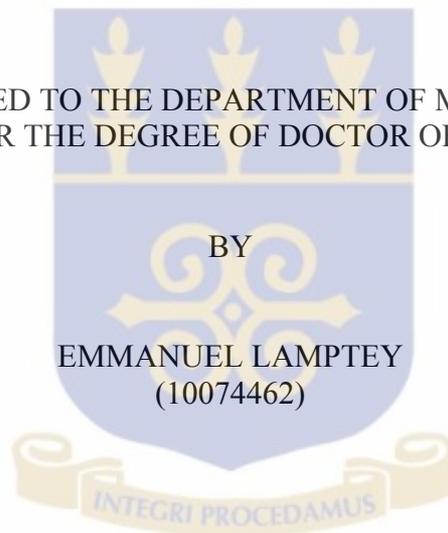




UNIVERSITY OF GHANA

**ECO-FUNCTIONAL BENTHIC BIODIVERSITY ASSEMBLAGE
PATTERNS IN THE GUINEA CURRENT LARGE MARINE
ECOSYSTEM**

A THESIS SUBMITTED TO THE DEPARTMENT OF MARINE & FISHERIES
SCIENCES FOR THE DEGREE OF DOCTOR OF PHILOSOPHY



BY

EMMANUEL LAMPTEY
(10074462)

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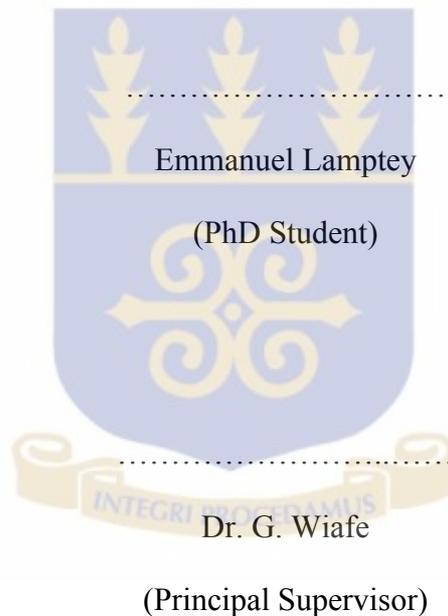
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PhD. OCEANOGRAPHY

DECEMBER, 2015

DECLARATION

This PhD thesis is original and independent research work conducted under supervision of Dr. George Wiafe, Prof. Elvis Nyarko and Mr. A.K. Armah of the Department of Marine and Fisheries Sciences. This research has not been included in any thesis or dissertation submitted to other institution for a degree, or any other qualifications. Authors whose works were used have been duly referenced/recognised.



.....
Prof. Elvis Nyarko
(Supervisor)

.....
Mr. A.K. Armah
(Supervisor)

DEDICATION

I dedicate this piece of work to God Almighty and my family.



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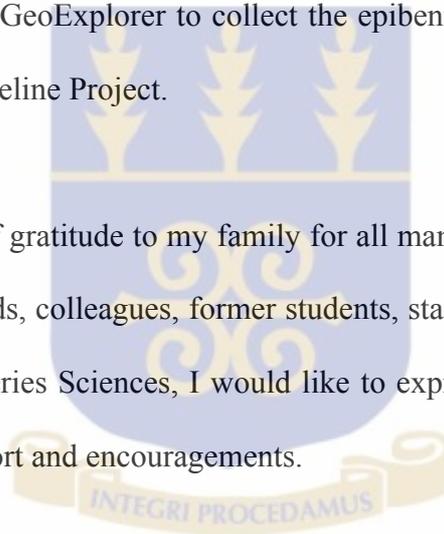


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LIST OF ABBREVIATIONS AND ACRONYMS

ABC:	Abundance-Biomass Comparison
ABC:	Abundance Biomass Curve
ANOSIM:	Analysis of Similarities
ANOVA:	Analysis of Variance
BC:	Benguela Current
B-EF:	Biodiversity Ecosystem Function
BIO-ENV:	Biological and Environment
BN:	Benin
BTA:	Biological Trait Analysis
CANOCO:	Canonical Community Ordination
CBD:	Convention on Biological Diversity
CC:	Canary Current
CCA:	Canonical Correspondence Analysis
CD:	Cote D'ivoire
CI:	Chlorine Index
CR:	Cameroon
DBM:	Dendrogram Based Measure
EA:	Equatorial Anticyclonic
EAF:	Ecosystem Approach to Fisheries
EAM:	Ecosystem Approach to Management
EcoQO's:	Ecological Quality Objectives
FAD:	Functional Attribute Diversity
FD:	Functional Diversity

FE:	Functional Evenness
FGR:	Functional Group Richness
FR:	Functional Richness
FS:	Functional structure
FWHM:	Full Width at Half Maximum
GA:	Gabon
GB:	Guinea Bissau
GC:	Guinea Current
GCE:	Guinea Current Ecosystem
GCLME:	Guinea Current Large Marine Ecosystem
GH:	Ghana
GNP:	Gross National Product
GU:	Guinea
HCL:	Hydro Chloric Acid
HPGe:	High Purity Germanium
INAA:	Instrumental Neutron Activation Analysis
ITCZ:	Intertropical Convergence Zone
KCl:	Potassium Chloride
LI:	Liberia
MCA:	Multi Channel Analyzer
MDS:	Multi-dimensional Scaling
MFAD:	Modified Functional Attribute Diversity
MLRA:	Multiple Linear Regression Analysis
MNSR:	Miniature Neutron Source Reactor
NAS:	North Atlantic Subtropical

NEC:	North Equatorial Cyclonic
NECC:	North Equatorial Counter Current
NG:	Nigeria
OC:	Organic Carbon
OM:	Organic Matter
POC:	Particulate Organic Carbon
RDA:	Redundancy Analysis
SEC:	South Equatorial Cyclone
SECC:	South Equatorial Counter Current
SIMPER:	Similarity Percentages
SL:	Sierra Leone
SOPs:	Standard Operation Procedures
SR:	Species Richness
STA:	Species Trait Analysis
TG:	Togo
TG-BN:	Togo-Benin
TOC:	Total Organic Carbon
TN:	Total Nitrogen

ABSTRACT

Functional diversity, an important component of biodiversity, has in recent years engaged global attention. This is in great part due to the mechanistic understanding achieved from functional diversity studies in the face of accelerated global biodiversity changes ascribed primarily to anthropogenic drivers. The exigency of the situation has stimulated biodiversity-ecosystem functions (B-EF) studies to elucidate ecosystem processes and services that are at threat notably in the marine ecosystem. The marine benthos is the largest ecosystem on earth and supports the highest phylogenetic diversity but has rather witnessed comparatively low attention in the B-EF studies than the terrestrial counterpart. This thesis is aimed at i) quantifying benthic functional diversity (using biological trait analysis) and assemblages along abiotic gradients in the Guinea Current Large Marine Ecosystem (GCLME); and ii) examining the impact of bottom trawling for demersal fishes on the functional structure of epibenthic fauna along bathymetric gradients.

In achieving the above-mentioned objectives, epibenthic fauna of bottom trawl samples were collected from Ghana to western Nigeria's continental shelf in 2003. Further, macrobenthic infauna and abiotic samples were collected from coastal waters of Guinea Bissau to Gabon in 2007. Each processed dataset was treated as a stand-alone in the thesis. In decomposing the assemblage patterns, suites of univariate and multivariate statistics were employed. The results indicated 381 macobenthic species comprising polychaetes (61.15% richness and 55.15% abundance), crustaceans (18.64% richness and 28.02% abundance), molluscs (9.19% richness and 2.23% abundance), echinoderms (2.63% richness and 1.84% abundance) and 'others' (8.39% richness and 12.76% abundance). Functional diversity analysis indicated spatial differences in eco-functional traits namely small

body size, solitary lifestyle, burrowing and deposit-feeding, and these traits dominated the assemblage especially from Ghana to Benin. The results suggest that these areas are potential surrogates of allochthonous organic material possibly driving pelagic productivity that is translated to the benthos. Significant ($p < 0.05$) relationship was found between functional traits (also species diversity) and sediment parameters (i.e., nitrate, calcium, magnesium, organic carbon, silt & clay). These abiotic variables largely implicate productivity and climate change models as principal community drivers, and are likely to impact ecosystem functions directly by altering B-EF relationship. Inferentially, the results indicated an unstable, dynamic, productive and low biomass-supported ecosystem Guinea Current Large Marine Ecosystem (GCLME), reflecting in the small body size solitary burrow-dwelling deposit-feeding organisms, which potentially exert the strongest influence on ecosystem processes (e.g., nutrient remineralization). These species used multiple adaptative strategies including trophic, lifestyle, anatomical and morphological in the prevailing environment.

Bottom trawled epibenthic sample analysis showed significant difference ($p = 0.002$; ANOSIM) of assemblages along bathymetric gradient, notably between shallow-depth (11-30m) and deep-depth (51-70m). Functional analyses showed dominance of carnivores (28% contribution), opportunistic/scavenging (9%) and herbivore (9%) in shallow waters, while filter-feeders (18%) dominated deep waters suggesting gradient in structuring forces. The high abundance of motile epibenthic fauna (64%) is suggestive of an unstable substrate and turbulent system supporting motile carnivores and filter-feeding organisms. The evidence of trophic interactions between demersal fishes and epibenthic fauna occurred ideally in most tolerable and favorable zone (i.e. mid-depth). Abundance-Biomass Comparison (ABC) analyses

indicated an ecosystem which is stressed (66.56%) with the degree of stress inversely related to increasing water depth. The findings of this thesis have important implications for marine biodiversity conservation and resource management approach in the GCLME.

CHAPTER ONE

GENERAL INTRODUCTION

Biodiversity, from genes through species to ecosystems, play an important role in the evaluation of the resilience of natural systems to environmental changes (Naeem *et al.*, 1999; Mant *et al.*, 2014). Understanding the patterns and processes of biodiversity at the primary, secondary and tertiary trophic levels is fundamental to sustainable management of marine living resources (Sherman and Duda, 1999; Costello, 2000; Hooper *et al.*, 2005). Biodiversity loss is defined as a sudden change to natural ecosystem setting due to human interventions. This is because natural changes of biodiversity are a much slower and longer-term process (Kessler *et al.*, 2007), which may be reversible. Human activities have contributed to variability in global climate, land cover and biodiversity at unprecedented rates (Steffen *et al.*, 2004). Human activities that affect biodiversity are referred to as *critical environmental issues* (National Research Council, 1995). The world is facing accelerated and apparently inevitable loss of species (Pimm *et al.*, 1995) and populations (Hughes *et al.*, 1997) through anthropogenic impact on the world's ecosystems.

The socioeconomic consequences of global biodiversity changes from *critical environmental issues* will depend on how they translate into altered ecosystem processes and services (Costanza *et al.*, 1997; Balmford *et al.*, 2002; Millennium Ecosystem Assessment, 2003). Impact of biodiversity loss under economic terms will mean that humankind will have to technically compensate for the services ecosystems provide (e.g. CO₂/O₂ gas regulation, food production, raw material

production, prevention of soil erosion, genetic resources for pharmacy development, regulation of hydrological flows) (Costanza, *et al.*, 1998; Edwards and Abivardi, 1998). Nonetheless, the ecological impacts of biodiversity loss are poorly understood (Solan *et al.*, 2004).

Concerns of biodiversity loss are more amplified in the marine ecosystem due to the uncertainties associated with the effects of the loss on the basic functioning of the ecosystem and the oceans' capacity to withstand multiple human disturbances (Snelgrove *et al.*, 1997). Available information indicates that the oceans account for approximately two-thirds of the value of global ecosystem services (Snelgrove, 1999), which is estimated to average \$33 trillion US dollars/yr compared to the Global GNP of \$18 trillion/yr (Costanza *et al.*, 1997). As a result, of the ecosystem services, a large and increasing proportion of the world's population lives close to the coast; thus the loss of services such as flood control and waste detoxification can have disastrous consequences to coastal dwellers (Danielsen *et al.*, 2005; Adger *et al.*, 2005). The marine seafloor is the largest ecosystem on earth (Snelgrove *et al.*, 1997) supporting high phylogenetic diversity (Snelgrove, 1999; Giller *et al.*, 2004) and key ecosystem services (Bremner, 2008) and as a consequence biodiversity alterations/changes may have wider ecological and socio-economic implications. Marine ecosystems provide a wide variety of goods and services, including food resources for millions of people (Peterson and Lubchenco, 1997; Holmlund and Hammer, 1999). The maritime domain has also been used by society for different activities including fishing, aquaculture, shipping, tourism, renewable energies, extraction of minerals etc. (Borja *et al.*, 2013).

Marine biodiversity alterations at both local and global scales can disrupt the ecological functions that species assemblages perform (Hughes *et al.*, 2003). These changes make differentiation between effects of species richness *per se*, and the effects of functional group richness (i.e., functional diversity) on ecosystem function a major issue in ecology (Solan *et al.*, 2004). This is because, although biodiversity generally enhances many process rates, such as resource use or biomass production, across a wide spectrum of organisms and ecosystems, the evidence for positive effects of biodiversity on ecosystem functioning (i.e., ecosystem processes, properties and their maintenance, (Reiss *et al.*, 2009) is neither ubiquitous nor unequivocal (Thompson and Starzomski, 2007; Jiang *et al.*, 2008).

Marine benthic faunal diversity, therefore, provides an ideal tool for exploring the relationship between biodiversity and ecosystem functioning in the marine environment (Snelgrove, 1999). Ecosystem functioning involves several processes, which can be summarized as production, consumption and transfer of organic matter to higher trophic levels, organic matter decomposition, and nutrient regeneration (Danovaro *et al.*, 2008). According to Jax (2005) ecosystem functioning refers to the overall performance of ecosystem, and has been variously defined as incorporating, individually or in combination, ecosystem processes (such as biogeochemical cycles), properties (e.g. pools of organic matter), goods (food and medicines) and services (e.g. regulating climate or cleansing air and water) as well as temporal resistance or resilience of these factors over time in response to disturbance (Biles *et al.*, 2002; Hooper *et al.*, 2005; Duffy and Stachowicz, 2006).

The assemblage patterns of the marine macrobenthos and associated functional diversity, and their spatial and temporal variations as well as the drivers of functional traits remain poorly understood. The importance of the marine macrobenthic functional diversity includes roles in the structure and functioning of the systems, particularly their productivity and resilience in the potential human-induced disturbances/perturbations context (Solan *et al.*, 2006). Essentially, the global biodiversity concerns, exemplified by the predictions that species loss might impair the functioning and sustainability of ecosystems (Naeem *et al.*, 1994; Sala *et al.*, 2000; Loreau *et al.*, 2001; Hooper *et al.*, 2005; Worm *et al.*, 2006;) have stimulated ecosystem-based and experimental efforts to: i) understand the synergy between biodiversity and ecosystem functioning, and ii) devise sustainable management strategies (Levin, 2001).

The apparent failure of diversity conservation tactics (Soulé, 1991; Faith, 2011), and the need to gain more profound understanding about the factors governing and/or governed by biodiversity is urgent and crucial. Diversity indices are relevant tools on which far-reaching decisions are based on in conservation science (Walker and Faith, 1994; Reid *et al.*, 2004). Indices derived from phylogeny play an important role in this area, where decisions frequently have to be taken on basis of a limited data about the system in question. Previously, the tendency was to focus on species diversity in one dimension using a single parameter (e.g., species richness) (Gaston, 2000). However, current studies employ different descriptors, and example of two of such descriptors that are improving description and understanding of diversity are *macrophysiology* and *trait* approaches. Macrophysiology describes how physiological traits are distributed in space (Chown *et al.*, 2004); while

morphological traits enable exploration selection pressures between different species assemblages (Vermeij, 1978; Ricklefs and Miles, 1994; Roy *et al.*, 2004; McGill *et al.*, 2006). The functional trait approach is interested in explaining the abundances and distributions of species (McGill *et al.*, 2006). It advocates for the examination of numerous functional traits and also species' abundance and trait distributions across environmental gradients (McGill *et al.*, 2006). The goal of the functional trait approach is to explore how the fundamental niche is determined by physiological and morphological traits and consequently how organismal traits and the fundamental niche are related to the realized niche (McGill *et al.*, 2006). A functional trait is defined as an attribute of an organisms' morphology or physiology that affects fitness indirectly via growth, reproduction and survival (Violle *et al.*, 2007). A trait-based approach in combination with an understanding of where species occur in relation to environmental gradients may provide new perspectives to species diversity; especially because most spatial and temporal patterns of diversity are based solely on the unit of species richness (Roy *et al.*, 2004).

Morphological traits are useful tools for detecting different selection pressures at species-rich and species-poor systems (Vermeij, 1978). For example, gastropod shell armour is more elaborate in species-rich tropical system than in species-poor temperate rocky intertidal environments (Vermeij, 1978). This relationship infers a gradient of protection against predation to tropical species (Vermeij, 1978). Although most diversity measures are likely to correlate with species richness, e.g. genetic diversity, in some cases the relationship between species richness and the traits of species can be complex and non-linear (Foote, 1997; Roy and Foote, 1997). Morphological diversity in most species-rich systems is not higher than in systems

with half the number of species, suggesting that species-poor systems can still harbor a great variety of morphological trait diversity (Roy *et al.*, 2001). Morphological traits have also been used to examine differences between species-rich and species-poor systems (Ricklefs and Miles, 1994). From basic principles, morphological traits of species in species-rich systems, relative to species-poor systems, could be expected to display either (a) increased morphological trait variety, i.e., a greater occupied morphospace, and trait differences between species, (b) minimized trait differences between species within a larger or similar occupied morphospace as temperate species or (c) have similar traits, i.e. show morphological overlap, in an occupied morphospace similar to temperate species (MacArthur, 1972; Ricklefs and Miles, 1994).

Measures of ecological functioning emphasize the roles played by organisms and include information on their interactions with their chemical and physical environment (Bremner, 2005). Measuring changes in the rates of ecological processes in the presence of anthropogenic impacts will, therefore, incorporate information on the chemical and biological components of ecosystems (Bremner, 2005). Hence, investigation of ecological functioning focus on the types of taxa present in marine communities and their responses to anthropogenic impacts. Taxa interact in various ways with their physical and chemical environment depending on the characteristics they express, and changes in the occurrence of these taxa have implications for ecological processes (Bremner, 2005). Organisms sharing particular characteristics are not always affected in the same way (Ramsay *et al.*, 1996) and as the methods also do not examine the responses of every taxon expressing a particular characteristic; it is difficult to determine their general responses. This thus

compromises the ability of the methods to determine anthropogenic effects at the ecosystem level (Bremner, 2005).

Nonetheless, a promising method for evaluating the ecological functioning of marine benthic assemblages is the use of biological traits analysis (Bremner; 2005), which originated from terrestrial and freshwater ecosystems studies (Olf *et al.*, 1994; Townsend and Hildrew, 1994; McIntyre *et al.*, 1995). Many terrestrial ecosystem studies have found positive effects of plant diversity on ecosystem processes, but this pattern has been less general in marine systems, where many studies find weak or no effects (Stachowicz *et al.*, 2007). The biological trait analysis approach explicitly incorporates information on the attributes of all members of the species assemblage, and on a wide range of attributes connected to organisms' interactions with each other and their physical and chemical environments, as well as their perceived responses to anthropogenic stress (Bremner, 2005). It can also accommodate intraspecific variation in trait expression (Chevenet *et al.*, 1994); thereby overcoming the problems encountered in trophic or functional group analyses where taxa fit into more than one functional category. Characters such as reproduction type, larval type, body size, movement, body form, growth rate, feeding type, attachment etc. are substituted for species names and multivariate analyses are conducted (Fleddum, 2010). Ostensibly, several factors influence the number of traits selected for inclusion in biological trait analysis, such as the length of the taxon list utilized, the amount of information available on biological characteristics of these taxa and the time required for gathering the information (Bremner, 2005). The use of the biological trait analysis (BTA) makes it possible to compare assemblage patterns of species and traits analyses, and also can reveal relationship of structure and

functional properties (Chevenet *et al.*, 1994; Charvet *et al.*, 2000; Bremner *et al.*, 2003b). The BTA can better discriminate environmental differences in comparison with taxonomic composition. The traditional biodiversity data analysis methods tend to underestimate the importance of rare species although it has provided useful information of benthic community structure over the years (Bremner, 2005; Fleddum, 2010). The use of BTA together with traditional biodiversity analysis is helpful in identifying impact-driven alterations to ecological functioning as well as providing information for ecosystem monitoring, management and conservation (Fleddum, 2010). For example, Bremner *et al.* (2003b) compared traditional analysis technique using relative taxa composition and trophic guilds with BTA in investigating the functioning diversity of macrobenthic fauna in the southern North Sea and eastern English Channel. They concluded that BTA can offer information on assessing ecosystem functioning in benthic environments on both large and small scales, and that there is a significant relationship between habitat and traits.

According to Usseglio-Polatera (2000b) the species trait approach has the potential to evaluate the actual state of ecosystems, discriminate among different types of human impact, and help to develop monitoring tools for ecological communities. However, the use of the BTA in the marine benthic ecosystems has received little attention (Bremner, 2005) and lags behind the freshwater and terrestrial counterparts (Bremner, 2008). Of much concern is the lack of study in the Guinea Current Large Marine Ecosystem (GCLME) focusing on functional species assemblages employing the BTA approach. Where information on general benthic biodiversity in the region has been carried out, the literature is widely dispersed and inadequate. The GCLME is one of the productive large marine ecosystems in the world's ocean (Ukwe, 2003;

Ukwe *et al.*, 2006). The fishery and the plankton have received some attention (Bainbrige, 1972; Bakun, 1978; Mensah, 1995; Koranteng, 1998; Wiafe, 2002; Wiafe 2008). However, very little is known about the dynamics of the macrobenthic community, especially its functional diversity and community structure. Knowledge of macrobenthic functional diversity and community structure will contribute immensely to understanding the overall trophic dynamics, biodiversity and ecosystem functioning of the GCLME.

1.1 Study Objectives and Hypothesis

The primary aim of this research is to investigate macrobenthic functional traits diversity and community assemblages along spatial scales in the GCLME. The research further explored whether environmental gradient, on spatial scale, correlated with local species diversity and their functional attributes. The study aimed at testing the hypothesis that the marine benthic functional biodiversity effects on ecosystem processes/properties were the results of established environment gradient in the ecosystem . Specifically, the following predictions were tested as part of the overall hypothesis:

- Dominant macrobenthic functional trait assemblages rather than species richness exert the strongest control on ecosystem properties/process; and
- abiotic stressors/drivers/factors select for differences in functional traits and species assemblages.

In order to evaluate the central predictions of the study hypotheses, the following objectives were formulated:

- Identify and quantify dominant functional traits and elucidate their influence on ecosystem functions;

- Ascertain how macrobenthic faunal communities and eco-functional trait assemblages are influenced by abiotic factors. This will assist in understanding and predicting how benthic communities and ecosystem properties might be affected by environmental variability and disturbance;
- Identify dominant epibenthic functional traits across bathymetric gradients;
- Investigate the effects of bottom trawling for demersal fishes on species diversity and functional structure of epibenthic communities; and
- Evaluate the ecological quality status of the GCLME using epibenthic macrofauna species.

1.2 Study Justification

The past several decades have witnessed a soaring research interest on earth's biodiversity across all environments, including studies that assessed trends in biodiversity and the underlying mechanisms that produced and maintained such trends. Escalating concerns over the loss of marine biodiversity and associated consequences have increased the urgency for research for a better mechanistic understanding.

Many of such studies/research have been carried out in short-term and on local scale with findings (species diversity and the driven forces) which still limit our understanding. Nonetheless, a growing body of research has addressed the functional consequences of diversity for ecosystem processes (Stachowicz *et al.*, 2008). The primary goals of Biodiversity-Ecosystem functioning research have been to investigate how biodiversity and ecosystem functioning are linked and to understand the mechanisms that inform such relationships. In accordance, recent biodiversity

researches have principally focused on important links between number of species and ecosystem functioning (Hooper *et al.*, 2005; Worm *et al.*, 2006; Solan *et al.*, 2008, 2009).

Earlier studies on biodiversity-ecosystem functioning tested whether ecosystem functioning was enhanced in species-rich versus depauperated assemblages (Srivastava and Vellend, 2005), but was demonstrated that biodiversity generally enhances many process rates such as resources use or biomass production, across a wide spectrum of organisms and ecosystems (Balvanera *et al.*, 2006). However, the evidence for positive effects of biodiversity of ecosystem functioning is neither ubiquitous nor unequivocal (Thompson and Starzomski, 2007; Jiang *et al.*, 2008), stimulating conservable scientific debate (Loreau *et al.*, 2002). Following from this, four research themes namely: functional traits, environmental gradients, interactions milieu and performance currencies have been suggested (McGill *et al.*, 2006) as a cornerstone of modern ecology in order to fully understand the biodiversity–ecosystem functioning.

There have been many studies investigating the relationship between species diversity, functional diversity and ecosystem function (Petchey and Gaston, 2002; Petchey and Gaston, 2006; Bremner, 2008). In marine benthic ecosystems, however, only a few studies have examined that relationship and most of them have shown a strong correlation between species diversity and functional diversity (Bremner *et al.*, 2003b; Micheli and Halpern, 2005; Hewitt *et al.*, 2008). Furthermore, there are studies investigating how biotic and abiotic components affect the temporal and spatial variability in functional diversity (Emmerson *et al.*, 2001; Raffaelli *et al.*,

2003; Micheli and Halpern, 2005; Ieno *et al.*, 2006; Bell, 2007; Norling *et al.*, 2007), but it seems that such processes affect species diversity and functional diversity in a similar way (Bremner *et al.*, 2003b; Micheli and Halpern, 2005; Hewitt *et al.*, 2008).

1.3 Datasets for the Thesis

The datasets used for this thesis research included the following:

- Epibenthic trawl samples collected along the continental shelves of Ghana, Togo, Benin and western part of Nigeria in 2003 as part of the West Africa Gas Pipeline Project (WAPCo, 2003). This data was used for the assessment of the impacts of bottom trawling on epibenthic functional assemblage patterns.
- Macrobenthic fauna and sediment samples collected from Guinea Bissau to Gabon in 2007 as part of the Guinea Current Large Marine Ecosystem (GCLME) project comprising 16 countries (GCLME, 2006). This data was used to investigate soft-bottom macrobenthic infauna functional assemblage patterns and their response to environmental variability.

1.4 Organization of Thesis

The thesis comprises five chapters. Chapter 1 presents a general introduction to the thesis, with a brief background information on marine biodiversity, functional diversity, trait analysis, level of macrobenthic information in the GCLME, scientific hypothesis and study objectives. The various data sets used in the analyses have also been presented. Chapter 2 presents a detailed review of relevant literature on the subject, biodiversity structure and functions of macrobenthic communities as well as environmental factors influencing benthic biodiversity assemblages. Chapter 3

describes the 'macrobenthic functional traits diversity and community structure along environmental gradient. Chapter 4 focuses on impact of demersal fish trawling on the structure and functional assemblages of epibenthic fauna along bathymetric gradient. Chapter 5 gives general conclusions and recommendations. The species list and biological trait database are presented as Appendices I & II. Appendix III shows the carbon:nitrate ratios and the sources of organic load, while statistical descriptions are annotated in Appendix IV.

CHAPTER TWO

LITERATURE REVIEW

2.1 Marine Benthic Biodiversity

The idea of biodiversity has taken hold on science and society with its multifaceted concepts (Zajac, 2008) and has also emerged as a major field within ecological research. Biodiversity has been variously defined as the variety of life and collectively referred to variation at all levels of biological organization (Sheppard, 2006). According to Harper and Hawksworth (1994), biodiversity refers to the extent of genetic, taxonomic and ecological diversity over all spatial and temporal scales. However, the Convention on Biological Diversity (CBD) gave the most important and far-reaching definition in its Article 2 to mean '*the variability among living organisms from all sources including, inter alia, terrestrial, marine and other aquatic ecosystems and the ecological complexes of which they are part; this include diversity within species, between species and of ecosystem*' (Convention on Biological Diversity, 1992). In seeking to describe the "variety of life" or "nature," biodiversity includes three components of diversity, namely, "within species," "between species" and "of ecosystems" (Costello, 2000). The usage of the term is value laden connoting that biodiversity is *per se* a good thing, that its loss is bad, and that something should be done to maintain it.

Diversity is usually designed as being α -diversity (the diversity within a given habitat), β -diversity (the degree to which communities show spatial variability in species composition from place to place) and γ -diversity (the overall diversity in a whole region; (Whittaker, 1975). At the species level in a given assemblage, α -

diversity can be regarded as either the number of species present (“species richness”), the proportional abundance or homogeneity of individual species (“evenness” or “equitability”) or more commonly a combination of both (Terlizzi and Schiel, 2009).

The marine benthic biodiversity comprise organisms that span a wide range of sizes, including micro-, meio-, macro- and megafauna (Clarke and Warwick, 1994; Dittmann, 1995; Zajac, 2008). These organisms are operationally classified as microbenthos (< 63 μm), meiobenthos (from 63 μm to 500 μm) and macrobenthos (> 500 μm or > 1000 μm) according to the sieve mesh size used for extracting them from sediment cores or grabs. The macrofaunal forms are by far the better known and are the main essential component of environmental impact studies (Clarke and Warwick, 1994). Marine macrobenthos are a diverse group of organisms composed mainly of molluscs (bivalves and snails), polychaetes (bristle worms), crustaceans (amphipods, shrimps, and crabs) and echinoderms (sea cucumbers, brittle stars, sea urchins) (Gray, 1981a). These organisms are central elements of marine ecosystems and provide excellent indicators of environmental health. They also play multiple ecological roles within the marine ecosystem and are a critical part of environmental monitoring and evaluation programmes. Most macrobenthic animals are relatively long lived (several years) and thus integrate changes and fluctuations in the environment over a longer period of time. Changes in soft bottom zoobenthic communities in response to the environmental impact have been successfully implemented world-wide in pollution assessment studies and monitoring programs (Pearson and Rosenberg, 1978).

Variations in species composition, abundance and biomass can be used to assess environmental disturbance. Comparatively rich and diverse shallow-water benthic communities are amenable for more sensitive analyses of eutrophication effects. The potential benefits of using macro-invertebrates include quick detection of pollution through differences between predicted and actual faunal assemblages (Ormerod and Edwards, 1987). Of relative importance, benthic invertebrates are relatively sessile (therefore allowing spatial patterns to imply causation), can be sampled quantitatively without high cost, are well described taxonomically, and reveal ecologically meaningful and important patterns, even at coarse levels of taxonomic discrimination (Warwick, 1988c). Analysis of differences in macrobenthic community structure is one of the mainstays of detecting and monitoring the biological effects of marine pollution and habitat disturbance (Warwick and Clarke, 1993) as well as for ecological modeling (Tumbiolo and Downing, 1994; Josefson and Rasmussen, 2000).

In most environmental studies of impacts, benthic invertebrates are the principal targeted organisms (78 percent of all studies), reflecting their suitability as ecological indicators (Clarke and Warwick, 1994; Peterson and Bishop, 2005). The macrobenthic infaunal communities are especially suited for long-term comparative investigations since many of the constituent species are of low mobility, relatively long lived and integrate effects of environmental changes over time. Consequently, macrobenthic fauna constitute good biological candidates for monitoring ecosystem health and processes. Cury and Roy (2002) have stressed that studies that link the different components of the trophic web or the spatial and temporal dynamics of the

interaction between the environment and marine resources are needed as they have important implication for managing the resources.

Marine biodiversity is of direct benefit to society as a food source, potential pharmacopoeia (Hunt and Vincent, 2006), stabilizer of inshore environments (Jie *et al.*, 2001) and regulator of atmospheric processes (Murphy and Duffus, 1996). Marine biodiversity provides indirect benefits to society through ecological stability (Menge *et al.*, 1999) and benthic-pelagic coupling (Ponder *et al.*, 2002) which contribute to self-sustaining marine ecosystems. Marine biodiversity also has recreational, aesthetic and intrinsic value (Wilson, 1994; Ponder *et al.*, 2002).

2.2 Functional Role of Benthic Communities

Benthic communities perform numerous ecological functions to the systems they inhabit. Benthic organisms continually process, transport, and modify marine sediments. There are those that bind, protect and stabilize near-surface sediment and those that loose and destabilize the sediment (Nichols and Boon, 1994). They also play a vital role in organic matter processing and nutrient cycling at the water/sediment interface (Aller and Yingst, 1985; Rosenberg, 2001) and decomposition of dead matter or waste materials (Snelgrove *et al.*, 1997). Sediment organic matter is a causal factor of infaunal distribution (Snelgrove and Butman, 1994) being the dominant source of food for deposit-feeders (Pearson and Rosenberg, 1978), and indirectly (e.g., through re-suspension) for suspension feeders (Snelgrove and Butman, 1994). Benthic organisms also improve the conditions within the sediment, such as oxygenation (Reise, 1985) and loosen subsurface sediments and render them inhabitable by other macrofauna (Flint and Kalke, 1986).

Benthic invertebrate assemblages are heavily involved in the regulation of ecosystem processes (Snelgrove, 1998), so provide a useful study unit. Functioning in these assemblages will be dependent on the biological characteristics, or traits, exhibited by constituent species, because these determine how the species contribute to ecological processes.

Woodin and Jackson (1979) have proposed five functional groups of benthic organisms in relation to their effects on the sediment: (i) mobile burrowers that destabilize the sediment (including their feeding activity) such as crustaceans, amphipods & tanaids, and Maldanid polychaetes; (ii) sedentary organisms that cause the sediment to be more easily resuspended (e.g., infaunal holothurian, *Molpadia oolitica*, Crustacean *Callinassa*); (iii) sedentary organisms that do not inhabit tubes that still straddle the sediment-water interface and modify the local hydrography such as to reduce re-suspension and, by virtue of buried parts, bind the subsurface particles together (e.g., seagrasses such *Thalassia* & *Zostera*, Sabelid polychaete worms); (iv) tube builders that stabilize the sediment by incorporating it, often in mucus-bound form into their tubes (e.g., mud snail *Illyanasa obsoleta*, polychaete *Polydora*); and (v) neutral species having no impact on sediment deposition or re-suspension. The feeding type of the benthic community is considered as an adaptation to the sediment characteristics (Rosenberg, 1995).

However, it has been suggested that animal and sediment correlation is a result of hydrological and geological processes associated with sediment granulometry rather than a function of organism in available space within sediment (Parry *et al.*, 1999). For macro-invertebrates, the requirements of life in unconsolidated sediments

inevitably involve the need to move particles around in some way, whether as a consequence of locomotion through the sediments, or feeding upon the organic material associated with them. This is known as bio-turbation (Hall, 1994). Bio-turbation occurring in sediments regulates carbon degradation and benthic-pelagic nitrogen cycling (Biles *et al.*, 2002; Widdicombe *et al.*, 2004).

Benthic species also affect the microbial processes in the sediments by modifying particle distribution, sediment porosity, and solute transport (Krantzberg, 1985). Bio-turbation of sediments by burrowing or deposit-feeders through processes such as irrigation, pelletization and tube construction, usually increases sediment pore space and thus, water content in the upper sediment layer (Rhoads, 1974; Rhoads and Young, 1970). Bio-turbation lowers erosion resistance of the surface, and thus destabilizes the bed sediment. Bio-turbation can be important in excluding particles and pore water nutrients across the sediment-water interface as well as through various vertical chemical gradients in the sediment (Nichols and Boon, 1994).

