28
	• S	0.34	29.78	10.09
	• sG	0.14	221.99	31.28
	• sM	0.58	0.55	0.32
	• **Total**	**0.17**	**370.9**	**61.1**

Table 6.17 shows a breakdown of the benthic macrofaunal productivity values for some of the studies in Table 6.2. From Table 6.17 we can see that the overall productivity value for the southern Irish Sea is 61.1 g AFDW m^{-2} yr^{-1}, with productivity values for the Folk sediment categories ranging from 0.31 g AFDW m^{-2} yr^{-1} and 0.32 g AFDW m^{-2} yr^{-1} respectively in 'slightly gravelly muddy sands' and 'sandy muds' to 31.28 g AFDW m^{-2} yr^{-1} in 'sandy gravels'. The

productivity of the Irish Sea seems to be high compared to the total North Sea (10.1 g AFDW m^{-2} yr^{-1}) and the other seas (see Table 6.17). Only the Wadden Sea has a higher productivity (468 g AFDW m^{-2} yr^{-1}) (see Table 6.17). The high productivity value for the southern Irish Sea is most likely because the most productive species in the Irish Sea, *Modiolus modiolus* and *Glycymeris glycymeris*, are large species (which results in low P:B values). Small *Modiolus modiolus* are selectively consumed by predators such as crabs and starfish (Seed and Brown, 1978, Anwar et al., 1990). They divert most of their energy into rapid somatic growth, but larger *Modiolus modiolus* effectively grow beyond a size range that is vunerable to attack from predators and divert their energy into reproductive growth (Seed and Brown, 1978, Anwar et al., 1990). The P:B ratio, therefore, may be a better measure of the food available in the southern Irish Sea than productivity, as smaller more productive species may be more consumable.

Table 6.18: Comparison of species P:B values used in this study and those found in López Jamar et al. (1986).

Species	Phylum	This Study P:B	López-Jamar et al. (1986) P:B
Abra alba	Mollusca	0.70	0.69
			0.62
Abra nitida	Mollusca	0.74	0.73
Cylichna cylindracea	Mollusca	0.94	1.18
Fabulina / Tellina fabula	Mollusca	0.62	1.42
		0.62	2.77
Lumbrineris gracilis	Annelida	0.90	0.58
Mediomastus fragilis	Annelida	1.86	2.13
Mysella bidentata	Mollusca	1.25	2.28
			2.45
Ophryotrocha sp.	Annelida	0.80	5.01
Owenia fusiformis	Annelida	0.92	1.36
Polycirrus spp.	Annelida	0.73	1.01
Thracia phaseolina	Mollusca	0.67	0.67
Thyasira flexuosa	Mollusca	1.28	0.95
			1.50
Spiophanes bombyx	Annelida	1.35	1.63
Glycymeris glycymeris	Mollusca	0.14	0.41

Table 6.18 compares P:B values used for some species in this study with values from the study of López-Jamar (1986). The P:B values for many species agree well, e.g. *Abra alba, Abra nitida* and *Spiophanes bombyx*. The biggest discrepancies are between *Ophryotrocha* sp. and *Fabulina/ Tellina fabula*. *Ophryotrocha* sp. may have used different species accounting for the differences in the

values. *Fabulina / Tellina fabula* also shows quite large differences, indicating that juveniles or smaller specimens may have been analysed in the López-Jamar (1986) study. Individual weights (kJ) for *Tellina fabula* from Salzwedel (1979) (Brey, 1995), when converted into P:B values show lower P:B values than López-Jamar (1986), of 0.99 – 1.31, which are closer to the values used in this study.

Several studies have examined the effect of fishing on benthic macrofaunal distribution and production (Kaiser et al., 1996, Kaiser and Spencer, 1996, Kenchington et al., 2001, Duplisea et al., 2002, Hiddink, 2006, Hiddink et al., 2006, Dounas et al., 2007). Fishing could be a cause of the low benthic productivity in the southern Irish Sea. Kaiser et al. (1996) found that the use of scallop dredges and beam trawls in the Irish Sea reduced the abundance of epifauna. Beam trawling led to a 58% decrease in the mean abundance of certain infaunal taxa and to a 50% reduction in the mean number of species per sample in the north-eastern Irish Sea (Kaiser and Spencer, 1996). Reduced biomass, production and species richness in trawled areas in the North Sea and in Welsh coastal waters were found both in field and in modelled data (Hiddink, 2006, Hiddink et al., 2006). Duplisea et al. (2002) found that beam trawling in soft sediments in the central North Sea had a greater effect on faunal size distribution than had sediment particle size or water depth, and that total biomass and production decreased with increased and sustained trawling activity (Duplisea et al., 2002). This study suggests that while there is a high productivity in the southern Irish Sea, the most productive species are large species which may be less available for consumption. The low P:B value for the southern Irish Sea (0.17) supports the view that perhaps the reason there is less fishing and fish yields are lower in the Irish Sea in the Irish Sea than in the North Sea is because there is less available food in the Irish Sea (Brander and Dickson, 1984, Kaiser et al., 1996). Fish yields are most likely lower in the Irish Sea as the macrofauna in the Irish Sea (P:B range 0.13 – 0.58) are less productive than the North Sea macrofauna (P:B range 0.1 – 5.0) and thus there is less food available fro fish in the Irish Sea (Steele, 1974, McLusky and McIntyre, 1988, Duineveld et al., 1991, Christensen, 1995).

Chapter 7

7 Overall Conclusions

7.1 Conclusions

This study has analysed sediment, foraminiferal and macrofaunal data, from chemical sediment characteristics and organic content to foraminiferal assemblages and macrofaunal productivity in the southern Irish Sea, characteristics that are not usually used in benthic habitat mapping. These characteristics could be included in hierarchical benthic habitat classification systems but further investigation is required due to the limited sample sizes involved. Additional physical, chemical and biological characteristics could be introduced at different levels of hierarchical classification systems, such as the European Union Information System (EUNIS) and the Marine Nature Classification Review (MNCR), to produce an ecosystem classification, incorporating different levels of biotic and abiotic information where available.

It was shown that in a homogenous environment, repeatable results are achievable for the chemical sediment characteristics of calcium carbonate, organic matter, organic carbon and organic nitrogen using the long armed continuous warped 0.1m^2 Van Veen grab. The Dublin Bay study found that there was no difference between groups (e.g. grab and site) or within groups (e.g. grab) for calcium carbonate, organic carbon and organic nitrogen. These results indicate that there is no difference between the means of samples from within the grab, from grabs within a single site or from different sites within a homogenous habitat. There was no difference between grab, site and habitat samples for organic matter. There were differences between samples within grabs and within sites for mean grain size but not between site and habitat or between grab and habitat.

The Arklow Bank area was dominated by gravelly sands and slightly gravelly sands. The Celtic Deep graded from sandy gravels in the north through gravelly sands and muddy sands to sandy muds in the southern part of the transect. Both the muddiest sediments and the highest levels of organic matter were found in the southern part of the Celtic Deep. Caernarfon Bay contained a mix of sediments mainly sandy gravels, slightly gravelly muddy sands and slightly gravelly sands. St. George's Channels North and South transects were comprised mainly of gravelly sands and sandy gravels.

Substantial differences were found for sediment type between this study and the BGS modified Folk map of the southern Irish Sea. The physical and chemical sediment characteristics from

stations sampled previously during the BIOMÔR and SWISS projects were often found to differ in their physical and chemical sediment characteristics. However, it is unlikely, due to factors such to tides, winds and currents that the exact same location was sampled in each study, so it was unclear if this was due to changes in habitat type. Strong correlations were found both between organic matter and silt/clay and organic carbon and silt clay. Muddy sediments and gravelly sediments were found to have high levels of calcium carbonate, attributed to foraminifera and mollusc shells respectively.

Depth, gravel, silt/clay and organic content (correlation = 0.546) best explained the separation of the HABMAP macrofaunal assemblages in the southern Irish Sea. The high levels of organic carbon and calcium carbonate content for the 'muddy sandy gravel' Folk category could be explained by the presence of the bivalve *Modiolus modiolus*. This resulted in a large amount of shell which contributed to the gravel component and a large amount of faeces which contributed to the mud component. Particle size alone is not the only factor affecting sediment type and the chemical characteristics of the sediment type should be taken into account where possible. A combination of physical and chemical sediment characteristics from the marine environment may provide a better real time view of the type of habitat than hydrographical factors, which are often derived from either modelled data or a single sample.

The foraminiferal assemblages were divided into two main groups. Foraminiferal assemblage I was clearly associated with the more muddy sites comprising and was dominated by calcareous foraminiferal species such as *Bulimina* sp., *Stainforthia fusiformis*, and *Hyalinea balthica*. Foraminiferal species-based assemblage I resembled the living western assemblage found by Murray (1970) in the North Celtic Sea, the western Celtic assemblage identified by Murray (1979) and the stratified assemblage found by Scott et al. (2003). Assemblage I also bears a resemblance to Le Calvez's (1958) muddy group in the 'Les fonds sablo-vaseux' group comprising Buliminidae, *Hyalinea balthica* and *Nonionella* species. Assemblage II was associated with coarser sediment and was dominated by *Cibicides* sp and agglutinated *Textularia* species. Foraminiferal assemblage II compared favourably with the dead eastern assemblage, dominated by *Textularia sagittula* group and *Cibicides lobatulus* found by Murray (1979) in the Celtic Sea. These assemblages are also closest to Scott et al.'s (2003) mixed assemblage which was dominated by *Cibicides lobatulus, Textularia bockii, Spiroplectammina wrightii, Ammonia batavus* and *Quinqueloculina seminulum*. Assemblage II also compared favourably with Le Calvez's (1958) 'Les fonds détritiques' assemblages.

Two distinct groups were found in both the foraminiferal and macrofaunal species-based assemblages of the Celtic Deep, one group consisting of the more southerly and muddier sites and the second consisting of the sandier and more northerly sites. Taxonomic resolution of the foraminiferal data could be limited to superfamily but more taxonomic work would be required. There is no single identification guide which incorporates all foraminifera.

While predictions of the presence and absence of macrofaunal abundance-based assemblages were not always valid, it was clear that biological assemblages based on abundance were not only linked to particle size but also to the chemical properties of the sediments. Median grain size featured as a predictor in only two assemblages in each dataset, indicating that particle size alone is not sufficient to predict biological assemblages based on total abundance. Environmental variables can be used to predict the presence or absence of macrofaunal abundance-based assemblages. There were no consistent predictors from assemblage to assemblage in the logistic regression analysis. The set of environmental variables cannot be reduced to one or two predictors for all assemblages. The inclusion of more stations would increase the confidence of the predictions. There was a clear link between 'slightly gravelly sands' and 'muddy sands' and low total benthic macrofaunal biomass and production, and between 'muddy sandy gravels' and 'sandy gravels' and high total benthic macrofaunal biomass and production. The distribution of benthic biomass contradicted that produced by Hiddink's (2006) water based model.

Multiple regression analyses were found to be effective for the benthic macrofaunal biomass and production models. It was not possible to produce a model for benthic macrofaunal abundance. Mean grain size and sorting contributed significantly to the biomass-based model, while only mean grain size contributed significantly to the production-based model. Mean grain size decreased with increases in total benthic biomass and productivity. Sorting increased with increased total benthic biomass. In the multiple regression analysis, particle size was a better predictor of total benthic biomass and benthic productivity, than chemical sediment characteristics. Binary logistic regression analysis predicted benthic macrofaunal abundance and biomass with reasonable success. It was unsuccessful in predicting benthic macrofaunal production. The biomass binary logistic regression model was able to explain more of the variance in assemblages than mean grain size and sorting could explain in the multiple regression biomass and production models. The binary logistic regression model would therefore be preferred. However, it is unsuccessful when the number of sites in an assemblage is low. There is an indication that logistic regression is better at predicting macrofaunal abundance-based assemblages than macrofaunal biomass-based assemblages. The binary logistic regression analysis would have benefited from an increased sample size.

The highest P:B values found for sediment categories in the Irish Sea, 'slightly gravelly muddy sand' (0.53) and 'sandy mud' (0.58) are close to the values found in other studies in the Central North Sea (0.6) and Northern North Sea (0.7). These southern Irish Sea sediments were dominated by smaller fauna with high P:B values. P:B values for the other Irish Sea sediment categories were very close to the values found in previous studies for the Wadden Sea (0.36), North Norway (0.29), Chile (0.2) and the Weddell Sea (0.3). The high productivity value but low P:B value for the southern Irish Sea suggests that there is less available food in the Irish Sea than the North Sea as large species such as *Modiolus modiolus* dominate the biomass in the Irish Sea. Fish yields are lower in the Irish Sea than the North Sea, most likely due to the fact that the total benthic macrofauna in the Irish Sea (P:B range in this study - 0.13 – 0.58) have lower P:B values than in the North Sea (P:B range 0.1 – 5.0).

Broadscale benthic habitat maps are a crucial component in the selection process for Marine Protected Areas (MPAs). They enable managers to identify the number, range and diversity of both distinct and representative habitats, ensuring that 'an ecologically coherent network of well-managed marine protected areas' can be established (OSPAR Commission, 2009). Benthic habitat maps can be used, together with stakeholder information on the uses and pressures facing habitats, to inform marine spatial planning. The involvement of stakeholders (individuals, groups and organisations) who will be directly or indirectly affected by an MPA at the beginning of the planning process is crucial.

Today's marine environment is facing many threats including ocean acidification due to rising carbon dioxide levels, rising temperatures, habitat loss, over-fishing, invasive species and pollution. Benthic marine habitat maps are essential in assessing the vulnerability of today's habitats to these threats. While the management and conservation of marine habitats is an essential process, it must be remembered that marine benthic habitats have never been static. The dynamics of marine communities are constantly changing and are always vulnerable to natural disturbances such as storms, predation and competition. The aim of conservation should not necessarily be to maintain the status quo but to protect habitats to allow them to evolve naturally over time free from anthropogenic disturbance. By establishing reference areas which are completely free from anthropogenic disturbance, the effect of activities on the benthos can be measured.