The impacts of invertebrates on biogeochemical processes are often due to biogenic structure in marine sediments (Aller and Aller, 1986, Kristensen *et al.*, 1991; Mayer *et al.*, 1995; François *et al.*, 1997) and infaunal activity (Holst and Grunwald, 2001). Biogenic structures can modify organic matter distribution and solute transport at the water-sediment interface (Krantzberg 1985, de Vaugelas and Buscail, 1990). Solute transport is enhanced by animal movement and burrow ventilation, which is a process known as bio-irrigation (Riisgård and Banta, 1998). Bioturbation (i.e., sediment biogenic activities) does not only play a crucial role in the stabilization of marine benthic environments (Woodin and Jackson, 1979; Kristensen *et al.*, 1985)

but, also in recycling of nutrients that enhance ocean productivity. Oceanic productivity is related to abundance of commercially important species such as fishes thereby depicting a coupling between benthic biodiversity (functional effects) and fisheries (Hodson *et al.*, 1981; Bell and Woodin, 1984; Josefson and Rasmussen, 2000) through primary production (Kjerve, 1994).

The health of marine ecosystems is often assessed in terms of the taxon composition of faunal communities, or on the distribution of abundance/biomass between the species present (e.g., Warwick and Clarke, 1991; Bonsdorff and Blomqvist, 1993). Marine macrobenthic fauna are used in pollution and ecosystem health monitoring studies to ascertain pollution effects on the ecosystem (Sherman and Anderson, 2002). Potential benefits of research on macro-invertebrates include quick assessment of biological resources for conservation purposes and the detection of pollution through differences between predicted and actual faunal assemblages (Ormerod and Edwards, 1987). Macrobenthic communities have the capabilities to integrate into their system both short-, and long-term environmental changes and thus are excellent candidates for monitoring environmental impacts (Borja *et al.*, 2000). Snelgrove (1998) reported that the roles performed by benthic species are important in regulating ecosystem processes and that these roles can be portrayed by biological traits they exhibit.

2.3 Biodiversity Indices and Measurements

Measurements of biodiversity are often used as bases for making decisions on planning and conservation actions. In conservation, diversity indices become mighty tools on which far-reaching decisions are based on (Walker and Faith 1994; Reid *et*

al., 2004). It is evident from the biodiversity definition that there could be no clear single all-embracing measure of biological diversity owing to its great complexity. The breadth of ways in which differences can be expressed is infinite. The most practical and relevant measures of biodiversity within species are the phenotypic or visible attributes of populations. Nevertheless, measurements of biodiversity are based on three assumptions (<http://www.coastalwiki.org>):

- *All species are equal in abundance*: meaning that richness measurement makes no distinctions amongst species and treats the species that are exceptionally abundant in the same way as those that are extremely rare species. The relative abundance of species in an assemblage is the only factor that determines its importance in a diversity measure.
- *All individuals are equal in size*: this means that there is no distinction between the largest and the smallest individual; in practice however the smallest animals can often escape for example by sampling with nets. Taxonomic and functional diversity measures, however, do not necessarily treat all species and individuals as equal.
- *Species abundance has been recorded in using appropriate and comparable units*. It is clearly unwise to use different types of abundance measure, such as the number of individuals and the biomass, in the same investigation. Diversity estimates based on different units are not directly comparable.

Biodiversity has many facets, yet three generally different concepts in its quantification can be distinguished (Purvis and Hector, 2000):

- (i) Richness: was probably the first measure used for assessing diversity. Counting the number of taxa in the sample under consideration is always

the first step. Often richness or an estimate of it is the only measure available for large unexplored regions;

- (ii) Evenness- often the individuals are not evenly distributed among species. A site containing dozens of species may not seem particularly diverse if 99.9% of the individuals belong to the same species. Evenness is defined as the ratio of observed diversity to maximal possible diversity if all species in a sample were equally abundant (Purvis and Hector, 2000); and
- (iii) (iii) Phylogeny: difference between the observed organisms is another facet of diversity. Phenotypic and genetic variability are reflected in phylogeny. A community consisting of 30 species of polychaeta is intuitively less diverse than one consisting of 30 benthic macrofaunal species of 5 different classes. These three principal concepts can be applied not only at the species level, the definition of the term species being a problem of its own (Hey, 2001), but also on higher taxonomic levels or arbitrary divisions like functional groups. Species is the unit of diversity most easily conceptualized and is therefore most commonly considered (Willig *et al.*, 2003).

Many diversity indices combine two or even all three concepts into one number, in order to summarize information for decisions and comparisons. However, information is always lost in this process and none of the three concepts should be held in low regard.

2.3.1 Diversity Indices

Species richness: The oldest and most straightforward measure, where: s , the sum of species in the sample, d' , Margalef's species richness, n , number of individual species, and \log_e is the natural logarithm. Margalef (1958) proposed a richness index which is standardized against the n in the formula below, following information theory.

$$d = \frac{s - 1}{\log_e n} \quad (\text{Margalef, 1958})$$

Shannon's diversity index: The Shannon-Weaver diversity index is one of a so called family of heterogeneity indices. These indices do not only take taxa richness into account but also depend on the relative distribution of individuals. The logarithm can be taken to any base but taken to the base of two gives H' a special meaning: bits per species. It is the mean number of binary decisions necessary to determine the taxum of an individual. Originally derived from communication theory (Shannon and Weaver, 1949), this index was severely criticized by Hurlbert (1971) for containing no ecologically valuable information. Apart from the problem of interpreting the ecological meaning of bits per species, all heterogeneity indices share the drawback that information is lost by merging two concepts. It is not possible to tell from the final value, if it is high or low due to species richness or relative abundances or a combination of both.

$$H' = -\sum_{i=1}^s p_i \log_2 p_i \quad (\text{Shannon and Weaver, 1949})$$

Simpson's index of diversity: The Simpson's index D also belongs to the class of heterogeneity indices and is a probability measure. Therefore it ranges between 0 and 1 but it appears in three similar formulations: D , $1-D$ and $1/D$. Each one has its

own name but often they all use the symbol D and are simply called Simpson's index, so attention is advisable at comparisons. In the formulation of 1-D, the Simpson's index of diversity is the probability of encountering two different species when randomly picking two individuals of a sample.

$$D = 1 - \sum_{i=1}^s p_i^2 \quad (\text{Simpson, 1951})$$

Pielou's evenness: Pielou (1966) defined this equitability measure for the Shannon weaver index. J' will approach 1 if H' will approach the maximal possible value for the given set of species, meaning that all species in the sample will be equally abundant.

$$J' = \frac{H'}{H'_{max}} = \frac{H'}{\log_2 s} \quad (\text{Pielou, 1966})$$

Taxonomic diversity Δ : Proposed by Warwick and Clarke (1995), the taxonomic diversity index delta is derived from the Simpson index. ω_{ij} is the "distinctness weight" and has no fixed syntax. It could be simple as a number for relatedness (1=same genus, 2= different genus same family, etc.) or a measure of distance between species in a phylogenetic tree.

$$\Delta = \frac{\sum_{i=1}^s \sum_{j=1}^s \omega_{ij} x_i x_j}{\binom{n(n-1)}{2}} \quad (\text{Warwick and Clarke, 1995})$$

Taxonomic distinctness $\Delta +$: Taxonomic diversity calculated only on presence/absence data. If all x_i are assumed to equate to unity then taxonomic diversity reduces to taxonomic distinctness.

$$\Delta + = \frac{\sum_{i=1}^s \sum_{j=1}^s \omega_{ij}}{\left(\frac{s(s-1)}{2} \right)}$$

(Warwick and Clarke, 1995)

Sum of phylogenetic diversity $\Phi +z$: Introduced by Faith (1992). The total branch length of the phylogenetic tree.

Average phylogenetic diversity $\Phi +$: This is simply the total phylogenetic diversity divided by the number of species.

Although this is not exhaustive list, the selection shows representation of all the three concepts (richness, evenness, difference), as well as indices which incorporate concepts. Other common indices have not been used because they are in one way or the other inappropriate for the dataset, like Fisher's α , which assumes a log series distribution of species abundances, or the rarefaction method of Saunders which allows comparisons of samples of unequal size.

2.3.2 *Functional Diversity*

With the unprecedented nature of biodiversity changes, science is faced with the challenge of predicting how ecological systems will respond. Predicting future changes based on relationships and patterns in the current environment records offers one way to address this question. While this approach has yielded important insights, it is largely correlational, making the identification of the roles of specific drivers of change (e.g. climate, atmospheric chemistry, land use, biota) difficult (Osmond *et al.*, 2004). A complementary approach is to identify the functional or mechanistic basis of the links between ecosystem functioning and global changes by scaling processes (Woodward *et al.*, 1991; Field *et al.*, 1992; Iverson and Prasad, 2001).

Functional diversity can be quantified using a variety of indices that capture different aspects of the distribution of trait values within a community (Bóttta-Dukàt, 2005; Ricotta, 2005; Petchey and Gaston, 2006). Functional groups describe organisms that share a similar physiological or ecological function e.g. deposit-feeders, bioturbators, predators (Bonsdorff and Pearson, 1999). The validity of using functional groups has been questioned because analyses based on such divisions may be meaningless without more comprehensive knowledge about life history and biology of marine biota than is currently available for most species (Pearson, 2001). In addition, some evidence points to species identity being closely linked to ecosystem services such as bioturbation (Norling *et al.*, 2007).

In a broad scale functional diversity research, Naeem and Wright (2003) proposed four step-wise factors:

- i. determination of species composition across sites through regional biotic inventory of species pool and application of environmental filters (Woodward and Diament, 1991; Keddy, 1992) (hierarchy of abiotic and biotic factors that constrain the distribution and abundance of the species, see Diaz *et al.*, 1999; Lavorel and Garnier, 2002) to obtain local species composition.
- ii. Species abundance determination through relative abundance or common and rarity.
- iii. Determination of functional traits by selecting driver of biodiversity impacts, ecosystem process, screening the local biota for relevant functional traits, establishing response traits relevant to the selected driver, and also establishing effect traits relevant to selected ecosystem function.
- iv. Determination of ecosystem functioning.

Nonetheless, functional diversity (utilizing functional/biological traits analysis) has assumed increased prominence in biodiversity ecosystem function (e.g. Petchey and Gaston, 2002; Bremner, 2006). According to Mason *et al.*, (2005), functional diversity is a measure (or group of measures) of the distribution of species and abundance of a community in functional attribute space that represents the following:

- the amount of functional attribute space filled by species in the community (*functional richness*),
- the evenness of abundance distribution in filled niche space (*functional evenness*), and
- the degree to which abundance distribution in niche space maximizes divergence in functional attributes within the community (*functional divergence*).

In their perspective, Tilman, (2001) and Hooper *et al.* (2005) refer to functional diversity to mean the range and value of organism traits that can influence ecosystem properties. According to Hooper *et al.* (2005), functional diversity can be expressed in a variety of ways including the number and relative abundance of functional groups (Tilman *et al.*, 1997, Hooper and Vitousek, 1998) and (Spehn *et al.*, 2000), the variety of interactions with ecological processes (Martinez, 1996), and the average difference among species in functionally related traits (Walker *et al.*, 1999). Functional groups are defined as groups of taxa which share a range of similar attributes and have analogous effects on major ecosystem processes (Bonsdorff and Pearson, 1999).

Functional diversity results from the different ways by which different species exhibit similar functional traits, or the number of different functional groups sharing biological traits (Wright *et al.*, 2006). Functional attributes of species are therefore crucial to understanding the effects of marine biodiversity and its role in ecological patterns and processes. Functional categorization of marine species is a useful approach for comparing communities over large scales in a way that transcends taxonomic boundaries, and for linking changes in structure to effects on ecological function (e.g. Bellwood *et al.* 2003; Floeter *et al.* 2004; Micheli and Halpern, 2005). An effective functional classification could be a cost-effective way of predicting effects of loss (or restoration) of particular taxa on ecosystem functioning and could have valuable implications for management and conservation (Micheli and Halpern, 2005). Functional classifications can enable meaningful comparison of the roles of biodiversity in different ecosystems as they transcend taxonomic differences (Micheli and Halpern, 2005; Bremner, 2006).

Functional classification of organisms can also improve mechanistic understanding of community assembly (Micheli and Halpern, 2005). This is because diversity is manifest in species identities (e.g., variations in form and functions) and therefore variations in species traits is a key element in biological diversity (Crowe and Russell, 2009). Reiss *et al.* (2009) emphasized that biodiversity-ecosystem functioning (B-EF) experiments regarding traits, could hold species identity constant, and alter traits and functional diversity to demonstrate whether species provide unique contributions to ecosystem processes. Ecosystem functions (e.g., nutrient cycling, sediment stabilization etc.) are moderated by the functional attributes of species in a community. To understand how an ecosystem will function

and its ability to provide crucial ecosystem services as well as its capacity to respond to environmental changes, functional diversity of the assemblages are critical fundamental steps.

Thus, there have been increased interests in examining ecosystem consequences of biodiversity loss in marine systems (e.g., Emmerson and Raffaelli, 2000; Duffy *et al.*, 2001, Emmerson *et al.*, 2001; Stachowicz *et al.*, 2002; Solan *et al.*, 2004; Hooper *et al.*, 2005; Worm *et al.* 2006; Bracken *et al.*, 2008) especially in high latitude locations. However, the biodiversity ecosystem function (B-EF) relationship can be dependent on environmental conditions for specific ecosystem functions (Hiddink *et al.*, 2009), which differ in spatial scales. Functional diversity incorporates interactions between organisms and their environment into a concept that can portray ecosystem level structure in marine environments (Bremner *et al.*, 2003a). The functional traits of benthic species are modified on many temporal and spatial scales (Solan *et al.*, 2004) due to the effects of physical, chemical and biological characteristics. Environmental gradients may form geographic patterns of diversity by influencing local processes such as predation, resource partitioning, competitive exclusion, and facilitations that determine species co-existence (Levin *et al.*, 2001).

2.3.3 Functional Diversity Indices

Recently, several methods have been proposed and described on how to calculate functional diversity (Mason *et al.*, 2003, 2005; Botta-Dukát, 2005; Ricotta, 2005; Petchey and Gaston, 2006; de Bello *et al.*, 2006). Some consider species presence/absence, whereas others are based on abundance data (e.g., Bady *et al.*, 2005; Botta-Dukát, 2005; Mason *et al.*, 2005). However, incorporating species

abundances into a measure of functional diversity poses several questions on weighing the relative contribution of richness and evenness components (Hurlbert, 1971), and on the relationship of trait dissimilarity (Walker *et al.*, 1999) to the ecological diversity of species (Magurran, 1988). It is therefore a more complex problem than previously thought (Mouillot *et al.*, 2005; Ricotta 2005; Petchey and Gaston, 2006).

Petchey *et al.* (2004) compared four presence/absence measures of functional diversity: (i) species richness (SR), (ii) functional group richness (FGR), (iii) a dendrogram-based measure (DBM) and (iv) functional attribute diversity (FAD). Although the simplest measure is SR, it assumes that all species are equally different and the contribution of each species to functional diversity is independent of species richness (Petchey *et al.*, 2004). Functional group richness (FGR) is the number of functional groups present in the community. FGR assumes that the species within the same group are identical in function (Lawton and Brown, 1993) and assigning a species into a category is unambiguous. However, many animal species use, for instance, a variety of feeding strategies and show omnivory (Lancaster *et al.*, 2005; Woodward *et al.*, 2005ab). Thus, measuring functional diversity based on FGR is not always meaningful, even if its application can be fruitful when no taxonomical information on the fauna of the study area is available (Cummins *et al.*, 2005).

A further problem is that the number of functional groups is arbitrarily determined. Petchey and Gaston (2002) applied cluster analysis from a matrix of functional traits, and then used the sum of branch lengths of the dendrogram as a multivariate measure of functional diversity (DBM). This function does not suffer from the problem of

species categorization since it uses the functional traits of the species (Walker *et al.*, 1999; Petchey and Gaston, 2002; Petchey *et al.*, 2004; Botta-Dukát, 2005; Ricotta, 2005; Podani and Schmera, 2006), and can be defined as a continuous measure (Petchey and Gaston, 2006). However, DBM also has limitations. For instance, Petchey and Gaston (2002) suggest that after removing a group of species from the community, the functional diversity of the new community should be calculated by deleting those parts of the dendrogram which pertain to the removed objects and then by summing the branch lengths for the remaining part. When a new group of species is captured, a new dendrogram should be calculated for all species (i.e., the original species and the new species). Accordingly, the same community could have different functional diversity if measured by the DBM value, depending upon the original community and the dendrogram from which it was derived.

Functional attribute diversity (FAD) (Walker *et al.*, 1999; Petchey *et al.* 2004) is the sum of the pairwise functional dissimilarities of species. FAD can be calculated as follows

$$FAD = \sum_{h=1}^S \sum_{k=1}^S d_{hk},$$

(Walker *et al.*, 1999):

where S is the number of species, and d_{hk} is the dissimilarity between species h and k. Thus, FAD measures the dispersion of species in the functional traits space (Ricotta, 2005) and similarly to DBM, it is also a continuous measure of functional diversity (Petchey and Gaston, 2006).

Among the many methods, the Rao coefficient (another measure of functional diversity proposed by Rao, (1982)) is gaining currency as a good candidate as an

efficient functional diversity index, because it is a generalization of the Simpson's index of diversity, it is easy intuitively understandable, and it can be used with various measures of dissimilarity between species (both those based on a single trait, and those based on many traits (Ricotta, 2005; Petchey and Gaston, 2006). However, when intending to quantify the functional diversity, various methodological decisions such as how many and which traits to use, how to weight them, how to combine traits that are measured at different scales and how to quantify the species' relative abundances in a community have to be made.

The Rao index uses species traits to calculate dissimilarity among species (Botta-Dukát, 2005; Lepš *et al.*, 2006; Lavorel *et al.* 2008). The Rao index generally reflects the probability that, picking randomly two individuals in a community (i.e., a sample), they are different. For trait diversity, the Rao index represents the probability that they are functionally different (e.g. for single traits, either they have different trait values or different trait categories). The Rao coefficient is very flexible, and can be used with various dissimilarity measures. For example, Shimatani (2001) used it with taxonomic dissimilarity when exploring taxonomic diversity and amino acid diversity; asymmetrical measures can be also used. The main methodological decisions are mainly i) how to measure the species dissimilarity, and ii) how to characterize the proportion of a species in the community. These methodological decisions are also made even if other indices of functional diversity other than Rao's coefficient are being used (Lepš *et al.*, 2006).

The mechanistic models concerning the functional consequences of diversity have been based on the fact that species differ from each other (and thus function

differently; MacArthur, 1955). Similarly, the importance of the differences among species for maintaining species coexistence was explicitly expressed by the concept of limiting similarity (MacArthur and Levins, 1967). Ecologists have thus progressively realized that species differ from each other in terms of some traits (Díaz and Cabido, 2001) and thus that the effect of ecological diversity might be based on the “extent of trait dissimilarity among species in a community” (or functional diversity; Tilman, 2001; Petchey and Gaston, 2002). Traditionally, species diversity has been considered a surrogate for functional diversity in most studies linking biodiversity to ecosystem functioning (Díaz and Cabido, 2001; Loreau *et al.*, 2003). However, some pairs of species are very similar to each other, while some are very different. Consequently, the relationship between species diversity and functional diversity is expected to be positive (Petchey and Gaston, 2002) but not necessarily very tight (Díaz and Cabido, 2001; Petchey and Gaston, 2006).

Other two widely used continuous measures of functional diversity are the dendrogram-based measure (DBM) and the functional attribute diversity (FAD). In contrast to DBM, FAD does not require the knowledge of the entire species pool before the analysis, and hence FAD is a more ideal tool for measuring functional diversity. However, the original form of FAD and its variants have several undesirable properties (Schmera *et al.*, 2009). A modified FAD (denoted by MFAD) has therefore been suggested (Schmera *et al.*, 2009). The MFAD allows for calculating functional diversity without violating the twinning and monotonicity criteria such that the number of species collected is compensated for (Schmera *et al.*, 2009). These requirements are met by replacing the original species by so-called functional species and then by dividing FAD by the number of functional units.

Accordingly, MFAD measures the dispersion of species in the functional traits space so that MFAD values for different communities can directly be compared if the same set of functional trait is used.

2.3.4 Functional Trait Analysis

One of the most promising of the recently proposed approaches to measure functional diversity is biological traits analysis (BTA) (Statzner *et al.*, 1994). A biological trait is a character of an organism that may be inherited or environmentally determined. The character can be genotypic or phenotypic i.e., size, body form, movement, feeding, larval type. These characteristics strongly influence ecosystem properties. The contribution of a benthic species to ecosystem processes may be determined by a suite of biological characteristics (Webb and Eyre, 2004a), suggesting the involvement of a number of traits in ecological functioning.

Biological traits analysis uses a series of life history, morphological and behavioural characteristics of species present in assemblages to indicate aspects of their ecological functioning (here defined as the maintenance and regulation of ecosystem processes (Naeem *et al.* 1999)). The roles performed by benthic species are important for regulating ecosystem processes (Snelgrove, 1998) and these roles are determined by the biological traits species exhibit (Bremner *et al.*, 2006). Several characteristics can be involved in organisms' responses to individual environmental variables. For example, responses to benthic trawling have been linked to traits such as feeding methods, body size, flexibility, mobility and burrowing activities (Kaiser *et al.*, 1998; Rumohr and Kujawski, 2000; Bradshaw *et al.*, 2002; Thrush and Dayton, 2002).

The approach aims to provide a description of multiple aspects of functioning based on features of the biological ecosystem component. It does this by utilising specific species traits as indicators of functioning (Diaz and Cabido, 2001) and examining the occurrence of these traits over assemblages (Bremner, 2008). Biological Traits Analysis (BTA) is based on habitat templet theory, which states that species' characteristics evolve in response to habitat constraint (Southwood, 1977). Community structure is governed by habitat variability and the biological traits exhibited by organisms will provide information about how they behave and respond to stress (Lavorel *et al.*, 1997), thereby indicating the state of the environment (Usseglio-Polatera *et al.*, 2000b). BTA uses multivariate ordination to describe patterns of biological trait composition over entire assemblages (i.e., the types of trait present in assemblages and the relative frequency with which they occur) (Bremner *et al.*, 2006).

Species trait analysis (STA) focuses on defining biological and ecological characteristics of faunal assemblages. It incorporates information on species' distributions and the biological characteristics they exhibit, to produce a summary of the biological trait composition of assemblages (Bremner *et al.*, 2005). The approach provides a link between species, environments and ecosystem processes, and is potentially useful for the investigation of anthropogenic impacts on ecological functioning (Bremner *et al.*, 2005). Species diversity indices do not take into account functional differences between species, though some authors pointed out the necessity of including these differences between species to estimate a diversity related to changes in environmental conditions or influencing ecosystem processes (Diaz and Cabido, 2001; Mouillot *et al.*, 2005). Alternative groups, functional

diversity and productivity descriptors are proposed (Bremner *et al.*, 2003; Mouillot *et al.*, 2006). These methods offer the opportunity to compare sites with different taxonomic compositions and allow derivation of indicators related to ecological status of communities under scrutiny.

Ecological functions can be described by a variety of biological traits that reflect the adaptations of species to environmental conditions (Townsend and Hildrew, 1994). It is thus promising to quantify the functional diversity in ecological communities to study both the response of diversity to environmental gradients and the effects of diversity on ecosystem functioning (Leps̃ *et al.*, 2006). The distinction between functional effect groups and functional response groups is directly analogous to the distinction between the functional and habitat niche concept (e.g., Leibold, 1995) where the functional niche encompasses the effects that a species has on community and ecosystem dynamics, and the habitat niche encompasses the environmental parameters necessary for species survival (Hooper *et al.*, 2005).

Changes in the environment can affect ecosystem processes directly through effects on abiotic controls and indirectly through effects on the physiology, morphology, and behavior of individual organisms, the structure of populations, and the composition of communities (Suding *et al.*, 2008). Changes of the functional components of the communities represent the adaptations of the organisms to the environment and their response to stress (de Juan *et al.*, 2007). For instance, the response of benthic fauna to organic enrichment depends on the biological traits of the organisms (Papageorgiou, *et al.*, 2009; Villnäs *et al.*, 2011). Different species have different activity patterns and the importance of faunal activities for system

regulation is frequently associated with individual species traits (Norling *et al.*, 2007). For example, opportunistic species are less affected by sedimentation and likely to respond positively to it (Tomassetti and Porrello, 2005).

2.4 Disturbance of Marine Biodiversity

Disturbance relates to the disruption of system's stability resulting from events including natural and anthropogenic. It is often not possible to decide what has been changed by anthropogenic stress and what is natural. This is because anthropogenic stresses are superimposed on stresses caused by natural environmental factors (Raffaelli and Hawkins, 1996). Anthropogenic stress is the response of a biological entity (individual, population, community etc.) to an anthropogenic disturbance or stressor. Stress can be any factor that negatively affects the physiology, growth, reproduction and survival of an organism or that has consequences affecting populations or communities (Shiel, 2009). Stress at one level of organization (e.g. individual, population) may also have an impact on other levels, for example, causing alterations in community structure. However, it is sometimes difficult to detect the effects of anthropogenic stress at the level of individual organisms, and impacts are more often investigated at a population or community level (Crowe *et al.*, 2000).

There is little doubt that anthropogenic disturbance have extensively altered the global environment, leading to a decrease in biodiversity. Changes in marine biodiversity are directly caused by exploitation, pollution and habitat destruction, or indirectly through climate change and related perturbations of ocean biogeochemistry (Jackson *et al.*, 2001; Dulvy *et al.*, 2003; Lötze *et al.*, 2006).

Disturbance of the community by physical and biological factors may reduce the number of organisms in the community to the point at which there is less competition for resources, and hence less competitive exclusion and greater species diversity (Dether, 1984).

Jackson and Chapman (2009) indicated a tendency to associate current biodiversity changes with contemporary causes such as pollution, global warming and invading species. In reality, impacts may be temporally disconnected from their causes; long-term or historic activities may have precipitated chains of events, causing what we see today. Anthropogenic influence and their consequences may also be disconnected spatially (Jackson and Chapman, 2009).

Useful conclusions of Worm *et al.* (2006) indicate that high biodiversity in the marine environment is associated with ecosystem stability and resilience, and with the productivity and recovery potential of vital fisheries, although this was criticized for two shortcomings (Hölker *et al.*, 2007). In the marine environment, changes are often assumed to be smaller, more localized or more easily reversed, although this may not be the case-e.g., large fishing grounds take decades to recover (Thrush and Dayton, 2002). Many impacts on ecosystem have now become global in scale (e.g., declines in major fisheries; Brander, 2007); others are limited to a local sphere of influence. According to Worm *et al.* (2006) and Hölker, *et al.* (2007) the number of overexploited or depleted fish stocks has been increasing over several decades and the United Nations Food and Agriculture Organization (FAO) reports an increase from about 10% in the mid-1970s to around 25% in the early 1990s (FAO, 2006). The FAO data indicate, however, that the increasing trend has stabilized since the

early 1990s, whereas the Worm *et al.* (2006) data indicate that the increasing trend continues.

Enhanced fisheries recovery occur at high diversity due to the fact fishers can switch more readily among target species, potentially providing overfished taxa with a chance to recover (Worm *et al.*, 2006). Also taxonomically related species play complementary functional roles in supporting fisheries productivity and recovery (Worm *et al.*, 2006). Another useful finding from Worm *et al.* (2006) indicated that collapse of LME fisheries occurred at a higher rate in species-poor ecosystem compared with species-rich ones, giving credence to the effects of biodiversity loss on the ecosystem. Removal of mature fish affects the supply of juveniles elsewhere in the system, with consequences for species richness and diversity, marine predator populations, and food web functionality (Worm *et al.*, 2006) that extend over a far greater area and range of ecosystems than the fishing activity itself.

Recent evidence suggests that coastal and open-water systems can rapidly flip from being dominated by fish (that keep jellyfish in check through competition or predation) to a less desirable 'gelatinous' state (Richardson *et al.*, 2009). This new ecosystem state is resistant to returning to its original state because jellyfish are voracious predators of fish eggs and larvae, and effectively prevent fish from returning. This flip to a jellyfish-dominated system once a critical threshold is reached has been termed 'the jellyfish joyride'. Thus, natural ecosystems can be slowly degraded by the combination of continued overfishing, eutrophication and climate change to one where there are few fish, marine mammals and seabirds (Fig.

2.1). This change to jellyfish is consistent with the ‘rise of slime’ (Pandolfi *et al.*, 2005).

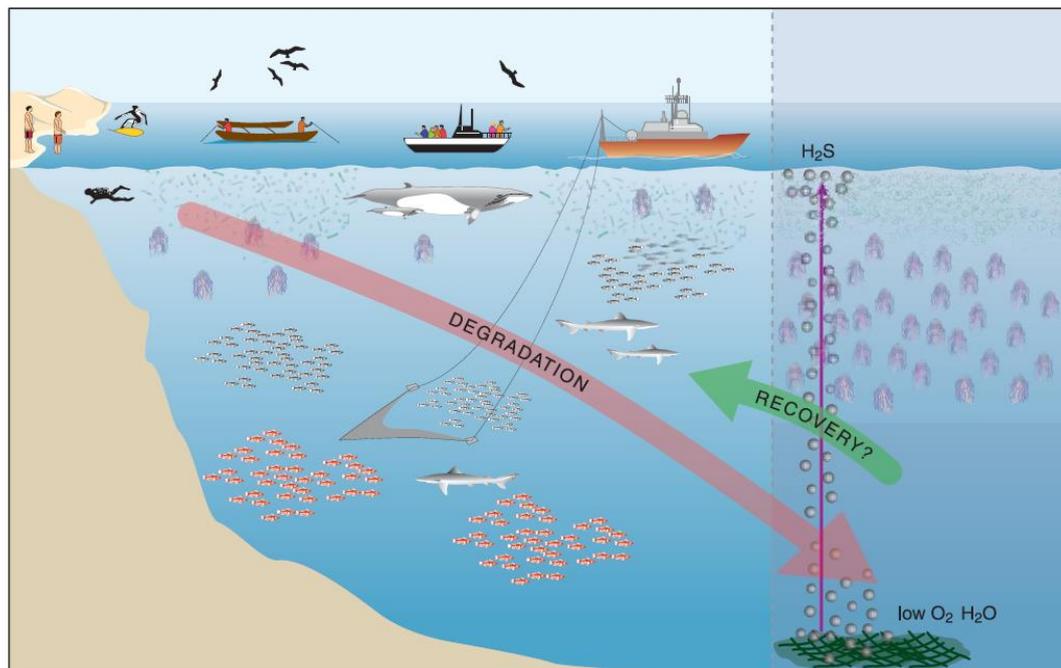


Figure 2.1 Human-induced processes of change from fish to jelly-fish domination (after Richardson *et al.*, 2009).

These tipping points for ecosystems (illustrated in Figure 2.1) are generally unknown and the new ecosystem state is resistant to returning to its original state (Richardson *et al.*, 2009). A pervasive and irreversible impact of human activity on natural marine ecosystem is introduction of non-indigenous species. The opportunities for species introduction have steadily increased over recent centuries (Hewitt and Campbell, 2007). Non-indigenous species are now common inhabitants of most geographic regions of the world. For example, up to 230 introduced species have been documented for a single estuary (Loxahatchee River estuary in Florida, USA) and about 400 are established in marine and estuarine habitats in the US alone (Ruiz *et al.*, 1997). Although the ecological effects of introduced species to the native assemblage are not clearly fully understood, they pose a significant stress to marine

communities, particularly in areas already stressed by loss of habitat or high levels of contamination (Clynick *et al.*, 2009).

The degrading effects of fishing, habitat destruction, introduced species, and eutrophication reinforce each other through positive feedbacks (Jackson, 2001; Jackson *et al.*, 2001; Lötze *et al.*, 2006). For example, oysters were nearly eliminated by overfishing, but their recovery is now hampered by hypoxia due to eutrophication, by introduced species that compete for space and cause disease, and by the explosive rise of formerly uncommon predators that were previously kept in check by now overfished species in the Neuse River estuary, North Carolina, USA (Lenihan and Peterson, 1998; Myers *et al.*, 2007). Much of the overall decline of the 80 species reviewed by Lötze *et al.* (2006) was due to multiple suites of drivers: 45% of depletions and 42% of extinctions involved multiple impacts. Nowhere have these drivers been brought under effective regulation or control.

Trawling is the most important factor affecting the structure and function of soft-bottom communities globally (Watling and Norse, 1998; Thrush and Dayton, 2002; Gray *et al.*, 2006). A number of studies have investigated the impacts of trawling on different components of the marine ecosystem (e.g., Drabsch *et al.*, 2001; Spark-McConkey and Watling 2001; Thrush and Dayton, 2002; Nilsson and Rosenberg, 2003; Rosenberg *et al.*, 2003). McConnaughey *et al.* (2000) further demonstrated that there are chronic effects, which result in lower diversity in the sedentary macrofauna in the heavily trawled areas of the eastern Bering Sea. Tillin *et al.* (2006) found that chronic bottom trawling can lead to large-scale shifts in the functional

composition of benthic communities, with likely effects on the functioning of coastal ecosystems.

Another important factor of disturbance to benthic communities is eutrophication.

Benthic eutrophication is defined as an increase in the rate of supply of organic matter to benthic environment (Nixon, 1995). One of the most important effects of eutrophication on aquatic organisms is the reduction in the concentration of dissolved oxygen. Hypoxia or anoxia (low or nil oxygen content) can cause direct mortality and reduced growth rates in organisms (Weston, 1990). Many studies have documented changes in biodiversity of macrofaunal benthic communities under hypoxia conditions (Nilsson and Rosenberg, 1994; Ritter and Montagna, 1999; Craig *et al.*, 2000; Meyers *et al.*, 2000; Nilsson and Rosenberg, 2000; Rosenberg *et al.*, 2001) and into the behavioral or physiological responses of species to hypoxia (Rosenberg *et al.*, 1991; Holmes *et al.*, 2002; Wu and Or, 2005). These studies showed decreased biodiversity, alterations of species composition and reductions in biological responses, when the benthic environment is subjected to short or long-term hypoxia events. Although the effects of hypoxia on biodiversity, physiology and behavioral responses have been extensively studied (Widdows *et al.*, 1989; Vaquel-Sunyer and Duarte, 2008; Hondorp *et al.*, 2010), there has not been any research into the combined effects of trawling and hypoxia on the biological traits of benthic communities.

The intermediate disturbance hypothesis of Connell (1978) predicts maximum biodiversity at a frequency of disturbance where recruitment is able to replace lost individuals but inter-specific processes do not have time to exclude species. This

response has been recorded in many marine systems (Begon *et al.*, 1996; Svensson *et al.*, 2007). Disturbance, both anthropogenic and natural, may act as a potential abiotic drivers/surrogate for diversity at an appropriate spatial scale and temporal scale (Harris *et al.*, 2008). The stability of the seabed sediment surface exerts a major control on benthic community structure (Newell *et al.*, 1998). Species diversity tends to be highest on stable rocky shores and on cohesive muddy shores, with the more mobile sandy or fine gravel substrates typically showing much lower richness. Sediment stability is dependent on slope, particle size and the degree of water motion on the bed (Bagnold, 1963). The shape and roundness of sediment grains are additional properties that determine the stability of a deposit (Lewis and McConchie, 1994) but grain shape is difficult to measure and is rarely recorded despite its likely importance. Stability may also be influenced by the presence of biota through biological armouring of the bed and binding of sediment by faunal mucus (Murray *et al.*, 2002). The stability of a sediment surface as a habitat is difficult to quantify, particularly given that one of the key proxies, sediment grain size, is determined on disaggregated samples which have been dislodged from their environment and may have little physical resemblance to what an organism actually encounters (Snelgrove and Butman, 1994).

2.5 Environmental Drivers of Marine Benthic Diversity

The goal of ecological research is to determine which easily measured characteristics best describe the species assemblage of a particular space and time (Moore *et al.*, 1991). Models which have been suggested for understanding community dynamics or species assemblages include “environmental stress models” and either “nutrient/productivity models” or the “food chain dynamics hypothesis” (Connell,

1975; Oksanen *et al.*, 1981; Fretwell, 1987; Menge and Olson, 1990; Menge, 2000). Environmental stress models assume that community structure results from species interactions and disturbances, and how these are modified by underlying gradients of environmental stress (where stress is a consequence of environmental conditions such as temperature, moisture, salinity) (Menge *et al.*, 2002). The two models postulate that communities can be ordered along environmental gradient. McGill *et al.* (2006) argued that general principle in community ecology may not be achieved if research continues to focus on pair-wise species interactions independent of the environment. Global species distributions are generally believed to be determined by abiotic influences related to oceanographic and physiographic properties (Sanders, 1968; Ricklefs and Schluter, 1993). For instance, water motion affects biology by acting as a transport mechanism for organisms and their propagules, as a dynamic boundary between regimes, and as a force to which organisms must adapt or respond, for example, in their feeding and locomotor activities (Nowell and Jumars, 1984; Denny, 1993).

The abiotic characteristics are expected to act as predictors of species assemblages in unexplored areas (Franklin, 1995). Pitcher *et al.* (2007) identified grain size, carbonate composition, available space, benthic irradiance, sheer stress, bathymetry, bottom water physical properties, nutrient concentrations and turbidity as abiotic surrogates of biotic distributions on the Great Barrier Reef; but these variables, while useful predictors, may not be the forces driving the patterns they describe. The influence of abiotic factors on species assemblages is due to the effect they exert on fundamental niches. A species' fundamental niche was defined by Austin *et al.* (1990) as "that hypervolume defined by environmental dimensions within which a species can survive and reproduce." Fundamental niches are rarely fully realized by

species because interspecific competition, disease and disturbance events displace individuals and populations, resulting in a reduced occupied hypervolume, often referred to as the realized niche (Austin and Smith, 1989).

The environmental gradients that describe a species' fundamental niche can be broadly grouped into resource gradients – e.g. chemicals or energy consumed by a species; direct gradients – variables with a physiological influence on a species but not consumed by it – e.g. sediment grain size or temperature; and indirect gradients – variables correlated with direct and resource gradients but with no physiological connection to the species – e.g. depth and latitude (Meynard and Quinn, 2007). When niche theory was first proposed, species were expected to exhibit a Gaussian distribution to environmental gradients but skewed distributions are more common in ecological studies as the effects of additional variables express their influence (Karadzic *et al.*, 2003).

The abiotic variables which have been historically ascribed the greatest direct influence over benthic organism distributions are temperature, salinity, oxygen concentration, light availability and sediment composition (Snelgrove, 2001). Environmental variables (such as sediment structure, organic matter content, temperature, salinity, dissolved oxygen, nutrient concentrations, pH, turbidity, water transparency and depth) have been found to correlate with abundance, density and diversity of macrofauna and these variables may vary seasonally (Nicolaidou *et al.*, 1988; Arvanitidis *et al.*, 1999; Hagberg and Tunberg, 2000; Mistri *et al.*, 2000; Mistri *et al.*, 2001).

A model describing the influences of these factors and some of their potential synergies is given in Figure 2.2. The figure depicts the influence of interdependency of physical processes and potential surrogate abiotic drivers on biological community structure. Olabarria (2006) found depth accounted for as much as a quarter of the variance in benthic diversity in deep systems but, as benthic organisms lack an apparent mechanism for measuring depth, some correlated water quality parameter or seafloor characteristic most likely influences the settlement, recruitment and survival processes that result in the observed depth related patterns. Lamptey *et al.*, (2010) identified nitrate-nitrogen, dissolved oxygen, salinity and water temperature as suite of abiotic drivers of rocky intertidal biodiversity in Ghana. Gray (2002) reduced Snelgrove's list of direct drivers (2001) to productivity, temperature and sediment composition as the dominant variables in determining regional benthic richness, noting that temperature and productivity are often correlated to depth and latitude. Combinations of these driving influences occur with varying spatial and temporal consistency, in turn producing semi-regular patterns of biodiversity. The validity and origin of several identified general benthic biodiversity patterns are the focus of much recent debate. For example, the latitudinal (spatial) richness gradient, widely accepted as a rule for benthic fauna since the mid twentieth century (Thorson, 1957) has been shown to be weaker than previously thought (Snelgrove, 2001) or entirely incorrect for some taxa or systems (Rex *et al.*, 2005) due to the driving influence of complex biotic and abiotic factors.

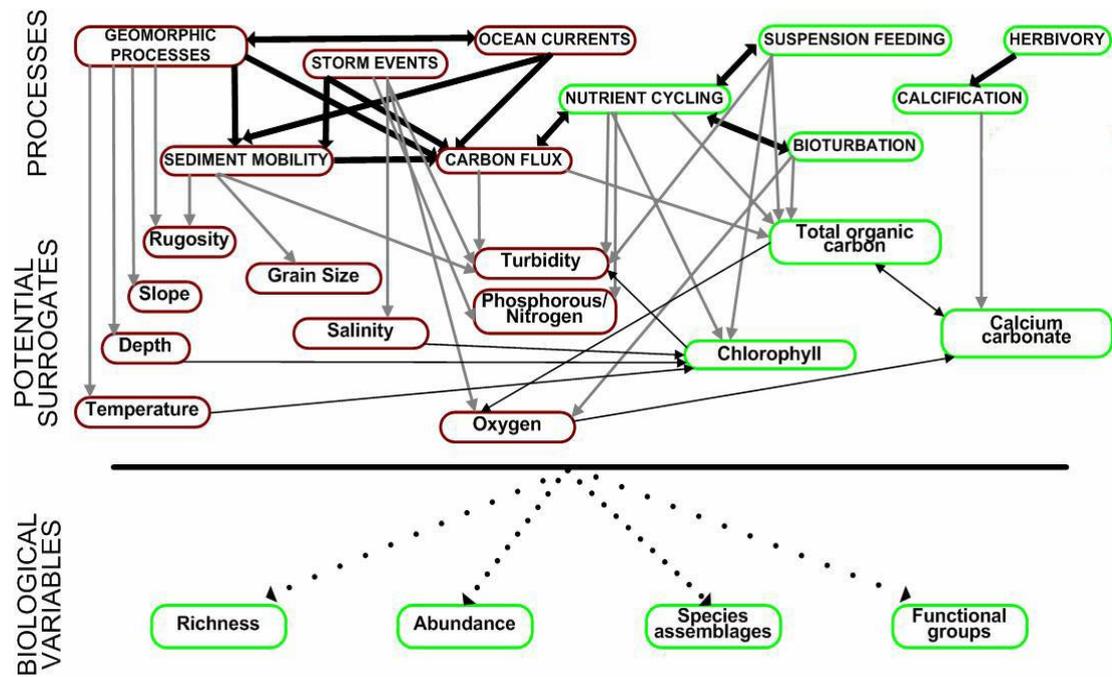


Figure 2.2. Conceptual map of the relationships between drivers of biodiversity in marine systems and potential surrogates (after McArthur *et al.*, 2009).

2.5.1 Spatial and Temporal Patterns of Environmental Drivers

An important goal in community ecology is to understand factors contributing to species assemblage patterns at variety of spatial and temporal scales. Benthic faunal communities vary considerably in time and space (Carriker, 1967; Boesch, 1973), due, in great part, to the patchiness of species occurrences (Pearson and Rosenberg, 1978) and overall heterogeneity of the benthic habitat (Mistri *et al.*, 2000). This heterogeneity has been ascribed to such factors as bottom sediment, spatial variability (Tenore, 1972), climatic irregularity (Hessle and Sanders, 1967; Bourcier, 1995), anthropogenic perturbations (Rosenberg, 1973; Kröncke *et al.*, 1992) and biogenic structures (Woodin, 1981). According to Alongi (1990), temporal and spatial patterns of benthos are determined by primary production in the water column and by sediment types and associated physico-chemical conditions. Changes in

environmental conditions promote changes in species assemblages at variety of spatial scales (Lamprey *et al.*, 2010). Many environmental factors affecting species performance and interactions vary with spatial scale (Noda, 2009). There is, however, no particular scales of change that are consistent among taxa (Burrows *et al.*, 2002), congruently demanding ambitious ecological models to decipher spatial patterns. Physical or environmental factors, such as water depth and sediment type and movement, are considered to determine large-scale patterns of distribution (e.g. Thorson, 1957; Barry and Dayton, 1991). Within these patterns, however, spatial heterogeneity exists at various scales, forming a mosaic of patches.

Spatial heterogeneity is often cited as a diversity driver, with high inshore species richness being promoted by the variety of habitats available on a broad scale and deep water benthic and planktonic richness occurring in spite of low biomass as a result of small scale shifts in sediment or water composition in habitats which otherwise appear homogenous (Snelgrove, 2001). Spatial pattern is difficult to quantify and often refers to the spatial character and arrangement, position or orientation of patches within a landscape (Li and Reynolds, 1993).

A greater understanding of the distribution and complexity of benthic habitats and a common approach to measuring and describing this complexity will provide a spatial framework within which to properly address spatially explicit research and management goals (Kendall *et al.*, 2005). The decline of many species has been linked directly to habitat loss and fragmentation. Identifying what characteristics make an area preferentially habitable for particular species has been examined by many landscape ecologists and is being increasingly taken up by marine ecologists to

describe patterns of benthic diversity (Barrett *et al.*, 2001). Recent advances in image processing and GIS technologies have made it possible to link indices of landscape pattern to ecological functions. However, the uncertainties in mapping the pattern and extent of marine habitats have, until recently, been behind the rarity of habitat-scale studies in marine ecology

Increasing species richness with increasing proximity to the equator is a long recognized biogeographic pattern (Cox and Moore, 2005). While this pattern has been documented in the marine environment (Attrill *et al.*, 2001) it has recently been found to be less general than previously thought (Gray, 2001). Hawkins *et al.* (2003) and Willig *et al.* (2003) each cite thirty hypotheses to explain latitudinal richness gradients. These were categorized by Mittelbach *et al.* (2007) into ecological, historical and evolutionary groups. The ecological hypotheses concentrate on the different adaptive challenges faced by organisms living in different climatic zones: polar and temperate organisms must adapt to environmental conditions (Schemske, 2002) while tropical organisms, dealing with less harsh abiotic extremes, adapt to biotic interactions (Crame, 2000). Historical explanations concentrate on the age and stability of richness hotspots (Alongi, 1990).

Evolutionary models incorporate several possible drivers for high rates of speciation including the wide variety of microhabitats available in tropical regions (Rex *et al.*, 2005) and higher rates of molecular evolution (Kerswell, 2006). Attempts to measure and explain the extent of a latitudinal richness gradient in taxa other than molluscs on broad geographic scales have found less evidence for a marine equivalent to the terrestrial pattern (Gray, 2001) and brought into question the treatment of data in

describing such patterns. For example, Thorson's (1956) pattern of increasing richness in benthic epifauna toward the equator was based only on the 140,000 marine taxa known at the time (Snelgrove, 2001). Diversity responses to pure spatial gradients can vary depending on how assemblage data are treated. Ellingsen *et al.* (2005) determined that latitude could account for variance in richness of molluscs (11.8 % explained), annelids (9.6 %) and crustaceans (13.7 %) in Norwegian shelf benthos.

2.5.2 Water Depth

Water depth has been a consistently powerful explanatory variable in benthic studies (Nicolaidou and Papadopoulou, 1989; Gogina *et al.*, 2010). When generalizing from shallow to deep, intertidal and estuarine systems exhibit high biomass and low species richness caused by high productivity and extreme environmental conditions (Edgar, 2001), coastal shelves have moderate biomass and species richness (Snelgrove, 2001), and the deep sea shows a decrease in biomass and increase in richness (Levin *et al.*, 2001). Peak benthic species richness values have been recorded seaward of the continental rise, excluding the deep sea (Snelgrove, 2001). The lower slope and abyssal plains become comparatively depauperate for some groups, and species turnover tends to be high (Paterson *et al.*, 1992). Levin *et al.* (2001) stated that the deep sea houses greater diversity than coastal shelf systems, although at far lower abundances. Areas with low abundance and high species turnover require greater sampling effort to reliably account for diversity (Etter and Mullineaux, 2001).

2.5.3 *Substrate Types*

Numerous studies have provided evidence to show significant differences in the species composition between ‘hard’ and ‘soft’ substrata (Beaman *et al.*, 2005; Beaman and Harris, 2007; Williams and Bax 2001). For practical purposes, ‘soft substrate’ is usually defined as detrital mineral or biogenic sediment comprising grains with a mean diameter less than 2 mm, although gravel size fractions are often included (Lewis and McConchie, 1994). The term ‘hard substrate’ is typically used to represent rock outcrops but may include sediments with large grain size (e.g. cobbles, boulders) since these materials can provide a surface that is functionally comparable to bedrock. While the contrast between soft and hard substratum is conceptually simple, defining the boundary between soft and hard substrates can be complex in practice because some rock types are friable or semi consolidated and may be partly covered by sediment (Ryan *et al.*, 2007). In addition, because the boundaries between adjacent soft-sediment environments are not always sharp as those across hard and soft substrate features, the associated boundaries between biological assemblages may be gradational and spatially complex (Beaman and Harris, 2007).

Sediment particle size distribution and composition on the seabed express a strong influence on the morphology and life history of species living in soft sediments (Jones, 1950). These variables are determined by complex interactions between local geology, rates of sediment production and supply, actions of bioeroders, current and wave induced bed stress, and slope (Reineck and Singh, 1980). Generally, in high-energy areas, coarse sediments (gravel) will predominate, whereas lower energy (depositional) areas are muddy, although there are exceptions (Foster, 2001; Hart

and Kench, 2007) which have led to a highly complex and variable distribution of seabed sediment types on the shelf and slope. Although several sediment surrogacy relationships are well documented (Brown *et al.*, 2001; Beaman and Harris, 2007; Degraer *et al.*, 2008), the nature and strength of sedimentary surrogates for species composition within soft sediment environments remains a subject of debate (Dye 2006; Inoue *et al.*, 2008; Stevens and Connolly, 2004). Soft substrates are home to epifauna and infauna and plant life may include sea grasses (and their epiphytes) or microphytic algae occurring at the sediment-water interface. Hard substrates can act as habitat for epifauna and encrusting or macro-algae, but infauna are excluded.

The most basic way of characterizing any community is by the habitat type and for benthic community habitat normally means sediment type (Hall, 1994). The distribution of many of the benthic communities shows a clear correlation with sediment type. Early studies suggested that macrobenthic communities could be distinguished on the basis of sediment composition (Thorson, 1957; Buchanan *et al.*, 1978; van Dalssen *et al.*, 2000). Other studies, however, have shown little correlation (Day *et al.*, 1971; Sneiderer and Newell, 1999) and suggested that the distribution of macrofauna in many sedimentary habitats is controlled by complex interaction between physical and biological factors at the sediment–water interface, rather than by the granulometric properties of the sediments themselves (Snelgrove and Butma, 1994). However, density-dependent variables play a minor role in structuring the macrobenthic communities, which were probably affected more by other variables, such as the kind of habitat and sediment structure (Mistri *et al.*, 2000). Many apparent relationships between sediment type and biota remain untested in an

experimental sense (Whitlatch, 1981) and have been challenged (Snelgrove and Butman, 1994).

Storms and current eddies may contribute to primary space being made available in a system in two fashions: increasing sheer stress at the benthos/water interface, which can remove sediment, algal cover and motile fauna; and mechanical abrasion or damage caused by moving sediment or projectiles (Sousa, 2001). Benthic organisms continually process, transport, and modify seafloor bed sediments. There are those that bind, protect and stabilize near-surface sediment and those that loose and destabilize the sediment (Nichols and Boon, 1994).

Depending upon its life style, an organism may require a given size range of sediment for tube building, burrowing or feeding (Wieser, 1959). The feeding type of the benthic community is considered as an adaptation to the sediment characteristics (Rosenberg, 1995). Certain mechanisms result in sediment-specific distribution. One of these is the preferential ingestion or retention of specific grain sizes during feeding. Adults of a variety of deposit-feeders have been shown to ingest specific grain sizes of sediments (Whitlatch, 1977; 1980). For instance, newly settled larvae may be restricted to feeding on the finest material within the bed or on particular rich food items (Jumars *et al.*, 1990) thus, optimal grain size may be different for settling larvae and adults. Larger particles may be preferred by larger organisms within a given species (Whitlatch and Weinberg, 1982 cited in Snelgrove and Butman, 1994). Some species show little affinity with any one particular sediment type, and the fauna within different sediment environments invariably

show some degree of overlap, which might be due to the grain size being a correlate of the actual causative factor(s) (Snelgrove and Butman, 1994).

Much of the potential food for benthic organisms are located within the upper 2 cm of the sediment (Whitlatch, 1977, 1980) and most of the organisms produce faecal pellets that are deposited at or near the sediment surface. This process may result in a change in the grain size of surface sediments (Hall, 1994). In mud, for instance, this can result in a pelletised silt-clay matrix. It is therefore, evident that physical processes impact upon biological features to structure the benthic organisms and its habitat. Habitat selection based on the availability of a preferred grain size in feeding is difficult to conceptualise in view of the ontogenic and hydrodynamic changes in feeding behaviour and particle selectivity (Snelgrove and Butman, 1994). It has been suggested that animal and sediment correlation is a result of hydrological and geological processes associated with sediment granulometry rather than a function of organism's available space within sediment (Parry *et al.*, 1999). Benthic space can also be made available in the wake of acute pollution events (Scanes *et al.*, 1993), fishing activity (Currie and Parry, 1996) and eutrophication (Tett *et al.*, 2007), but the effects tend to be locally focused.

2.5.4 Primary Productivity

Contrary to observed patterns in terrestrial systems (Currie *et al.*, 2004), high primary productivity in near shore waters tends to promote low species richness (Snelgrove, 2001) and high evenness (Hillebrand *et al.*, 2007). In these areas, the role of producer tends to be dominated by a small number of species able to monopolise resources under ambient conditions. Corresponding benthic communities

are dominated by the taxa best able to use the associated products (Lenihan and Micheli, 2001) or withstand periods of anoxia imposed by excess organic input (Dell'Anno *et al.*, 2002). In contrast, oligotrophic waters are often home to low biomass assemblages with high species richness, including a large proportion of endemic taxa (Poore *et al.*, 2008). Coral reefs, areas of high biomass and species richness occurring in oligotrophic waters, are an exception. The symbiosis between coral polyps and their resident zooxanthellae allows higher productivity than would otherwise occur in the ambient conditions and the spatial complexity and diversity of habitats provided by hard corals competing for space and light promotes a high corresponding richness of invertebrate and fish life, in turn supporting a rich community of predators (Cribb *et al.*, 1994). Primary production can be estimated from satellite or airborne spectral analysis of chlorophyll in surface waters (Parmar *et al.*, 2006). While productivity is directly linked to marine biodiversity, the relationship has yet to be fully explored as a predictive surrogate over large scales.

2.5.5 Organic Carbon

Detrital matter derived from primary productivity and the wastes of secondary production comprise a valuable resource in the photic zone and, excepting chemosynthetic systems, almost the only energy input to the aphotic zone (Vetter, 1995; Carney, 2005). This material settles in particles of various sizes, among which larger particles such as faecal pellets (Angel, 1984) and marine snow (Alldredge and Silver, 1988) are particularly important. It is generally accepted that the flux of particulate organic carbon (POC) from the euphotic zone controls the biomass and abundance of deep-sea benthos. This notion was originally based on observations of high benthic standing-crops beneath productive equatorial and near-shore waters,

and low standing-crops underlying oligotrophic gyres (Belyayev *et al.*, 1973; Gage and Tyler, 1991; Rowe *et al.*, 1991; Blake and Hilbig, 1994). However, a direct coupling between pulse-like sedimentation events and the activity of benthic fauna has become clear (Aberle and Witte, 2003 and references therein). The detailed nature of this coupling remains poorly understood because there have been few studies which combine both types of measurements. One good example is a study by Smith *et al.* (1997) in the equatorial Pacific, in which strong and significant correlations ($r^2 > 0.9$) were found between both megafaunal (phototransects) and macrofaunal (enumerated from box core samples) abundances and annual POC fluxes.

An interesting conclusion from this study was that macrofaunal abundance might potentially serve as a proxy (i.e., surrogate) for POC flux in low energy abyssal habitats, implying that the macrofauna themselves are either more widely or more easily measured than POC fluxes (see also Rowe *et al.*, 1991; Cosson *et al.*, 1997). The main technique to directly measure POC fluxes is using sediment traps. Seiter *et al.* (2005) drew on particle-trap data from 61 locations, and produced a global map of minimum POC flux to the seafloor which was based on global estimates of diffusive oxygen uptake. This map, and the global map of total organic carbon (TOC) concentrations that underpins it (Seiter *et al.*, 2004), may prove useful in making first order approximations of benthic productivity over broad scales, assuming that benthic communities are not compromised by sediment de-oxygenation. Indeed, the relationships between diversity and POC fluxes (or other productivity proxies) are scale-dependent and may be complicated by other variables

that influence diversity including bottom-water oxygen concentration, hydrodynamic regime and the stability of the physical environment (Levin *et al.*, 2001).

Proxies of POC fluxes such as TOC, TOC:TN (total nitrogen) ratios, biochemical markers and pigments in sediment have proven useful in explaining more localized patterns of biodiversity. TOC is undoubtedly the most widely measured of these parameters (Seiter *et al.*, 2005), and, where a consistent and robust method (Galy *et al.*, 2007) has been applied to its measurement, TOC can be a useful surrogate for biomass, deposit-feeding taxa, and community structure (Gogina *et al.*, 2010). However, its application is limited to interpolations from physical samples (Levin and Gage, 1998) as no remote sensing proxy is available. Moreover, correlations between TOC and diversity measures are not always found (Cartes *et al.*, 2002) because a large proportion of TOC in sediment may be refractory and thus resistant to bacterial degradation. Sediment grain size can also affect the amount of biologically available organic matter (OM) in shallow soft sediments (Taghon, 1982). Small particles have larger surface area per unit volume than large particles, offering greater habitat for micro-organisms (Fauchald and Jumars, 1979; Petch, 1986; Neira and Hoepner, 1994) and associated organic matter. Some deposit-feeding species use size-specific foraging mechanisms to select and ingest fine sediments (Butman and Grassle, 1992; Sebesvari *et al.*, 2006), but both selective and non-selective deposit-feeders exhibit settlement preferences for sediments with high concentrations of readily available organic carbon (Snelgrove and Butman, 1994; Post *et al.*, 2006).

The organic matter content of bottom sediments may be a more likely causal factor than sediment grain size in determining infaunal distribution (Snelgrove and

Butman, 1994). This is because it is a dominant source of food for deposit-feeders (Pearson and Rosenberg, 1978), indirectly (e.g., through resuspension) for suspension feeders (Snelgrove and Butman, 1994). The sediment must be considered as an indicator of the availability of food, and not as a first order factor directly determining the distribution of feeding types (Snelgrove and Butman, 1994). Nichols (1970) and Field (1971) have suggested that there is a strong relationship not only between animal and grain-size distribution but also between animal and organic-carbon distributions as well. However, a similarity between the type of sediment and the percentage of organic matter, which have been ascribed to the hydrodynamic conditions established during heavy rains, has been observed (Estacio *et al.*, 1999).

Several deposit-feeding opportunistic species have been shown to colonize, preferentially, organic-rich sediments over non-enriched sediments with comparable grain size in shallow-water (Grassle *et al.*, 1985; Tsutsumi *et al.*, 1990) and in associated slow water movements (Mistri *et al.*, 2001). Organic matter was also found to be correlated with annelid distribution (Arvanitidis *et al.*, 1999). Seasonal variations in particulate organic matter are greatly influenced by monsoonal rains. Total organic matter levels decrease during the monsoon season as a result of increase in river discharge and scouring of surface silt and clay and associated organic matter (Alongi, 1990). The highest concentrations of organic matter in sediments are in regions of upwelling and in proximity to rivers and more generally, relate to the patterns of pelagic primary production (Alongi, 1990).

The availability, freshness or quality of organic matter (OM) pertains to the labile fraction, which consists mainly of lipids, carbohydrates, proteins and nucleic acids

(Danavaro *et al.*, 1993, 1995, 2001). Several useful biochemical parameters have been derived to describe the lability of OM (Danavaro *et al.*, 1995; Dauwe *et al.*, 1999), and some of these have proven useful for explaining different diversity indices (Cartes *et al.*, 2002). Such measures, however, often require a high degree of discipline expertise (and advanced techniques), and as such are unlikely to be widely employed in the capacity of surrogates. However, the Chlorin Index (CI) (Schubert *et al.*, 2005) is a simple analytic measurement of OM lability, whose reliability has been demonstrated by comparison to more advanced techniques (e.g., Dauwe Index, total hydrolysable amino acids, and % β -alanine as non-protein amino-acid, and sulfate reduction rates) (Schubert *et al.*, 2005). The Chlorin Index (CI) is a measure of the amount of chlorophyll (and its degradation products) that could be transformed to phaeophytin, and is expressed as the ratio of the fluorescence intensity of a sediment sample extracted in acetone and subject to HCl treatment to that of the original sediment sample (Schubert *et al.*, 2005). CIs have been found to correlate well with an index of track richness developed from photographic stills of seabed sediments, which conveyed differences in the diversity of tracks, faecal casts, burrows and mounds of benthic biota in deep-sea sediments of the Lord Howe Rise (Dundas and Przeslawski, 2009). Comparison with this index shows a greater diversity of animal traces, and potentially more metazoan activity, in sediments of apparently higher food quality. CIs thus show promise as an easily measured geochemical surrogate of biodiversity for regions where organic loads are not expected to give rise to significant sediment anoxia.

2.5.6 *General Oceanography*

Oceanographers measure and model variables that directly influence the physiology and behavior of marine organisms (temperature, salinity, pH), variables affecting productivity (nutrient concentrations, temperature and light intensity: see section 2.5.4 on productivity) and the currents that affect larval distributions. Some factors such as pH and salinity vary sufficiently over regional and global scales to show correspondence to biological patterns (Williams and Bax, 2001) but are sufficiently uniform at a local scale (with the exception of estuarine systems) to preclude their use in local surrogacy analyses (Bamber *et al.*, 2008). Dissolved oxygen has been identified as a key predictor of biodiversity in deep sea sediments (Levin and Gage, 1998).

In addition to determining local water properties and delivering food and oxygen, ocean currents are important to the dispersal of many marine organisms which, in turn, determines the potential distribution of many benthic taxa. Most larvae and algal propagules spend their early development adrift and must attempt to settle where the prevailing currents take them. With larval periods ranging from hours (e.g., tropical ascidians in Cloney *et al.*, 2006) to four and a half years (e.g., gastropod of the Tropical Atlantic Ocean in Strathmann and Strathmann, 2007), the scope for currents to act as a surrogate for potential richness is substantial where both life histories and water movements are well known. The relative rarity of long larval life histories make local currents (~tens of kilometers) more important than regional currents in determining benthic larval supply (Palumbi, 2001), but even groups with well-known life histories have frustrated attempts to predict geographic assemblies (Shulman and Bermingham, 1995). Stevens and Connolly (2004)

considered local scale current speed as an abiotic variable in their assessment of surrogates in Moreton Bay, Australia, but found its predictive capacity negligible. In addition to understanding larval supply patterns, the proximity of any given sample to diversity hotspots must be taken into consideration (Bellwood *et al.*, 2005). Further information on biodiversity patterns as they relate to oceanographic variables can be found in reviews by Hall (1994), Wolanski (2001), and Levin *et al.* (2001).

2.5.7 The Guinea Current Ecosystem

The oceanography of the Guinea Current Ecosystem (GCE) is dominated by the Guinea Current (GC), but also the Benguela Current (South Equatorial), the Canary (Counter Equatorial) play important roles in the regional oceanography that influence coastal upwelling. The GCE and adjacent areas of the eastern tropical Atlantic, bounded to the north by the Canary Current (CC) coastal upwelling region and to the south by the Benguela Current (BC) coastal upwelling region, are affected by five major basin-wide wind-driven cells of ocean circulation (Longhurst, 1962). These are the North Atlantic Subtropical (NAS), North Equatorial Cyclonic (NEC), Equatorial Anticyclonic (EA), and South Equatorial Cyclonic (SEC) gyres (Henin *et al.*, 1986). The circulation cells are formed due to latitudinal variations in the wind stress that is due to the existence of the subtropical anticyclones and Intertropical Convergence Zone (ITCZ), which separates the belts of the northeast and southwest trade winds.

The major surface currents forming the peripheries of the gyres are the North Equatorial Current (NEC), South Equatorial Current (SEC), North Equatorial Counter Current (NECC), South Equatorial Counter Current (SECC), GC, and

Angola Current (Moroshkin *et al.*, 1970; Stramma and Schott 1999). Other current systems that may affect near surface circulation in the region are the equator-ward CC feeding the NEC in the north and the BC feeding the SEC in the south (Arnault, 1987). The NEC, SEC, NECC, and SECC are the westward and eastward cross-basin flows while the CC, GC, AC, and BC form the system of the tropical eastern boundary currents (Richardson and Walsh, 1986).

Three narrow coastal sedimentary basins, with a few volcanic intrusions and outcrops of hard rock forming the major capes, have developed on the edges of the coastline along the GCE: from north to south, they include the Cote d'Ivoire basin, the Niger basin (Delta) and the coastal basins from Gabon to Angola (Allen and Wells, 1962, Quellenec, 1984). The Volta, Niger and Congo basins dominate the coastal geology of the GCE. The continental shelf widens towards the east reaching its widest part of about 90 km off Cape Coast in Ghana. The shelf narrows again further eastwards between Tema (Ghana) and Lagos (Nigeria). Off Nigeria, the middle shelf configuration is modified by the Avon, Mahin and Calabar canyons, as well as pockets of dead Holocene coral banks (Awosika and Ibe, 1998). East of Lagos, the shelf widens to about 85 km off the Niger Delta beyond which it narrows to an average width of 30–40 km. The shelf generally breaks at depths of between 100 and 120m (Awosika and Ibe, 1998).

Generally, the northern subsystem of GCE is thermally unstable and is characterized by intensive seasonal upwelling (around Cote d'Ivoire—Ghana) while the southern subsystem is mostly stable depending on nutrient input originating from land drainage and river flood and oceanic turbulent diffusion, although periodic

upwellings have been reported (Bakun, 1978; Ukwe, 2003). The GC is a geostrophically balanced current with isotherms sloping upwards towards the coast and as the current intensifies, the slope becomes steeper bringing the thermocline closer to the surface near the coast (Henin *et al.*, 1986). The coastal upwelling and the boreal summer intensification of the GC are thus related (Philander, 1979)

Although oceanography has been identified as a major driver of benthic biodiversity, there are limited studies in the GC relating it to biodiversity distribution. Lœuff and Cosel (1998) in their investigation of the benthic biodiversity pattern across hydroclimatic conditions in the Tropical eastern Atlantic concluded the following:

- i) five different hydroclimatic regions existed in the tropical eastern Atlantic namely: the northern altemance region (Cape Blanc -Cape Verga), the atypical tropical region (Cape Palmas - border Benin/Nigeria), the southern altemance region (Cape Lopez - Cape Frio), all with periodical upwelling of colder water, and two intercalated typical tropical regions with warm water and reduced salinity.
- ii) the faunal richness in the regions with upwelling is higher than in the typical tropical regions because many benthic species avoid warm and reduced salinity water;
- iii) faunistic exchange and affinity are greater between the upwelling zones and the areas bordering temperate zones;
- iv) the cold regions are also more similar in faunal composition;
- v) benthic communities in both tropical and temperate eastern Atlantic are not fundamentally different;

- vi) species diversity of benthic invertebrates in tropical West Africa is about the same order of magnitude as in Europe and the Mediterranean; and
- vii) hydro-climatic conditions do not favor the establishment of stenohaline and stenotherm fauna in West Africa. Lœuff and Zabi (2002) also demonstrated the existence of major types of faunal bionomic variations at different spatial and temporal scales in benthic ecosystem of tropical Atlantic coast of Africa.



Figure 2.3. Guinea Current Ecosystem Region (Google Earth Image).

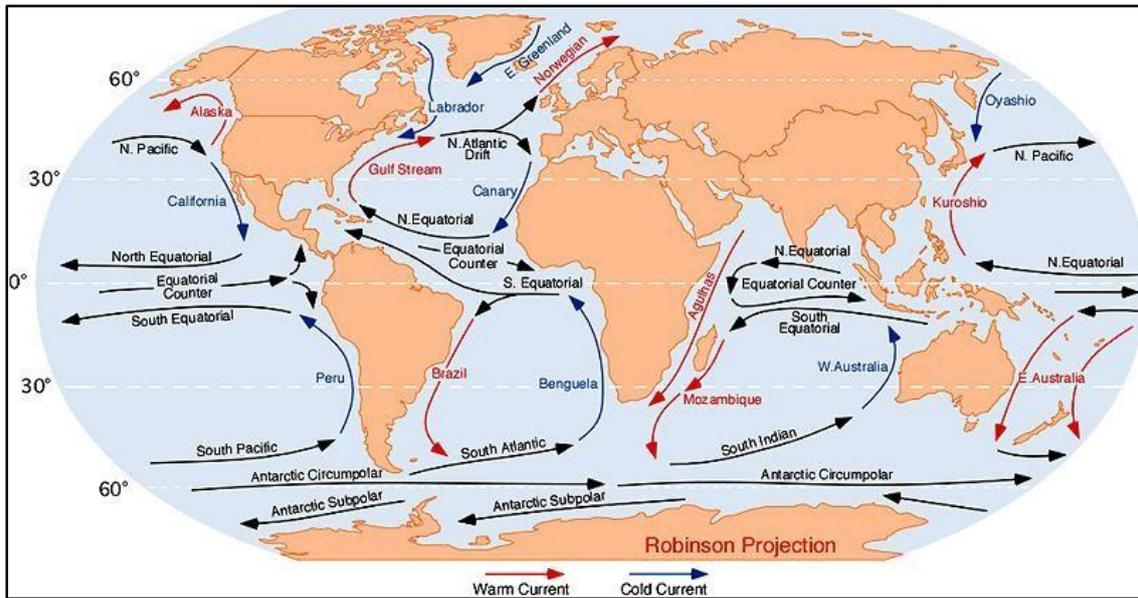


Figure 2.4. Large-scale oceanic circulation in the Atlantic Ocean including the Guinea Current Ecosystem region. (Image Source: NASA)

CHAPTER THREE

MACROBENTHIC FUNCTIONAL TRAIT DIVERSITY AND COMMUNITY STRUCTURE ALONG ENVIRONMENTAL GRADIENT

3.1 Introduction

The distribution of species and species' traits across environmental gradients can provide an understanding of how assemblages that differ in diversity are composed and their relative selection pressures (McGill *et al.*, 2006). Comparing assemblages at local scales can often yield more insights into processes that drive diversity compared to global or regional scales (Gaston, 2000). However, a challenge to understanding various local processes is the comparison of assemblages with differing abundances in space and time, different histories (Underwood and Petraitis, 1993) and differing climatic and environmental settings. One approach for comparing diversity is to compare the spatial distributions of species at different geographic localities to look for generalities in community composition or habitat use (MacArthur, 1972; Warwick and Ruswahyuni, 1987, Thrush *et al.*, 2005). Many of these approaches have been employed in most terrestrial ecosystems with the marine counterparts lagging behind.