Legislation is a vital component in the attempt to protect the marine environment from anthropogenic disturbance. International conventions and European Directives are essential in

compelling European governments to protect the marine environment. Member States which do not meet their requirements under EU legislation are subject to hefty fines. The advent of marine surveillance and monitoring programmes which will take place in the EU to meet the requirements of the Marine Strategy Framework Directive provide a unique opportunity to increase our knowledge of marine benthic ecosystems in European waters. These programmes could be used to substantially increase our knowledge and perhaps change our understanding of the most important elements in the construction of predictive marine benthic maps.

Benthic habitat mapping generally focuses on today's environment; however foraminifera can be used to create benthic habitat maps for past environments. These maps could help us to better understand how changes in the marine environment will be likely to affect benthic fauna in the future. Foraminifera, unlike macrofauna, provide an excellent historical record of the marine environment, reflecting changes in both the physical and the chemical environment.

Predictive seabed habitat mapping, like the habitats themselves, evolves over time as new techniques become available and more information is gathered on the composition, structure and function of biological ecosystems. In the past, the focus has been on the use of abiotic conditions to produce predictive benthic habitat maps. Hierarchical habitat classification systems, such as EUNIS, could by their nature, be adapted to include more characteristics at different levels of their hierarchy. The inclusion of more variables, while making the classification systems more complex by incorporating different aspects of the structure and function of a habitat, would lead to a more ecosystem-based mapping approach.

7.2 *Future recommendations*

- Foraminifera from replicate samples taken at stations in the Celtic Deep and from samples taken in Caernarfon Bay should be identified. The Caernarfon Bay samples shoud be analysed to see if similar patterns can also be found between the formainifernal and macrofaunal assemablages in Caernarfon Bay.
- More abiotic variables (e.g. seabed temperature and bed shear stress) should be included in the binary logistic and multiple regression models for macrofaunal abundance, biomass and productivity, as these variables could be stronger predictors of biological conditions than chemical variables. The physical environment controls the type of biological communities which can exist; the amount of energy species are exposed to, the substrate they live in or on and the temperature of the water could all be limiting factors to the settlement and survival of species.
- Stations from areas of coarser and muddier sediments should be included in the binary logistic and multiple regression models. This may require the integration of quantitative and qualitative sampling data. The stusy was limited by the fact that the Van Veen grab sampler does not work well in coarse sediments and no mud samples were taken during the study. This limits the habitats which are being studied.
- The binary logistic regression analysis was limited by sample size, it is recommended that this type of analysis be used to test habitat data from the Marine Recorder database in the UK; this would increase the sample size to tens of thousands.
- Regular monitoring of benthic stations in the southern Irish Sea should take place to enable the observation of temporal change in the structure and function of the benthos.
- Benthic habitat maps should be produced with associated confidence maps to allow people to judge the quality of the maps they are view.

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Appendix 1 – Spatial variability of Van Veen grab samplers

Table 1: Sediment characteristics for the Dublin Bay sediments

Ref	Type	Calcium carbonate %	Organic carbon %	Organic nitrogen %	Organic matter %	Gravel %	Sand %	Mud %
1GS	Grab	14.8747	0.087	0.017	1.87	0.66	94.32	5.01
2G S	Grab	14.1025	0.233	0.039	1.87	2.23	92.71	5.07
3GS	Grab	12.8348	0.107	0.027	1.75	0.88	92.98	6.15
4GS	Grab	14.275	0.313	0.039	1.94	1.65	93.27	5.08
5GS	Grab	14.2223	0.087	0.018	2.01	11.75	84.59	3.67
6GS	Grab	17.4197	0.218	0.048	1.93	1.26	91.57	7.17
7GS	Grab	13.9296	0.159	0.058	2.08	1.53	92.17	6.30
8GS	Grab	14.3125	0.124	0.027	1.78	0.84	92.31	6.85
9GS	Grab	13.1488	0.266	0.044	1.7	1.75	92.53	5.73
10SS	Grab	17.4286	0.119	0.032	1.62	1.99	93.52	4.49
11SS	Site	13.797	0.184	0.057	1.47	1.70	89.91	8.40
12SS	Site	15.6534	0.302	0.052	1.51	0.98	89.76	9.26
13SS	Site	14.4304	0.227	0.023	1.56	0.43	92.05	7.52
14SS	Site	14.7648	0.23	0.029	1.89	0.65	87.94	11.40
15SS	Site	13.291	0.29	0.045	1.46	3.13	89.34	7.52
16SS	Site	13.4764	0.212	0.049	1.55	0.23	91.64	8.13
17SS	Site	14.2729	0.335	0.034	1.65	0.33	89.26	10.41
18SS	Site	13.8582	0.176	0.038	1.9	1.13	88.46	10.41
19SS	Site	14.2713	0.203	0.044	1.76	0.78	92.01	7.22
20SS	Site	15.8675	0.324	0.055	2.12	3.14	86.16	10.70
22BS	Habitat	14.4873	0.251	0.057	1.78	0.14	88.88	10.98
23BS	Habitat	15.1083	0.342	0.074	2.19	0.36	87.60	12.04
24BS	Habitat	13.2201	0.237	0.045	1.66	1.44	90.18	8.38
25BS	Habitat	14.0131	0.316	0.07	2.02	0.44	89.46	10.10
26BS	Habitat	12.2082	0.15	0.039	1.2	4.05	90.34	5.61
27BS	Habitat	12.4653	0.191	0.045	1.63	3.15	84.60	12.25
28BS	Habitat	12.4463	0.103	0.022	1.25	0.74	93.56	5.70
29BS	Habitat	14.0508	0.125	0.03	1.24	1.82	92.50	5.68
30BS	Habitat	16.73	0.246	0.056	1.96	1.75	79.64	18.61
20BS	Habitat	15.8675	0.324	0.055	2.12	0.66	94.32	5.01

Table 2: Particle size breakdown for the Dublin Bay sediments

	> 8mm	8 - 4 mm	4 – 2 mm	2 - 1 mm	1 - 0.5 mm	500 -250 µm	250 – 125 µm	125 – 63 µm	63 - 32 µm	< 32 µm
1GS	0.00	0.00	0.20	0.46	4.22	24.91	51.86	13.33	1.42	3.59
2GS	0.00	0.46	0.97	0.80	4.30	25.77	48.29	14.35	1.77	3.29
3GS	0.00	0.00	0.50	0.38	3.60	24.93	51.39	13.05	1.61	4.53
4GS	0.00	0.00	0.71	0.94	4.52	24.44	52.04	12.27	1.45	3.63
5GS	0.00	4.19	3.70	3.86	3.66	16.52	49.73	14.67	1.43	2.24
6GS	0.00	0.44	0.32	0.50	2.96	24.49	50.82	13.30	1.89	5.29
7GS	0.00	0.24	0.46	0.84	5.19	28.47	46.03	12.49	1.80	4.49
8GS	0.00	0.00	0.36	0.48	3.42	24.52	50.79	13.59	1.86	5.00
9GS	0.73	0.00	0.36	0.65	2.34	13.68	63.78	12.72	1.91	3.82
10SS	0.00	0.45	0.79	0.75	3.96	23.64	52.22	13.70	1.36	3.13
11SS	0.00	0.00	1.46	0.23	5.19	19.28	50.98	14.45	2.13	6.27
12SS	0.00	0.88	0.00	0.10	1.15	7.34	65.34	15.93	2.96	6.30
13SS	0.00	0.00	0.14	0.29	4.63	23.91	47.55	15.97	2.06	5.46
14SS	0.00	0.00	0.17	0.49	2.29	11.58	55.88	18.18	3.11	8.29
15SS	0.00	0.07	0.20	2.86	2.66	18.48	52.43	15.77	1.94	5.58
16SS	0.00	0.00	0.05	0.18	1.87	16.05	56.78	16.94	1.88	6.24
17SS	0.00	0.00	0.15	0.18	3.50	15.64	52.69	17.43	2.87	7.54
18SS	0.00	0.85	0.13	0.16	3.38	14.12	55.22	15.74	2.69	7.72
19SS	0.00	0.09	0.31	0.38	4.99	21.58	49.82	15.61	1.97	5.25
20SS	1.55	0.73	0.42	0.44	2.30	14.78	52.56	16.52	2.44	8.26
22BS	0.00	0.00	0.00	0.14	4.14	25.53	41.83	17.38	3.08	7.90
23BS	0.00	0.25	0.00	0.11	3.48	19.72	46.13	18.26	3.35	8.70
24BS	0.00	0.00	1.42	0.03	5.85	24.85	45.77	13.71	2.19	6.18
25BS	0.00	0.25	0.12	0.06	4.78	24.83	47.25	12.60	2.28	7.82
26BS	0.00	3.54	0.12	0.39	4.60	22.70	51.28	11.76	1.60	4.01
27BS	0.00	3.03	0.07	0.06	3.52	15.17	49.69	16.22	2.80	9.45
28BS	0.22	0.14	0.17	0.22	5.93	26.71	52.87	8.04	1.08	4.62
29BS	0.66	0.31	0.50	0.35	6.20	26.07	50.98	9.25	1.30	4.38
30BS	0.00	0.00	1.37	0.38	3.35	16.36	43.59	16.34	4.20	14.41

Appendix 2 –HABMAP sediments of the southern Irish Sea

Table 1: Descriptive statistics for the HABMAP sediments, N = number and SD = standard deviation.

Folk		Gravel (%)	Sand (%)	Mud (%)	Calcium carbonate (%)	Organic matter (%)	Organic Carbon (%)
(g)mS	N	4	4	4	4	4	4
	Mean	1.41	84.71	13.88	19.72	2.77	0.41
	S.D.	1.02	2.08	1.68	9.17	1.33	0.31
(g)S	N	8	8	8	8	8	8
	Mean	2.47	94.52	3.01	14.05	1.12	0.21
	S. D.	1.29	3.08	3.25	4.01	0.20	0.23
gS	N	16	16	16	16	16	16
	Mean	11.79	87.18	1.02	22.51	1.09	0.26
	S. D.	6.14	6.37	0.59	10.40	0.30	0.25
mS	N	5	5	5	5	5	5
	Mean	0.19	80.03	19.78	22.97	4.30	0.69
	S. D.	0.19	12.01	12.10	12.86	4.03	0.67
msG	N	2	2	2	2	2	2
	Mean	5.02	81.49	13.49	32.32	3.66	1.05
	S. D.	2.62	4.54	1.92	4.75	0.04	0.24
S	N	9	9	9	9	9	9
	Mean	0.13	97.08	2.78	10.32	0.94	0.14
	S. D.	0.14	2.47	2.45	2.93	0.35	0.16
sG	N	20	20	20	20	20	20
	Mean	33.33	64.68	1.99	32.25	1.61	0.68
	S. D.	11.44	11.61	1.74	14.84	0.51	0.68
sM	N	4	4	4	4	4	4
	Mean	0.10	24.28	75.61	34.99	9.40	1.60
	S. D.	0.20	4.75	4.90	4.89	1.29	0.56
Total	N	68	68	68	68	68	68
	Mean	13.14	78.20	8.66	23.66	2.13	0.50
	S. D.	15.40	19.73	18.10	13.14	2.34	0.58

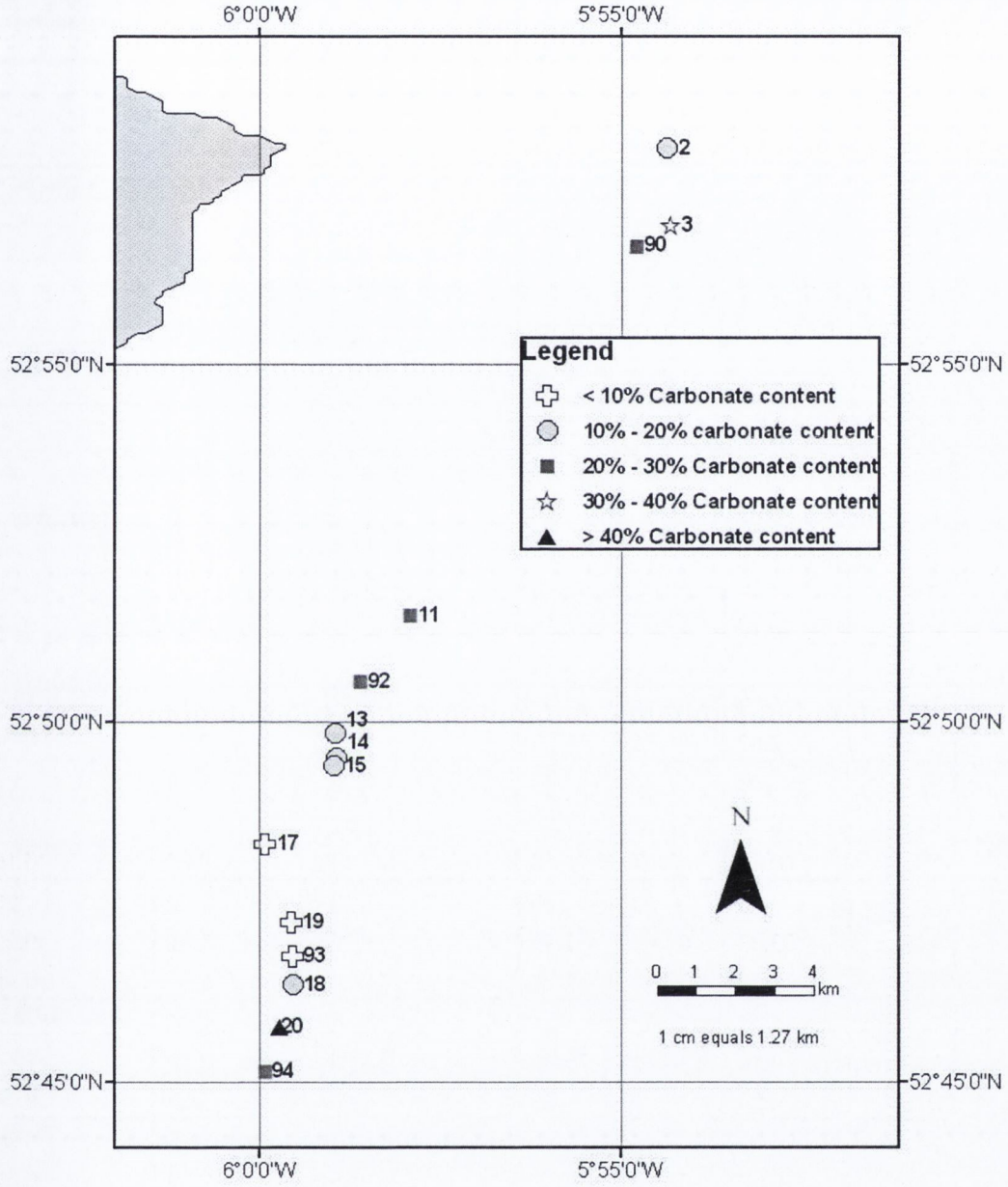

Figure 1: Distribution of Calcium carbonate at stations from the Arklow Bank.

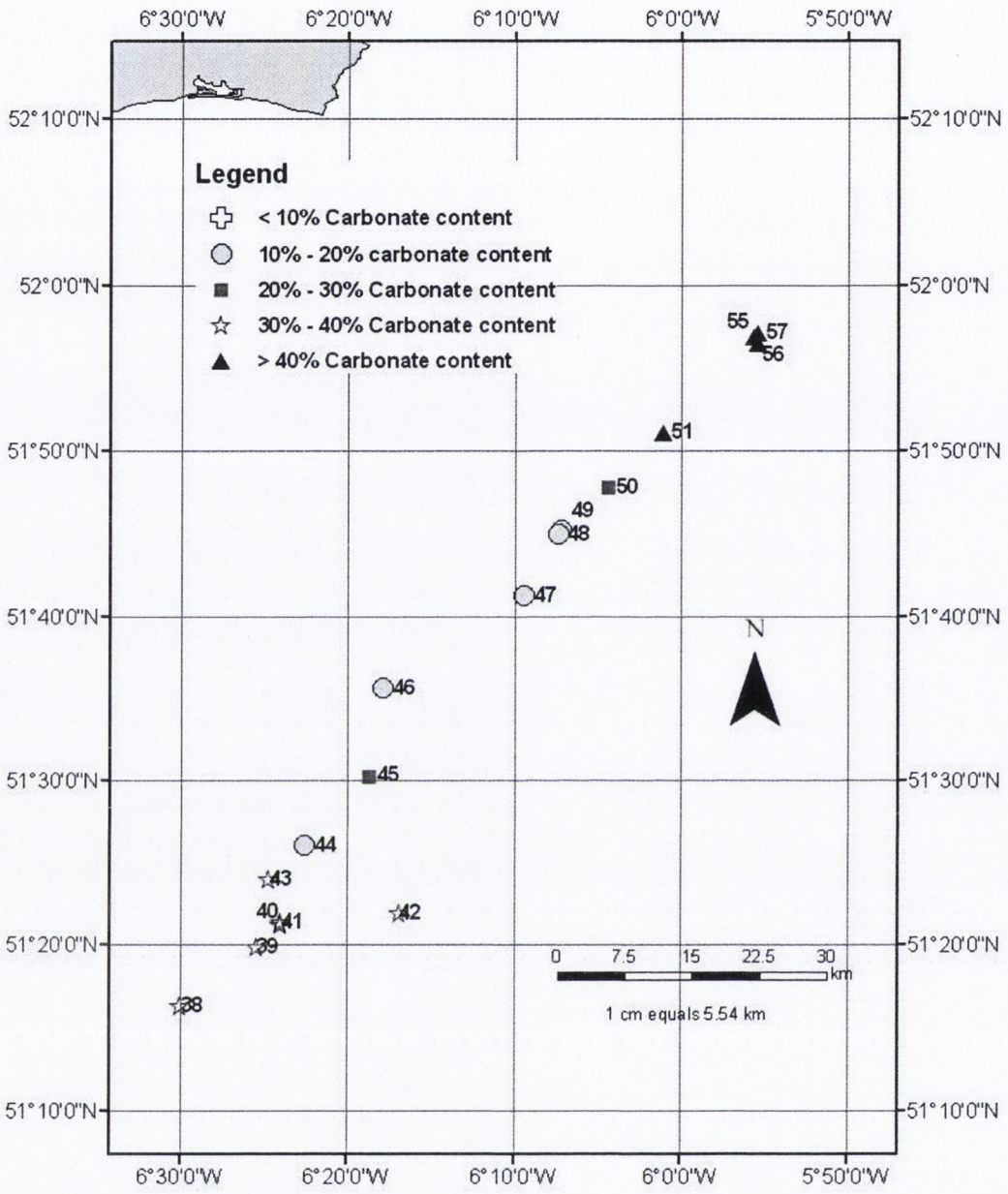

Figure 2: Distribution of Calcium carbonate at stations from the Celtic Deep.

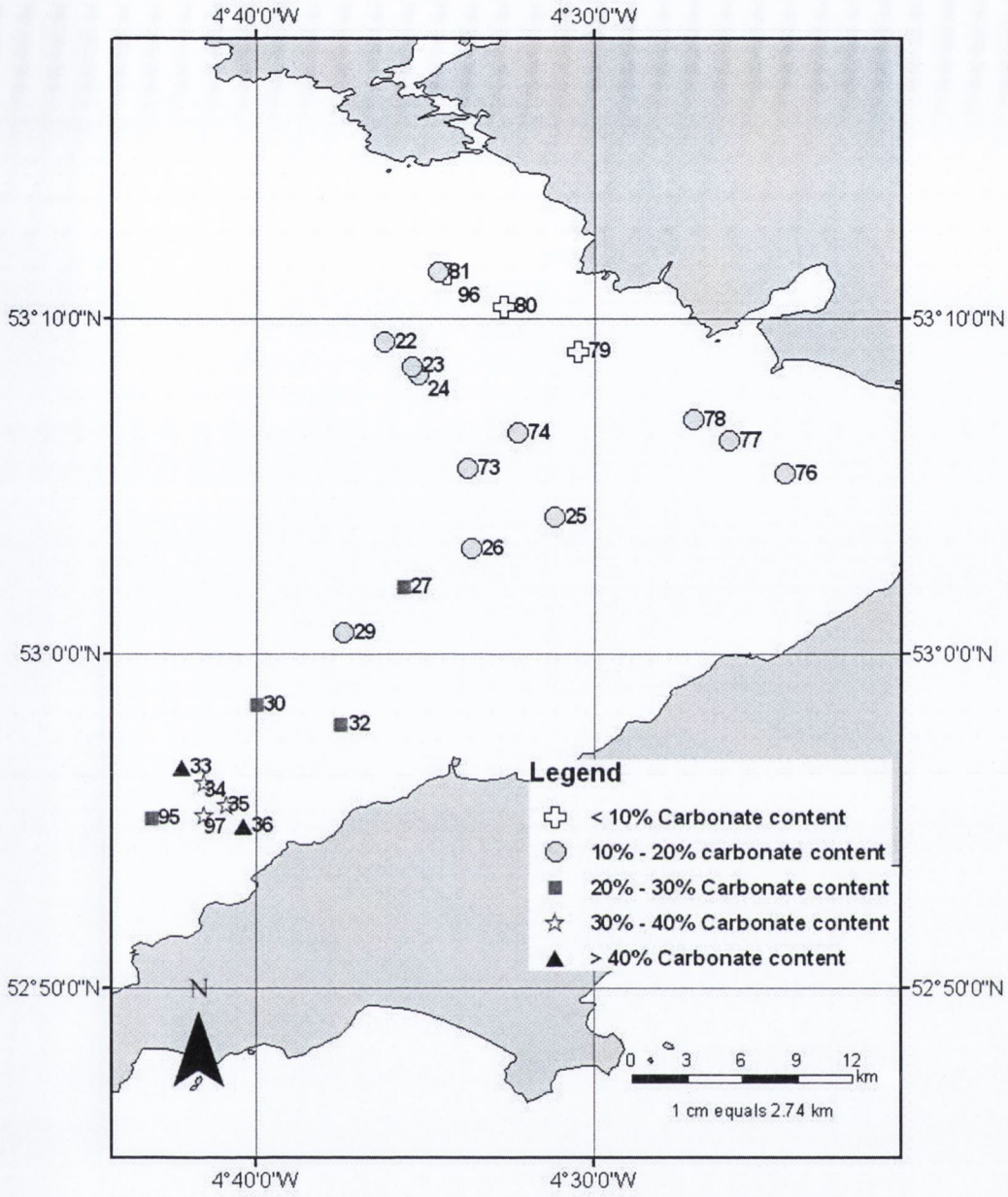

Figure 3: Distribution of Calcium carbonate at stations from Caernarfon Bay.

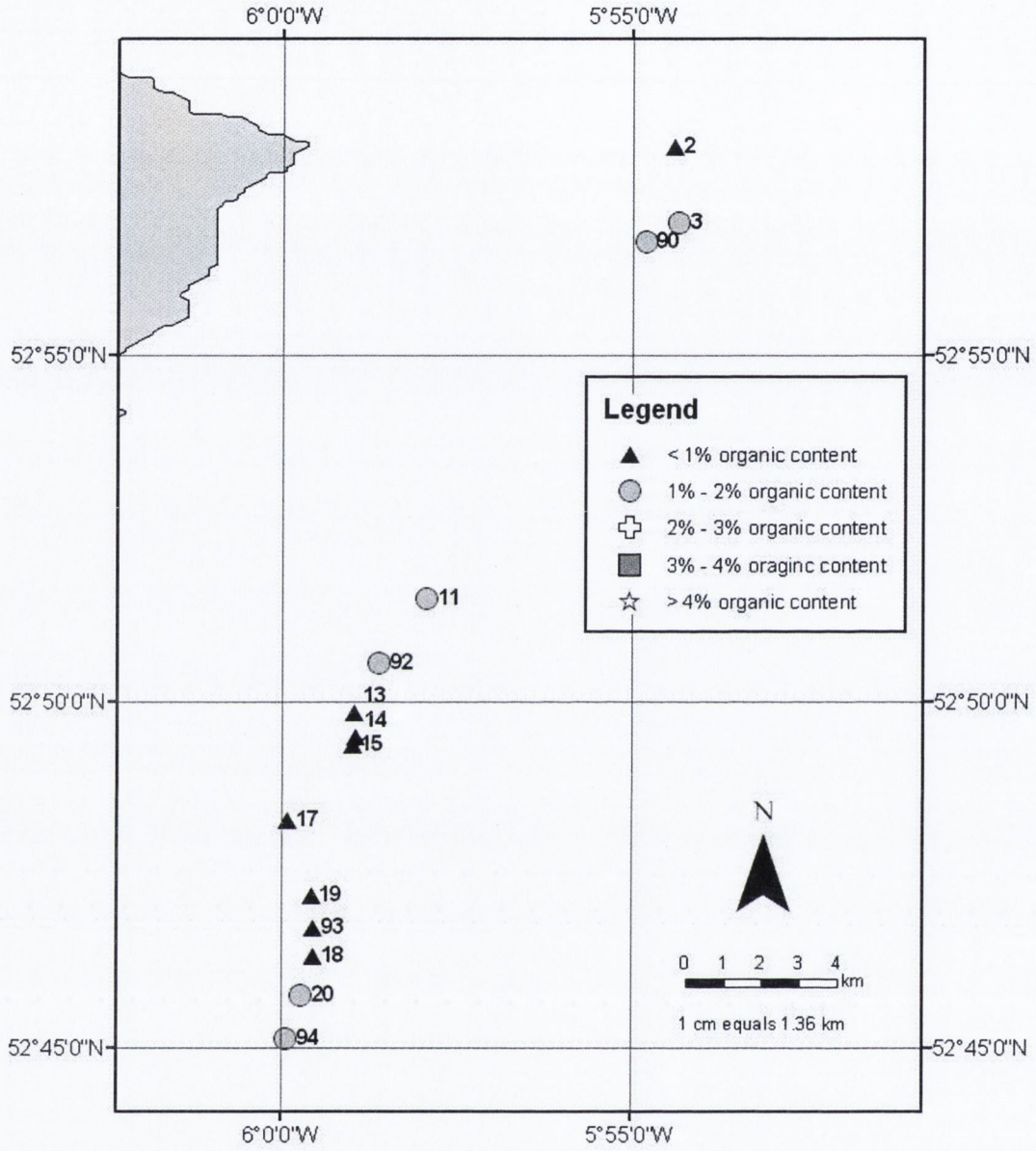

Figure 4: Distribution of organic content at stations from the Arklow Bank.