The marine ecosystems are composed of three units: (i) the physical environment (e.g. seabed structure, sediment composition, waves, currents and water temperature), (ii) the chemical environment (e.g. substances such as carbon, oxygen, nitrogen and phosphorus and properties such as salinity and pH) and (iii) the biotic environment (the assemblages of living organisms present in the system, ranging

from micro-organisms up to macroalgae, large marine mammals and humans) (Bremner, 2005). Recent evidence suggests that environmental conditions are intricately linked to biological traits, and hence ecological functioning (Bremner, 2006). Environmental conditions are all the things outside an organism that affect it but, in contrast to resources, are not consumed by it (Begon *et al.*, 1990). The environment of an organism consists of all those phenomena outside an organism that influence it, whether those factors are physical (abiotic) or are other organisms (biotic) (Olf *et al.*, 2009). Increasing moderation in environmental conditions leads to increased abundances, more complex trophic structure, and increased influence of species interactions on structure (Menge, 2000; Menge and Branch, 2001).

The main environmental gradients that have been associated with variation in species diversity are energy-related variables (*i.e.*, temperature), precipitation, productivity and habitat heterogeneity (Currie, 1991; Rahbek and Graves, 2001; Hawkins *et al.*, 2003). Models which have been suggested for understanding community dynamics include “environmental stress models” and either “nutrient/productivity models” or the “food chain dynamics hypothesis” (Connell, 1975; Oksanen *et al.*, 1981; Fretwell, 1987; Menge and Olson, 1990; Menge, 2000). Environmental stress models assume that community structure results from species interactions and disturbances, and how these are modified by underlying gradients of environmental stress (where stress is a consequence of environmental conditions such as temperature, moisture, salinity, etc.) (Menge *et al.*, 2002).

The two models postulate that communities can be ordered along environmental gradient. McGill *et al.* (2006) argued that general principle in community ecology

may not be achieved if research continues to focus on pair-wise species interactions independent of the environment. They suggested four research themes: functional traits, environmental gradients, interactions milieu and performance currencies, in order to bring general patterns to community ecology. Relatively few studies have explicitly incorporated structuring abiotic (environmental gradient) and biotic (movement, dispersal) features that are key to species co-existence and vital for the maintenance of species diversity (Loreau *et al.*, 2003). The number of species in a community are influenced by a variety of factors (e.g., physical stress, nutrient availability, consumer pressure, habitat destruction), which result in non-random diversity gradient in natural habitats (Zavaleta, 2004; Srivastava and Vellend, 2005).

From a theoretical point of view, functional diversity decreases with increasing environmental constraints or stress (Mouillot *et al.*, 2006). When environmental constraints increase, coexisting species are more likely to be similar to one another because environmental conditions (i.e., abiotic properties of the habitat) act as a filter, allowing only a narrow spectrum of species to survive. The species that make it through the environmental filters are likely to share many biological/ecological characteristics through the niche filtering concept (Franzen, 2004; Statzner *et al.*, 2004). More precisely, environmental factors could limit the presence of certain functional traits at certain sites and thus decrease functional diversity of local communities in sites under environmental pressure such as confined parts in lagoons (Mouillot *et al.*, 2006).

Global species distributions are generally believed to be determined by abiotic influences related to oceanographic and physiographic properties (Sanders, 1968;

Richlefs and Schluter, 1993). For instance, water motion affects biology by acting as a transport mechanism for organisms and their propagules, as a dynamic boundary between regimes, and as a force to which organisms must adapt or respond, for example, in their feeding and locomotor activities (Nowell and Jumars, 1984; Denny, 1993). Thus mechanisms of species assemblages depend strongly on various environmental conditions. However, the variability of species along major environmental gradients in many components of biodiversity remains poorly understood.

Nevertheless, environmental conditions and processes that occur at a variety of spatial scales are critical elements to understand patterns of species assemblages. Analysis of spatial patterns along environmental gradient at different scales is seen as a logical requirement to deal with spatial and temporal confounding (Hurlbert, 1984), and provides tests for generality of models of species assemblages. There are limited studies that have tested the consistency of patterns along sharp environmental gradients at hierarchies of spatial scales (e.g., Benedetti-Cecchi, 2001). A better understanding of the role played by abiotic factors is a key prerequisite for forecasting the effects of shifts in environmental conditions on species diversity (or species traits), as a result of human pressure, and for setting up adequate policies for marine conservation and management (Terlizzi and Schiel, 2009).

The use of traits to predict functional response to environmental change has developed rapidly over the last two decades (Grime *et al.*, 1988; Woodward and Diament, 1991; Chapin *et al.*, 1993; McIntyre *et al.*, 1995; Gitay and Noble, 1997; Poff, 1997; Purvis *et al.*, 2000), including studies on traits related to the probability of extinction (e.g. Davies *et al.*, 2000; Williams *et al.*, 2005) and invasion (e.g.

Grotkopp *et al.*, 2002; Hamilton *et al.*, 2005; Olden *et al.*, 2006). The community assemblage that will affect ecosystem properties is the result of sorting processes among individuals with appropriate response traits (Weiher *et al.*, 1998; Grime, 2006). These response traits may encompass response to environmental change, directly and response through compensatory dynamics due to consequent changes in species interactions. The altered community will impact ecosystem processes via changes in the representation of ecosystem-effect traits. Suites of effect on traits are often reliable predictors of ecosystem function (Chapin *et al.*, 1996; Diaz and Cabido, 2001; Garnier *et al.*, 2004) across a wide range of ecosystem types (Grime *et al.*, 1997; Reich *et al.*, 2003; Diaz *et al.*, 2004; Kremen, 2005), and understanding of how traits affect various ecosystem properties is a currently growing area of research (Suding *et al.*, 2008).

The species trait diversity effects on ecosystem processes are the degree to which abiotic conditions constrain the functional variations within communities that influence the processes within the system (Hopper *et al.*, 2002). Consequently, merging our understanding of ecosystem level controls with our understanding of community dynamics and assembly is an important focus of future study (Thompson *et al.*, 2001). Functional diversity is increasingly used to understand the biodiversity-environment relation and biodiversity-ecosystem functioning and to decipher the effect of anthropogenic activities on ecosystem (Dimitriadis and Koutsoubas, 2011).

Studies using functional traits to test the strength of different processes of community assembly often find that habitat filtering plays a key role in the communities' formation (Paine *et al.*, 2011; Katabuchi *et al.*, 2012; Shipley *et al.*,

2012). However, it is important to recognize that in many cases there is also evidence that in varying degrees, other processes (e.g. limiting similarity, dispersal limitation) play a role in the formation of the community structure (Cornwell and Ackerly 2009; Katabuchi *et al.*, 2012; Shipley *et al.*, 2012).

There has been an overall lack of studies accounting for the fact that communities assemble across environmental gradients (McGill *et al.*, 2006). This chapter of the thesis focuses on quantifying assemblage patterns of functional traits and assesses whether those patterns are the results of gradient in abiotic factors. The study hypothesizes that multiple functional traits influence macrobenthic community structure, and that traits relating to primary strategy or ‘ecological syndrome’ (sets of traits that are collectively associated with adaptation to particular environment change (or gradient) (see Grime, 2001; Lavorel *et al.*, 2007), will be similar among species; and also, the dominant traits exert the strongest control on ecosystem processes.

3.2 Materials and Methods

3.2.1 Study Area

The study locality is within the Guinea Current Large Marine Ecosystem (GCLME) which borders 16 countries from Bissagos Island in Guinea Bissau to Angola in Western Africa. It is number 28 of the 66 globally delineated large marine ecosystems (LMEs) (IOC, 2013). The sampling extended from Bissagos Island to Cape Lopex in Gabon and comprised of 11 countries (Figs. 2.3 and 3.1).

The GCLME is characterized by distinctive bathymetry, hydrography, chemistry and trophodynamics. The Guinea Current System represents a Large Marine Ecosystem (LME) ranked among the five most productive coastal and offshore waters in the world with rich fishery resources, oil and gas reserves, precious minerals, a high potential for tourism and serves as an important reservoir of marine biological diversity of global significance (Sherman, 1993; Ukwe, 2003).

3.2.2 Field Sampling

Soft-bottom macrobenthic fauna samples were collected in replicate from the Bissagos Island (Guinea Bissau) in the north to Cape Lopez (Gabon) in the south of the GCLME onboard RV Fritdjorf Nansen as part of the GCLME fisheries resource survey from May to July 2007. In all four stations were sampled for sediment in each of the GCLME country, using a van Veen grab of surface area of 0.1m^2 . At each station, two replicate sediment samples were in order to ensure sample representativeness due to the patchiness in the macrobenthic community.

The sediment samples were washed through a 0.5 mm mesh size sieve using filtered seawater.

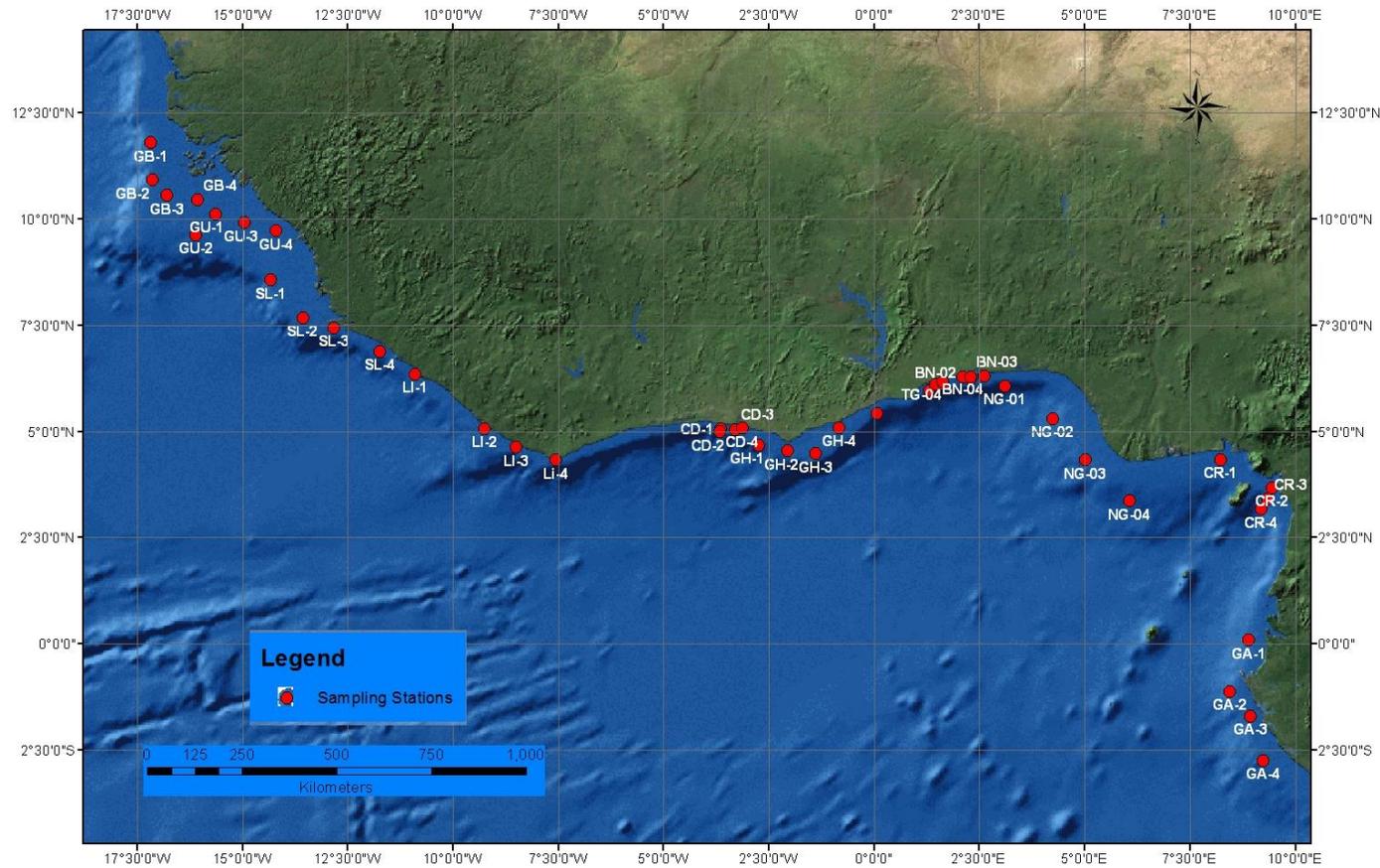


Figure 3.1 Map of the study area showing sampling points.

The retained samples on the sieve were transferred in turns into inner and outer-labeled wide neck plastic sample holding containers and fixed with borax pre-buffered with 10% formaldehyde solution for taxonomic identification in the laboratory. The labeling followed a format of the station name and number (i.e. country first 2 initial letters), date, replicate type, and fixative used (e.g. GB-03, 08/05/06, 1/3, Formalin). Each grab sample was evaluated on suitability of acceptance as good grab sample. For instance, an acceptable grab sample has the top layer of the sediment intact and not disturbed and also if +51% of the sample were retrieved from the grab (Holme and McIntyre, 1971; Eleftheriou and Holme, 1984).

The top 2cm of each sediment sample was sub-sampled for physical and chemical analyses. This was done using a 2 cm deep Kynar-coated scoop and placed into separate jars as follows:

- 500 ml container for organic carbon content analysis (samples were frozen);
- 250 ml container for chemical analyses (samples were frozen);
- ziplock bag for grain size analyses.

3.2.3 Field Quality Control

Basic quality control measures were followed for sediment macro-infauna sampling. These measures were based on internationally accepted Standard Operation Procedures (SOPs) in benthic sampling to ensure quality of the information gathered (Holme and McIntyre, 1971; Eleftheriou and Holme, 1984; ASTM, 2006). Among others, the following field quality control procedures and measures were observed:

- Sediment samples collected at each station were ensured that they meet international sample acceptance criteria. These include:

- Incomplete closure of grab
- Inadequate sediment samples
- Lack of surficial water
- Only experienced persons assisted with the sediment sampling, sieving, fixation and preservation.
- Sediment was sieved with gentle flowing water hose to avoid squashing of organisms.
- All sieves were backwashed into storage containers after sieving to ensure that organisms at the crevices of the sieve are removed.
- Chemicals solutions such as formalin and ethanol for fixation and preservation respectively were carefully and properly prepared.
- Injurious and harmful chemicals were adequately labelled and stored in appropriate cabinet.

3.2.4 Laboratory Processing of Samples

The processing and analyses of samples were performed in the Department of Fisheries and Marine Science , University of Ghana laboratory for the sediment biota and the activities included sorting of organisms (picking target organisms from the sediment grains), preservation and taxonomic identification. For the abiotic component both physical and chemical analyses were carried out on the sediment samples and these are described in section 3.4.

The sample sorting involved emptying the contents of the fixed samples into 0.5 mm mesh sieves and thoroughly washing with fresh water to get rid of all silt/clay particles, as well as the formaldehyde fixative. The samples were then put into a tray

with a white background and macrobenthic faunal organisms sorted into preservation vials containing 70% ethanol premixed with glycerol to prevent evaporation of the ethanol.

3.2.4.1 Taxonomic Identification

The preserved organisms were put into petri dishes and identified to the lowest taxonomic units as possible using Leica 2000 dissecting and compound microscopes. Enumeration of individual species was carried out after the identification. Various taxonomic guides were used in the species identification including Day, (1967ab); LeLœuff and Intes, (1974); Fauchald, (1977); Edmunds, (1978); Intes and Lœuff (1984); Kirkegaard, (1988); Cosel, (2006) and Rakel, (2007).

With regards to taxonomic identification, quality assurance measures were observed in the laboratory to ensure that the quality and the integrity of the data from the laboratory processes were not compromised. The following procedures were used.

- Each sorted sample was crosschecked by other benthic expert to ensure that all organisms had been picked before sample was discarded.
- Species identification was verified independently by a colleague expert.
- Unidentified species were assigned the genus name followed by 'sp.' (if only one species, e.g. *Glycera* sp.) or 'spp.' (i.e. more than one species, e.g. *Eunice* spp.) and put separately into vials for later identification.
- Organisms preserved in vials were annotated with relevant information on non-wettable sheets.
- Data entering into computers were verified by another person to avoid wrong entering.

3.2.4.2 Laboratory Analysis of Abiotic Data

The abiotic data collected were physical (grains size), and chemical (total organic carbon, nutrients [i.e. nitrate, phosphate], calcium, sodium, potassium and magnesium).

3.2.4.3 Analyses of Physical Parameters

Prior to the sediment grain size fraction analysis, the sediment samples were air-dried, sieved through 200 mm mesh size sieve. The Bouyoucos Methods (Bouyoucos, 1934) was used for the grain-size analysis. The method is based on the principle that sediment particles were expected to settle in water at a speed directly related to the square of their diameter and inversely related to the viscosity of the water. As regards the Bouyoucos Method, forty grams (40 g) of the air-dried, homogenized and sieved samples were transferred into polyethylene containers and then 100 ml of calgon solution was added to disperse the particles. The solution was stirred on a mechanical shaker for 90 minutes and then transferred into a sedimentation cylinder after sieving through 45 μm .

The retained sand fraction was put in a moisturizing container and 5ml of hydrogen peroxide was added to dissolve any organic matter present. The sample was oven dried overnight at a temperature of 105° C, each sample was weighed afterwards. The suspension was poured into a cylinder and made up to the 1 litre mark with distilled water. The sediment particles were thoroughly stirred with a hand stirrer and after five hours a hydrometer was carefully inserted into the suspensions and the readings were taken. The hydrometer readings for a blank were also taken. This was subtracted from the original hydrometer readings to give the actual weight of the

clay fractions. The weights of both the clay and sand fractions were calculated in terms of percentages with respect to the initial weight taken, and the sum of their combined weight was subtracted from 100 to give the percentage weight of the silt.

3.2.4.4 Chemical Analysis

Total Organic Carbon

The organic carbon content determination was carried out at the Ecological Laboratory of the University of Ghana using the ELTRA 5500 C-S determinator. The samples were pretreated with 10% hydrochloric acid to remove the inorganic carbonates. The sediment samples were oven-dried at 60°C for 12 hours to get rid of the moisture. The samples were then weighed individually and transferred into a weighing boat of size 1.5 x 0.15 cm. The samples were then sent into an ELTRA C5500 C-S determinator, with a furnace combustion temperature of about 1100°C. After the combustion the percent organic carbon of the samples were determined and recorded.

Sediment Nutrient Determination

Five grams (5 g) of each sediment sample was weighed into a beaker and 0.75M KCl solution was added for extraction, after which the samples were shaken vigorously for 1 hour. The resultant solution was filtered and 25ml of it taken for analysis of nitrate and using the HACH DR/2010 Spectrophotometer following the methods in A.P.H.A. *et al.*, (1998). However, for phosphate analysis the EDTA method (Golterman, 1996) was used for the P-extraction.

Elemental Analysis

The sediments were first dried to get rid of excess water and later oven-dried at a temperature of 50°C to attain a constant mass. Sediments were then pounded into powder form using a mortar and pestle. They were later passed through a 63µm sieve (silt fraction) and later kept in labeled transparent polythene bags for analysis. One hundred milligrams (100 mg) of each sample was enveloped via thermal sealing inside 5×5 cm² polyethylene thin film, which was heat-sealed in 8.9 cm³ rabbit capsule for irradiation. Initially, the polyethylene film and rabbit capsules were cleaned by soaking them into dilute nitric acid for three days and washed with de-ionized water.

The sediment samples were analyzed by Instrumental Neutron Activation Analysis (INAA). The neutron flux used for the irradiation was approximately $5.0 \cdot 10^{11} \text{ n} \cdot \text{cm}^{-2} \cdot \text{s}^{-1}$. The samples were sent into the Miniature Neutron Source Reactor (MNSR) by means of a pneumatic transfer system operating at a pressure of 25 atmospheres. The scheme of the irradiation was chosen so as to take into account the half-lives of the radionuclides under investigation. In that regard, the following irradiation times were selected: 10 seconds for the short-lived radionuclides; 3600 seconds for the intermediate radionuclides; and 14400 seconds for long-lived elements.

After a short decay period the activity of the gamma-ray emitting radionuclides with short and medium half-lives were measured. The measurements of the gamma-ray spectral intensities were made using a spectroscopy system of high purity germanium (HPGe) N-type coaxial detector Model GR 2518; high voltage power supply Model 3105; and a spectroscopy amplifier Model 2020 (all manufactured by Canberra Industries, Inc.). The detector system at fixed geometry was coupled to an 8k Ortec multichannel analyzer (MCA) emulation card and a 486 microcomputer.

The resolution of the detector system which operates at a bias voltage of -3000 V full width at half maximum (FWHM) was 1.8 keV for ^{60}Co 1332 keV gamma-ray with 25% relative efficiency.

The output spectral intensities of both the analytical samples and the standards were processed and stored in the microcomputer software by means of the MCA card. Qualitative analysis of the radioisotopes was achieved by means of identifying their spectral intensities. The evaluations of the areas through integration under the photo peaks of the identified elements were converted into their concentrations using the comparator method (Dampare *et al.*, 2005).

3.2.5 Functional Trait Analysis

The statistical analyses of the data was preceded by functional trait categorization as described in the ensuing sections. The macrobenthic fauna species were categorized using biological traits. The selection of biological traits and their categorization was dictated by i) available information, ii) ecological functions and iii) perceived sensitivities to environmental disturbance. The selected biological traits reflect morphology (e.g. body size and form) and behaviour (adult mobility, sociability and feeding habit). Some of these traits directly reflect ecological functions (e.g. food and feeding habits), whereas others are indirect indicators. For example, body size indicates the ratio of production/biomass and of production/respiration, because for invertebrate populations in most aquatic systems, the ratios of production/biomass and of production/respiration are closely related to the maximum size achieved by the different taxa (Statzner, 1987). Size also has implications for many other ecological functions and considered to be an important trait of organisms because it

correlates with many aspects of its biology (e.g. metabolism, growth and reproduction) (Calder, 1984). The selected biological traits were further divided into categories as indicated in Table 3.1.

Table 3.1 Biological traits categorization

Numbers	Adult Body Size [BS]	Adult Mobility [AM]	Feeding Habit [FH]	Feeding Structure [FS]	Sociability [S]	Adult Body Form [BF]
1	0.5-20mm	Sessile	Deposit-feeding	Mandible	Solitary	Vermiform
2	20.5-40mm	Crawl	Filter/suspension	Jaw	Gregarious	Cylindrical
3	40.5-60mm	Burrow	Opportunist/scavenger	Proboscis	Colonial	Slender
4	60.5-80mm	Swim	Predator	Palp	Commensal	Flattened
5	80.5-100mm	Creep	Herbivore	Pharyngeal		Elongated
6	>120mm	Glide	Omnivore	Tentacle		Tapered

3.2.5.1 Ecological and Biological Traits

Characteristics describing living modes of the organisms were classified in the ecological traits. These traits have a strong effect on ecosystem functioning and occur in most of the macrobenthic organisms. Mobility was described in the scale of the capacity of the organisms to move in and outside of the sediment. Semi-mobile organisms have the ability to move but they do so only if necessary and usually very slowly. Mobility is an important ecological trait because it affects the capture method of prey organisms or other food resources and defines the trophic relationships of a benthic community.

The chosen morphological traits are important indicators of sediment condition (sediment type and organic loading concentration). The average weight of an adult individual was used to assign the organisms to the body size categories. The second characteristic of the morphological traits was the body form. The attribute “shell” describes all the organisms having external protecting structures while vermiform are considered all the worm-like organisms with or without segmentation (length >> width) (Papageorgiou *et al.*, 2009).

3.2.5.2 Functional Trait Classification and Categorization

For every species, information was assigned in each trait category. The data on the species traits was gathered from a variety of literature and internet sources. The functional composition of the samples was determined using biological (morphological) and ecological traits based on the fact that traits that affect resources use (e.g., energy and nutrients), feeding interactions, habitats modification

(bioturbation and habitat providers) are recognized for their functional importance (Pearson, 2001; Meysman *et al.*, 2006; Hastings *et al.*, 2007) and are wide ranging (Bremner, 2008). As a result, six biological and ecological traits were used in the functional classification analysis. These described the morphology and behaviour of the macrobenthic invertebrates, reflecting their involvement in ecosystem processes and perceived sensitivities to environmental disturbance (see Snelgrove *et al.*, 1997; Jennings and Kaiser, 1998; Bolam *et al.*, 2002; Coleman and Williams, 2002; Thrush and Dayton, 2002). Each of the six traits were sub-divided into categories, for example the trait 'feeding habit' contained the categories deposit-feeder, filter/suspension feeder, opportunist/scavenger and predator (Table 3.1). As a result, each species at each sampled station was assigned its biological and ecological traits (see Appendices I & II), and the total traits were determined for each station under each of the selected trait in Table 3.1. Further, statistical analyses of the traits and their categorization were carried out as described in section 3.3.

The selected traits are likely to bring out the effect and response to environmental drivers. For instance traits such as adult size is likely to change with severity of disturbance (Pearson and Rosenberg, 1978), feeding type of the species determine its ability to utilize/tolerate a new diet (Fauchald and Jumars, 1979). Mobility and sociability can be related to recovery patterns and resilience to disturbance (Thrush and Whitlatch, 2001). Size and living habits indicate the ability to rework the sediment affecting sediment biogeochemistry (Michaud *et al.*, 2006) providing a link to ecosystem function.

3.3 Statistical Analysis

The data sets were analysed using suites of univariate and multivariate statistics. Basic statistics of the species abundance were calculated as well as distributional trends of the major macrobenthic taxa and dominant functional traits across the sampled stations. Macrobenthic species abundance data were grouped into major taxa namely polychaeta, mollusca, crustacea, echinodermata and 'Others'. Wet-weight biomass of these major taxa were determined across the stations.

The frequency of occurrence of the data sets (taxonomic diversity and functional richness) were calculated using the F index described by Guille (1970):

$$F = p_a / P \times 100 \quad (1)$$

where: p_a , is the number of stations where the species occurred and P is the total number of stations. Using this formula the species (and also functional traits) data were classified as: constant ($F > 50\%$), common ($10\% < F < 49\%$) and rare species or traits ($F < 10\%$). The data sets were refined and all the rare taxonomic species and functional traits ($F < 10\%$) were eliminated from the data sets as they could potentially introduce 'noise' in the statistical analyses. In certain instances, only data for constant taxonomic species and functional traits were used in the statistical analyses. These have been indicated in the appropriate sections of the thesis.

For multivariate analysis, dendrograms of Bray-Curtis similarity index of the composite station data for the GCLME countries were calculated for taxonomic species abundance and functional trait richness using the PRIMER v6 package (Clarke and Gorley, 2006). The data sets were first fourth-root transformed to stabilize and normalize the variance (Clarke and Green, 1988). Using a complete

linkage, sample (country and biological traits) classifications were produced and thereafter samples (i.e., countries and traits) related to each other identified based on the resulting similarity matrix. The differences in the samples (i.e., GCLME countries) were assessed with one-way ANOSIM (Clarke and Warwick, 1994).

In order to demonstrate the most important abiotic variables related to assemblage patterns of the taxonomic and functional traits, various statistical tools were employed. Forward selection in a Canonical Correspondence Analysis (CCA) and Redundancy Analysis (RDA) ordinations in the CANOCO package and rank correlations between cluster matrix with the program BIO-ENV (Clarke and Ainsworth, 1993) in the PRIMER package and Multiple Linear Regression Analysis (MLRA) were utilized.

In the CCA and RDA analyses, the proportion of the total faunal variance (= sum of all eigenvalues, called total inertia in CANOCO) which can be accounted for by the environmental variables can be estimated as the ratio of eigenvalues of constrained versus unconstrained axes. From this ratio, the percentage value which indicates the percentage explanation of each separate environmental variable to the total fauna and trait variance was calculated. Constrained axes are constructed to maximise the fit with linear combinations of environmental variables, and remaining, unconstrained axes represent a residual variation in data after extracting the constrained axes.

For the functional trait data, the RDA was performed (Ter Braak, 1986) for only identified dominant functional trait data (the identified dominant trait contributed

35.6% and their selection as dominant traits was based on the F index, i.e., $F > 85\%$) (Guille, 1970) and trait richness $> 4\%$. This technique ensured that rare traits and/or traits with low spatial occurrence and contribution were eliminated so that the analysis was refined and 'noisy' data were not included. It is the author's view that functional traits (or taxonomic species) with the highest spatial coverage (based on the F-index) possess valuable ecological information, having adapted naturally possibly through ecological filtering to the varied environmental gradient, are key in unearthing the main environmental drivers of community assemblages.

The RDA was run using the package CANOCO 4.5 (Ter Braak and Smilauer, 2002), which combines both ordination and regression to ascertain relationships between species (and also species traits) and environmental variables (Ter Braak, 1986). None of the environmental variables utilized reported inflation factor > 20 (Ter Braak and Smilauer, 2002) and as a result none was eliminated from the RDA and CCA analyses. All the environmental variables used for the analysis were transformed ($\text{Log}(x + 1)$) to stabilize and normalize the variance. In the RDA biplot, the first and second axes represent the most important environmental gradient along which the macrobenthic functional traits are linearly distributed. The direction of each environmental vector represents the maximum rate of change for that particular environmental variable and its length indicates the relative importance to the ordination.

The significance of all primary RDA axes was determined by a Monte Carlo permutation test (199 permutations) of the eigenvalues (Ter Braak and Smilauer,

2002). A forward selection procedure ordered the environmental variables according to the amount of variance they captured in the trait data (Ter Braak and Verdonschot, 1995). In the first step of this method, all environmental variables were ranked on the basis of the fit for each separate variable. Each variable was treated as the sole predictor variable and all other variables were ignored; hence, the variance explained represents marginal effects. At the end of the first step of the forward selection, the best variable was selected. Hereafter, all remaining environmental variables were ranked on the basis of the fit (amount of variance explained) that each separate variable gave in conjunction with the variable(s) (covariables) already selected (conditional or unique effects). At each step, the statistical significance of the variable added was tested using a Monte Carlo permutation test (199 unrestricted permutations) (Ter Braak and Smilauer, 1998). This description of RDA is similar to the CCA used for the taxonomic species and functional trait data sets except that the RDA is a linear ordination whilst CCA is unimodal (weighted averaging).

Bio-Env analysis was the second method used for extracting important explanatory variables from the taxonomic species and functional traits data. This harmonic analysis uses a weighted Spearman's rank correlation between the resulting ranked similarity matrices which underlie the MDS ordinations (or the dendrogram) of species or traits and correlation-based. The variable or combinations of variables which give the highest correlation coefficient is assumed to be the most important explanatory variable(s).

In order to confirm the explanatory variables and develop a simple model, the taxonomic species and functional traits data were subjected to step-wise linear multiple regression analysis. The analysis not only select the best explanatory

environmental variable to the dependent variable (ie., species diversity, functional richness, and dominant functional traits) but also create a significant predictive model of the dependent variables.

3.4 RESULTS

3.4.1 Macrobenthic Fauna Community Structure

The analysis of the taxa resulted in a numerical abundance of 3,048 individuals (mean density = 693 ± 579 indi/m²) comprising 381 species that belong to five major taxonomic groups namely: Polychaeta, Crustacea, Mollusca, Echinodermata and 'Others'. Of the total numerical abundance, polychaetes contributed 55.15%, crustaceans accounted for 28.02%; 12.76% was contributed by species placed in "Others" category, while molluscs and echinoderms accounted for 2.23% and 1.84% respectively (Table 3.2). Species placed in 'Others' category included cnidarians, sponges, sipunculids etc.

In terms of number of species, polychaetes comprised 233 species (61.32%), crustaceans consisted 71 species (18.64%), 35 species (9.19%) were molluscs, whereas echinoderms and "others" category constituted 10 (2.63%) and 32 (8.39%) species respectively. Polychaetes taxa contributed substantially and ranked highest in terms of species richness and numerical abundance among the major macrobenthic taxa in the study area. Crustaceans ranked second highest in terms of species richness and numerical abundance. The dominant polychaete and crustacean species could constitute important food resources for many commercially important demersal fish species.

Table 3.2 Abundance and richness of major macrobenthic faunal groups.

Taxa	No. of Species	Abundance (No. of indi.)	Abundance (%)
Polychaeta	233	1681	55.15
Crustacea	71	854	28.02
Mollusca	35	68	2.23
Echinodermata	10	56	1.84
Others	32	389	12.76
Total	380	3048	100

The distribution pattern of these macrobenthic fauna may therefore determine the abundance of demersal fish stocks on the continental shelves of the GCLME as the fish prey on these. The spatial pattern of all the major macrobenthic faunal taxa is shown in Figures 3.2-3.13. The distribution pattern generally depicts two abundance peaks especially for polychaetes, crustaceans and molluscs (Fig. 3.2). The lowest abundances were noted from Guinea Bissau to Sierra Leone, with Guinea being exception, while the highest abundances occurred in the central sections from Ghana to Benin. Cameroon and Gabon recorded the lowest numerical abundance (Fig. 3.2). The highest abundance of echinoderms occurred at Guinea Bissau (Fig. 3.2) but with low species richness (Fig. 3.3) depicting dominance of few species, which could suggest conditions tolerable to few species. The highest crustacean abundance and richness was noted at Guinea (Figs. 3.2 and 3.3). Nonetheless, the composite abundance and richness data indicated that Togo, Benin and Ghana, and Guinea ranked highest. The composite data indicated considerable differences in species abundances and richness in Togo, Benin, Ghana and Guinea with the other GCLME countries (Figs. 3.2 and 3.3).