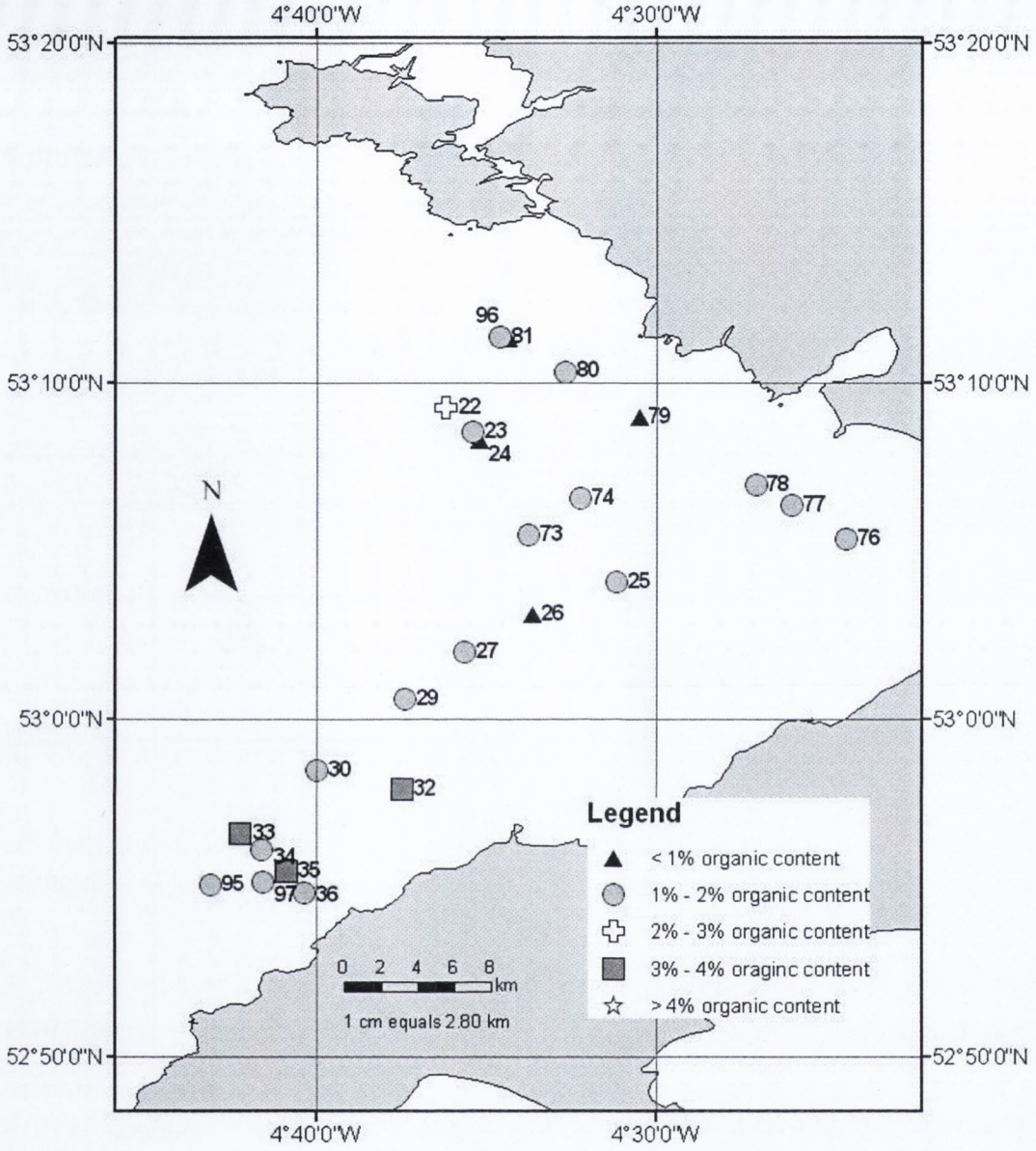

Figure 5: Distribution of organic content at stations from Caernarfon Bay.

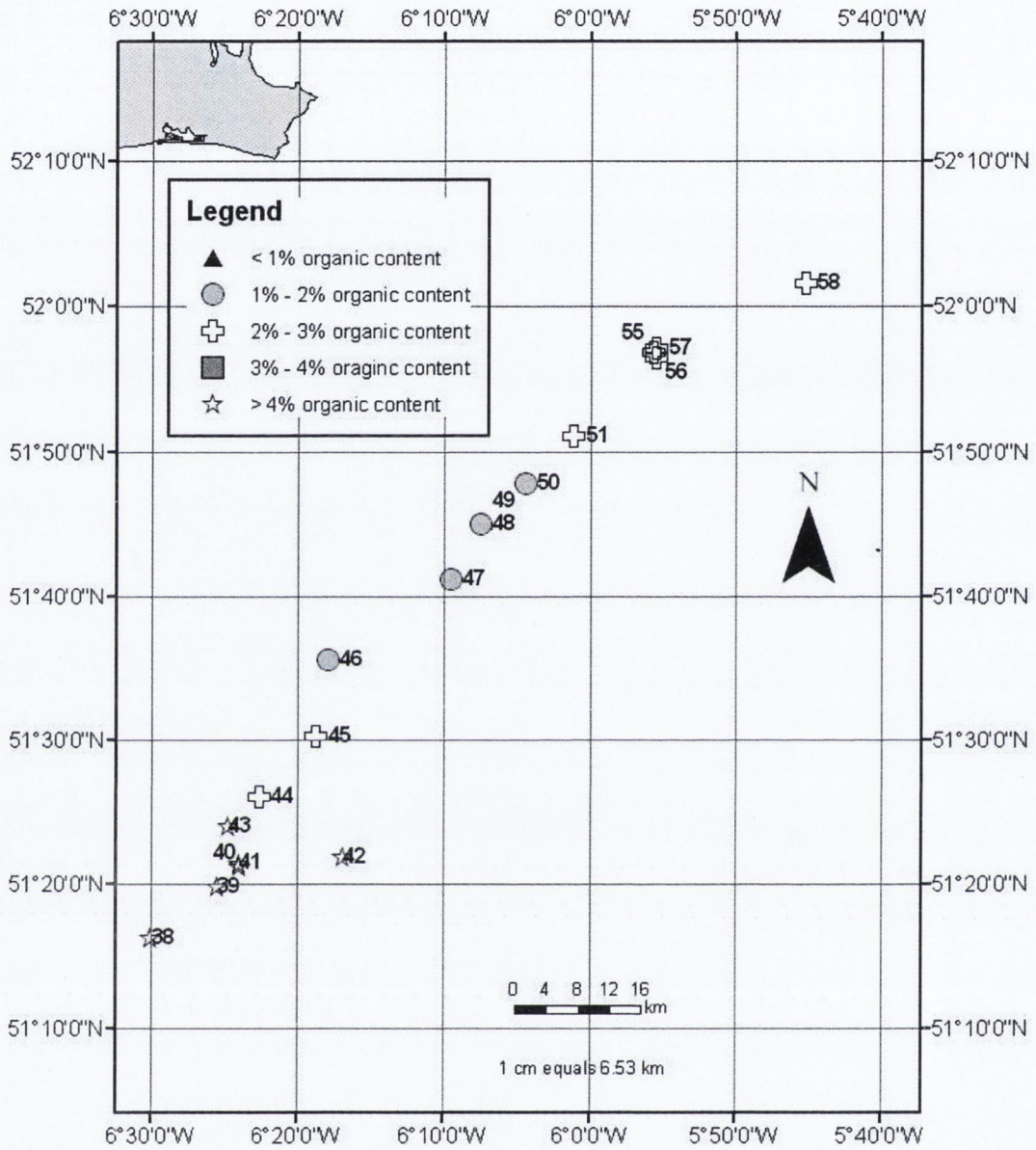

Figure 6: Distribution of organic content at stations from the Celtic Deep.

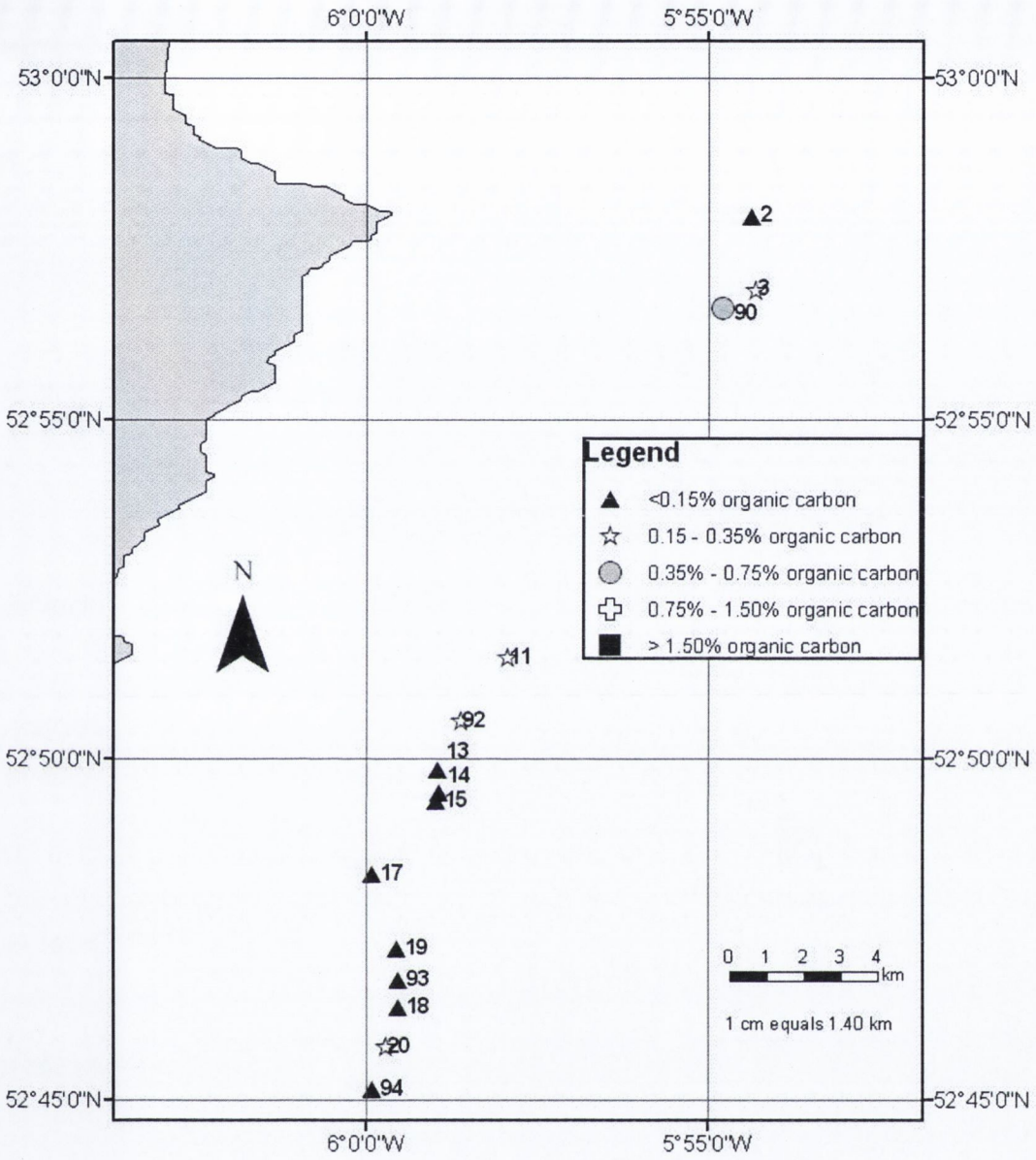

Figure 7: Distribution of organic carbon at stations from the Arklow Bank.

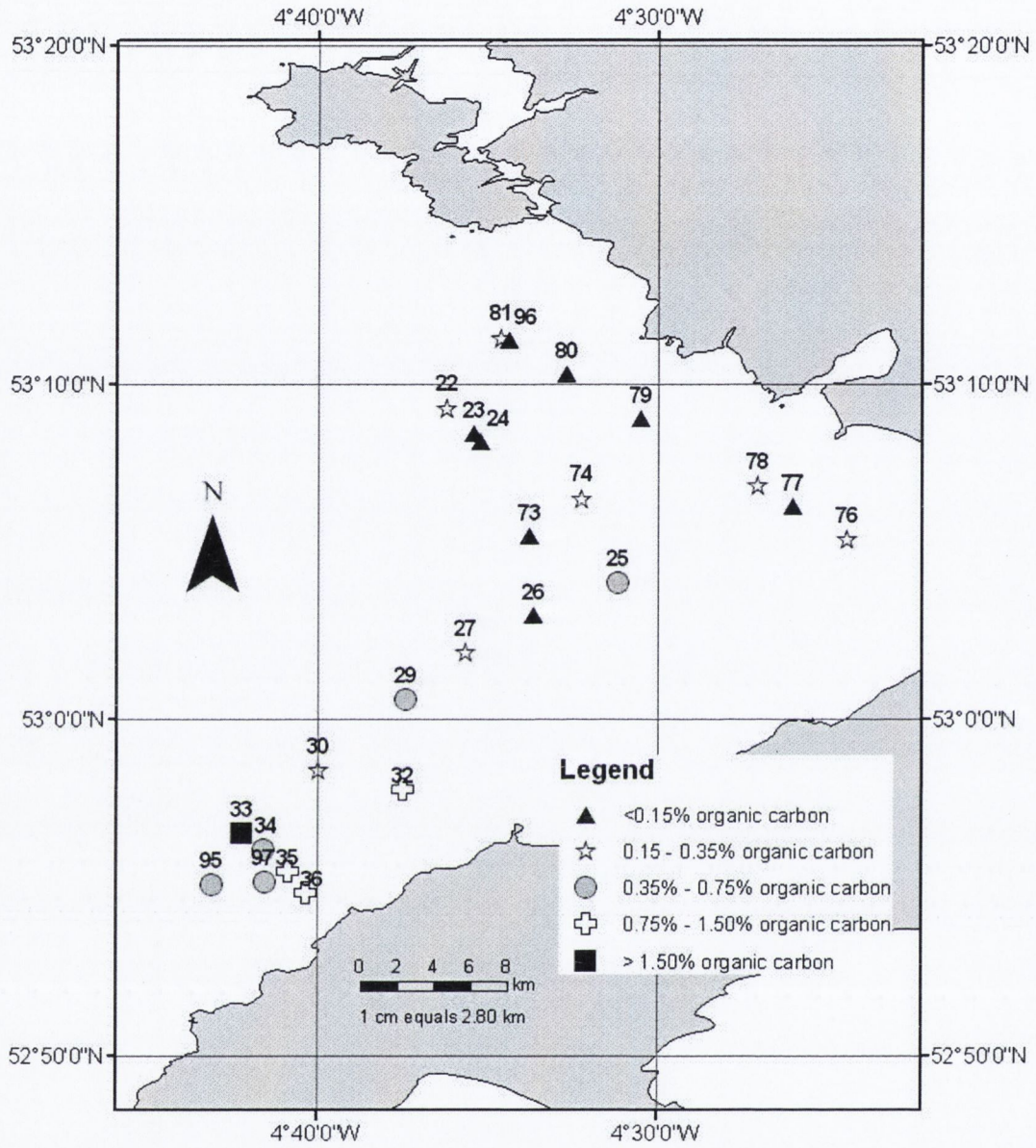

Figure 8: Distribution of organic carbon at stations from Caernarfon Bay.