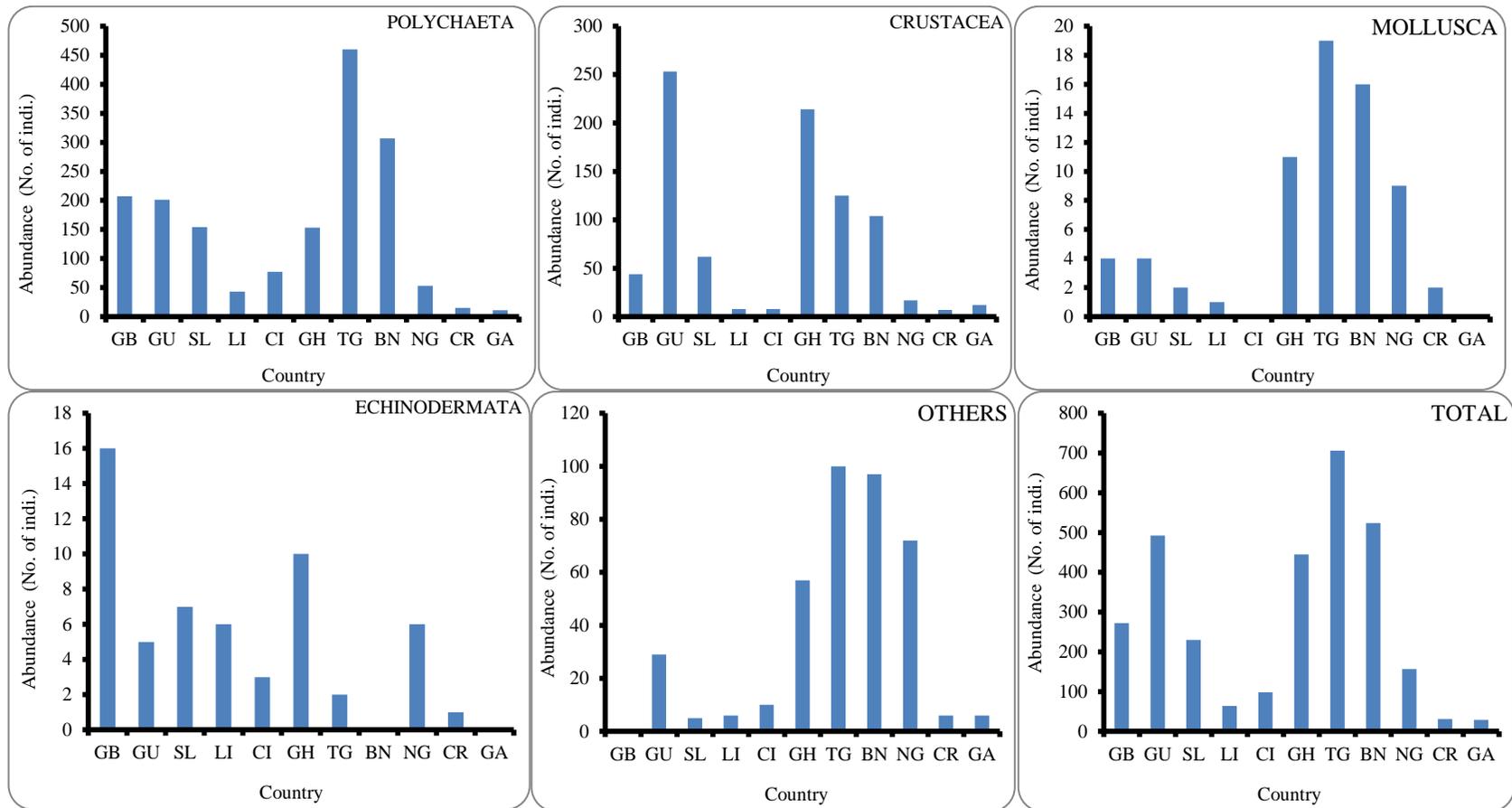


Figure 3.2 Spatial distribution of major macrobenthic fauna abundance on the continental shelves of the GCLME countries. See Table 3.3 for the codes used on the x-axis.

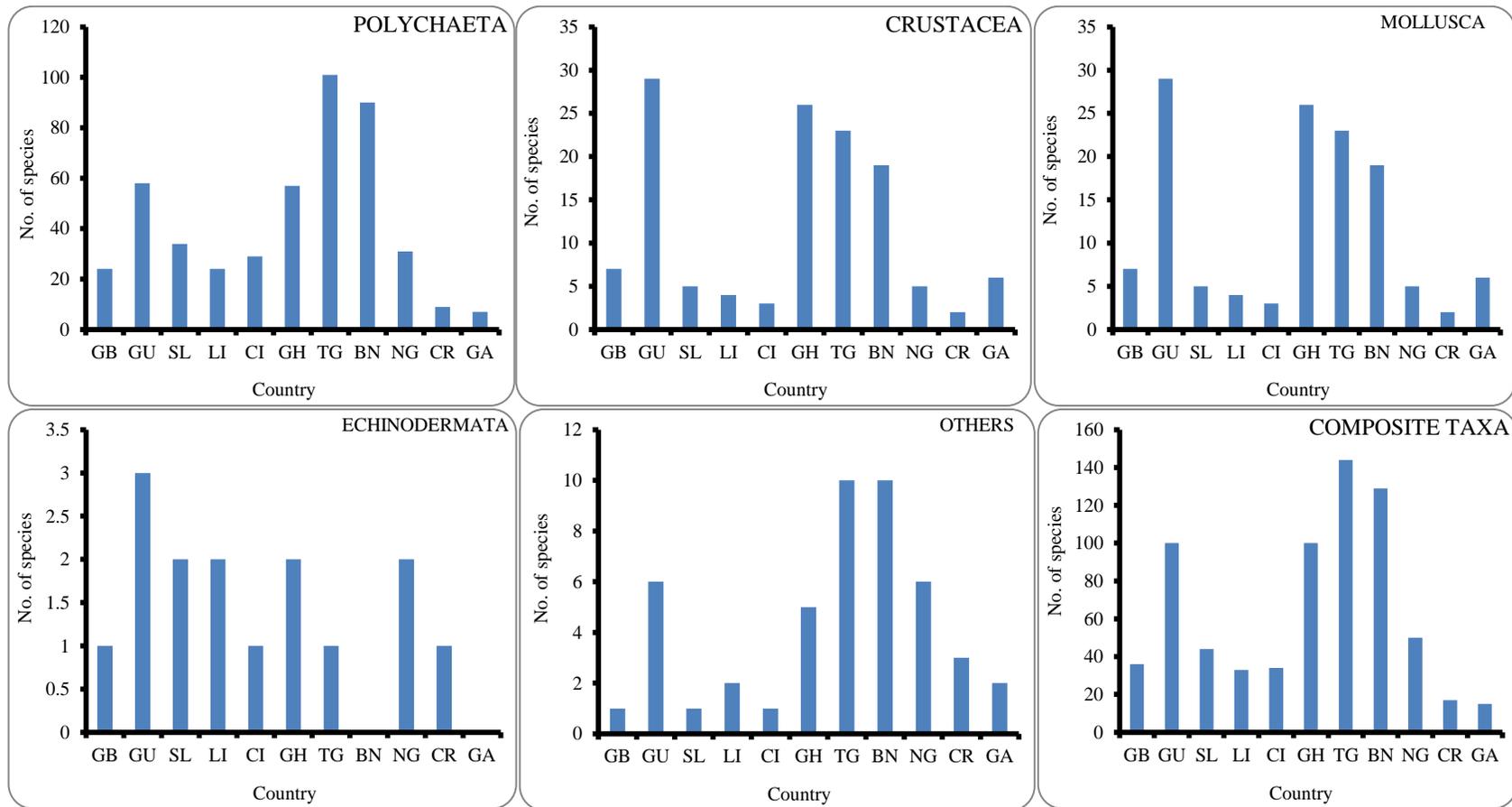


Figure 3.3 Spatial distribution of number of species (species richness) across continental shelf of the GCLME countries. See Table 3.3 for the codes used on the x-axis

3.4.2 Macrobenthic Faunistic Density

The total densities for the respective countries are presented in Table 3.3. The overall total density for the study area was 9,525 indi/m² (mean density = 865.9±723.2 indi/m²). The highest densities were sequentially observed with polychaetes, crustaceans, 'other' taxa, molluscs and echinoderms, which are consistent with the pattern of the species abundance data. The densities of polychaetes, crustaceans and molluscs across the GCLME countries showed similar patterns to that of the species abundance (Figure 3.2). The patterns indicated two peaks and troughs. The highest densities occurred between Ghana and Benin, followed by Guinea Bissau to Sierra Leone, while lowest densities were noted between Liberia-Cote d'Ivoire, and Cameroon-Gabon

Table 3.3 Densities (Ind./m²) of major macrobenthic faunal groups in the continental shelves of countries bordering the GCLME.

Country	Country ID	Polychaeta	Crustacea	Mollusca	Echinodermata	'Others'	Total
Guinea Bissau	GB	647	138	13	50	3	850
Guinea	GU	628	791	13	16	91	1538
Sierra Leone	SL	481	194	6	22	16	719
Liberia	LI	134	25	3	19	19	200
Cote d'Ivoire	CD	241	25	0	9	31	306
Ghana	GH	478	669	34	31	178	1391
Togo	TG	1438	391	59	6	313	2206
Benin	BN	959	325	50	0	303	1638
Nigeria	NG	166	53	28	19	225	491
Cameroon	CR	47	22	6	3	19	97
Gabon	GA	34	38	0	0	19	91

3.4.3 Dominant Macrobenthic Taxa

The analysis of frequency of occurrence (F-index) of the 381 identified macrobenthic faunal species across the 44 sampling locations, indicated that 15 species (contributed 35% to species abundance) occurred in >20% of the sampling stations. They may constitute cosmopolitan species with greater geographical coverage and could be excellent biological candidates for monitoring the health of the GCLME. These species were predominantly polychaetes, however, the highest occurrence species (59.0%) was noted for a crustacean, *Ampelisca* spp. The polychaete with the highest frequency of occurrence was *Glycera* sp. and *Eunice vittata* in that order with 41% and 39% respectively (Table 3.4).

Table 3.4 Frequency of Occurrence for 15 numerical dominant macrobenthic fauna. For brevity only taxa contributing >20% were selected. P= Polychaete, C=Crustacean, O= 'Others' taxa .

Taxa	Frequency of Occurrence (%)
<i>Ampelisca</i> spp. (C)	59.0
<i>Glycera</i> sp.(P)	41.0
<i>Eunice vittata</i> (P)	39.0
<i>Sipunculid</i> spp. (O)	39.0
<i>Lumbrinereis aberrans</i> (P)	32.0
<i>Tanaid</i> spp. (C)	30.0
<i>Mysid</i> sp. (C)	27.0
<i>Armandia intermedia</i> (P)	25.0
<i>Prionospio pinnata</i> (P)	25.0
<i>Scoloplos madagascariensis</i> (P)	25.0
<i>Aricidea fauveli</i> (P)	23.0
<i>Lumbrinereis latrelli</i> (P)	23.0
<i>Lumbrinereis coccinea</i> (P)	23.0
<i>Nephtys lyrochaeta</i> (P)	23.0
<i>Prionospio sexoculata</i> (P)	23.0

The spatial distribution of the abundance of the 15 most occurred species is presented as Figure 3.4. A striking feature of the distribution was the high numbers of *Prionospio pinnata* (Spionidae) at Guinea Bissau (Fig. 3.4), which also revealed higher numerical abundance for echinoderm but low taxa richness (Figs. 3.2 and 3.3) suggesting the existence microhabitats that support certain species. *Eunice vittata* (Spionidae) was also highest at Togo followed by Guinea Bissau (Fig. 3.4).

There were numerical dominance of different species across the GCLME countries suggesting the existence of abiotic gradients supporting organismal life. *Ampelisca* spp. for instance ranked highest in Togo followed by Guinea. Ostensibly, the 3 most occurred crustaceans (*Ampelisca* spp., Tanaid & mysid) were collectively dominant numerically in Guinea, which thus rank the country highest in terms of crustacean abundance. *Sipunculid* spp. was dominant in Ghana but was visibly absent in Guinea Bissau, Togo, Benin and Nigeria (Fig. 3.4). The countries with the lowest representation of these most occurred species were Nigeria, Gabon, Cameroon, Liberia, Cote d' Ivoire and to some extent Sierra Leone.

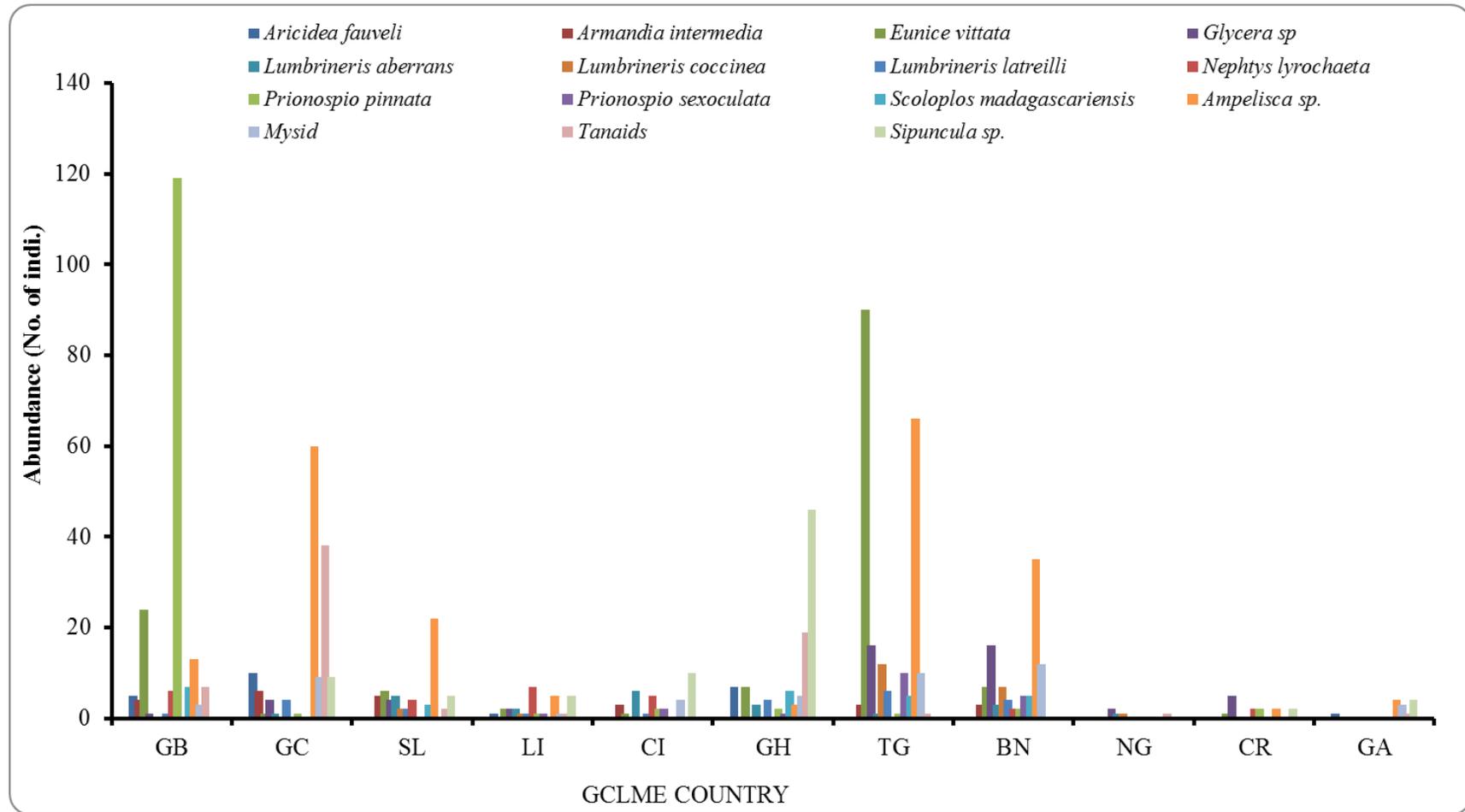


Figure 3.4 Distribution of abundance of dominant macrobenthic faunal species across GCLME countries using F-index, F>20. Codes on x-axis are provided in Table 3.3.

3.4.4 Spatial Pattern of Sediment Abiotic Variables

The water depth for the various sample stations ranged between 16 m and 153 m (Appendix V) with the mean water depth of 54.7 ± 33.7 m. However, 50% of the stations had an average depth of 49 m.

The mean concentration levels and the distribution of the sediment abiotic variables are presented in Figure 3.5. All the sediment parameters showed spatial differences with peaking and troughing between the countries, but without discernible east-west pattern. Average nitrate levels were higher at both west (Guinea Bissau, Guinea and Sierra Leone) and east (Nigeria, Cameroon and Gabon) of GCLME than at the central (Benin, Togo, Ghana, Cote d'Ivoire and Liberia). There were considerable within country spatial variations in the sediment parameters. Certain GCLME countries, reported the highest mean concentrations namely phosphate in Benin, sodium and organic carbon in Ghana, nitrate in Guinea Bissau, and silt in Cameroon

Calcium showed three spatial peaks at Sierra Leone, Gabon and Ghana in that decreasing order. The lowest concentrations of calcium were noted at Togo, Benin and Nigeria. However, the levels within Nigeria depicted the highest variations. Total organic carbon and clay showed relatively similar pattern with Ghana recording the highest mean concentrations.

Magnesium levels ranked highest at the western sections of the GCLME depicting a similar pattern to calcium distribution. The lowest magnesium and calcium levels occurred in Togo and Benin, which also depicted the highest species and dominant

trait richness. Higher phosphate levels were noted at Togo, Benin and Ghana (Fig. 3.5b).

Table 3.5 Average water depth of the sampled GCLME countries

Country	Country Code	Average (m)	Standard Deviation
Guinea Bissau	GB	89.8	58.9
Guinea	GU	47.5	32.0
Sierra Leone	SL	40.5	12.0
Liberia	LI	41.5	15.0
Cote d'Ivoire	CD	59.5	32.6
Ghana	GH	66.3	29.8
Togo	TG	32.8	19.2
Benin	BN	21.3	5.4
Nigeria	NG	58.2	23.6
Cameroon	CR	51.5	36.8
Gabon	GA	92.8	25.5

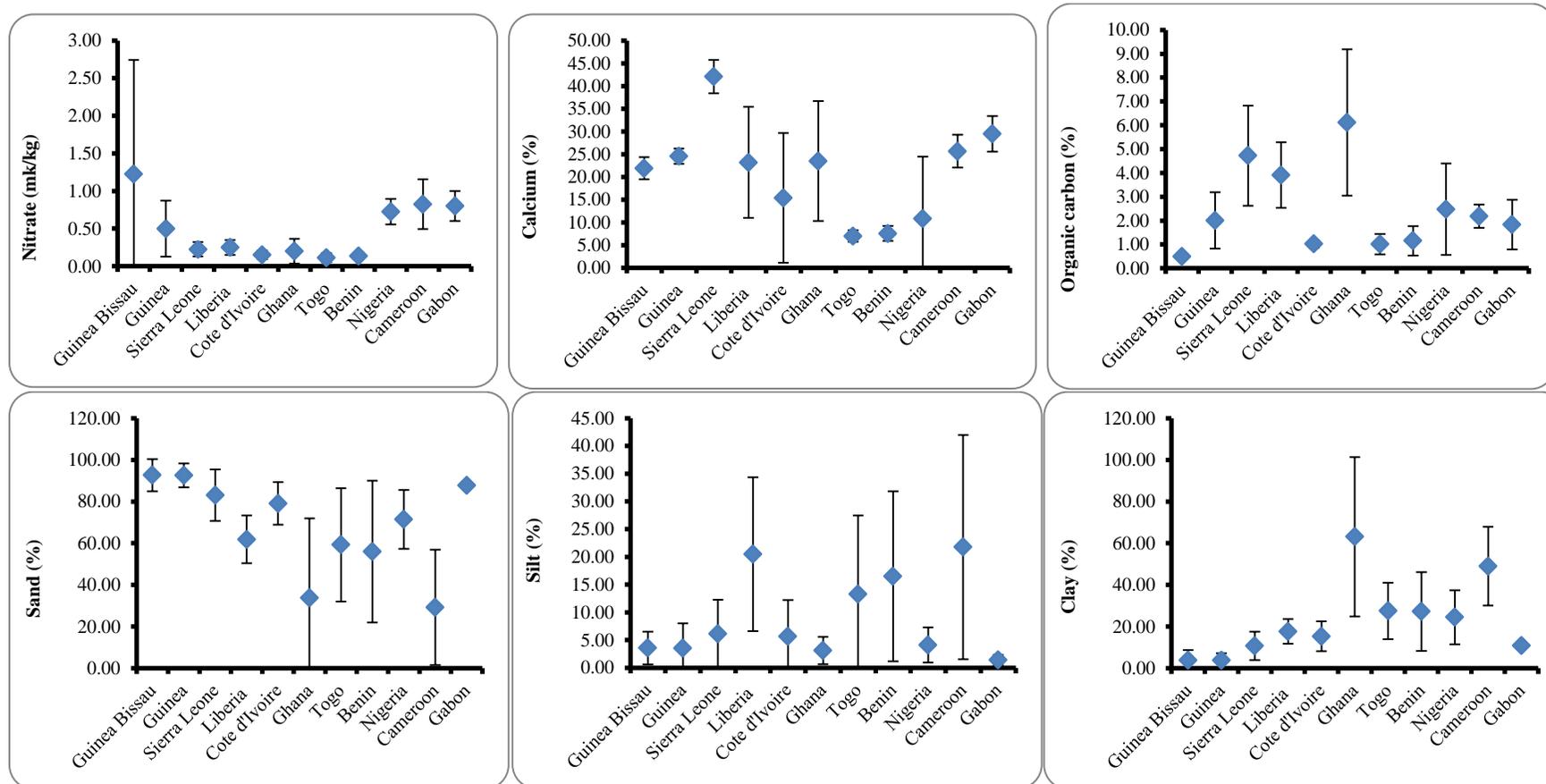


Figure 3.5a. Mean concentration of nitrate, calcium, organic carbon, sand, silt and clay contents of sediments across the GCLME countries. The error bars indicate 95% confidence intervals.

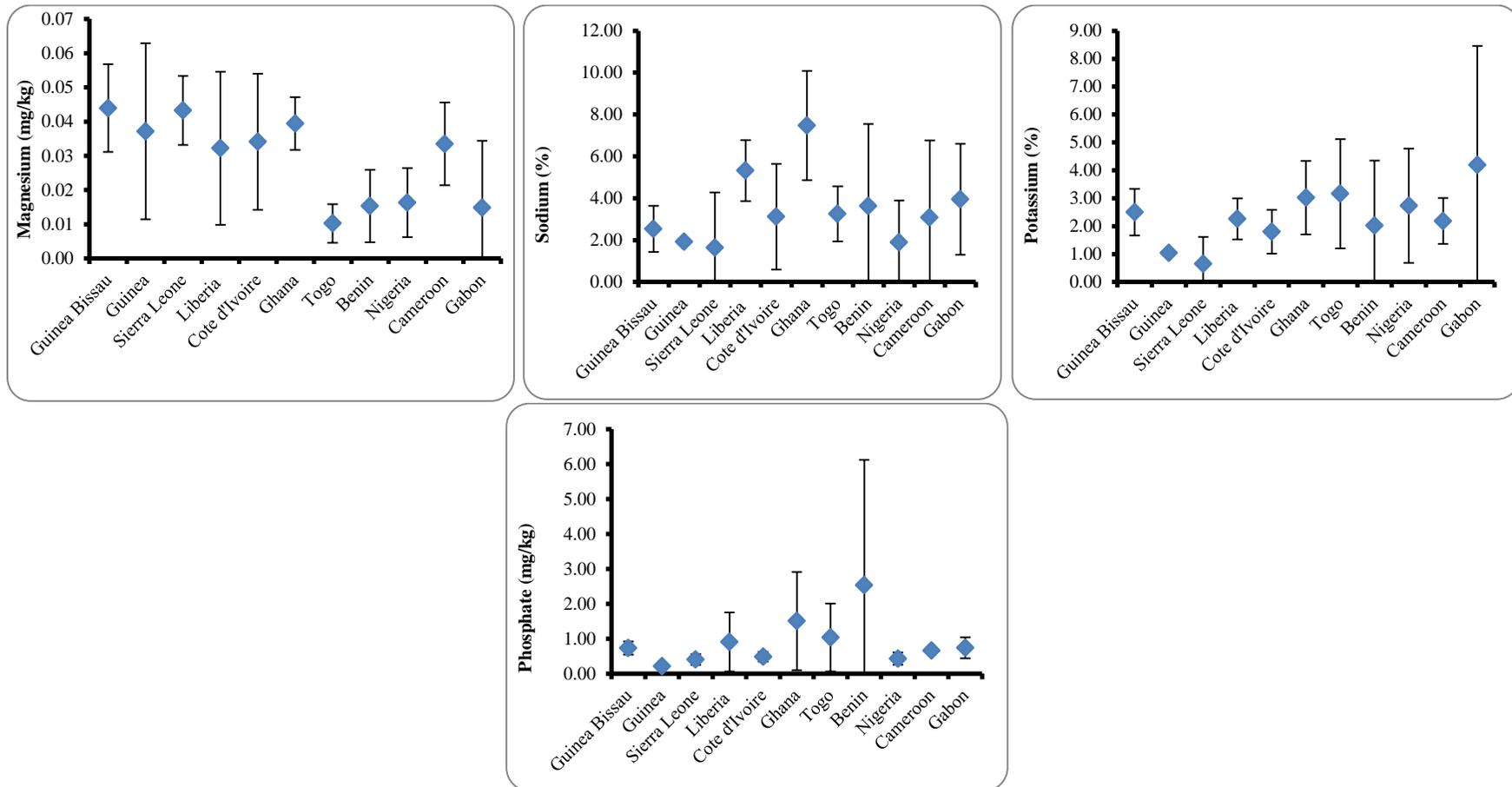


Figure 3.5b. Mean concentrations of magnesium, sodium, potassium and phosphate across the GCLME countries. The error bars indicate 95% confidence intervals.

3.4.5 Community Structural Analysis

An agglomerative Bray–Curtis similarity dendrogram of the pooled station species abundance data to represent countries revealed three significant ($p < 0.05$) groupings based on the faunistic data (Fig. 3.6). Only Nigeria showed non-significant faunistic structure with the other countries indicating either unique condition supporting unique fauna or a stressful ecosystem. The first cluster ground (Group A) comprised Cameroon, Liberia and Gabon. Cluster Group B is made up countries located at the western part of the GCLME namely Guinea Bissau, Guinea, Sierra Leone, Cote d’Ivoire and Ghana. Ghana and Cote d’Ivoire formed one sub-group under Group B just as Guinea Bissau, Guinea and Sierra Leone. The last cluster Group C composed of Benin and Togo, which showed the highest similarity index of 58%, followed by Sierra Leone and Guinea at 54%, and together with Guinea Bissau at 47% (Fig. 3.6). Liberia and Cameroon followed at 43% similarity before Ghana and Cote d’Ivoire 36%. The pattern shows high degree of spatial differences in the macrobenthic fauna composition and abundance possibly due to prevailing gradients in environmental conditions creating varied tolerable regimes for the organisms.

In order to test the level of similarity between the countries, the analysis of similarity (ANOSIM) test was run and the results indicated significant differences ($p = 0.001$) between the countries with the global $R = 51.2\%$ (Table 3.6). However, the pairwise test showed non-significant differences ($p > 0.05$) between some countries notably those bordering the western sections of the GCLME suggesting that the macrobenthic fauna composition at those countries are relatively similar than the central and eastern sections of the GCLME.

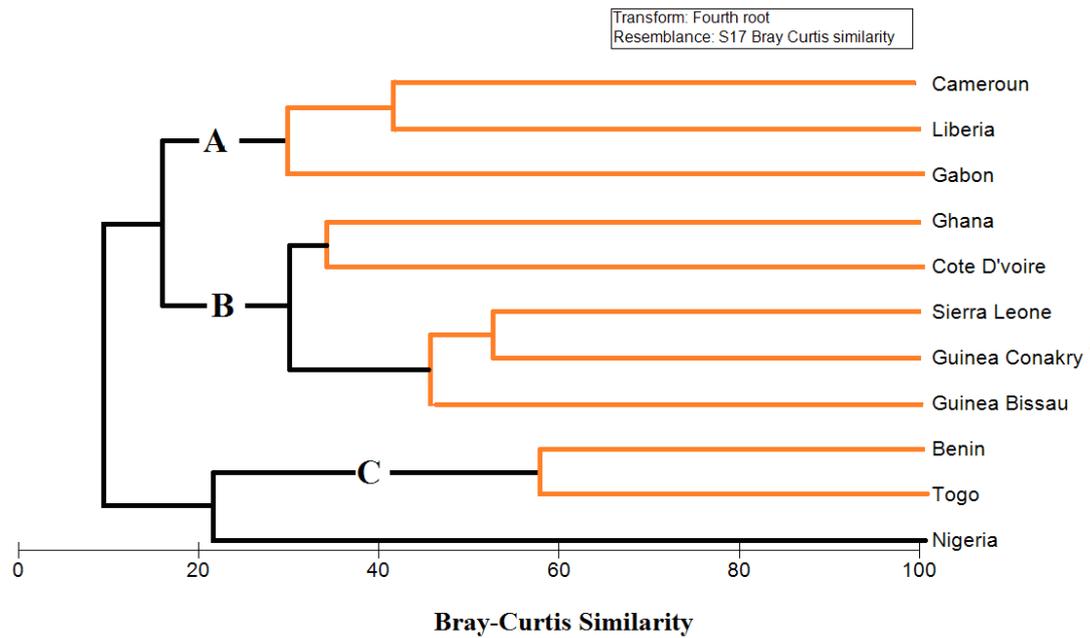


Figure 3.6 Complete-linkage of agglomerative dendrogram of Bray–Curtis similarity of macrobenthic faunal abundance data for GCLME countries. Thin red lines indicate significant evidence of structure (SIMPROF test, $p < 0.05$) and thick black lines indicate no evidence of structure.

Table 3.6 Pairwise ANOSIM analysis

Global Test

Sample statistic (Global R): 0.512

Significance level of sample statistic: 0.1%

Number of permutations: 999 (Random sample from a large number)

Number of permuted statistics greater than or equal to Global R: 0

Pair Country	R Statistic	Significance level (%)	Significance
Guinea Bissau, Cote d' Ivoire	0.672	2.9	Yes
Guinea Bissau, Ghana	0.516	2.9	Yes
Guinea Bissau, Togo	0.766	2.9	Yes
Guinea Bissau, Benin	0.771	2.9	Yes
Guinea Bissau, Nigeria	0.635	2.9	Yes
Guinea Bissau, Cameroon	0.479	2.9	Yes
Guinea, Cote d' Ivoire	0.625	2.9	Yes
Guinea, Togo	0.719	2.9	Yes
Guinea, Benin	0.750	2.9	Yes
Guinea, Nigeria	0.740	2.9	Yes
Sierra Leone, Ghana	0.427	2.9	Yes
Sierra Leone, Togo	0.615	2.9	Yes
Sierra Leone, Benin	0.677	2.9	Yes
Sierra Leone, Nigeria	0.604	2.9	Yes
Sierra Leone, Cameroon	0.339	2.9	Yes
Liberia, Ghana	0.604	2.9	Yes
Liberia, Togo	0.958	2.9	Yes
Liberia, Benin	0.958	2.9	Yes
Liberia, Nigeria	0.677	2.9	Yes
Cote d' Ivoire, Ghana	0.469	2.9	Yes
Cote d' Ivoire, Togo	0.969	2.9	Yes
Cote d' Ivoire, Benin	0.969	2.9	Yes
Cote d' Ivoire, Nigeria	0.740	2.9	Yes
Cote d' Ivoire, Gabon	0.385	2.9	Yes
Cote d' Ivoire, Cameroon	0.557	2.9	Yes
Ghana, Togo	0.927	2.9	Yes
Ghana, Benin	0.917	2.9	Yes
Ghana, Nigeria	0.719	2.9	Yes
Ghana, Gabon	0.333	2.9	Yes
Ghana, Cameroon	0.776	2.9	Yes
Togo, Nigeria	0.635	2.9	Yes
Togo, Gabon	0.458	2.9	Yes
Togo, Cameroon	0.854	2.9	Yes
Benin, Nigeria	0.625	2.9	Yes

Benin, Gabon	0.479	2.9	Yes
Benin, Cameroon	0.828	2.9	Yes
Nigeria, Cameroon	0.693	2.9	Yes
Guinea Bissau, Guinea	0.078	25.7	No
Guinea Bissau, Sierra Leone	0.005	57.1	No
Guinea Bissau, Liberia	0.490	8.6	No
Guinea, Ghana	0.323	5.7	No
Guinea, Sierra Leone	-0.042	60	No
Guinea, Liberia	-0.073	74.3	No
Guinea, Gabon	0.036	37.1	No
Guinea, Cameroon	0.266	8.6	No
Sierra Leone, Liberia	-0.219	94.3	No
Sierra Leone, Cote d' Ivoire	0.396	8.6	No
Sierra Leone, Gabon	0.198	17.1	No
Liberia, Cote d' Ivoire	0.313	8.6	No
Liberia, Gabon	0.146	14.3	No
Liberia, Cameroon	0.292	5.7	No
Togo, Benin	0.146	25.7	No
Nigeria, Gabon	0.375	8.6	No
Gabon, Cameroon	0.167	20	No

3.4.5.1 Community Structure-Environmental Relation

The relationship between benthic macrofaunal community structure and the abiotic variables were determined using suite of multivariate statistical analysis including BIO-ENV routine in PRIMER software v6. This was done to obtain best combination of explanatory environmental variables for the species assemblages. Further, canonical correspondence analysis (CCA) in CANOCO package was used for ordination and correlation of environmental variables, and lastly a multiple linear regression model for a predictive model of species diversity.

The results of the BIO-ENV analysis indicated four environmental variables (silt, nitrate, sodium and calcium) as best explanation variables for the data of the 'constant' species (constant species are based on F-index, with $F > 50$) with

Spearman's correlation of 24.3% (Table 3.7). Silt and nitrate combination gave a significant ($p < 0.05$) correlation of 23.5%. However, when only the ten most occurred species (i.e., species with the highest occurrence) were used in the analysis, similar abiotic variables (i.e., silt, nitrate, sodium and calcium) combined to give a correlation of 28.6% although the overall analysis was not significant ($p = 0.164$).

Table 3.7 BIO-ENV results for dominant 'constant' species with $F > 20$.

No of variables	Best variable Combination	Correlation (p_w)
<u>'Constant' Species with $F > 20$ ($p = 0.047$; $Rho = 0.243$)</u>		
4	Silt-Nitrate-Sodium-Calcium	0.243
3	Silt-Nitrate-Calcium	0.241
2	Silt-Nitrate	0.235
<u>Ten Most Dominant 'Constant' Species with $F > 25$ ($p = 0.164$; $Rho = 0.204$)</u>		
4	Silt-Nitrate-Sodium-Calcium	0.286
1	Nitrate	0.201
2	Silt-Nitrate	0.199

The forward selection of the CCA indicated that six environmental variables namely magnesium, organic carbon, nitrate, sand, sodium and silt explained significant variations in the species abundance data ('constant' species). The highest significantly ($p = 0.005$) explained species variance was the effect of magnesium (35%), total organic carbon (31%) and nitrate (18%) (see Table 3.8). In the CCA ordination the first two ordination axes showed 66.2% relationship between the

species and environment indicating that the species data is constrained on the environment data. The first axis alone explained 19.2% variance in the species data and together with the second axis 33.6% of the species variance data is explained. The Monte Carlo test indicated that the first axis was significant ($p=0.01$) while all the four axes showed higher significance ($p=0.005$). All the four axes indicated 92% relation between the species and environment data but only 46.7% variation in the species data was explained (Table 3.9).

Table 3.8 Canonical Correspondence Analysis (CCA) results. Marginal effects denote percentage variance explained (percentage of the total variance in the species data explained) by using each environmental variable as the sole predictor variable. Conditional (unique) effects denote variance explained by each environmental variable with the variable (s) already selected and treated as covariable(s) based on forward selection. Environmental variables are listed by the order of their inclusion into the model. Significant levels are based on a Monte Carlo permutation test with 199 restricted permutations.

Abiotic variable	Marginal Effect	Conditional	p -value	F -ratio
	Lambda1	Effect Lambda1		
Magnesium	0.35	0.35	0.005*	6.40
Organic carbon	0.33	0.31	0.005*	6.25
Nitrate	0.18	0.18	0.005*	4.00
Sand	0.11	0.12	0.025*	2.67
Sodium	0.16	0.13	0.005*	3.15
Silt	0.13	0.09	0.015*	2.17
Clay	0.08	0.07	0.070	1.83
Potassium	0.18	0.04	0.375	1.12
Calcium	0.19	0.02	0.870	0.51
Phosphate	0.06	0.02	0.945	0.41

The ordination biplot (Fig. 3.7) showed important correlations between organic carbon and *Lumbrineria aberrans*, tanaid spp. and mysid spp. These species showed preference to higher sediment organic carbon. *Ampelisca* spp. *Glycera* spp. and *Amandia intermedia* also showed positive preference for clay, whereas higher silt content correlated with *Eunice vittata* and *Scoloplos madagascariensis*.

Table 3.9 Summary of CCA results.

Axes	1	2	3	4	Total inertia
Eigenvalues	0.502	0.378	0.202	0.141	2.622
Species-environment correlations :	0.887	0.848	0.751	0.715	
Cumulative percentage variance					
of species data:	19.2	33.6	41.3	46.7	
of species-environment	37.8	66.2	81.4	92.0	
Sum of all eigenvalues					2.622
Sum of all canonical eigenvalues					1.330

*** Monte Carlo test ***

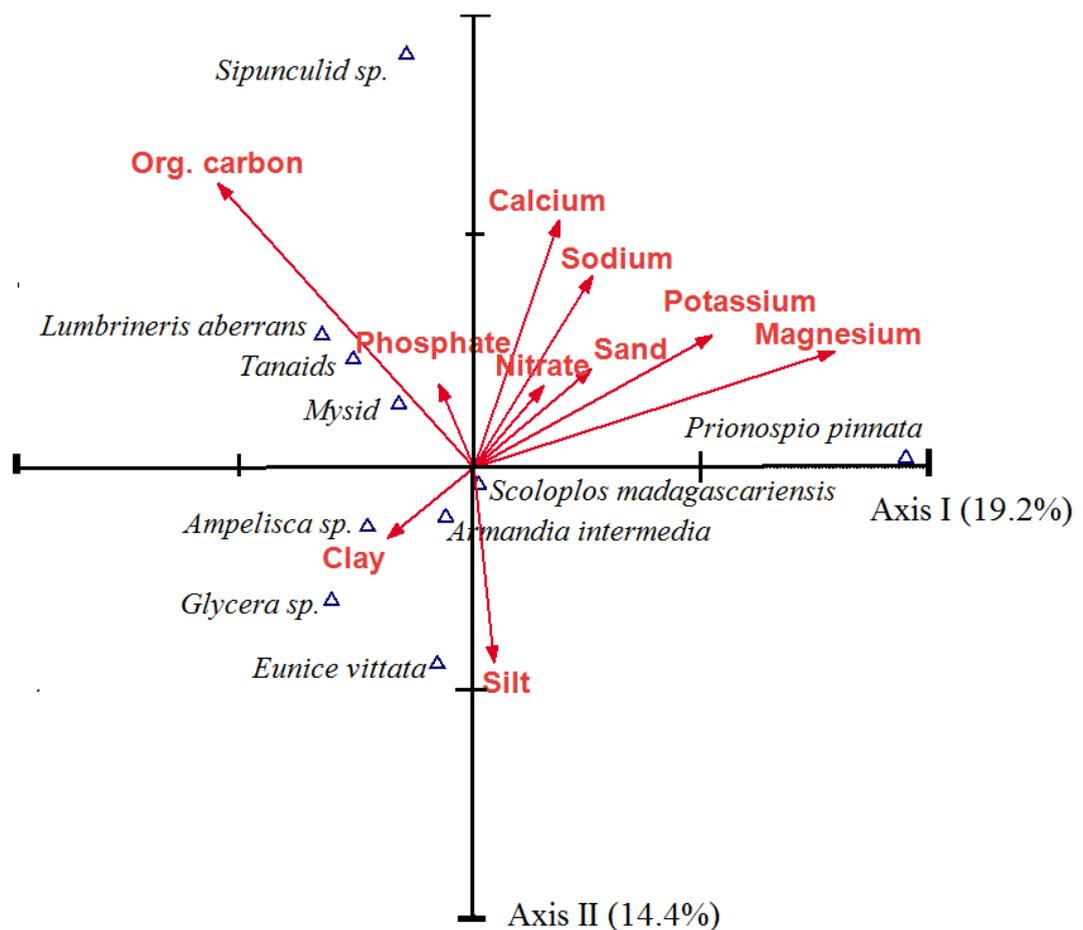
Significance of first canonical axis: eigenvalue ($p = 0.010$; $F\text{-ratio} = 7.585$)Significance of all canonical axes : ($p = 0.005$; $F\text{-ratio} = 3.293$)

Figure 3.7 CCA ordination biplot for taxon-environment relationship

Predictive Linear Regression Model

To further test the interactions between diversity indices (species assemblages) and abiotic variables, a multiple predictive regression model was run using the Business Spreadsheet Excel software. The result of this analysis showed that species assemblages were significantly influenced by suite of abiotic variables ($p < 0.05$). Shannon-Wiener species diversity index was influenced by nitrate and calcium, and these two variables explained 41.37% of the variance in the data (Table 3.10) and are therefore important parameters predicting Shannon-Wiener's diversity in the GCLME. The regression model depicted that the independent variables of nitrate and calcium were correlated negatively with the dependent variable. This suggests that low levels of the variables influence the species diversity but there could be a threshold to these low levels. The variations in Margelef's species richness were also explained by nitrate and calcium accounting for 41.71%. The model relationships were indirect (negative) for nitrate and calcium and similar explanation as in the Shannon-Wiener diversity could be adduced. Since none of the explained variances (R squared) were 100%, the unexplained variances could constitute surrogate of unmeasured environmental variables. This means that other factors such as biological (competition and predation), physical (waves and tides), chemical (pollutants), human disturbances, nature of the topography could all be critical in seeking influence of environmental gradients to species community assemblages.

Table 3.10 Step-wise multiple regression model (using the Business Spreadsheet Excel software) for taxon assemblages and abiotic variables, $p < 0.05$.

Diversity index	Equation (independent parameters)	R ²
Shannon-Wiener's diversity index	-1.13*nitrate + -0.50*calcium+ 4.06 ± 0.66	0.4137
Margalef's richness	-4.43*nitrate +-1.91*calcium+11.81 ± 2.55	0.4171

3.4.5.2 Functional Trait Richness And Distribution

The functional trait richness data were categorised into constant, common and rare traits using the F-index proposed by Guille (1970) (see Tables 3.11 and 3.12). The analysis showed that the highest functional trait group were sociability (solitary trait category dominate contributing 14.89% and F=92%); mobility (burrow traits being dominant category contributing 11.09% and F=90); adult body size (the dominant trait category was small adult size of 0.5-20 mm contributing 4.98% and F=85%); and feeding habit (deposit-feeding as the dominant category contributing 4.71% and F=81%) (see Table 3.12). The total contributions of the functional trait groups under the 'constant', 'common' and 'rare' categories were 72.72%, 23.65% and 3.63% respectively (Table 3.11). This indicates that the contributions to the functional group richness of the 'rare' species were marginal and will not influence the traits structural analyses, and to some extent the influence of the 'common' species to the analyses may be marginal. Essentially, the influence of the 'constant' functional traits to community assemblage is deemed important due to the total percent contribution and as such dominant traits within the category may exert the strongest influence on ecosystem processes in the GCLME region.

Of the biological traits (see Appendix II), the 4 most dominant were solitary, burrow, small body size and deposit-feeding, which together contributed 35.67% to the functional richness (Table 3.12). The dominant traits were selected based on an individual trait contribution >4% and $F > 80\%$ (Table 3.12). The individual and combined influences of these traits will determine to a very large extent the nature of the substrate, prevailing environment conditions, environmental drivers of community assemblages, effect and response of community and key ecosystem processes in the GCLME.

Table 3.11 Percentage functional trait group richness using the F-index described by Guille (1970): $F = p_a/P \times 100$, where: p_a , is the number of stations where the functional traits occurred and P is the total number of stations, thus classified as: constant ($F > 50\%$), common ($10\% < F < 49\%$) and rare traits ($F < 10\%$).

Trait Group	Constant	Common	Rare	TOTAL
Feeding Habit	12.03	4.62	0.23	16.88
Feeding Structure	8.48	6.98	0.98	16.44
Adult Mobility	14.44	2.08	0.28	16.79
Sociability	15.87	1.00	-	16.87
Adult Body Size	16.65	-	-	16.65
Adult Body Form	5.26	8.97	2.14	16.37
TOTAL	72.72	23.65	3.63	100

Table 3.12 Dominant traits with respective percent richness and frequency of occurrence. Trait category's richness contribution >4% and F>80% concurrently are highlighted.

Functional Trait Group	Trait Category	% Richness	% Freq. of occurrence
Feeding Habit	Deposit-feeder	4.71	81
	Carnivore	3.82	79
	Detritivore	1.44	65
Feeding Structure	Proboscis	2.12	67
	Mandible & Jaw	1.72	65
	Pharynges & Proboscis	1.08	63
Adult Mobility	Burrow	11.09	92
	Burrow & Sessile	1.02	54
	Burrow & Swim	0.91	50
Sociability	Solitary	14.89	92
	Commensal	0.98	56
Adult Body Size	0.5- 20mm	4.98	85
	20.5- 40mm	3.42	83
	40.5- 60mm	2.89	83
Adult Body Form	Vermiform & flattened	1.61	65
	Slender and Elongated	0.91	56
	Slender	0.83	50

The Bray-Curtis similarity clustering of the 'constant' functional traits revealed significantly important pairings that lend evidence/support to combined effect of trophic, lifestyle, anatomical and morphological adaptations to the prevailing environmental conditions. This may suggest that habitation and subsequent survival

of macrobenthic organisms in their environment require multiple adaptive strategies including biological and ecological, which may be determined by prevailing environmental conditions. The dendrogram clustering depicted the highest cluster pairs between mandibular palps (feeding structure) and laterally-flattened (adult body form) (Fig. 3.8) giving an indication of body form playing an important role in organism's feeding structure as well as the feeding type.

Further, the results may suggest that species with elongated and tapered body form are mainly carnivores or detritivores and that possibly facilitate their food acquisition mechanism. Slender and elongated species may also be commensal, which could mean better attachment to host to ensure efficient feeding or optimal foraging. The benthic solitary species and burrowing type (see Appendix I) indicated strong significant relationship (Fig. 3.8). The dendrogram also suggests that deposit-feeding species range from different body sizes (Fig. 3.8) due possibly to the different forms/types of organic carbon (refractory & labile) or sources (autochthonous and allochthonous) of organic carbon. The results also suggest that benthic carnivorous species in the GCLME are of medium body size (i.e., 20.5-40.0mm) possibly to facilitate quick movement for preys as well as adequate body size to handle the prey items. Filter-feeders are species with maximum body size (i.e., 100.5- 120mm) probably because they require greater amount of energy for active filter feeding in possibly the high water current.

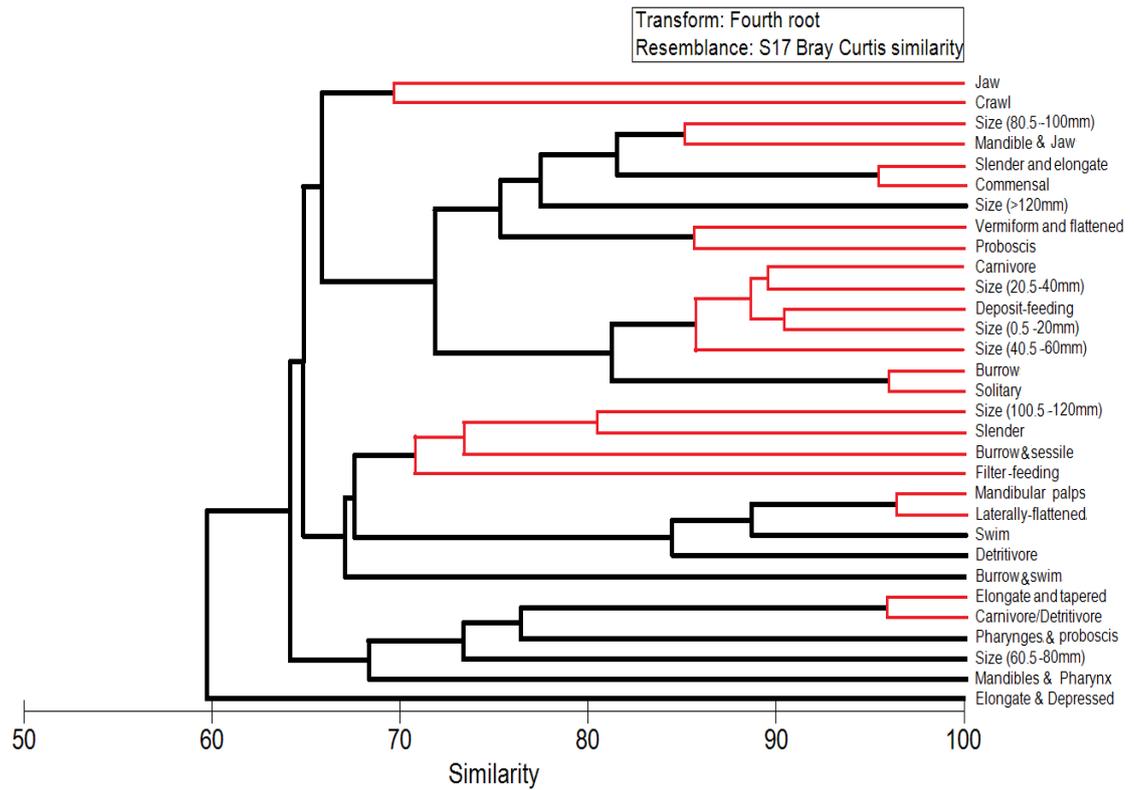


Figure 3.8 Group-average agglomerative dendrogram of Bray-Curtis similarity of 'constant' functional biological traits. Thin red lines indicate significant evidence of structure (SIMPROF test, $p < 0.05$) and thick black lines indicate no evidence of structure

3.4.5.3 Distribution of Most Dominant Functional Traits

The distribution of the 4 most dominant traits across the countries bordering the GCLME showed higher abundance of solitary trait followed by burrowing traits (Fig. 3.8). The sequence of dominance for the functional traits were solitary>burrow>small body size>deposit-feeding. The highest richness of the dominant traits occurred at Togo followed by Benin, Guinea and Ghana. The countries with the least in dominant trait richness were Gabon and Cameroon. The distribution pattern of the 4 most dominant traits (Fig. 3.9) is a resemblance of the distribution of taxonomic species abundance (Fig. 3.2), taxonomic species richness (Fig. 3.3) and the 15 most abundant species (Fig. 3.4) strongly suggesting that the dominant species reflect in dominant traits and exert the strongest influence on ecosystem properties/processes in the GCLME.

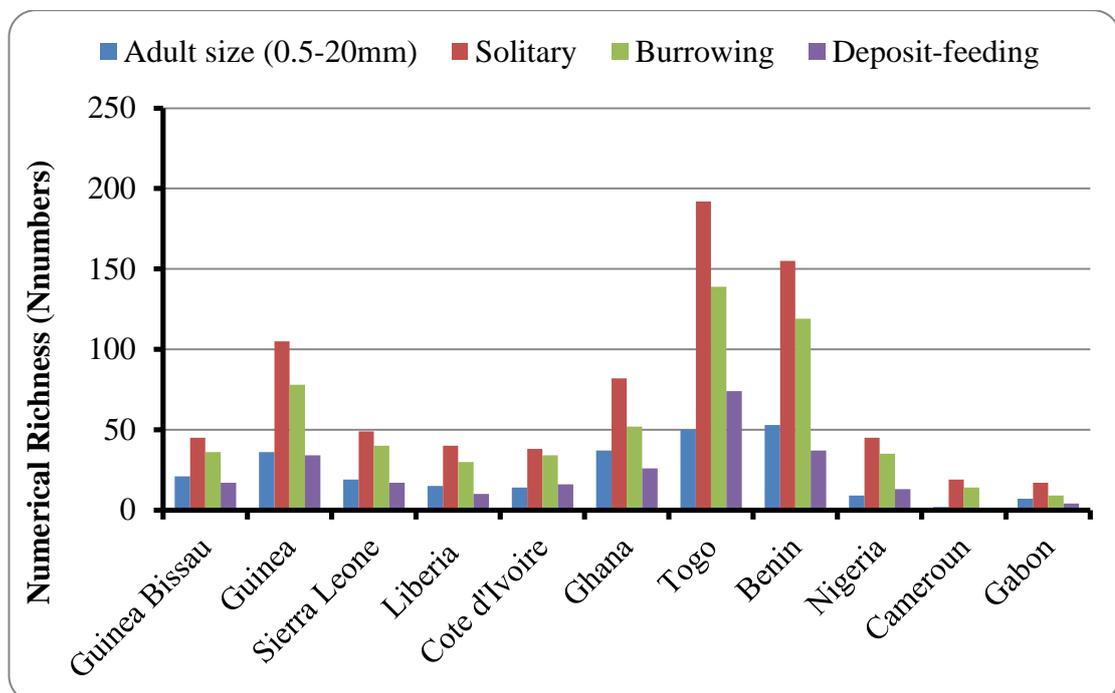


Figure 3.9 Distribution of dominant functional trait richness across GCLME country stations.

3.4.5.4 Multivariate Structural Analysis of Functional Traits

Bray-Curtis similarity analysis of the functional richness data for countries in the GCLME indicated two major significant ($p < 0.05$) cluster groups (Group A & B) distinguished at 52% similarity level. Group A comprised Cameroon and Gabon, located far east of the GCLME. Group B is made up of two subgroups namely B1 and B2, which is distinguished at 73% Bray-Curtis similarity level. Subgroup B1 comprised Liberia, Sierra Leone, Guinea Bissau, Nigeria and Cote d'Ivoire in that decreasing order of similarity, and these are mainly countries located west of the GCLME except for Nigeria (Fig. 3.10). Group B2 comprised Ghana, Guinea (subgroup B2i), Benin and Togo (subgroup B2ii), which with the exception of Guinea, are countries located at the central part of the GCLME. In effect, the analysis significantly categorized the countries bordering the GCLME into Eastern Zone (i.e., Gabon & Cameroon), Central Zone (Benin, Togo & Ghana) and Western Zone (Guinea Bissau, Sierra Leone, Liberia & Cote d'Ivoire). Guinea and Nigeria presented macrobenthic functional structure that mimic the Central Zone and Western Zone respectively. The similarity between the groups showed a sequential declension from Central GCLME > Western GCLME > Eastern GCLME. The analysis suggests that the eastern GCLME is low (poor) in benthic biodiversity, the western GCLME moderately rich benthic biodiversity and the central GCLME rich benthic biodiversity relatively.

Nonetheless, the highest Bray-Curtis similarity was noted between Togo and Benin clustering at 97%. This was followed by the similarity of 96% between Liberia and and Sierra Leone. Ghana and Guinea followed with 94% similarity (Fig. 3.10).

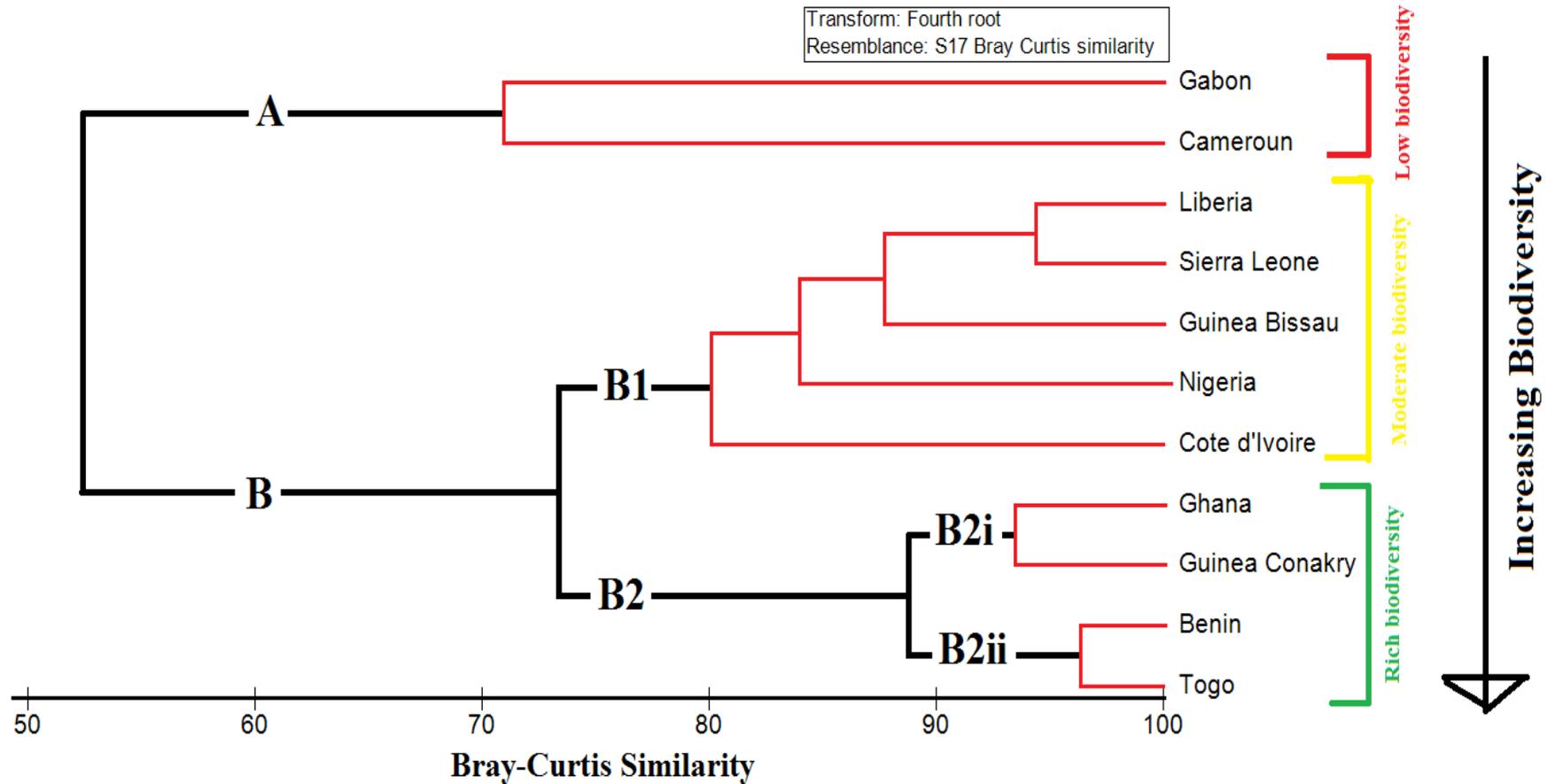


Figure 3.10 Complete-linkage of agglomerative dendrogram of Bray–Curtis similarity of GCLME countries based on functional richness data of ‘constant’ trait. Thin red lines indicate significant evidence of structure (SIMPROF test, $p < 0.05$) and thick black lines indicate no evidence of structure.

3.4.6 Functional Trait-Environment Interactions

The relationships between the functional trait and environment were examined using the BIO-ENV procedures in the PRIMER v6 program (Clarke and Gorley, 2006). The BIO-ENV procedure identified two variables as ‘best explaining’ the dominant benthic functional traits assemblages in the study area (Table 3.13). Nitrate and magnesium produced the highest significant correlation ($p=0.005$) of 34.8%. Nitrate alone showed 34.7% correlation with the dominant functional traits. However, for the 4 dominant functional trait distribution, the ‘best match’ was obtained with sand, nitrate and potassium ($\rho_w=0.286$) (Table 3.13). Here also, nitrate alone indicated good correlation ($\rho_w=0.275$).

Table 3.13 Bio-Env results for ‘constant’ functional traits.

No of variables	Best variable Combination	Correlation (ρ_w)
<u>‘Constant’ Traits ($p=0.005$; Rho=0.348)</u>		
2	Nitrate-Magnesium	0.348
1	Nitrate	0.347
4	Silt-Nitrate-Potassium-Magnesium	0.210
<u>Four Most Dominant ‘Constant’ Traits ($p=0.042$; Rho=0.286)</u>		
3	Sand-Nitrate-Potassium	0.286
4	Sand-Nitrate-Potassium-Sodium	0.278
1	Nitrate	0.275

In the RDA, the environmental variables are shown as arrows, the lengths of which indicate the relative importance and the directions of which are obtained from the correlation of the variable to the axes. The orthogonal projection of a trait linear to an environmental arrow represents the approximate center of the traits distribution along that particular environmental gradient.

In the RDA, the first four ordination axes accounted for 50.1% of explained total variance in the dominant trait richness data. The first ordination axis accounted for 49.5% of the trait variance, but the ordination axes showed 98.7% relationship between the traits and environment indicating that the trait data is strongly constrained on the environment data. The first ordination together with the second axis accounted for 49.9% of the variance and 99.5% of the variance explained by the environmental variables. This indicates that the first axis alone and the environmental variables associated with it are important in explaining large portion of the trait variance. The first ordination axis reflected environmental samples with a gradient largely related to nitrate, calcium, organic carbon, magnesium and sand at the positive end of the axis, which are linearly related to all the dominant traits at the negative end of the axis (Fig. 3.11). The entire RDA analysis resulted in a significant model as depicted by the Monte Carlo test ($p \leq 0.005$) (Table 3.15).

The results of forward selection environmental explanatory covariable(s) (marginal effect) was significantly ($p < 0.05$) noted for nitrate (21% explained variance), organic carbon (11% explained variance) and clay (6% explained variance) (Table 3.14). However, for the sole predictor environmental variables (marginal effect), the

highest explained variances were noted for nitrate (21%), calcium (18%), organic carbon (8%), magnesium and silt (each 5%) (Table 3.14).

Table 3.14 Results of Redundancy Analysis (RDA). Marginal effects denote percentage variance explained (percentage of the total variance in the functional trait data explained) by using each environmental variable as the sole predictor variable. Conditional (unique) effects denote variance explained by each environmental variable with the variable (s) already selected and treated as covariable(s) based on forward selection. Environmental variables are listed by the order of their inclusion into the model. Significant levels are based on a Monte Carlo permutation test with 199 restricted permutations

Environmental variable	Marginal Effect	Conditional Effect	<i>p</i> -value	<i>F</i> -ratio
	Lambda1	Lambda1		
Nitrate	0.21	0.21	0.005*	11.08
Organic carbon	0.08	0.11	0.010*	6.78
Magnesium	0.05	0.05	0.065	3.29
Sand	0.01	0.05	0.100	3.25
Clay	0.01	0.06	0.035*	4.48
Phosphate	0.02	0.01	0.575	0.62
Silt	0.05	0.01	0.180	0.48
Potassium	0.00	0.00	0.620	0.21
Sodium	0.01	0.00	0.000	0.05
Calcium	0.18	0.00	1.000	0.01

Table 3.15 Summary of Redundancy Analysis (RDA) results:

Axes	1	2	3	4	Total variance
Eigenvalues	0.495	0.004	0.002	0.001	1.000
Traits-environment correlations:	0.715	0.543	0.334	0.376	
Cumulative percentage variance					
of traits data:	49.5	49.9	50.0	50.1	
of traits-environment :	98.7	99.5	99.8	100.0	
Sum of all eigenvalues					1.000
Sum of all canonical eigenvalues					0.501

*** Summary of Monte Carlo test ***

Significance of first canonical axis:

(*p* = 0.005; *F*-ratio = 32.32)

Significance of all canonical axes:

(*p* = 0.005; *F*-ratio = 3.32)

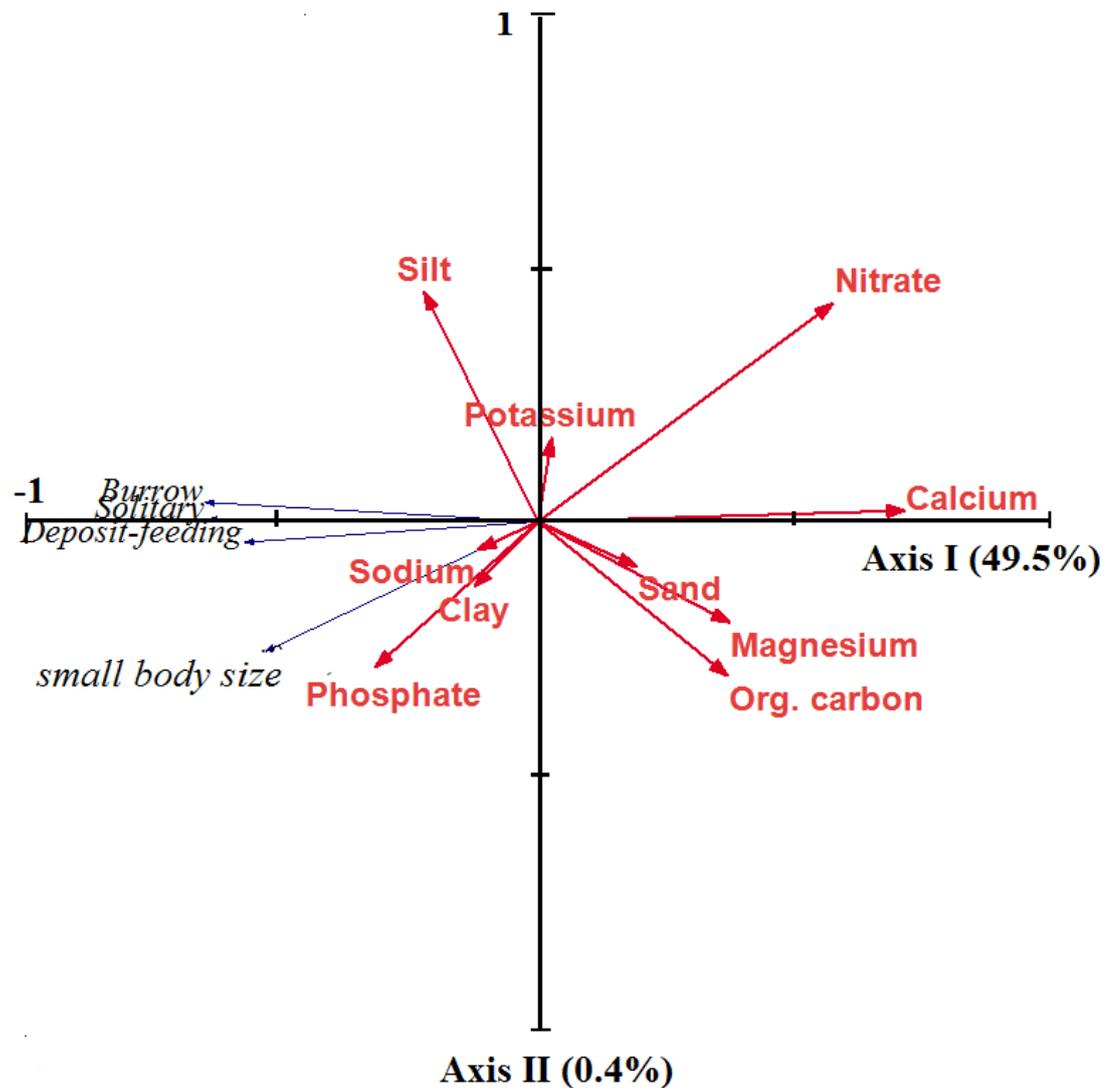


Figure 3.11 RDA ordination of functional trait-environment biplot.

3.4.6.1 Functional Trait-Environment Model

The functional trait assemblage and their relationship with the environmental variables were modeled using the Business Spreadsheet Excel software for multiple linear predictive regression. The regression models were run for the functional richness and diversity for the composite data sets and also for 'constant' data only. The result showed that functional assemblage (i.e., functional richness and diversity) for the composite data were explained by three environmental variables namely nitrate, calcium and silt, whereas the 'constant' functional trait assemblage was

explained by nitrate and silt (Table 3.16). The model was significant ($p < 0.05$) and thus the explanatory variables could predict the assemblage patterns of these traits (Table 3.16). Nonetheless, the percent explained variance for the two scenarios were relatively low, although in all cases marginally higher in the functional richness than the functional diversity.

Table 3.16 Step-wise multiple regression model (using the Business Spreadsheet Excel software) for dominant functional trait and abiotic variables, $p < 0.05$.

Functional Assemblage	Trait	Model for independent environmental variables	R-squared
Functional (composite traits)	Richness	$-6.83 \cdot \text{nitrate} + -1.63 \cdot \text{calcium} + 0.55 \cdot \text{silt} + 17.44 \pm 3.93$	0.3401
Functional (composite traits)	Diversity	$-0.98 \cdot \text{nitrate} + -0.6 \cdot \text{calcium} + 0.07 \cdot \text{silt} + 4.33 \pm 0.54$	0.3142
Functional (constant traits)	Richness	$-2.94 \cdot \text{nitrate} + 0.26 \cdot \text{silt} + 6.81 \pm 1.37$	0.3343
Functional (constant traits)	Diversity	$-0.84 \cdot \text{Nit} + 0.06 \cdot \text{Silt} + 3.15 \pm 3.96$	0.2825

The step-wise multiple linear regression model was also developed for the the dominant functional traits namely burrow (adult mobility), solitary (sociability/degree of attachment), small adult body size (0.5-20mm) and deposit-feeding (feeding habit). The model results showed nitrate, organic carbon and calcium as significant abiotic variables explaining the trait variance and could predict the numerical abundance of these dominant functional traits (Table 3.17).

The model indicated that for burrowing trait, nitrate, total organic carbon and calcium were the main environmental factors that could predict their richness (Table 3.17). All these variables depicted inverse relationship with the burrowing trait. The results were also consistent with the other dominant traits, viz. deposit-feeding, solitary, and small body size but with varying degrees of explained predictive variances. The low R-squared values suggest the influence of other important variables biological (competition and predation), physical (currents and temperatures), chemical (organic and inorganic substances), and anthropogenic disturbances as surrogates, which were probably not assessed in this study.