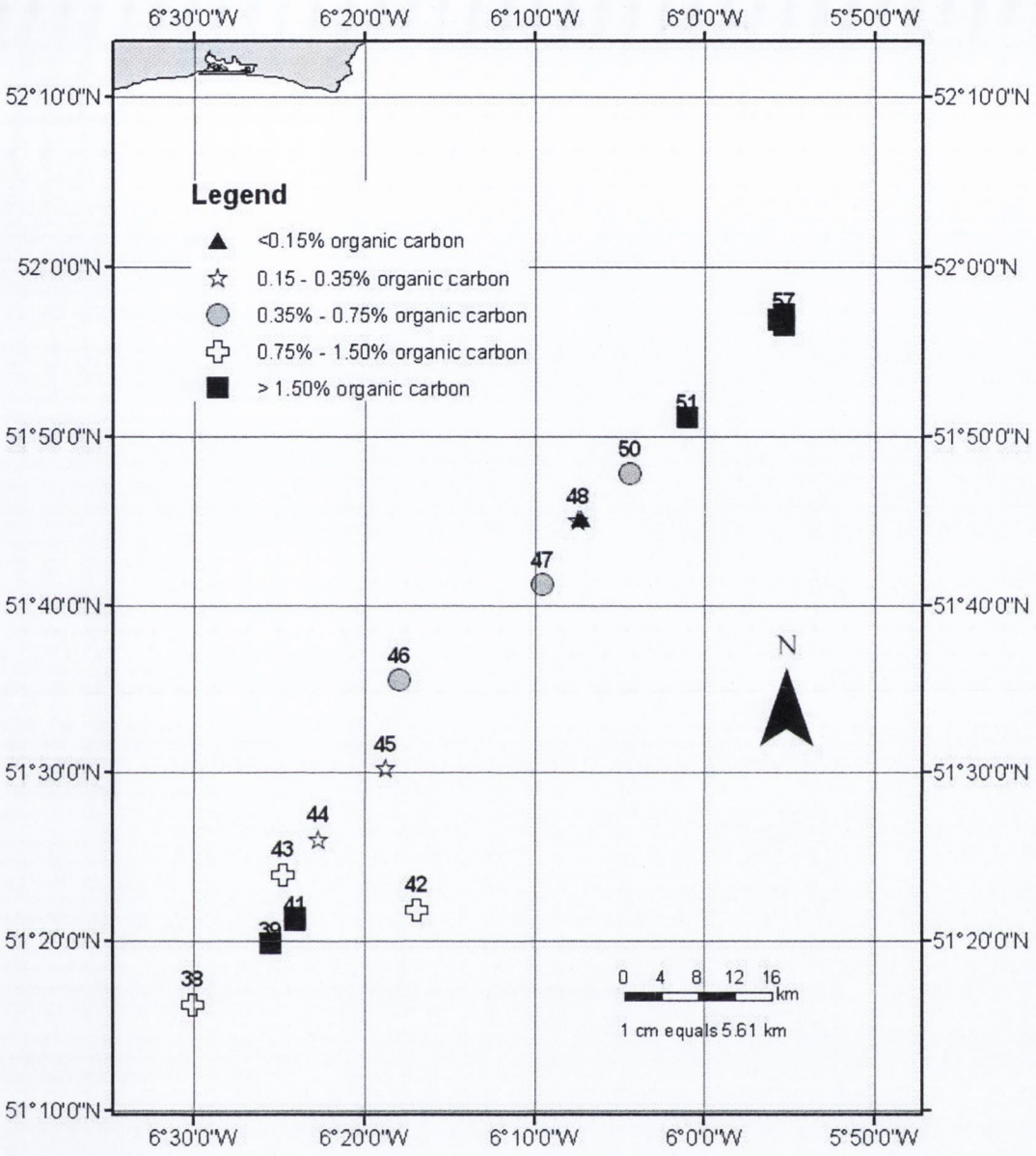

Figure 9: Distribution of organic carbon at stations from the Celtic Deep.

Appendix 3 – Foraminifera of the Celtic Deep

Table 1: Foraminifera species list for stations in the Celtic Deep

Species	Stations																
	38	39	40	41	42	43	44	45	46	47	48	49	50	51	55	56	57
Agglutinated sp.	5	1	0	2	0	0	2	2	11	2	1	0	0	1	5	4	1
Ammonia batavus	2	8	1	1	3	7	5	12	4	10	4	9	15	34	21	31	29
Ammonia sp.	2	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Ammonia sp. 2	0	0	3	0	0	1	2	2	3	2	3	3	2	2	2	7	4
Ammonia sp. 3	0	0	0	0	1	0	0	0	0	0	1	0	0	0	0	1	2
Amphicoryna scalaris	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0
Astacolus sp.	0	0	0	0	0	0	0	0	0	0	1	1	1	3	1	0	0
Asterigerinata mamilla	0	0	0	0	0	0	0	0	6	12	4	0	11	7	3	8	8
Biloculinella depressa	0	0	0	0	0	0	0	0	0	1	2	0	0	0	0	0	0
Bulimina sp.	106	203	118	178	0	216	170	81	69	3	0	2	3	0	6	9	3
Cancris auriculus	2	2	0	2	2	4	1	1	1	2	2	4	5	3	2	5	5
Cibicides sp.	6	3	18	6	2	2	10	26	86	114	81	111	101	72	76	61	91
Cribrostomoides jeffreysii	0	0	0	0	0	0	0	0	1	0	1	0	0	1	8	4	0
Dentalina sp.	0	0	0	0	0	0	0	1	0	0	0	0	0	1	0	1	0
Eggerelloides scaber	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0
Elphidium crispum	0	0	0	0	0	0	0	0	0	0	1	1	0	0	0	0	0
Elphidium sp.	1	1	0	0	2	3	2	0	5	0	0	0	0	0	5	2	3
Elphidium sp. 3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Epistomella sp. 1	0	0	0	0	0	0	0	0	0	1	2	1	1	1	0	3	0
Fissurina sp.	1	4	2	3	2	2	4	6	6	0	0	0	0	0	0	0	0
Gaudryina rudis	0	0	0	0	0	0	0	0	0	0	0	0	1	7	3	8	14

Species	Stations																
	38	39	40	41	42	43	44	45	46	47	48	49	50	51	55	56	57
Globulina sp.	0	0	0	0	0	0	0	0	2	0	0	1	2	0	1	0	1
Haplophragmoides bradyi	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0
Haynesina sp.	2	0	2	0	1	1	2	0	1	0	1	0	0	0	0	7	0
Hyalinea balthica	32	24	3	10	48	15	2	6	2	0	0	0	0	0	0	0	0
Hyalinonetrion clavatum	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0
Lagena sp.	0	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0
Lagena sp. 1	0	0	0	0	0	0	1	2	1	0	0	0	0	0	0	1	0
Lagena sp. 2	0	0	0	0	0	0	1	1	0	0	0	0	0	2	1	0	0
Lagena sp. 3	1	0	0	0	0	2	0	1	0	0	0	0	0	0	0	0	0
Lagena sp. 4	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0
Lagena sp. 5	0	0	0	0	1	1	0	0	0	0	0	0	0	0	0	0	0
Lagena sp. 6	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0
Lenticulina sp.	1	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0
Melonis pompilioides	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0
Melonis sp.	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0
Miliolina sp.	0	0	1	0	0	0	1	4	6	8	7	1	0	0	0	1	1
Miliolinella subrotunda	0	0	0	0	0	0	1	1	4	3	3	0	0	0	0	0	1
Nodosaria sp.2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Nonionella auricula	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Nonionella sp.	0	0	1	0	0	1	0	0	0	0	0	0	0	0	0	6	4
Nonionella turgida	10	4	1	5	15	12	8	4	3	3	0	0	0	0	3	0	0
Oolina sp.	0	0	2	0	0	0	0	0	1	0	0	0	0	0	1	0	0
Oolina sp. 1	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	1
Oolina sp. 2	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0
Oolina sp. 3	0	0	0	0	0	0	0	0	0	1	3	4	6	3	4	4	5

Species	Stations																
	38	39	40	41	42	43	44	45	46	47	48	49	50	51	55	56	57
Oolina sp. 4	0	0	0	0	0	1	0	0	0	0	0	0	1	0	0	0	0
Oolina sp. 5	0	0	0	0	0	0	2	0	0	0	1	0	0	0	0	0	0
Planorbulina mediterranenis	0	0	0	0	2	0	0	5	3	0	1	2	1	0	7	3	3
Pullenia sp. 1	1	1	0	1	0	0	1	1	0	0	0	0	0	0	1	1	0
Pyrgo sp.	0	0	0	0	1	1	0	1	0	0	0	0	0	0	0	0	0
Quinqueloculina bicornis	0	0	0	0	0	0	0	0	0	6	3	0	0	0	0	0	0
Quinqueloculina seminulum	1	0	1	1	2	2	5	15	15	9	39	14	0	0	0	0	0
Quinqueloculina sp.	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Reophax sp.	0	0	0	0	0	0	0	0	1	0	1	0	1	0	0	0	0
Rosalina sp.	0	0	16	2	1	0	2	2	0	0	0	0	0	0	2	0	0
Rosalina sp. 1	0	0	0	0	1	0	0	2	1	0	1	0	1	0	2	1	3
Rosalina sp. 10	0	0	0	0	0	0	0	0	1	2	10	3	2	2	5	4	1
Rosalina sp. 11	0	0	0	0	0	0	0	1	0	0	0	5	5	1	4	6	0
Rosalina sp. 12	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Rosalina sp. 13	0	0	0	1	2	1	0	0	2	0	0	1	0	0	1	0	0
Rosalina sp. 14	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0
Rosalina sp. 15	21	7	14	6	4	7	11	2	0	0	0	0	0	0	0	0	0
Rosalina sp. 2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	3	2	1
Rosalina sp. 3	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
Rosalina sp. 4	1	0	0	0	0	0	0	1	0	0	0	0	0	0	2	1	1
Rosalina sp. 5	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
Rosalina sp. 6	1	1	0	0	0	0	0	0	0	0	0	0	0	0	1	0	1
Rosalina sp. 7	0	0	0	0	0	0	0	2	1	0	1	0	0	3	10	10	3
Rosalina sp. 8	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
Rosalina sp. 9	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2
Species A	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	2

Species	Stations																
	38	39	40	41	42	43	44	45	46	47	48	49	50	51	55	56	57
Species B	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0
Species C	1	0	6	0	5	1	6	3	1	0	0	0	0	0	2	1	0
Species D	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0
Species E	0	0	0	0	0	0	0	0	0	1	3	0	0	0	1	0	0
Species F	1	1	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0
Species G	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0
Species H	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0
Species I	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0
Species J	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0
Species K	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0
Species L	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0
Species M	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0
Species N	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Species X	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Species Y	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Spiroculina sp.	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0
Stainforthia fusiformis	46	24	13	38	12	9	25	34	5	1	0	0	1	1	19	6	4
Textularia sagittula	1	0	0	0	0	0	0	0	0	17	27	22	35	33	15	11	11
Textularia sp.	1	0	0	0	0	0	0	0	0	0	2	0	4	3	0	0	0
Textularia sp. 1	0	0	0	0	0	0	1	0	1	5	4	17	10	8	3	3	7
Textularia sp. 10	3	0	0	0	0	0	2	4	0	0	0	0	0	0	0	0	0
Textularia sp. 2	0	0	0	1	0	0	1	0	6	27	44	53	31	54	23	32	24
Textularia sp. 3	3	1	1	1	0	1	4	6	1	0	1	1	7	3	4	14	16
Textularia sp. 4	0	0	0	0	0	0	1	0	0	3	0	0	1	5	0	3	8

Species	Stations																
	38	39	40	41	42	43	44	45	46	47	48	49	50	51	55	56	57
Haplophragmoides bradyi	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0
Haynesina sp.	2	0	2	0	1	1	2	0	1	0	1	0	0	0	0	7	0
Hyalinea balthica	32	24	3	10	48	15	2	6	2	0	0	0	0	0	0	0	0
Hyalinonetrion clavatum	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0
Lagena sp.	0	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0
Lagena sp. 1	0	0	0	0	0	0	1	2	1	0	0	0	0	0	0	1	0
Lagena sp. 2	0	0	0	0	0	0	1	1	0	0	0	0	0	2	1	0	0
Lagena sp. 3	1	0	0	0	0	2	0	1	0	0	0	0	0	0	0	0	0
Lagena sp. 4	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0
Lagena sp. 5	0	0	0	0	1	1	0	0	0	0	0	0	0	0	0	0	0

Table 2: List of species, including orders, superfamilys and familys.