Table 3.17 Step-wise multiple regression model for dominant functional trait and abiotic variables. TOC=total organic carbon

Dependent Functional Trait	Model for independent environmental variables	R-squared
Burrow	$-17.48*\text{nitrate} + -5.24*\text{TOC} + -3.48*\text{calcium} + 34.92 \pm 9.09$	0.3796
Solitary	$-23.30*\text{nitrate} + -6.42*\text{TOC} + -4.72*\text{calcium} + 46.29 \pm 12.55$	0.3580
Small Body Size (0.5-20mm)	$-8.72*\text{nitrate} + -1.62*\text{TOC} + -1.09*\text{calcium} + 13.83 \pm 3.96$	0.3617
Deposit-feeding	$-8.68*\text{nitrate} + -3.19*\text{TOC} + -1.08*\text{calcium} + 15.18 \pm 5.04$	0.3068

3.6 Discussion

3.6.1 Species Composition and Abundance

The species composition and dominance were noted for the polychaetes, crustaceans and molluscs with numerical abundance, richness and density varying spatially across the countries in the GCLME. Ecological variability is regarded as ubiquitous patterns in marine benthos regardless of the habitats or taxa especially on the small-scale level (Fraschetti *et al.*, 2005). However, according to Benedetti-Cecchi (2009) it is pertinent to address the issues of the variability of the processes driving the change in the species assemblage (i.e., ecological drivers), and the variables that are influenced by the forces (i.e., ecological response). The environmental changes promoting fluctuations in species and assemblages are important ecological forces (Benedetti-Cecchi, 2009), as spatial heterogeneity in species assemblage may enhance productivity and increase resistance to disturbance (Hutchison *et al.*, 2003).

The species assemblage (notably polychaete, crustaceans and molluscs) patterns across sampled stations (countries) showed variations with higher taxa abundances, richness and densities occurring in the central section of the GCLME (Benin, Togo and Ghana) (see Figs. 3.2-3.3 and Table 3.2 and 3.3). These areas (country stations) corresponded with moderate levels of sediment nitrate, calcium, magnesium and higher total organic carbon at some areas. These areas showed surrogates of allochthonous and autochthonous organic matter input (Appendix III). The macrobenthic community structure was influenced by the abiotic variables namely: nitrate, total organic carbon, silt, calcium and magnesium. These variables may be influenced by the interactions with other environmental factors to create favourable conditions for the organisms. For instance, the primary food source for benthos

originates, with a few localized exceptions, in euphotic surface waters. The movement of water driven by currents, wind and other forces transports food particles in the water mass and causes resuspension of bottom sediments (Pearson and Rosenberg, 1987), which essentially distribute food to benthic animals. Essentially, benthic infaunal communities are organized structurally, numerically and functionally in relation to gradients of resource availability, and are modified by interactions with other environmental factors (Pearson and Rosenberg, 1987; Wieking and Kröncke, 2005). Thus species distribution may be recognised as a response to the varying effects of these modified environmental gradients in tandem with other factors. According to Angel (1984) sedimentation of faecal pellets is generally considered to be the major means of transporting phytoogeneous primary production to the benthos.

Nitrate is known to drive marine primary production (Camargo and Alonso, 2006), thus the low levels of nitrate observed to influence species diversity, could be the result of denitrification and nitrate uptake for pelagic primary production, with the latter driving benthic diversity. In marine sediments, nitrate is often consumed within the zone of denitrification (Lehmann *et al.*, 2005) possibly as a result of organic matter remineralization, which is also influenced by the conditions in the overlying water. The observation and interactions between the organisms and the abiotic variables suggest a more complex ecological driver-species assemblages relations in the GCLME. This is because the assumed reason for high nitrate abstraction and subsequent utilization reflecting in higher species abundance and diversity, could be the result of complex interactions. The low correlation values realized in the BIO-ENV matrix, CCA ordination and the predictive regression models (see Tables 3.7-

3.10, Fig. 3.6) support the assertion of a complex environmental stressors/drivers of species and functional assemblage patterns in the GCLME.

3.6.2 Functional Structure and Assemblage Patterns

Functional biodiversity encompassed functional richness (FR– the number of functional groups derived from a combination of functional feeding groups and habit trait groups), functional diversity (FD – the number of functional groups and division of individuals among these groups, and functional evenness (FE– the division of individuals among functional groups). Furthermore, functional structure (FS) comprised the composition and abundance of functional groups at each site. The results of the functional biodiversity analysis revealed dominance of small size (0.5-20 mm) burrow-dwelling solitary deposit-feeding organisms (dominated by polychaetes), which potentially exert the strongest influence on the ecosystem properties/processes in the GCLME region such as biogeochemical nutrient remineralization of nitrate from organic matter. These traits further provide clear indication/information about prevailing environmental conditions, nature of the substrate, key ecosystem processes and possible response to ecological disturbances. In the ecological processes, the interactions and feedback among species and their respective environment are important elements in elucidating synergies.

The prevalence and dominance of small body size (0.5-20 mm) traits inferred habitat instability (see Schwinghamer, 1983) and may result in high production relative to total biomass (given the high turnover rates of member organisms (Bougreau *et al.*, 1991). This suggests that the GCLME region is characterized by high productivity but low total biomass as a result of small adult body size dominance. Essentially, the

size structure of marine macrobenthic communities is affected by anthropogenic stressors such as organic enrichment (Pearson and Rosenberg, 1978; Gray, 1989; Weston, 1990; Warwick and Clarke, 1994) and trawling (Jennings *et al.*, 2001; Duplisea *et al.*, 2002), and thus size-dependent relationships provide objective basis for understanding ecology and predicting conservation outcomes (Calder, 2001). According to Calder (2001), adult body size exerts a quantitative dominance over how an animal lives and for how long and on its rate of living and extraction of resources from its environment, and consequently on how many of its kind can live simultaneously on a unit of habitat.

The small body size organisms are closely related to the burrow-dwelling species, and are well known to play key roles in ecosystem functioning of soft-bottom temperate habitats (Austen and Widdicombe, 1998; Amaro *et al.*, 2010). Macrobenthic burrowers can affect recruitment, growth and survival of a variety of organisms, and thus influence community biodiversity (Macdonald *et al.*, 2012). The profound effects of their burrowing and feeding activities can include the delivery of food and solutes (e.g., oxygen) to subsurface sediments, alteration of sediment geochemical and physical makeup (Braeckman *et al.*, 2011), and increased potential for grazing and subduction of smaller organisms (Needham *et al.*, 2011). The dominance of small body size burrow-dwelling species (e.g., *Prionospio sexoculata*, *Prionospio cirrobranchiata*, *Paraonides lyra capensis*) indicates characteristics of short lifespans due possibly to habitat instability as large surface burrowers have limitations on their ability to maintain an optimal burrow position in shifting sediments (Bromley, 1990).

Small size organisms are mainly opportunistic species that respond to habitat perturbations. According to Villnäs *et al.* (2011), such opportunistic species may endure stress and take advantage of extra resources through processing the uppermost layers of the sediments. Small body size burrow-dwelling traits are likely to influence secondary production due to their short generations and may play essential roles in sediment biogeochemistry (an important ecosystem process) due to their bioturbatory activities. Further, burrowing deposit-feeding traits give lucid indication of sediment characteristics including fine-grained soft substrate with potentially high organic matter (i.e., silt or clay) supporting burrowing and deposit-feeding. The retention for organic matter in sediment is influenced by the particle size (Milliman, 1994). Subsurface deposit-feeders tend to be common in muddier sediments (Macdonald *et al.*, 2012b). Deposit-feeders play important role in bioturbation, which is a critical process in biogeochemistry that ensures mineralization of nutrients (e.g., nitrate) to drive primary production. This thus makes the GCLME a productive ecosystem as acknowledged by Ukwe *et al.* (2006).

It has been demonstrated that macrobenthic fauna create burrow networks that penetrate the sediment anoxic zone (Anderson and Meadows, 1978) and create burrow ventilation (Webb and Eyre, 2004), which impact on the sediment (Rhoads, 1974) thus affecting sediment biogeochemistry (Aller and Aller, 1998; Wenzhöfer and Glud, 2004). The importance of benthic macrofauna in nutrient dynamics and benthic-pelagic coupling have been noted in several studies (Pilskaln *et al.*, 1998; Thrush and Dayton, 2002; Lohrer *et al.*, 2004) suggesting that benthic bioturbators have large-scale ecosystem implications (Bonsdoff and Rosenberg, 2007). The

results of this study lend potential evidence to benthic-pelagic coupling clearly demonstrating the functional significance of marine macrobenthic species.

3.6.3 Functional Trait-Environment Relationship

Marine benthic biodiversity–environment relationships are well-understood in the context of taxonomic species richness and species composition, whereas other component of biodiversity, including functional richness (FR) and functional diversity (FD) lag behind in scientific literature. Most studies to date have examined either taxonomic assemblage patterns with few giving prominence to functional diversity especially in the marine environment (Bremner *et al.*, 2005 and 2008). The relationships between functional diversity (and also taxonomic diversity) of marine macrobenthic fauna and environmental factors showed synergistic association and can give evidence of effect and response mechanisms. This present study established strong association between functional diversity (also taxonomic diversity) and suites of environmental parameters namely nitrate, calcium, organic carbon, manganese, silt and clay. These abiotic variables, which significantly influence the functional and taxonomic species diversities, are largely related to primary productivity and climate change factors. The spatial variations (or gradient) in these abiotic factors explained and can predict the species abundance and functional structure of macrobenthic organisms in the GCLME. It is possible that the functional and community assemblages of the macrobenthic fauna are tolerable to these abiotic variables, and have as such emerged as dominant component through the habitat filtration process (Mouillot *et al.*, 2006).

It has been indicated that the adaptation of certain species to unpredictable environments can be related in part to their life history (Grassle and Grassle, 1976) and biological traits characteristics (Mouillot *et al.*, 2006). Newell (1970) further pointed out that where the tolerance limits for a particular environmental variable have been determined for an organism, the organism's realized distribution is much more restricted than its potential distribution. It is reasonable, therefore, to presume that the gradients (spatial differences) in the environmental variables probably ensured that only tolerant species or traits are selected and hence their distribution.

Among the many best matched environmental factors with species and functional communities, sediment nitrate emerged as key abiotic driver. Nitrate is an important nutrient in primary production (Camargo and Alonso, 2006) and thus productivity models could be implicated here in influencing assemblage patterns. Nonetheless, the possible reasons for the nitrate influence may include:

- i) nitrogen is the most abundant chemical element on the earth atmosphere (almost 80%) and essential components of many key biomolecules (e.g., amino acids, nucleotides) (Camargo and Alonso, 2006) and also ranked fourth behind carbon, oxygen and hydrogen as the commonest chemical element in living tissues (Campbell, 1990);
- ii) most inorganic reactive nitrogen is in the form of nitrate and nitrate drives aquatic productivity by increasing cyanobacteria (an important autotroph) as they efficiently uptake nitrate for fast growth,, and
- iii) less toxicity of nitrate in seawater animals probably because of the ameliorating effect of water salinity (sodium, chloride, calcium and other ions) on the tolerance of aquatic animals. Also nitrate has to be converted

into nitrite under internal body conditions for its toxicity to be realized but owing to the low branchial permeability to nitrate ions by most marine organisms (Cheng and Chen, 2002), the nitrate uptake in aquatic animals is more limited than the nitrite uptake, thus contributing to the relatively low toxicity of nitrate (Jensen, 1996; Cheng and Chen, 2002; Alonso and Camargo, 2003; Camargo *et al.*, 2005a).

Nitrate has been found to be a strong predictor of marine benthic assemblages (Lamptey *et al.*, 2010) due in part to their influence on primary productivity. Aquatic animals are, in general, better adapted to relatively low levels of inorganic nitrogen since natural (unpolluted) ecosystems often are not N saturated (Camargo *et al.*, 2005a), and that explains the low nitrogen correlation with benthic biodiversity (see Tables 3.10 and 3.16).

Calcium and magnesium also emerged as important variables best explaining and predicting functional biodiversity patterns in the GCLME. These parameters implicate climate change effects on the benthic species and functional diversities. The main climate change impact on the marine ecosystem is triggered by the atmospheric CO₂ dissolution in the ocean. Absorption of CO₂ into the ocean leads to low pH and decreased concentration of CO₃⁻². The decreased concentration of CO₃⁻² means low CaCO₃ saturation, which is important in calcification of benthic organisms. According to Fabry *et al.* (2008), elevated partial pressure of CO₂ (*p*CO₂) in seawater (also known as hypercapnia) impact on marine organisms both via decreased CaCO₃ saturation, which affects calcification rates, and via disturbance to acid–base (metabolic) physiology. Some studies have indicated that the oceanic uptake of anthropogenic CO₂ and the concomitant changes in seawater chemistry

have adverse consequences for many calcifying organisms, and may result in changes to biodiversity, trophic interactions, and other ecosystem processes (Kleypas *et al.*, 2006; Royal Society, 2005). Evidence from freshwater systems suggests climate warming could also cause significant shifts in benthic community size structure (Yvon-Durocher *et al.*, 2011). Such shifts in size structure could have significant impacts on marine ecosystems, affecting sediment production, geochemistry, and the amount of food available to predators at higher trophic levels (Jennings and Kaiser, 1998).

Further, during calcification, element such as magnesium is incorporated into biogenic calcium carbonate (Dissard *et al.*, 2010) and thus decalcification would lead to the release of magnesium. Magnesium occurred in seawater to nearly constant ratios to calcium (for the last 1Myrs, Broecker and Peng, 1982) and variations in Mg/Ca in benthic shelly organisms (e.g., foraminiferans) on shorter timescale are shown to be mainly related to changes in temperature (Anand *et al.*, 2003; Reichart *et al.*, 2003; Barker *et al.*, 2004), which is resultant effect of climate change. Other environmental parameters such as pH or (CO_3^{2-}) may influence magnesium incorporation into shelly organisms (Dissard *et al.*, 2010). Higher temperature result in higher amounts of magnesium incorporated into the shell matrix (Fergusson *et al.*, 2008; Dissard *et al.*, 2010). Shells with higher Mg:Ca ratios are more soluble, so even organisms with primarily calcite (less soluble than aragonite) skeletons may be heavily impacted by future conditions.

The precipitation of CaCO_3 in the upper ocean through the formation of calcareous skeletons by marine organisms creates more acidic conditions which decrease the

capacity of the upper ocean to take up atmospheric CO₂ (Kleypas *et al.*, 2006). Conversely, the dissolution of marine carbonates at depth, including biogenic magnesium calcites (from coralline algae), aragonite (from corals and pteropods), and calcite (from coccolithophorids and foraminifera), raises pH and increases the capacity of the oceans to take up and store CO₂ from the atmosphere (Feely *et al.*, 2004). The results of the analysis herein indicated that the selection of magnesium and calcium as drivers of species and functional diversity supports the view of carbonates dissolution at depth leading to the possible release of magnesium and calcium.

In general, magnesium (Mg) calcite minerals with a significant mole percent (mol %) MgCO₃ are more soluble than aragonite and calcite, and it is therefore likely that Mg-calcite, high latitude and cold-water calcifying organisms will be the first to be affected by increasing ocean acidification (Andersson *et al.*, 2008). The mole percent of magnesium deposited by marine organisms varies from a few mol% to as much as 30 mol% between different species (Andersson *et al.*, 2008), resulting in a significant response variation among taxa to changing ambient conditions (Hoffmann *et al.*, 2008). In tropical and sub-tropical environments, the dependence of calcareous algae, and other important reef calcifiers like echinoderms and benthic foraminifera, on high-magnesium calcite, the most soluble of all calcium carbonate minerals, would make these likely early casualties of climate change effect. The importance of magnesium is seen on its influence on calcium carbonate precipitation. According to Holmes-Farley, 2003), magnesium binds to the calcium carbonate crystals' growing surface, when the latter begins to precipitate. The magnesium effectively clogs the crystals' surface so that they no longer look like calcium carbonate, making them

unable to attract more calcium and carbonate, so the precipitation stops. Without the magnesium, the abiotic (i.e. non-biological) precipitation of calcium carbonate would likely increase enough to prohibit the maintenance of calcium and alkalinity at natural levels.

Sea urchins and crustaceans, including lobsters and shrimp, exert higher biological control by gradually accumulating intracellular stocks of ions; between moults crustaceans are thought to harden their chitin and protein exoskeletons by continually depositing calcite minerals (Convention on Biological Diversity, 2009). The shell chemistry and mineralization of crustaceans suggest that they may withstand climate change effect (e.g., ocean acidification) and saturation state decreases better than molluscs, however the response of organisms is likely to be a function of individual history and genetic variability (Cooley and Doney, 2009).

Organic carbon and sediment particles have been demonstrated as playing important structuring role in marine species assemblages (Gray, 1989 and 2002; Lamptey and Armah, 2008; Pearson and Rosenberg, 1978 and 1987; Snelgrove and Butman, 1994) as they are associated with productivity and nutrition. It is therefore corroborating the selection of these abiotic factors as key environmental drivers of taxonomic and the functional assemblages in the GCLME. Organic matter is the main food source for deposit-feeders (Pearson and Rosenberg, 1978), which were the dominant feeding trait identified. The sediment type gives an indication of availability of food rather and not as a first order factor determining species assemblages (Snelgrove and Butman, 1994).

CHAPTER FOUR

IMPACT OF DEMERSAL FISH TRAWLING ON THE STRUCTURE AND FUNCTIONAL ASSEMBLAGES OF EPIBENTHIC FAUNA ALONG BATHYMETRIC GRADIENT IN THE GUINEA CURRENT LME

4.1 Introduction

The global biodiversity concerns (i.e., accelerated loss and decline) and the predictions of impaired ecosystem functioning and sustainability (Naeem *et al.* 1994; Sala *et al.*, 2000; Loreau *et al.*, 2001; Hughes *et al.*, 2003; Hooper *et al.*, 2005; Worm *et al.*, 2006; Hooper *et al.*, 2012), have increased interests of investigating the wider impacts of commercial fishing on non-target species (e.g. Alverson *et al.*, 1994; Dayton *et al.*, 1995). The effects of mobile fishing gears on marine benthic productivity and biodiversity are a global concern both for the fishing industry and government regulators (Dayton *et al.*, 1995; Auster and Langton, 1999; McConnaught *et al.*, 2000; Kaiser *et al.*, 2002; Hiddink *et al.*, 2007). The socioeconomic consequences of the biodiversity changes depend on how they translate into altered ecosystem processes and services (Costanza *et al.*, 1997; Balmford *et al.*, 2002; Millennium Ecosystem Assessment, 2003).

The marine benthic ecosystems are increasingly affected by environmental stress and degradation due to pollution (Halpern *et al.*, 2008) and other anthropogenic factors such as overfishing (Jackson, 2008), bottom trawling and dredging (Pauly *et al.*, 2005) and human-induced climate change (Bindoff *et al.*, 2007). Many of the expected responses to human activities in the marine environment may best be

monitored at the seafloor in the benthic communities (Jørgensen *et al.*, 2011). This is due to the fact that benthic organisms have limited locomotion; they are long-lived and able to integrate into their system both short-term and long-term environmental processes (Borja, 2000).

Increasing importance of marine biodiversity and fisheries in general have resulted in integrated approach, such as Ecosystem Approach to Management (EAM), which requires sustainable and ecosystem-based assessment. For instance, Ecosystem Approach to Fisheries (EAF) requires that managers take account of the ecosystem effects of fishing in management plans that are intended to achieve sustainable exploitation of target species (Kaiser *et al.*, 2002). Ecological Quality Objectives (EcoQO's) is now used to assist in the movement toward an ecosystem approach to management (Frid and Hall, 2001). Skjoldal *et al.* (1999) defined the EcoQ as *an overall expression of the structure and function of the aquatic systems*. It is therefore reasonable to assume that the development of ecosystem approaches to environmental management is to define the 'overall structure and function' desired for the ecosystem being considered. It also calls for integration of commercial marine resources (e.g., fish) and non-commercial communities (Brind'Amour *et al.*, 2009) such as epibenthic fauna.

Epifaunal component of the benthos includes organisms of high biomass and potentially of high ecosystem importance as they provide habitat structure, and potentially different functional components of the community (Jørgensen *et al.*, 2011). Larger fauna (e.g., epifauna) often represent long-lived and slowly reproducing species that are more prone to decline if mortality is increased due to

fishing (Witbaard and Klein, 1994). For the marine benthos, the issues that need to be considered include (i) aspects of the composition and structure of the benthic community – species diversity, species abundance patterns (i.e., how individuals are distributed between the species present), and biomass. Further, the functioning of this assemblage; and (ii) functional attributes such as the productivity of the community and the degree, rate and pathways of nutrient and carbon cycling. In coastal ecosystem, indicators integrating both the structural (i.e., species composition) and functional attributes of the communities are increasingly recognized as useful tools to assess change in these ecosystems (Elliott and Quintino, 2007).

A huge body of knowledge exists on the evidence of fishing effects on the marine macrobenthos (Jennings and Kaiser, 1998; Kaiser and De Groot, 2000; Trush and Dayton, 2002), however a lack of comparable quantitative data of fish and epifauna is still a concern and confounds our understanding of the extent of the fishing effects. Given the growing appreciation of the value of marine biodiversity as critical to the sustainability of commercially valuable ground fish stocks as well as for its own unique heritage (Bengtsson *et al.*, 1997; Costanza *et al.*, 1997; Freckman *et al.*, 1997; Gray, 1997; Schlapfer and Schmidt, 1999), there is now an increasing need to understand and sustain biodiversity as a part of any fisheries management plan.

Trawling is a common method for catching fish and bottom trawling is one kind of fishing practice with heavy nets connected to large trawl doors. The nets drag along the seafloor leaving deep visual marks on the sea bottom (Enticknap, 2002). The design and mode of operation of the trawling gear influences how it interacts with the seafloor and how many species are removed (Thrush and Dayton, 2002). The

otter trawl is an example of bottom trawl and is commonly used to catch fish and invertebrate species. The otter trawl can penetrate the sea bed down to 20 cm (Querios *et al.*, 2006). The beam trawl is held open by a steel beam fitted with chains and the penetration of the beam trawl and the amount of physical disturbance caused by beam trawl, depend on the weight of the gear, towing speed and bottom type (sediment), and varies between 3 mm and 6 cm (Lindeboom and de Groot, 1998a; Duplisea *et al.*, 2002).

Bottom trawling has been documented to cause extensive impacts on benthic communities and habitats, leading to reduced biomass, production and diversity (e.g. Kaiser and De Groot, 2000; Hiddink *et al.*, 2006). When heavy trawling gear is dragged along the seabed, some of the complex benthic structure that serves as refugia are damaged (Stone *et al.*, 2005). Bottom trawling is harmful to seafloor habitats and this effect has been well studied in marine systems (Kaiser *et al.*, 1998; McConnaughey *et al.*, 2000; Sparks-McConkey and Watling, 2001; Rosenberg *et al.*, 2003; Tillin *et al.*, 2006). Modifications of the composition of benthic assemblages may result in changes to the ecological functioning of the system (Bremner, 2006; Tillins *et al.*, 2006).

Relatively few studies have investigated the impact of bottom trawling on benthic ecosystem integrating fisheries and epibenthic data/information along bathymetric gradient. Nonetheless, most benthic biodiversity systems are stratified by water depth (Zmarzly *et al.*, 1994; Bergen, *et al.*, 2001). Study of that nature will unearth the influence of bathymetry on epibenthic fauna distribution and may obviate confounding issues of impact of bottom trawling on the epibenthic bottom dwellers.

Integrated assessment of fisheries requires studies that focus on the whole ecosystem and not only on single species, and that consider fishing activities as key pressures affecting several ecosystem components (Gaertner *et al.*, 2005; Massuti and Reñones, 2005). Therefore, it is highly necessary to develop studies like these, which identify the components, assemblage structure and functioning of ecosystems at a regional scale.

4.2 Study Objectives

The present study is the first attempt in the Gulf of Guinea to compositely describe the spatial distribution patterns of epibenthic fauna (treated as non-targeted species or by-catch from bottom trawl). The main objectives were to characterise epibenthic assemblages (i.e., composition and structure) caught by the beam trawl, establish the bathymetric relationships between demersal fish and epibenthic fauna distribution patterns in terms of abundance and biomass and ascertain the functional attributes (i.e., feeding and mobility) of epibenthic fauna along bathymetric gradients.

The findings of this study will attempt to answer the questions: i) what are the community structural differences in epifauna and fish in a bottom trawled samples?, ii) how do the assemblage patterns of fish trawl samples and epibenthic by-catch differ along bathymetric gradient? and iii) is the epifauna by-catch functionally significant to influence ecosystem functions and processes?

4.3 Materials and Methods

4.3.1 Study Area

The study was conducted in the Gulf of Guinea of the Guinea Current Large Marine Ecosystem along the continental shelves of Ghana, Togo, Benin and western part of Nigeria. The GCLME extends from approximately latitude 12⁰N south to about 16⁰S latitude, and varies from 20⁰ west to about 12⁰ east longitude (Fig. 2.3). It extends from Bissagos Island (Guinea Bissau) to Republic of Congo with its boundary extending in a north–south direction from the intense upwelling area of the Guinea Current (GC) south to the northern seasonal limit of the Benguela Current (BC). In an east–west sense, the GCLME includes the drainage basins of the major rivers seaward to the GC front delimiting the GC from open ocean waters (a time- and space-variable boundary).

4.3.2 Field Sampling

Epibenthic fauna samples were collected from beam trawl (Plate 4.1) catches carried out from 3-14 March 2003 aboard the *RV Geo-Explorer* scientific vessel during the West Africa Pipeline Project baseline studies from Ghana to Nigeria using a randomized stratified survey design (Fig. 4.1 & Table 4.1). Beam trawls are very effective in sampling vagile as well as epibenthic macrofauna and the latter may represent a large proportion (density and biomass) of the catches (Kaiser *et al.*, 1994; Till *et al.*, 2006). It should be noted that no trawl gear ever sample all the individuals present in the path of the net (Jorgensen *et al.*, 2011) and the beam trawl net based on the mesh-size will select certain size classes of the same epibenthic faunal taxa. As such, the actual epifauna abundance may have been grossly under-represented in the

sample collection and consequently the analysis likewise the fish data although fishes are relatively larger than epifauna.

Therefore the impressions of the epibenthic community gained from the analysis of the sample data is not that of the actual epifaunal community present at each sampled location, but rather it is a view of the community biased by the differential selectivity of the sampling gear for each species present at each location (Tillin *et al.*, 2006).

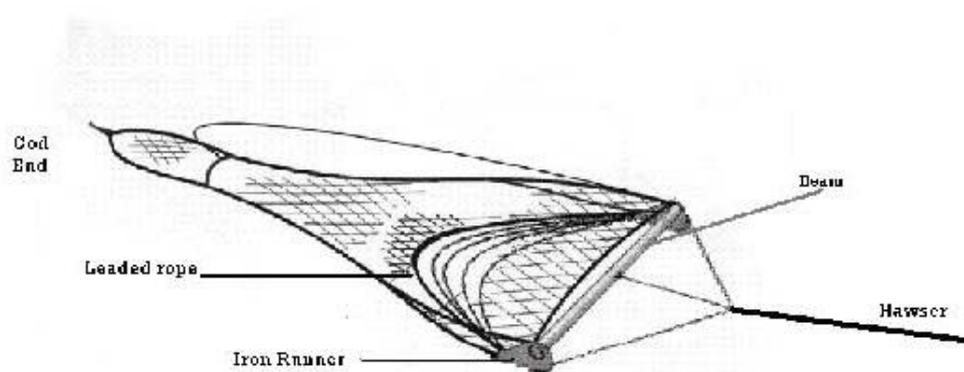


Plate 4.1 Beam trawl gear. (Source: ilvo.vlaanderen & Grantontrawlers)

A total of 18 trawls were made within a depth range of 10–70 m (Table 4.2). Of this, 7 hauls were carried out in the shelf of Ghana, 4 in Togo, 4 in Benin and 3 in the western shelf of Nigeria (Table 4.1). The sample stations were located at approximately 50 km intervals along predetermined defined areas, which were selected based on a prior geotechnical assessment by the West Africa Gas Pipeline Project. Each haul lasted for 30 minutes with a tow speed of 1.5 knots over the ground and covering appropriately a distance of 2.7 km.

Table 4.1: Length of coastline and number of hauls made per sector (WAPCo, 2003)

	Ghana	Togo	Benin	Nigeria
Length of coastline covered (km)	330	50	120	30
Maximum length of coastline (km)	550	50	120	853
Number of hauls	7	4	4	3

At each station, the trawl was hauled in, emptied and prepared for the next tow. As the catches were chuted to the processing area, the net and deck were examined carefully and all epibenthic fauna collected. The epibenthic samples from each trawl station were separated from the fish catches on a sorting table, put into labeled containers and fixed with 10% borax pre-buffered formaldehyde solution for later laboratory examination and taxonomic resolution. All the trawl fish samples were identified taxonomically onboard, counted and weighed for each haul.

4.3.3 Laboratory Processing of Samples

The epibenthic fauna were processed (i.e., washing & sorting) in the laboratory. The formaldehyde solution in the epibenthic samples was replaced with 70% ethanol until samples were ready for taxonomic identification. Species identification was carried

out to the lowest practicable taxonomic unit using various taxonomic manuals and guides namely Day, (1967ab); LeLœuff and Intes, (1974); Fauchald, (1977); Edmunds, (1978); Intes and Lœuff (1984); Kirkegaard, (1988); Cosel, (2006) and Rakel, (2007). Each species was counted and weighed (blotted wet weight in grams) to determine the biomass.

Table 4.2 Trawl station information and trawl distance covered during the West Africa Pipeline Project baseline studies.

Trawl Station	Country	Latitude	Longitude	Mean Depth (m)	Speed of tow (km/h)	Distance towed (m)
T 02	Nigeria	E2 ⁰ 59.1487	N6 ⁰ 11.9672	64	5.18	2.59
T 04	Nigeria	E2 ⁰ 47.7939	N6 ⁰ 11.5422	61	5.55	2.78
T 05	Nigeria	E2 ⁰ 26.5627	N6 ⁰ 10.9210	45	5.55	2.78
T 07	Benin	E2 ⁰ 20.5873	N6 ⁰ 14.4042	21	5.74	2.78
T 08	Benin	E2 ⁰ 10.5182	N6 ⁰ 09.7585	54	5.37	2.87
T 10	Benin	E1 ⁰ 42.0839	N6 ⁰ 05.6873	49	5.18	2.68
T 11	Benin	E1 ⁰ 16.5090	N6 ⁰ 04.7729	18	5.37	2.59
T 12	Togo	E1 ⁰ 18.9000	N6 ⁰ 01.5600	13	5.18	2.59
T 13	Togo	E1 ⁰ 21.5790	N5 ⁰ 58.3448	60	4.44	2.68
T 14	Togo	E0 ⁰ 52.4986	N5 ⁰ 41.8603	13	5.55	2.78
T 16	Togo	E0 ⁰ 07.2247	N5 ⁰ 30.6685	56	5.18	2.59
T 17	Ghana	E0 ⁰ 04.5541	N5 ⁰ 33.7917	39	5.55	2.78
T 19	Ghana	W0 ⁰ 41.1364	N5 ⁰ 07.6678	28	5.44	2.59
T 20	Ghana	W0 ⁰ 22.3600	N5 ⁰ 16.7100	36	5.55	2.78
T 22	Ghana	W1 ⁰ 34.8500	N4 ⁰ 58.1300	16	5.55	2.78
T 24	Ghana	W1 ⁰ 32.3500	N4 ⁰ 51.2900	32	5.92	2.96
T 25	Ghana	W1 ⁰ 25.1300	N4 ⁰ 34.9800	50	5.55	2.78
T 26	Ghana	W1 ⁰ 08.4700	N4 ⁰ 59.7600	26	5.37	2.68

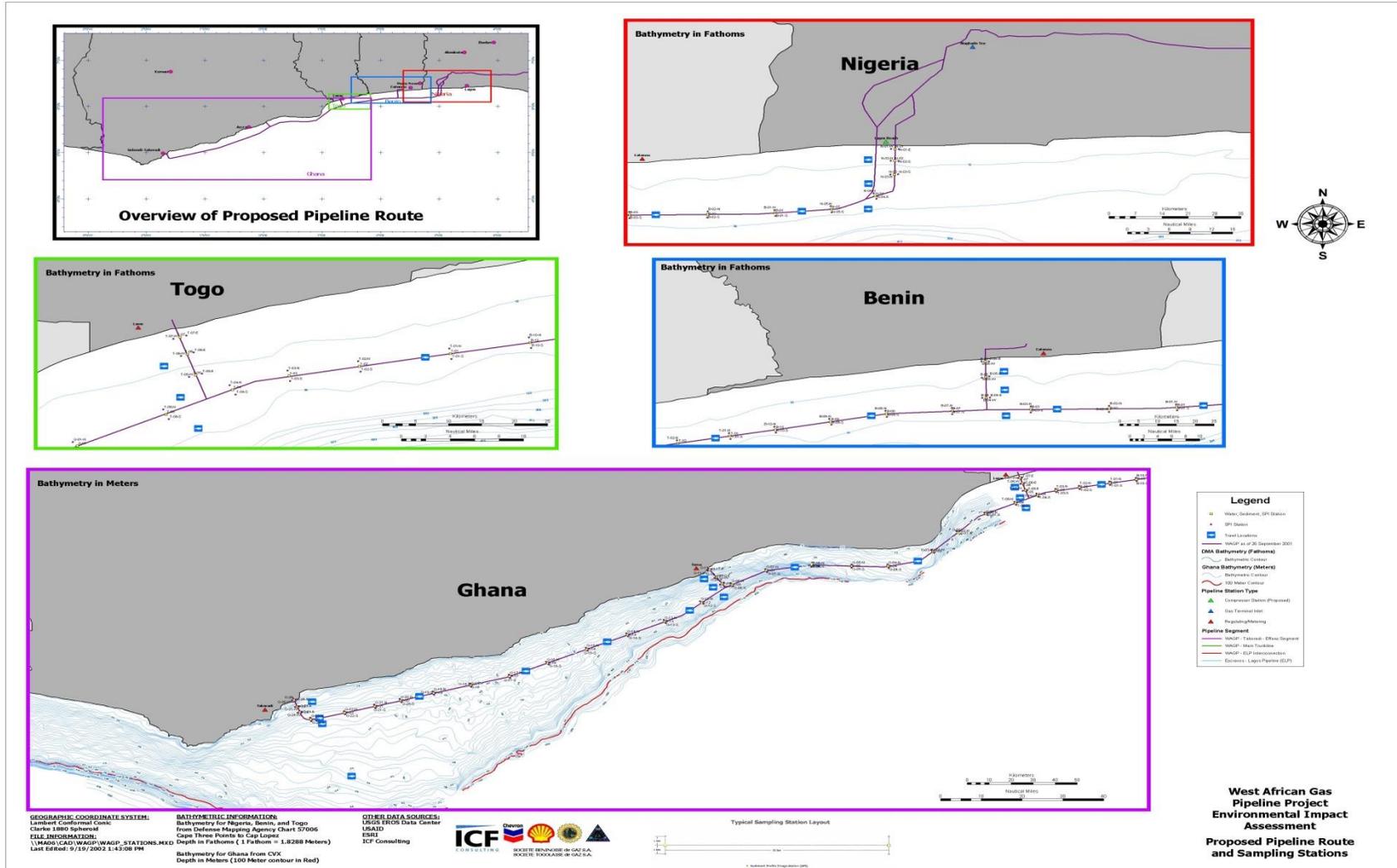


Figure 4.1 Map showing routes along which bottom trawling was carried out (WAPCo, 2003)

4.3.4 Statistical Analysis

All the epibenthic fauna identified and counted were categorized into polychaeta, mollusca, crustacea, echinodermata, and “others”. The ‘others’ category included cnidaria, nematoda, sipunculida, priapulida, brachiopoda and tunicata.