Species	Order	Superfamily	Family
Asterigerinata mamilla	*Rotaliida*	*Asterigerinacea*	*Asterigerinidae*
Bolivina sp.	*Buliminida*	*Bolivinacea*	*Bolivinidae*
Bulimina sp.	*Buliminida*	*Buliminacea*	*Buliminidae*
Trifarina sp.	*Buliminida*	*Buliminacea*	*Uvigerinidae*
Cancris auriculus	*Rotaliida*	*Discorbacea*	*Bagginidae*
Rosalina sp.	*Rotaliida*	*Discorbacea*	
Rosalina sp. 1	*Rotaliida*	*Discorbacea*	
Rosalina sp. 10	*Rotaliida*	*Discorbacea*	
Rosalina sp. 11	*Rotaliida*	*Discorbacea*	
Rosalina sp. 12	*Rotaliida*	*Discorbacea*	
Rosalina sp. 13	*Rotaliida*	*Discorbacea*	
Rosalina sp. 14	*Rotaliida*	*Discorbacea*	
Rosalina sp. 15	*Rotaliida*	*Discorbacea*	
Rosalina sp. 2	*Rotaliida*	*Discorbacea*	
Rosalina sp. 3	*Rotaliida*	*Discorbacea*	
Rosalina sp. 4	*Rotaliida*	*Discorbacea*	
Rosalina sp. 5	*Rotaliida*	*Discorbacea*	
Rosalina sp. 6	*Rotaliida*	*Discorbacea*	
Rosalina sp. 7	*Rotaliida*	*Discorbacea*	
Rosalina sp. 8	*Rotaliida*	*Discorbacea*	
Rosalina sp. 9	*Rotaliida*	*Discorbacea*	
Epistomella sp. 1	*Rotaliida*	*Discorbinellacea*	*Pseudoparrellidae*
Eggerelloides scaber	*Textulariida*	*Eggerellidae*	*Eggerella*
Reophax sp.	*Lituolida*	*Hormosinacea*	*Reophacidae*
Cribrostomoides jeffreysii	*Lituolida*	*Lituolacea*	*Haplophragmoididae*
Haplophragmoides bradyi	*Lituolida*	*Lituolacea*	*Haplophragmoididae*
Biloculinella depressa	*Miliolida*	*Miliolacea*	*Hauerinidae*
Miliolinella subrotunda	*Miliolida*	*Miliolacea*	*Hauerinidae*
Pyrgo depressa	*Miliolida*	*Miliolacea*	*Hauerinidae*
Pyrgo sp.	*Miliolida*	*Miliolacea*	*Hauerinidae*
Pyrgo williamsoni	*Miliolida*	*Miliolacea*	*Hauerinidae*
Quinqueloculina bicornis	*Miliolida*	*Miliolacea*	*Hauerinidae*
Quinqueloculina seminulum	*Miliolida*	*Miliolacea*	*Hauerinidae*
Quinqueloculina sp.	*Miliolida*	*Miliolacea*	*Hauerinidae*
Spiroculina sp.	*Miliolida*	*Miliolacea*	*Spiroloculinidae*
Amphicoryna scalaris	*Lagenida*	*Nodosariacea*	*Vaginulinidae*
Astacolus sp.	*Lagenida*	*Nodosariacea*	*Vaginulinidae*
Dentalina sp.	*Lagenida*	*Nodosariacea*	*Nodosariidae*
Hyalinonetrion clavatum	*Lagenida*	*Nodosariacea*	*Lagenidae*
Lagena sp.	*Lagenida*	*Nodosariacea*	*Lagenidae*
Lagena sp. 1	*Lagenida*	*Nodosariacea*	*Lagenidae*
Lagena sp. 2	*Lagenida*	*Nodosariacea*	*Lagenidae*
Lagena sp. 3	*Lagenida*	*Nodosariacea*	*Lagenidae*
Lagena sp. 4	*Lagenida*	*Nodosariacea*	*Lagenidae*
Lagena sp. 5	*Lagenida*	*Nodosariacea*	*Lagenidae*

Species	Order	Superfamily	Family
Lagena sp. 6	*Lagenida*	*Nodosariacea*	*Lagenidae*
Lenticulina sp.	*Lagenida*	*Nodosariacea*	*Vaginulinidae*
Nodosaria sp.2	*Lagenida*	*Nodosariacea*	*Nodosariidae*
Haynesina sp.	*Rotaliida*	*Nonionacea*	*Nonionidae*
Melonis pompilioides	*Rotaliida*	*Nonionacea*	*Nonionidae*
Melonis sp.	*Rotaliida*	*Nonionacea*	*Nonionidae*
Nonionella auricula	*Rotaliida*	*Nonionacea*	*Nonionidae*
Nonionella sp.	*Rotaliida*	*Nonionacea*	*Nonionidae*
Nonionella turgida	*Rotaliida*	*Nonionacea*	*Nonionidae*
Pullenia sp. 1	*Rotaliida*	*Nonionacea*	*Nonionidae*
Cibicides sp.	*Rotaliida*	*Planorbulinacea*	*Cibicididae*
Hyalinea balthica	*Rotaliida*	*Planorbulinacea*	*Hyalinea*
Planorbulina mediterranenis	*Rotaliida*	*Planorbulinacea*	*Planorbulina*
Fissurina sp.	*Lagenida*	*Polymorphinacea*	*Ellipsolagenidae*
Globulina sp.	*Lagenida*	*Polymorphinacea*	*Polymorphinidae*
Oolina sp.	*Lagenida*	*Polymorphinacea*	*Ellipsolagenidae*
Oolina sp. 1	*Lagenida*	*Polymorphinacea*	*Ellipsolagenidae*
Oolina sp. 2	*Lagenida*	*Polymorphinacea*	*Ellipsolagenidae*
Oolina sp. 3	*Lagenida*	*Polymorphinacea*	*Ellipsolagenidae*
Oolina sp. 4	*Lagenida*	*Polymorphinacea*	*Ellipsolagenidae*
Oolina sp. 5	*Lagenida*	*Polymorphinacea*	*Ellipsolagenidae*
Ammonia batavus	*Rotaliida*	*Rotaliacea*	*Rotaliidae*
Ammonia sp.	*Rotaliida*	*Rotaliacea*	*Rotaliidae*
Ammonia sp. 2	*Rotaliida*	*Rotaliacea*	*Rotaliidae*
Ammonia sp. 3	*Rotaliida*	*Rotaliacea*	*Rotaliidae*
Elphidium crispum	*Rotaliida*	*Rotaliacea*	*Elphidiidae*
Elphidium sp.	*Rotaliida*	*Rotaliacea*	*Elphidiidae*
Elphidium sp. 3	*Rotaliida*	*Rotaliacea*	*Elphidiidae*
Species A			
Species B			
Species C			
Species D			
Species E			
Species F			
Species G			
Species H			
Species I			
Species J			
Species K			
Species L			
Species M			
Species N			
Species X			
Species Y			
Textularia sagittula	*Textulariida*	*Textulariidae*	*Textularia*
Textularia sp.	*Textulariida*	*Textulariidae*	*Textularia*

Species	Order	Superfamily	Family
Textularia sp. 1	*Textulariida*	*Textulariidae*	*Textularia*
Textularia sp. 10	*Textulariida*	*Textulariidae*	*Textularia*
Textularia sp. 2	*Textulariida*	*Textulariidae*	*Textularia*
Textularia sp. 3	*Textulariida*	*Textulariidae*	*Textularia*
Textularia sp. 4	*Textulariida*	*Textulariidae*	*Textularia*
Textularia sp. 5	*Textulariida*	*Textulariidae*	*Textularia*
Textularia sp. 6	*Textulariida*	*Textulariidae*	*Textularia*
Textularia sp. 7	*Textulariida*	*Textulariidae*	*Textularia*
Textularia sp. 8	*Textulariida*	*Textulariidae*	*Textularia*
Textularia sp. 9	*Textulariida*	*Textulariidae*	*Textularia*
Stainforthia fusiformis	*Buliminida*	*Turrilinacea*	*Stainforthiidae*
Gaudryina rudis	*Lituolida*	*Verneuilinacea*	*Verneuilinidae*
Agglutinated sp.	*Litulolida*		
Miliolina sp.	*Miliolida*		

Appendix 4 – Sediment characteristics and benthic macrofaunal production of the southern Irish Sea

Table 1: Species individual biomass (g AFDW), production (g AFDW yr^{-1}) and P:B values AFDW values.

Species	Phylum	Class	Family	*B*	P	P:B
TUBIFICIDAE spp.	ANNELIDA	Oligochaeta	Tubificidae	0.0000	0.0000	0.8048
Tubificoides amplivasatus	ANNELIDA	Oligochaeta	Tubificidae	0.0001	0.0002	2.3901
Macrochaeta helgolandica	ANNELIDA	Polychaeta	Acrocirridae	0.0028	0.0022	0.8048
Ampharete falcata	ANNELIDA	Polychaeta	Ampharetidae	0.0045	0.0036	0.8048
Ampharete lindstroemi	ANNELIDA	Polychaeta	Ampharetidae	0.0036	0.0029	0.8048
Ampharete sp. B	ANNELIDA	Polychaeta	Ampharetidae	0.0057	0.0046	0.8048
Melinna palmata	ANNELIDA	Polychaeta	Ampharetidae	0.0004	0.0002	0.6823
Hermonia hystrix	ANNELIDA	Polychaeta	Aphroditidae	0.0002	0.0001	0.8048
Apistobranchus spp.	ANNELIDA	Polychaeta	Apistobranchidae	0.0028	0.0022	0.8048
Apistobranchus tenuis	ANNELIDA	Polychaeta	Apistobranchidae	0.0028	0.0022	0.8048
Mediomastus fragilis	ANNELIDA	Polychaeta	Capitellidae	0.0028	0.0052	1.8585
Aphelochaeta marioni	ANNELIDA	Polychaeta	Cirratulidae	0.0002	0.0003	1.3844
Caulleriella zetlandica	ANNELIDA	Polychaeta	Cirratulidae	0.0247	0.0199	0.8048
Chaetozone sp. A	ANNELIDA	Polychaeta	Cirratulidae	0.0059	0.0048	0.8048
Chaetozone sp. B	ANNELIDA	Polychaeta	Cirratulidae	0.0059	0.0048	0.8048
Tharyx killariensis	ANNELIDA	Polychaeta	Cirratulidae	0.0021	0.0036	1.7092
Ophryotrocha sp.	ANNELIDA	Polychaeta	Dorvilleidae	0.0003	0.0003	0.8048
Protodorvillea kefersteini	ANNELIDA	Polychaeta	Dorvilleidae	0.0028	0.0060	2.1463
Diplocirrus glaucus	ANNELIDA	Polychaeta	Flabelligeridae	0.0001	0.0001	1.1988
Glycera lapidum	ANNELIDA	Polychaeta	Glyceridae	0.0028	0.0024	0.8597
Glycera oxycephala	ANNELIDA	Polychaeta	Glyceridae	0.0036	0.0033	0.9136
Goniadella gracilis	ANNELIDA	Polychaeta	Goniadidae	0.0097	0.0078	0.8048
Lumbrineris gracilis	ANNELIDA	Polychaeta	Lumbrineridae	0.0002	0.0002	0.8950
Lumbrineris scopa	ANNELIDA	Polychaeta	Lumbrineridae	0.0097	0.0043	0.4445
Magelona filiformis	ANNELIDA	Polychaeta	Magelonidae	0.0028	0.0077	2.7735
Magelona minuta	ANNELIDA	Polychaeta	Magelonidae	0.0028	0.0059	2.1072
Magelona sp. A	ANNELIDA	Polychaeta	Magelonidae	0.0304	0.0244	0.8048
Clymenura tricirrata	ANNELIDA	Polychaeta	Maldanidae	0.0006	0.0009	1.4923
Praxillella affinis	ANNELIDA	Polychaeta	Maldanidae	0.0028	0.0024	0.8588
Nephtys cirrosa	ANNELIDA	Polychaeta	Nephtyidae	0.0127	0.0098	0.7719
Nephtys incisa	ANNELIDA	Polychaeta	Nephtyidae	0.0003	0.0002	0.4980
Nephtys longosetosa	ANNELIDA	Polychaeta	Nephtyidae	0.4025	0.1710	0.4249
Nephtys sp. indet.	ANNELIDA	Polychaeta	Nephtyidae	0.0097	0.0076	0.7806
Nereis zonata	ANNELIDA	Polychaeta	Nereididae	0.0001	0.0001	0.4595
Ophelia sp. juv.	ANNELIDA	Polychaeta	Opheliidae	0.0097	0.0078	0.8048

Species	Phylum	Class	Family	*B*	P	P:B
Ophelina sp. juv.	ANNELIDA	Polychaeta	Opheliidae	0.0017	0.0013	0.8048
Travisia forbesii	ANNELIDA	Polychaeta	Opheliidae	0.0002	0.0001	0.7176
Scoloplos armiger	ANNELIDA	Polychaeta	Orbiniidae	0.0008	0.0006	0.7315
Galathowenia sp.	ANNELIDA	Polychaeta	Oweniidae	0.0001	0.0002	2.9751
Galathowenia sp. A	ANNELIDA	Polychaeta	Oweniidae	0.0008	0.0007	0.8048
Owenia fusiformis	ANNELIDA	Polychaeta	Oweniidae	0.0304	0.0280	0.9217
Aricidea catherinae	ANNELIDA	Polychaeta	Paraonidae	0.0028	0.0071	2.5368
Aricidea minuta	ANNELIDA	Polychaeta	Paraonidae	0.0014	0.0016	1.1662
Levinsenia gracilis	ANNELIDA	Polychaeta	Paraonidae	0.0304	0.0646	2.1278
Levinsenia sp.	ANNELIDA	Polychaeta	Paraonidae	0.0304	0.0244	0.8048
Paradoneis cf. ilvana	ANNELIDA	Polychaeta	Paraonidae	0.0008	0.0022	2.9200
Paradoneis lyra	ANNELIDA	Polychaeta	Paraonidae	0.0059	0.0199	3.3632
Amphictene auricoma	ANNELIDA	Polychaeta	Pectinariidae	0.0002	0.0002	0.9960
Lagis koreni	ANNELIDA	Polychaeta	Pectinariidae	0.0002	0.0001	0.8363
Hesionura elongata	ANNELIDA	Polychaeta	Phyllodocidae	0.0028	0.0013	0.4509
Ancistrosyllis groenlandica	ANNELIDA	Polychaeta	Pilargidae	0.0304	0.0452	1.4905
Glyphohesione klatti	ANNELIDA	Polychaeta	Pilargidae	0.0028	0.0050	1.8024
Pisione remota	ANNELIDA	Polychaeta	Pisionidae	0.0012	0.0023	1.8722
Poecilochaetus serpens	ANNELIDA	Polychaeta	Poecilochaetidae	0.0304	0.0415	1.3676
Polygordius spp	ANNELIDA	Polychaeta	Polygordiidae	0.0005	0.0015	3.3654
HARMOTHOINAE indet.	ANNELIDA	Polychaeta	Polynoidae	0.0002	0.0002	0.8782
Lepidonotus squamatus	ANNELIDA	Polychaeta	Polynoidae	0.0001	0.0001	0.8394
Sabellaria spinulosa	ANNELIDA	Polychaeta	Sabellariidae	0.0001	0.0001	1.0958
Chone sp. B	ANNELIDA	Polychaeta	Sabellidae	0.0004	0.0003	0.8048
Saccocirrus papillocercus	ANNELIDA	Polychaeta	Saccocirridae	0.0097	0.0160	1.6466
Asclerocheilus spp.	ANNELIDA	Polychaeta	Scalibregmatidae	0.0005	0.0004	0.8048
Scalibregma inflatum	ANNELIDA	Polychaeta	Scalibregmatidae	0.0304	0.0253	0.8339
Filograna implexa	ANNELIDA	Polychaeta	Serpulidae	0.0028	0.0022	0.8048
Filogranula gracilis	ANNELIDA	Polychaeta	Serpulidae	0.0097	0.0078	0.8048
Josephella marenzelleri	ANNELIDA	Polychaeta	Serpulidae	0.0076	0.0183	2.4099
Placostegus tridentatus	ANNELIDA	Polychaeta	Serpulidae	0.3521	0.2833	0.8048
Pomatoceros lamarckii	ANNELIDA	Polychaeta	Serpulidae	0.0008	0.0006	0.8048
Aonides paucibranchiata	ANNELIDA	Polychaeta	Spionidae	0.0015	0.0020	1.2977
Atherospio disticha	ANNELIDA	Polychaeta	Spionidae	0.0022	0.0017	0.8048
Laonice bahusiensis	ANNELIDA	Polychaeta	Spionidae	0.0001	0.0002	1.3123
Polydora caulleryi	ANNELIDA	Polychaeta	Spionidae	0.0003	0.0008	2.5698
Prionospio banyulensis	ANNELIDA	Polychaeta	Spionidae	0.0066	0.0053	0.8048
Prionospio fallax	ANNELIDA	Polychaeta	Spionidae	0.0028	0.0093	3.3234
Prionospio multibranchiata	ANNELIDA	Polychaeta	Spionidae	0.0028	0.0055	1.9798

Species	Phylum	Class	Family	*B*	P	P:B
Prionospio sp.	ANNELIDA	Polychaeta	Spionidae	0.0000	0.0000	0.8048
Spio goniocephala	ANNELIDA	Polychaeta	Spionidae	0.8201	1.0570	1.2889
Spio sp. A	ANNELIDA	Polychaeta	Spionidae	0.0002	0.0004	2.1916
Spiophanes bombyx	ANNELIDA	Polychaeta	Spionidae	0.0028	0.0038	1.3505
Spiophanes kroyeri	ANNELIDA	Polychaeta	Spionidae	0.0002	0.0002	0.9688
Autolytus alexandri	ANNELIDA	Polychaeta	Syllidae	0.0126	0.0101	0.8048
Exogone hebes	ANNELIDA	Polychaeta	Syllidae	0.0005	0.0006	1.1977
Exogone verugera	ANNELIDA	Polychaeta	Syllidae	0.0028	0.0022	0.8048
Sphaerosyllis bulbosa	ANNELIDA	Polychaeta	Syllidae	0.0304	0.0465	1.5319
Sphaerosyllis sp.	ANNELIDA	Polychaeta	Syllidae	0.0022	0.0076	3.3654
Sphaerosyllis taylori	ANNELIDA	Polychaeta	Syllidae	0.0018	0.0053	2.8705
Syllis sp. E	ANNELIDA	Polychaeta	Syllidae	0.0097	0.0143	1.4789
Lanice conchilega	ANNELIDA	Polychaeta	Terebellidae	0.0097	0.0043	0.4479
Pista cristata	ANNELIDA	Polychaeta	Terebellidae	0.0059	0.0070	1.1890
Polycirrus spp.	ANNELIDA	Polychaeta	Terebellidae	0.0001	0.0001	0.7297
Terebellides stroemi	ANNELIDA	Polychaeta	Trichobranchidae	0.0001	0.0001	0.8390
Uncispio n.sp.	ANNELIDA	Polychaeta	Uncispionidae	0.0028	0.0022	0.8048
Balanus sp.	CRUSTACEA	Cirripedia	Balanidae	0.0006	0.0003	0.5942
Ampelisca spinipes	CRUSTACEA	Eumalacostraca	Ampeliscidae	0.0188	0.0181	0.9628
Ampelisca tenuicornis	CRUSTACEA	Eumalacostraca	Ampeliscidae	0.0010	0.0018	1.7114
Haploops tubicola	CRUSTACEA	Eumalacostraca	Ampeliscidae	0.0012	0.0026	2.1550
Araphura brevimana	CRUSTACEA	Eumalacostraca	Anarthruridae	0.0001	0.0000	0.5511
AORIDAE sp.	CRUSTACEA	Eumalacostraca	Aoridae	0.0011	0.0024	2.1019
Bodotria scorpioides	CRUSTACEA	Eumalacostraca	Bodotriidae	0.0001	0.0002	1.9587
Cumopsis fagei	CRUSTACEA	Eumalacostraca	Bodotriidae	0.0001	0.0001	1.9780
Cumopsis longipes	CRUSTACEA	Eumalacostraca	Bodotriidae	0.0028	0.0015	0.5511
Caprella linearis	CRUSTACEA	Eumalacostraca	Caprellidae	0.0028	0.0049	1.7598
Caprella sp.	CRUSTACEA	Eumalacostraca	Caprellidae	0.0001	0.0000	0.5511
Pariambus typicus	CRUSTACEA	Eumalacostraca	Caprellidae	0.0176	0.0448	2.5386
Eurydice spinigera	CRUSTACEA	Eumalacostraca	Cirolanidae	0.0002	0.0002	1.3920
Corophium affine	CRUSTACEA	Eumalacostraca	Corophiidae	0.0020	0.0031	1.5661
Siphonoecetes kroyeranus	CRUSTACEA	Eumalacostraca	Corophiidae	0.0067	0.0113	1.6818
Unciola planipes	CRUSTACEA	Eumalacostraca	Corophiidae	0.0001	0.0000	0.5511
Corystes cassivelaunus	CRUSTACEA	Eumalacostraca	Corystidae	0.0197	0.0035	0.1776
Cressa dubia	CRUSTACEA	Eumalacostraca	Cressidae	0.0304	0.0167	0.5511
Atylus falcatus	CRUSTACEA	Eumalacostraca	Dexaminidae	0.1908	0.1051	0.5511
Atylus swammerdamei	CRUSTACEA	Eumalacostraca	Dexaminidae	0.0025	0.0043	1.7488
Atylus vedlomensis	CRUSTACEA	Eumalacostraca	Dexaminidae	0.0192	0.0354	1.8450
Guernea coalita	CRUSTACEA	Eumalacostraca	Dexaminidae	0.0003	0.0002	0.5511
Diastylis sp.	CRUSTACEA	Eumalacostraca	Diastylidae	0.0000	0.0001	1.5454
Gammaropsis maculata	CRUSTACEA	Eumalacostraca	Isaeidae	0.0001	0.0003	2.2335
Gammaropsis palmate	CRUSTACEA	Eumalacostraca	Isaeidae	0.0048	0.0026	0.5511

Species	Phylum	Class	Family	*B*	P	P:B
Megamphopus cornutus	CRUSTACEA	Eumalacostraca	Isaeidae	0.0032	0.0065	2.0195
Microprotopus maculatus	CRUSTACEA	Eumalacostraca	Isaeidae	0.0228	0.0358	1.5679
Photis pollex	CRUSTACEA	Eumalacostraca	Isaeidae	0.0018	0.0010	0.5511
Protomedeia fasciata	CRUSTACEA	Eumalacostraca	Isaeidae	0.0028	0.0015	0.5511
Jassa (falcata) sp	CRUSTACEA	Eumalacostraca	Ischyroceridae	0.0007	0.0007	1.0624
Janira maculosa	CRUSTACEA	Eumalacostraca	Janiridae	0.0386	0.1374	3.5587
Tanaopsis graciloides	CRUSTACEA	Eumalacostraca	Leptognathiinae	0.0000	0.0000	0.5511
Eudorella truncatula	CRUSTACEA	Eumalacostraca	Leuconiidae	0.0001	0.0002	1.9892
Eudorellopsis deformis	CRUSTACEA	Eumalacostraca	Leuconiidae	0.0028	0.0044	1.5667
Leucon nasica	CRUSTACEA	Eumalacostraca	Leuconiidae	0.0040	0.0044	1.0996
Liljeborgia pallida	CRUSTACEA	Eumalacostraca	Liljeborgiidae	0.0396	0.0928	2.3407
Lysianassidae sp.	CRUSTACEA	Eumalacostraca	Lysianassidae	0.0004	0.0010	2.4377
Socarnes erythrophthalmus	CRUSTACEA	Eumalacostraca	Lysianassidae	0.0000	0.0000	0.5511
Gastrosaccus spinifer	CRUSTACEA	Eumalacostraca	Mysidae	0.0097	0.0115	1.1866
Schistomysis spiritus	CRUSTACEA	Eumalacostraca	Mysidae	0.0010	0.0006	0.5511
Tanaissus lilljeborgi	CRUSTACEA	Eumalacostraca	Nototanaidae	0.0000	0.0001	3.2123
Perioculodes longimanus	CRUSTACEA	Eumalacostraca	Oedicerotidae	0.0304	0.0624	2.0539
Pontocrates altamarinus	CRUSTACEA	Eumalacostraca	Oedicerotidae	0.0044	0.0074	1.7016
Pontocrates arcticus	CRUSTACEA	Eumalacostraca	Oedicerotidae	0.0017	0.0009	0.5511
Pontocrates arenarius	CRUSTACEA	Eumalacostraca	Oedicerotidae	0.0091	0.0160	1.7567
Synchelidium sp.	CRUSTACEA	Eumalacostraca	Oedicerotidae	0.0018	0.0010	0.5511
Harpinia antennaria	CRUSTACEA	Eumalacostraca	Phoxocephalidae	1.6811	3.1929	1.8993
Harpinia crenulata	CRUSTACEA	Eumalacostraca	Phoxocephalidae	0.0304	0.0837	2.7574
Harpinia pectinata	CRUSTACEA	Eumalacostraca	Phoxocephalidae	0.0449	0.1095	2.4377
Metaphoxus fultoni	CRUSTACEA	Eumalacostraca	Phoxocephalidae	0.0135	0.0075	0.5511
Bathyporeia elegans	CRUSTACEA	Eumalacostraca	Pontoporeiidae	0.0024	0.0046	1.8748
Bathyporeia nana	CRUSTACEA	Eumalacostraca	Pontoporeiidae	0.0304	0.0167	0.5511
Bathyporeia sp	CRUSTACEA	Eumalacostraca	Pontoporeiidae	0.0010	0.0020	2.0026
Pisidia longicornis	CRUSTACEA	Eumalacostraca	Porcellanidae	0.0304	0.0615	2.0255
Pseudocuma longicornis	CRUSTACEA	Eumalacostraca	Pseudocumatidae	0.0028	0.0050	1.7954
Pseudocuma similis	CRUSTACEA	Eumalacostraca	Pseudocumatidae	0.0004	0.0012	2.6374
Stenothoe marina	CRUSTACEA	Eumalacostraca	Stenothoidae	0.0059	0.0033	0.5511
Stenothoidae sp.	CRUSTACEA	Eumalacostraca	Stenothoidae	0.0028	0.0015	0.5511
Urothoe brevicornis	CRUSTACEA	Eumalacostraca	Urothoidae	0.0013	0.0019	1.5117
Urothoe elegans	CRUSTACEA	Eumalacostraca	Urothoidae	0.0304	0.0742	2.4441
Urothoe marina	CRUSTACEA	Eumalacostraca	Urothoidae	0.0001	0.0002	1.8641
AMPHIPODA sp.	CRUSTACEA	Eumalacostraca		0.0000	0.0000	0.8685
Mysidacea indet.	CRUSTACEA	Eumalacostraca		0.0031	0.0022	0.7201
Echinocyamus pusillus	ECHINODERMATA	Echinoidea	Fibulariidae	0.0028	0.0029	1.0338
Echinocardium indet.	ECHINODERMATA	Echinoidea	Loveniidae	0.0008	0.0005	0.6409
Spatangoida indet ju	ECHINODERMATA	Echinoidea	Spatangidae	0.0002	0.0002	0.6409

Species	Phylum	Class	Family	*B*	P	P:B
ECHINOIDEA juv.	ECHINODERMATA	Echinoidea		0.0005	0.0003	0.6409
SYNAPTIDAE sp.	ECHINODERMATA	Holothurioidea	Synaptidae	0.0097	0.0062	0.6409
Amphipholis squamata	ECHINODERMATA	Ophiuroidea	Amphiuridae	0.0056	0.0078	1.4003
Amphiura chiajei	ECHINODERMATA	Ophiuroidea	Amphiuridae	0.0003	0.0002	0.5094
Amphiura filiformis	ECHINODERMATA	Ophiuroidea	Amphiuridae	0.0097	0.0040	0.4146
Amphiura juv.	ECHINODERMATA	Ophiuroidea	Amphiuridae	0.0001	0.0001	0.6409
Amphiuridae juv.	ECHINODERMATA	Ophiuroidea	Amphiuridae	0.0002	0.0001	0.6409
Ophiactis balli	ECHINODERMATA	Ophiuroidea	Ophiactidae	0.0488	0.0687	1.4087
Ophiothrix fragilis	ECHINODERMATA	Ophiuroidea	Ophiotrichidae	0.0039	0.0042	1.0880
Ophiura albida	ECHINODERMATA	Ophiuroidea	Ophiuridae	0.0001	0.0000	0.6160
Ophiura sp.	ECHINODERMATA	Ophiuroidea	Ophiuridae	0.0000	0.0001	3.1150
Ophiuroidea sp. juv.	ECHINODERMATA	Ophiuroidea	Ophiuridae	0.0028	0.0018	0.6409
Caecum glabrum	MOLLUSCA	Gastropoda	Caecidae	0.0097	0.0038	0.3896
Vitreolina philippi	MOLLUSCA	Gastropoda	Eulimidae	0.0001	0.0000	0.4952
Polinices polianus	MOLLUSCA	Gastropoda	Naticidae	0.0011	0.0004	0.3373
Brachystomia eulimoides	MOLLUSCA	Gastropoda	Pyramidellidae	0.0001	0.0000	0.3896
Retusa umbilicata	MOLLUSCA	Gastropoda	Retusidae	0.0009	0.0004	0.3896
Alvania abyssicola	MOLLUSCA	Gastropoda	Rissoidae	0.0001	0.0001	0.3896
Cylichna cylindracea	MOLLUSCA	Gastropoda	Scaphandridae	0.0304	0.0286	0.9433
Dikoleps nitens	MOLLUSCA	Gastropoda	Skeneidae	0.0010	0.0004	0.3896
Gibbula tumida	MOLLUSCA	Gastropoda	Trochidae	0.0038	0.0015	0.3896
Turritella communis	MOLLUSCA	Gastropoda	Turritellidae	0.0004	0.0001	0.3885
Astarte sulcata	MOLLUSCA	Pelecypoda	Astartidae	0.0028	0.0021	0.7420
Goodallia triangularis	MOLLUSCA	Pelecypoda	Astartidae	0.0097	0.0164	1.6955
Parvicardium minimum	MOLLUSCA	Pelecypoda	Cardiidae	0.0097	0.0099	1.0247
Parvicardium sp.	MOLLUSCA	Pelecypoda	Cardiidae	0.0000	0.0000	0.3896
Corbula gibba	MOLLUSCA	Pelecypoda	Corbulidae	0.0001	0.0000	0.5083
Glycymeris glycymeris	MOLLUSCA	Pelecypoda	Glycymerididae	0.0002	0.00004	0.1430
Hiatella arctica	MOLLUSCA	Pelecypoda	Hiatellidae	0.0059	0.0064	1.0913
Laevicardium crassum	MOLLUSCA	Pelecypoda	Mactridae	0.0003	0.0001	0.2228
Lutraria lutraria	MOLLUSCA	Pelecypoda	Mactridae	0.0000	0.0000	0.3896
Spisula elliptica	MOLLUSCA	Pelecypoda	Mactridae	0.0051	0.0026	0.5196
Spisula solida	MOLLUSCA	Pelecypoda	Mactridae	0.0304	0.0069	0.2288
Spisula sp.	MOLLUSCA	Pelecypoda	Mactridae	0.0304	0.0118	0.3896
Spisula subtruncata	MOLLUSCA	Pelecypoda	Mactridae	0.0006	0.0003	0.5323
Mysella bidentata	MOLLUSCA	Pelecypoda	Montacutidae	0.0118	0.0147	1.2479
Tellimya ferruginosa	MOLLUSCA	Pelecypoda	Montacutidae	0.0021	0.0022	1.0656
Mya truncata	MOLLUSCA	Pelecypoda	Myidae	0.0015	0.0005	0.3622
Sphenia binghami	MOLLUSCA	Pelecypoda	Myidae	0.0002	0.0001	0.3896
Chlamys varia	MOLLUSCA	Pelecypoda	Mytilidae	0.0002	0.0001	0.3896
Modiolula phaseolina	MOLLUSCA	Pelecypoda	Mytilidae	0.0304	0.0316	1.0408
Modiolus modiolus	MOLLUSCA	Pelecypoda	Mytilidae	0.0006	0.0001	0.1150
Musculus discors	MOLLUSCA	Pelecypoda	Mytilidae	0.0005	0.0002	0.3459

Species	Phylum	Class	Family	*B*	P	P:B
Mytilus edulis	MOLLUSCA	Pelecypoda	Mytilidae	0.1749	0.0629	0.3593
Nucula hanleyi	MOLLUSCA	Pelecypoda	Nuculidae	0.0304	0.0118	0.3896
Nucula nitidosa	MOLLUSCA	Pelecypoda	Nuculidae	0.0109	0.0101	0.9261
Nucula nucleus	MOLLUSCA	Pelecypoda	Nuculidae	0.0097	0.0038	0.3896
Nucula sulcata	MOLLUSCA	Pelecypoda	Nuculidae	0.0097	0.0068	0.7021
Nuculoma tenuis	MOLLUSCA	Pelecypoda	Nuculidae	0.0004	0.0004	0.9370
Ophelia borealis	MOLLUSCA	Pelecypoda	Nuculidae	0.0059	0.0033	0.5615
Ensis ensis	MOLLUSCA	Pelecypoda	Pharidae	0.0003	0.0000	0.1850
Ensis JUV	MOLLUSCA	Pelecypoda	Pharidae	0.0025	0.0010	0.3896
Phaxas pellucidus	MOLLUSCA	Pelecypoda	Pharidae	0.0097	0.0063	0.6521
Gari tellinella	MOLLUSCA	Pelecypoda	Psammobiidae	0.0097	0.0038	0.3896
Abra alba	MOLLUSCA	Pelecypoda	Semelidae	0.0002	0.0001	0.6981
Abra nitida	MOLLUSCA	Pelecypoda	Semelidae	0.0023	0.0017	0.7444
Abra prismatica	MOLLUSCA	Pelecypoda	Semelidae	0.0028	0.0018	0.6468
Abra spp. JUV	MOLLUSCA	Pelecypoda	Semelidae	0.0000	0.0000	1.6799
Fabulina fabula	MOLLUSCA	Pelecypoda	Tellinidae	0.0304	0.0188	0.6198
Moerella donacina	MOLLUSCA	Pelecypoda	Tellinidae	0.0001	0.0000	0.3896
Tellina pygmaea or Tellina (Moerella) pygmaeus	MOLLUSCA	Pelecypoda	Tellinidae	0.0041	0.0046	1.1235
Thracia phaseolina	MOLLUSCA	Pelecypoda	Thraciidae	0.0028	0.0019	0.6715
Thracia spp.	MOLLUSCA	Pelecypoda	Thraciidae	0.0001	0.0000	0.3896
Thracia villosiuscula	MOLLUSCA	Pelecypoda	Thraciidae	0.0306	0.0119	0.3896
Thyasira flexuosa	MOLLUSCA	Pelecypoda	Thyasiridae	0.0097	0.0124	1.2776
Timoclea ovata	MOLLUSCA	Pelecypoda	Veneridae	0.0028	0.0025	0.8790
Leptochiton asellus	MOLLUSCA	Polyplacophora	Leptochitonidae	0.0000	0.0000	0.3896
Scaphopoda indet.	MOLLUSCA	Scaphopoda		0.0024	0.0009	0.3896
NEMERTEA spp.	NEMERTEA			0.0002	0.0003	1.4436
Phoronis spp.	Phoronida		Phoronidae	0.0138	0.0212	1.5356

Table 2: Total biomass and productivity values and Folk classifications for the BIOMÔR, SWISS (extrapolated annelid values) and HABMAP stations.

Station	Survey	Biomass g AFDW m^2	Productivity g AFDW m^2 yr^{-1}	Folk
1	BIOMOR	908.15	13.57	gmS
2	BIOMOR	5220.75	14.33	sG
4	BIOMOR	155.33	24.43	
6	BIOMOR	714.46	55.11	gS
7	BIOMOR	7.24	47.36	sM
8	BIOMOR	8.45	69.28	sM
9	BIOMOR	8.08	104.28	mS
10	BIOMOR	20.24	606.80	sM
11	BIOMOR	68.47	84.34	S
12	BIOMOR	55.13	175.28	S
13	BIOMOR	103.43	51.61	S
14	BIOMOR	664.46	38.49	sG
15	BIOMOR	4978.43	49.84	sG
16	BIOMOR	500.17	102.69	sG
17	BIOMOR	1281.76	89.41	gS
18	BIOMOR	51.12	122.48	(g)mS
19	BIOMOR	29.93	37.85	gmS
20	BIOMOR	53.02	48.22	mS
21	BIOMOR	258.78	55.38	(g)S
22	BIOMOR	96.24	54.80	S
23	BIOMOR	513.63	73.71	S
24	BIOMOR	30.22	58.79	mS
25	BIOMOR	63.46	55.75	S
26	BIOMOR	43.14	42.54	mS
27	BIOMOR	39.92	136.66	mS
28	BIOMOR	142.48	101.51	S
29	BIOMOR	53.76	63.93	sM
32	BIOMOR	32.19	95.35	S
33	BIOMOR	28.96	61.55	sG
34	BIOMOR	179.50	57.71	(g)mS
38	BIOMOR	433.11	64.17	sG
39	BIOMOR	40.58	64.47	sG
42	BIOMOR	167.95	68.24	S
43	BIOMOR	25.94	56.42	S
45	BIOMOR	15.93	111.00	S
46	BIOMOR	50.50	66.31	sG
47	BIOMOR	25.92	81.28	mS
48	BIOMOR	33.61	61.00	sG
49	BIOMOR	10.62	179.28	gmS
50	BIOMOR	89.25	98.04	gS
51	BIOMOR	28.98	153.05	gS
52	BIOMOR	183.04	81.65	S
54	BIOMOR	45.01	80.50	mS
55	BIOMOR	943.24	68.64	gS

Station	Survey	Biomass g AFDW m^2	Productivity g AFDW m^2 yr^{-1}	Folk
57	BIOMOR	274.80	76.18	sG
58	BIOMOR	675.98	85.35	gmS
59	BIOMOR	37.31	12.82	mS
60	BIOMOR	27.98	14.93	mS
61	BIOMOR	10.77	44.50	sM
62	BIOMOR	21.63	40.61	mS
63	BIOMOR	32.95	13.70	S
H11	HABMAP	302.97	40.95	sG
H13	HABMAP	317.11	38.75	gS
H14	HABMAP	51.98	16.69	gS
H15	HABMAP	75.57	31.52	(g)S
H17	HABMAP	0.94	98.50	S
H18	HABMAP	167.60	9.09	gS
H2	HABMAP	36.29	19.98	(g)S
H22	HABMAP	81.43	60.35	(g)mS
H23	HABMAP	56.50	44.72	(g)S
H24	HABMAP	131.67	107.29	S
H25	HABMAP	675.31	156.30	sG
H26	HABMAP	20.34	103.33	S
H27	HABMAP	203.76	379.96	sG
H29	HABMAP	139.37	209.11	gS
H3	HABMAP	45.69	0.47	gS
H32	HABMAP	614.88	50.10	msG
H33	HABMAP	890.27	10.14	sG
H34	HABMAP	663.10	5.00	sG
H35	HABMAP	3021.80	6.56	msG
H36	HABMAP	1507.19	6.58	sG
H38	HABMAP	100.11	10.55	(g)mS
H39	HABMAP	18.47	18.20	mS
H40	HABMAP	6.99	55.45	sM
H41	HABMAP	9.99	48.88	sM
H42	HABMAP	9.21	23.79	sM
H43	HABMAP	14.89	10.44	mS
H44	HABMAP	34.42	7.42	mS
H45	HABMAP	117.47	9.69	(g)mS
H46	HABMAP	93.78	42.50	S
H47	HABMAP	51.40	28.63	S
H48	HABMAP	30.51	24.81	(g)S
H49	HABMAP	12.30	123.44	gS
H50	HABMAP	16.95	77.02	(g)S
H51	HABMAP	223.69	110.79	gS
H52	HABMAP	156.92	189.48	sG
H55	HABMAP	81.16	4.40	sG
H56	HABMAP	982.34	10.53	sG
H57	HABMAP	535.59	13.17	sG

Station	Survey	Biomass g AFDW m^2	Productivity g AFDW m^2 yr^{-1}	Folk
H58	HABMAP	804.67	7.90	sG
H59	HABMAP	1214.77	21.10	sG
H60	HABMAP	8.17	39.81	gS
H61	HABMAP	44.48	16.79	gS
H62	HABMAP	77.46	12.31	gS
H63	HABMAP	27.77	5.60	sG
H65	HABMAP	96.75	58.10	gS
H66	HABMAP	237.84	36.76	sG
H67	HABMAP	61.30	157.27	sG
H68	HABMAP	37.11	138.27	gS
H69	HABMAP	10.88	11.03	(g)S
H73	HABMAP	197.69	110.20	S
H74	HABMAP	117.84	113.03	mS
H82BC	HABMAP	878.22	143.21	sG
H83AD	HABMAP	772.03	124.30	
H83BC	HABMAP	16.55	181.41	
74	SWISS	68.52	105.36	mS
75	SWISS	85.95	235.46	S
76	SWISS	126.66	83.79	S
77	SWISS	86.40	172.63	S
78	SWISS	204.29	89.98	S
79	SWISS	44.80	168.27	S
80	SWISS	397.62	120.77	mS
81	SWISS	4.86	186.81	S
82	SWISS	373.83	114.35	S
83	SWISS	12.02	95.38	S
84	SWISS	212.13	97.43	gS
85	SWISS	66.58	94.90	S
87	SWISS	310.75	108.88	S
88	SWISS	71.24	139.76	S
89	SWISS	51.43	203.31	gS
90	SWISS	12.78	107.07	S
91	SWISS	15.41	102.33	S
92	SWISS	51.46	107.16	mS
93	SWISS	76.71	108.98	mS
94	SWISS	205.38	178.24	
95	SWISS	17.33	469.03	mS
96	SWISS	10.31	144.43	mS
97	SWISS	14.45	121.16	S
98	SWISS	20.14	108.17	S
99	SWISS	578.25	130.34	mS
100	SWISS	3059.84	118.62	gS
101	SWISS	328.22	120.99	sG
103	SWISS	34.69	124.99	S
104	SWISS	7.76	119.17	M

Station	Survey	Biomass g AFDW m^2	Productivity g AFDW m^2 yr^{-1}	Folk
105	SWISS	45.16	122.70	S
106	SWISS	25.22	112.82	S
107	SWISS	63.54	136.30	S
108	SWISS	60.37	133.80	S
110	SWISS	56.06	117.49	S
111	SWISS	32.41	167.41	S
112	SWISS	1.40	122.87	S
113	SWISS	47.99	122.19	gmS
114	SWISS	47.77	122.52	S
116	SWISS	3.72	318.48	S
118	SWISS	304.06	152.88	gS
120	SWISS	19.18	220.16	S
121	SWISS	2.98	134.14	S
122	SWISS	0.88	131.76	S
126	SWISS	1008.93	176.69	S
127	SWISS	55.70	251.73	sM
128	SWISS	520.25	317.20	S
129	SWISS	15.78	135.67	S
130	SWISS	2.26	323.68	mS
131	SWISS	288.66	197.19	sG
132	SWISS	1005.12	167.77	gS
133	SWISS	1487.07	5981.46	gS
135	SWISS	0.97	558.10	S
137	SWISS	1518.74	3035.52	gS
140	SWISS	351.66	1371.51	sG
141	SWISS	98253.52	7783.65	