A frequency of occurrence of epifaunal taxa was calculated using the F-index described by Guille (1970): $F = p_a/P \times 100$, where: p_a , is the number of stations where the species occurred and P is the total number of stations. Using this formula the species were classified as: constant ($F > 50\%$), common ($10\% < F < 49\%$) and rare species ($F < 10\%$). Consequently, all the rare species ($F < 10\%$) were eliminated before the community structural analyses using suites of multivariate techniques with the PRIMER v6 package (Clarke and Gorley, 2006). Bray-Curtis similarity index was calculated. Prior to that, the data sets were fourth-root transformed to stabilize the variance. Using a complete linkage, sample classifications were achieved and thereafter samples related to each other identified based on the resulting non-parametric multidimensional scaling (MDS).

Changes of epifauna along bathymetric gradient were assessed with one-way ANOSIM (Clarke and Warwick, 1994). Thereafter, Similarity Percentage (SIMPER) analysis (Clarke and Gorley, 2006) was used to identify characteristic species, which contributed most to the statistical dissimilarity between the different bathymetric gradients among samples. For each sample, the Shannon–Wiener diversity index (H' , $\log e$) and Margalef's richness was determined from abundance data.

Functional group classification of the species was carried out using feeding type and mobility. The functional trait of feeding type (predator/scavenger, deposit feeder, filter/suspension feeder) and mobility (sessile/tube-dwelling/motile) according to a variety of references (Fauchald and Jumars, 1979; Barnes, 1987; Beesley *et al.*, 2000; Pechenik, 2000; Rouse and Pleijel, 2001; Brusca and Brusca, 2003) were used for the functional group classification. A functional group is a collection of organisms with similar suites of co-occurring functional attributes and as such has similar responses to external factors and/or effects on ecosystem processes (de Bello *et al.*, 2010).

4.4 Results

4.4.1 Epifauna Composition

A total of 3959 individual epibenthic fauna comprising 65 taxa from major taxonomic groups were encountered in the 18 trawl hauls (Table 4.3). The mean epifauna abundance per trawl haul was 792. The highest taxa abundance (3268 individuals) was noted for the mollusca due to the highest contribution of *Chlamys purpurata* (64.17%) and *Pecten jacobaeus* (30.02%) recorded at Stations T26 and T22 respectively. Mollusca contributed 82.55% to the total epifaunal numerical abundance. The other dominant groups were Crustacea and Echinodermata contributing 8.26% and 5.23% respectively to the total numerical abundance. The species placed in the 'others' category contributed 2.98%, while polychaetes accounted for 0.99%. These indicate the direct impact of beam trawling on the different epibenthic fauna taxa.

Of the total 65 taxa identified, molluscs, crustaceans and echinoderms recorded 28 (43%), 15 (23.08%) and 10 (15.39%) species respectively (Table 4.3), thus representing the major epibenthic faunal groups of the study area. However, in terms of biomass, the 'others' category ranked second with 34.88% after the molluscs with 36.90% (Table 4.3). The two numerical dominant species of the crustaceans were *Scyllarides herklotsii* (24.46%) and *Maja squinado* (13.76%). For the echinoderms, *Echinocardium caudatum* (36.23%) and *Diadema* sp. (29.47%) were the dominant species. The five most distributed species based on the F-index were *Portunus validus* (40%), *Scyllarides herklotsii* (40%), *Lithodes ferox* (40%), *Pagurus* sp. (40%) and *Stenorynchus lanceolatus* (35%).



From Left: *Strombus* sp., *Conus* sp., *Strombus* sp. *Tonna* sp., *Strombus* sp., & *Murex* sp.



Sea cucumber,



From left *Pagrus* sp. in *Tonna* shell; *Pentaceraster* spp., *Echinus* sp. and Barnacle

The taxa contribution to the total biomass of 3235.4 g was highest for the molluscs (36.90%) and species placed in the ‘others’ category (34.88%). The species *Prianpulus caudatum* contributed substantially (75.88%) to the total biomass of the ‘others’ category. The lowest biomass contribution (<1%) was noted for the Polychaeta (Table 4.3). The mean biomass per haul was ~162 g (wet wt.).

Table 4.3: Number of species , abundance and biomass of epibenthic fauna from 18 trawl hauls of the study area in March 2003. The percentage contribution of each taxa is given in parenthesis.

Taxa	No. Of species	Abundance (No. Of indi.)	Biomass (mass) (wet wt. g)
Mollusca	28 (43.08)	3268 (82.55)	1194 (36.90)
Crustacea	15 (23.08)	327 (8.26)	334.0 (10.32)
Echinodermata	10 (15.38)	207 (5.23)	552.5 (17.08)
Polychaeta	3 (4.62)	39 (0.99)	26.5 (0.82)
‘Others’	9 (13.85)	118 (2.98)	1128.4 (34.88)
Total	65	3959	3235

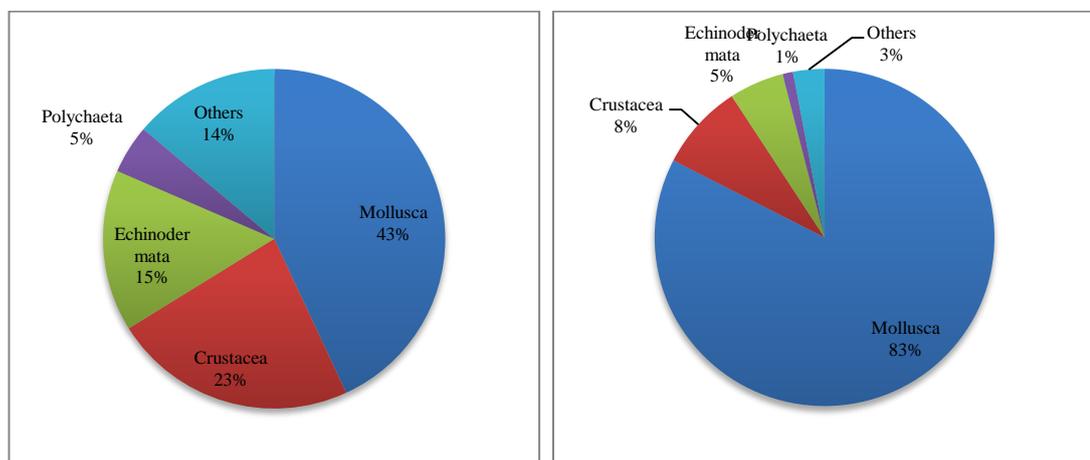


Figure 4.2 Percent distribution of major epibenthic faunal richness (left) and numerical abundance (right).

4.4.1.1 Comparison of Bathymetric Distribution of Epifauna and Fish Assemblage Structure

The distribution of taxa abundance across bathymetric gradient indicated a decrease in numerical abundance of epibenthic fauna with increasing water depth (Fig. 4.3). Abundance of fish on the other hand did not show any discernible bathymetric pattern except that the highest abundance occurred at mid-depth water (i.e., 31-50m). There were no significant differences ($p > 0.05$) in abundance of epifauna and fish at both mid-depth (31-50m) and deeper waters (51-70m), which suggests that for the study area impact of bottom trawling epifauna abundance could be inferred from fish catches, albeit comparatively fish abundances at these depths were relatively higher than the epifauna. The significant difference ($p < 0.05$, ANOVA) between abundances of fish and epibenthic fauna at shallow-dept (11-30m) suggests that trawling impact at this depth would be significant on the epibenthic fauna, since numerically epifauna ranked highest (Fig. 4.3).

For taxa biomass, the epifauna ranked highest across all the depth zones in comparison with the fish abundance. The highest biomass (catch by weight) was recorded at mid-depth (31-50m). The degree of variations in taxa biomass for both epifauna and fish assemblage decreased with increasing water depth (Fig. 4.4). This occurrence may suggest prevailing benign conditions at deeper depths or conversely a higher degree of disturbances at shallow depths. This dichotomy may have been due to the creation of different niches that have physiologically and ecologically adapted to the respective zones.

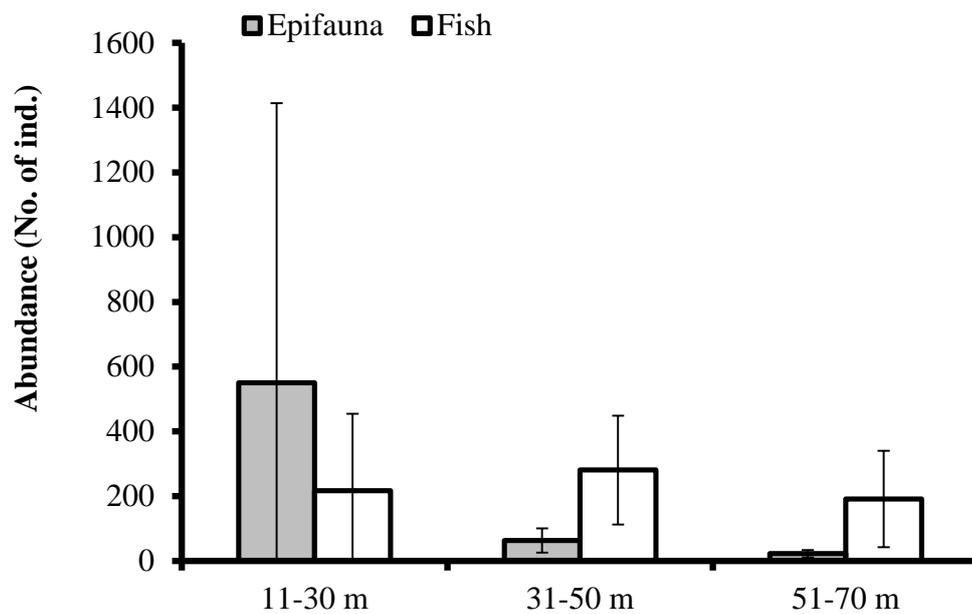


Figure 4.3 Bathymetric pattern of mean abundance (\pm SE) for epifauna and fish from trawl catches.

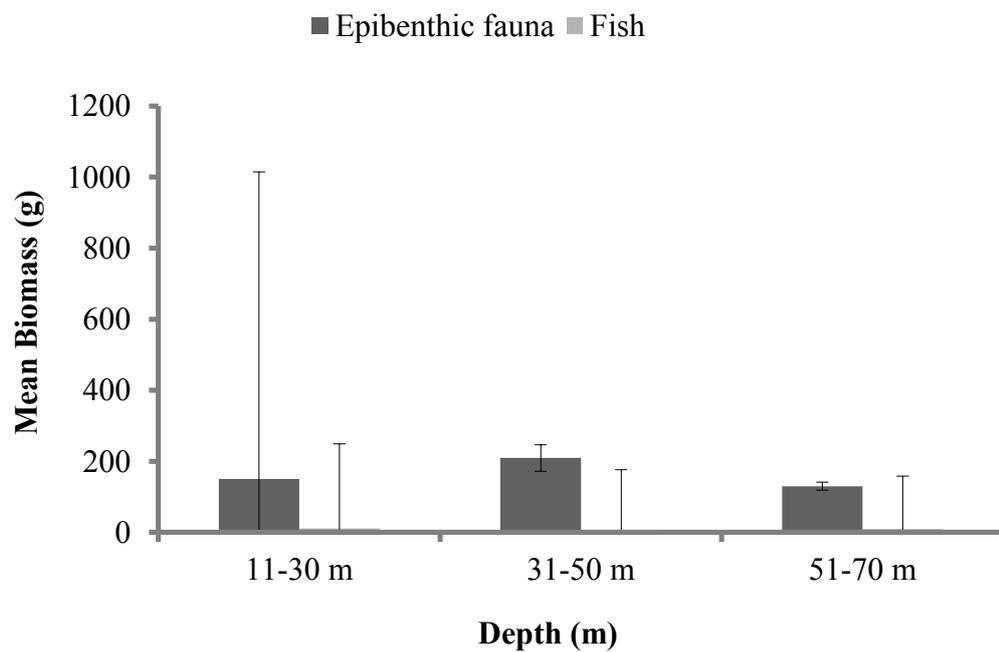


Figure 4.4 Bathymetric pattern of mean biomass (\pm SE) for epifauna and fish from trawl catches.

The taxa richness of fish species was higher than the epifauna across the bathymetric gradient (Fig. 4.5) although the differences were not statistically significant ($p>0.05$). The highest richness occurred within the mid-depth water (31-50m) for both fish and epifaunal taxa (Fig. 4.5) suggesting a synergistic trophic relationship.

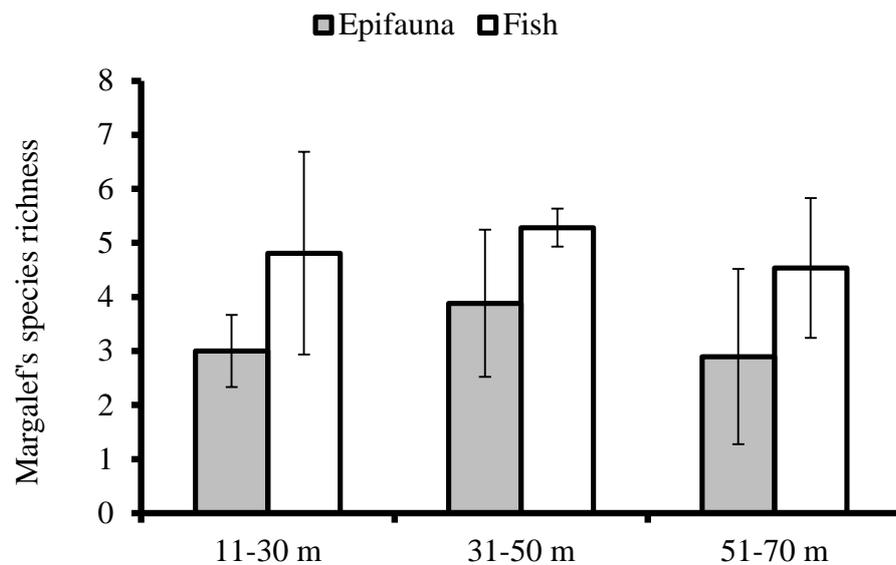


Figure 4.5 Distribution of Margalef's species richness index along depth gradient. The error bars indicate 95% confidence interval.

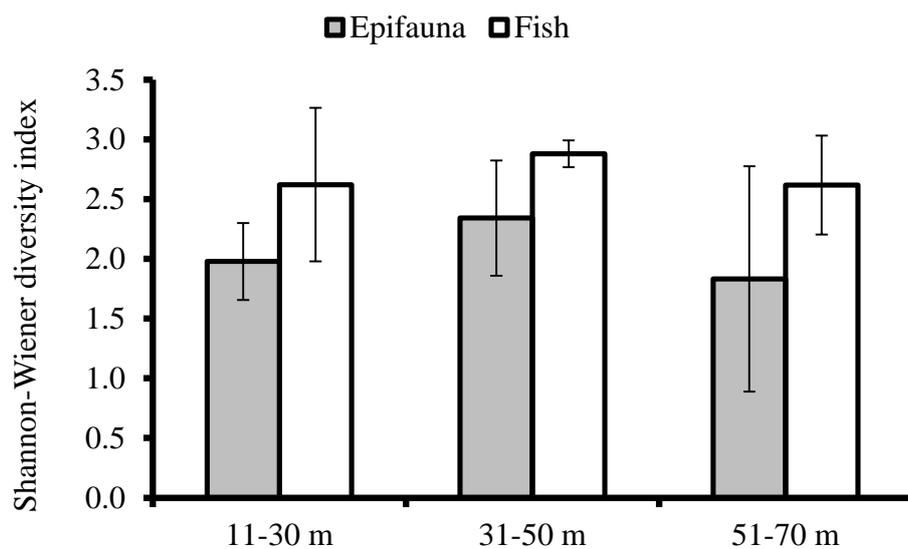
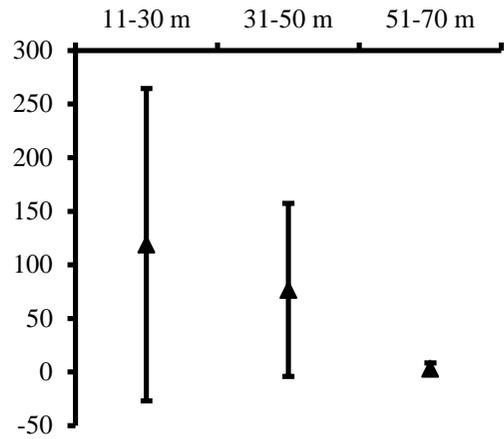


Figure 4.6 Distribution of Shannon-Wiener diversity index along depth gradient. The error bars indicate 95% confidence interval.

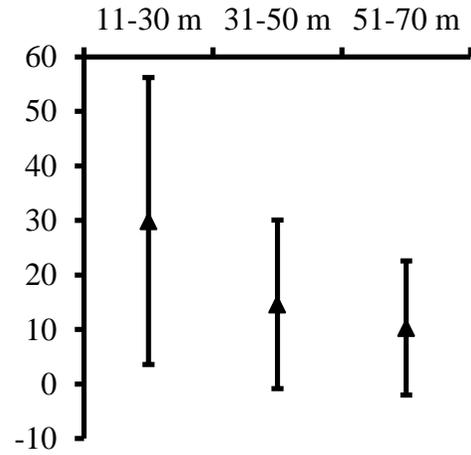
4.4.2 Pattern of Major Epifaunal Taxa

The patterns of distribution for the major epifauna groups showed a steady decrease in biomass for molluscs and crustaceans with increasing water depth (Fig. 4.7). Conversely, polychaetes, 'others' category and echinoderms revealed increases in biomass with increasing water depth except that the highest biomass for the echinoderms occurred at mid-depth. All but polychaetes did not reveal any discernible bathymetric pattern. The bathymetric pattern for the numerical abundance of the epifauna was different from the pattern depicted by the biomass. The striking observation was the highest numerical abundance at mid-depth (31-50m) for crustaceans, echinoderms and 'others' category (Fig. 4.7). The molluscs and polychaetes revealed similar pattern of abundance and biomass, with the abundance decreasing with increasing water depth while biomass increased with depth (Fig. 4.7).

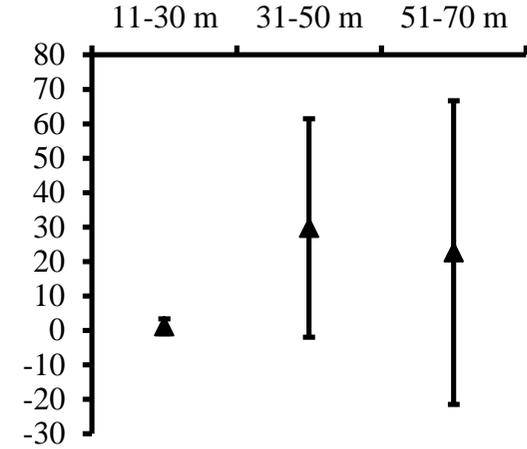
Mollusca



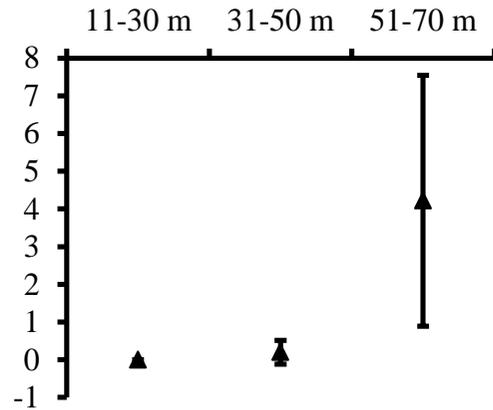
Crustacea



Echinodermata



Polychaeta



Others

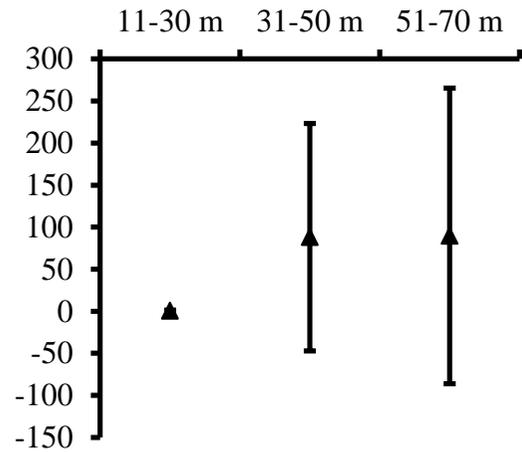


Figure 4.7 Mean biomass (±SE) of major epibenthic fauna along bathymetric gradient.

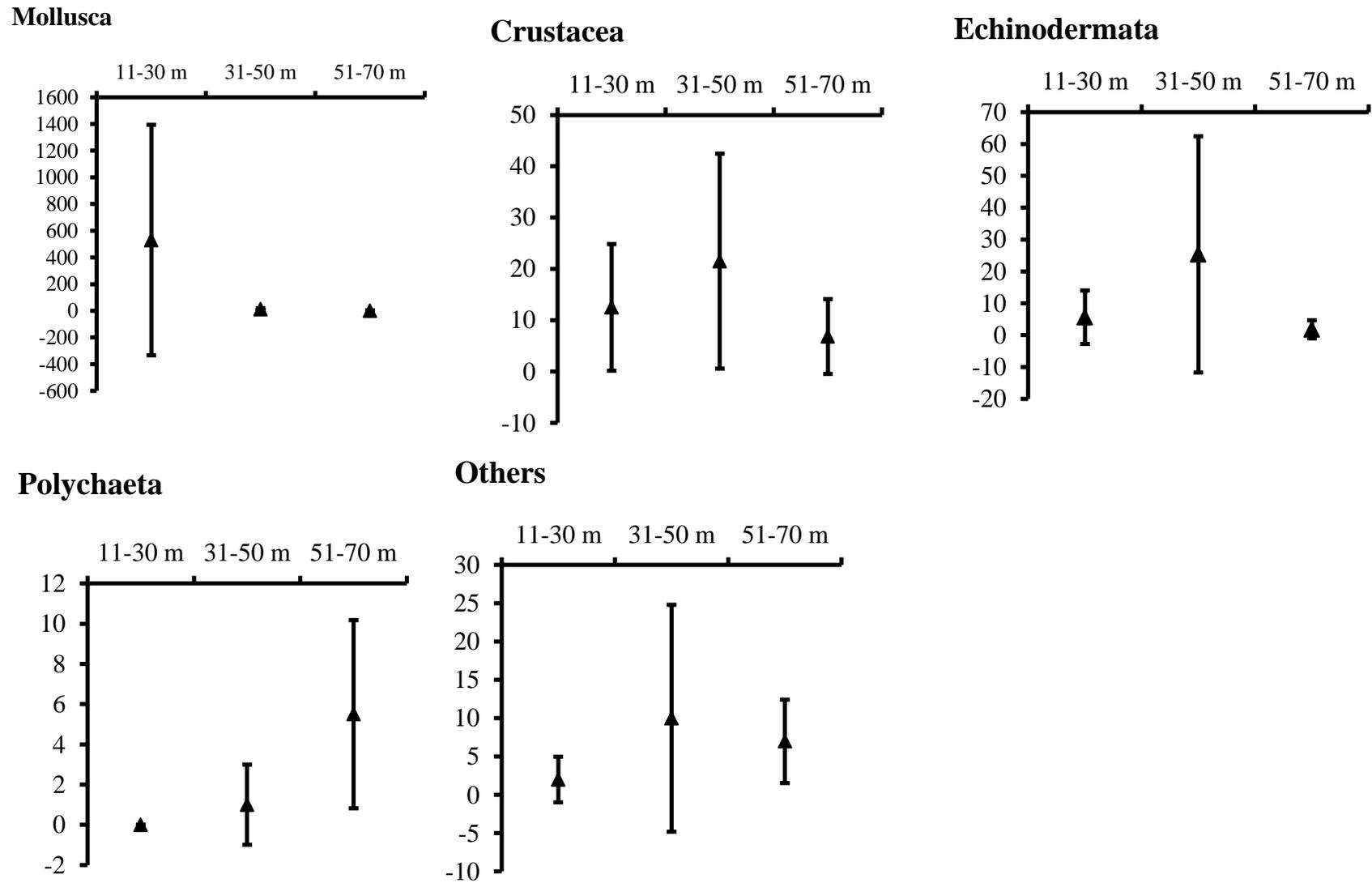


Figure 4.8 Mean abundance (\pm SE) of major epibenthic fauna along bathymetric gradient.

The abundance and biomass of the epifauna varied significantly with water depth (one-way ANOSIM, $p < 0.05$) (Table 4.4). Spatial (bathymetric) differences of the epifaunal abundance and biomass were particularly important (or significant) between 11-30m (Shallow zone) and 51-70m (Deep zone) (one-way ANOSIM, $p = 0.002$). Nonetheless, no significant difference existed between shallow and mid-depth zones, and also mid-depth and deep zones (Table 4.4).

Table 4.4: Pairwise ANOSIM test of epifaunal abundance and biomass

Depth (m)	Abundance		Biomass	
	R-statistic	Significance Level (p)	R-statistic	Significance Level (p)
11-30, 31-50	0.25	0.069	0.144	0.152
11-30, 51-70	0.47	0.002	0.491	0.002
31-50, 51-70	0.093	0.199	0.005	0.457

For taxa abundance; Global R= 0.271, $p = 0.5\%$; for taxa biomass; Global R= 0.213, $p = 1.9\%$.

The distribution pattern of the stations in the MDS ordination (Fig. 4.9) showed a clear separation of shallow depth stations (11-30m) and deep depth stations (51-70m). The pattern is consistent with the observation in the pairwise ANOSIM test (Table 4.4). The distribution of the stations shows strong spatial (east-west axis) and bathymetric patterns. The spatial pattern is indicative that stations located in each specific sampled country tend to cluster together (see Table 4.1), which also suggest the influence of surrogate abiotic water conditions.

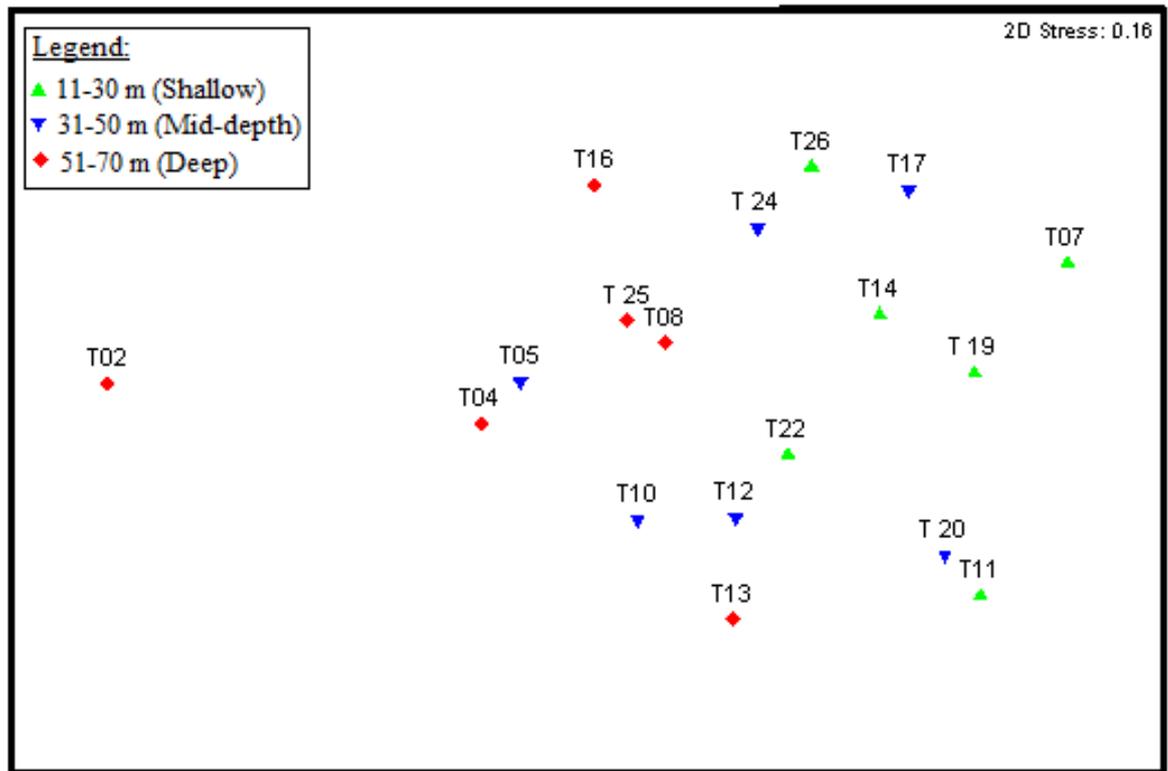


Figure 4.9 Non-parametric multidimensional scaling (MDS) of epibenthic faunal abundance data

SIMPER analysis (Table 4.5) showed that the significant difference between shallow stations (11-30m) and deep station (51-70m) was attributable to differing numerical abundance of 10 discriminating species that contributed 51.73% to the average dissimilarity of 89.04% (Table 4.5).

Table 4.5 SIMPER analysis results: species contributing to the average dissimilarity between shallow stations (11-30m), mid-depth (31-50m) and deep waters (51-70m) based on simultaneous analysis of taxa abundance data. δ_i : contribution of the i-th faunistic group to the average Bray-Curtis dissimilarity (δ) between depths, also expressed as a cumulative percentage ($\sum\delta_i\%$). Diss/SD is the ratio of dissimilarity to standard deviation. For brevity, only species that contributed to $\geq 3.0\%$ and cumulative percentage of $\geq 50\%$ are listed. The codes in the parenthesis after the species name indicate: 'C' crustacean, 'P' Polychaete, 'M' Mollusc, 'E' Echinoderm

Species	Ave. Abundance 11-30 m	Ave. Abundance 31-50m	Av.Diss	Diss/SD	δ_i	$\sum\delta_i\%$
Average dissimilarity 11-30m & 31-50m = 81.22%						
<i>Chlamys purpurata</i> (M)	1.13	0.27	4.88	0.54	6.01	6.01
<i>Astropecten</i> sp. (E)	0.52	0.77	3.88	0.98	4.78	10.79
<i>Pagurus</i> sp. (C)	0.93	0.49	3.80	1.35	4.68	15.47
<i>Lithodes ferox</i> (C)	0.00	1.02	3.79	1.26	4.66	20.13
<i>Strombus latus</i> (M)	0.17	0.70	3.67	0.92	4.52	24.65
<i>Diadema</i> sp. (E)	0.33	0.80	3.66	0.89	4.51	29.16
<i>Scyllarides herklotsii</i> (C)	0.20	0.96	3.54	1.00	4.36	33.51
<i>Portunus validus</i> (C)	0.94	0.65	3.53	1.14	4.35	37.86
<i>Turris</i> sp. (M)	0.66	0.49	3.46	0.99	4.26	42.12
<i>Chlamys</i> sp. (M)	0.76	0.00	3.19	0.64	3.92	46.04
<i>Philine</i> sp. (M)	0.00	0.75	2.82	0.95	3.47	49.52
<i>Stenorynchus lanceolatus</i> (C)	0.33	0.53	2.63	0.93	3.24	52.76
Species	Ave. Abundance 11-30 m	Ave. Abundance 51-70m	Av.Diss	Diss/SD	δ_i	$\sum\delta_i\%$
Average dissimilarity between 11-30m & 51-70m = 89.04%						
<i>Portunus validus</i> (C)	0.94	0.25	5.93	1.02	6.66	6.66
<i>Pagurus</i> sp.(C)	0.93	0.20	5.55	1.12	6.23	12.90

<i>Nereis</i> sp. (P)	0.00	1.02	5.26	1.25	5.91	18.81
<i>Chlamys purpurata</i> (M)	1.13	0.00	5.02	0.43	5.63	24.44
<i>Scyllarides herklotsii</i> (C)	0.20	0.93	4.55	1.17	5.11	29.55
<i>Maldanid</i> sp. (P)	0.00	0.63	4.39	0.79	4.93	34.48
<i>Chlamys</i> sp.(M)	0.76	0.00	4.14	0.62	4.65	39.14
<i>Turris</i> sp. (M)	0.66	0.00	4.04	0.86	4.54	43.67
<i>Astropecten</i> sp. (E)	0.52	0.24	3.65	0.73	4.10	47.78
<i>Lithodes ferox</i> (C)	0.00	0.70	3.52	1.26	3.96	51.73

Species	Ave. Abundance 31-50 m	Ave. Abundance 51-70m	Av.Diss	Diss/SD	δ_i	$\sum \delta_i\%$
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Average dissimilarity between 31-50m & 51-70m= 80.14%

<i>Scyllarides herklotsii</i> (C)	0.96	0.93	4.27	1.18	5.33	5.33
<i>Strombus latus</i> (M)	0.70	0.00	3.98	0.84	4.97	10.30
<i>Diadema</i> sp. (E)	0.80	0.25	3.97	0.87	4.95	15.25
<i>Nereis</i> sp. (P)	0.33	1.02	3.94	1.21	4.91	20.16
<i>Astropecten</i> sp. (E)	0.77	0.24	3.63	0.86	4.53	24.70
<i>Lithodes ferox</i> (C)	1.02	0.70	3.56	1.23	4.45	29.14
<i>Maldanid</i> sp. (P)	0.24	0.63	3.32	0.84	4.14	33.28
<i>Portunus validus</i> (C)	0.65	0.25	3.20	0.91	4.00	37.28
<i>Priapulus caudatus</i> (O)	0.55	0.27	3.11	0.73	3.88	41.16
<i>Pagurus</i> sp. (C)	0.49	0.20	2.97	0.65	3.71	44.87
<i>Philine</i> sp. (M)	0.75	0.00	2.87	0.93	3.59	48.45
<i>Stenorynchus lanceolatus</i> (C)	0.53	0.53	2.87	1.08	3.58	52.03

4.4.3 Species Dominance and Pollution Status

In order to ascertain the impact and the level of habitat stress possibly from bottom trawling or natural process, species abundance/biomass comparison (ABC) curves were determined as proposed by Warwick (1986). Warwick suggested on theoretical considerations that the distribution of the numbers of individuals among species should differ from the distribution of biomass among species when influenced by pollution-induced disturbance. This difference can be shown by *K-dominance* plots (Lambshead *et al.*, 1983; Shaw *et al.*, 1983). The curves rank species in order of importance on the x-axis and show the percentage of each species or the total numbers or biomass on a cumulative scale (called percentage dominance) on the y-axis. There are three scenarios of the ABC curves. These are:

- i) when the community is approaching equilibrium, the biomass becomes increasingly dominated by one or a few large species, each represented by few individuals. The numerical dominants are generally smaller species. Hence, when plotted as *K-dominance* curves, 'numerical diversity' is greater than 'biomass diversity', so that the line for abundance lies well below the line for biomass, since one species forms a much larger proportion of the total biomass than it does of the total numbers.
- ii) Under stress (natural physical and biological or pollution-induced disturbances), large competitive dominants are eliminated and biomass and abundance curves are close together and crossing one or several times.
- iii) Under severe disturbance, benthic communities become increasingly dominated by one or a few very small species (usually annelids such as *Capitella* spp. or oligochaetes) and few larger species are present. Hence 'numerical diversity' is lower than 'biomass diversity'.

These three cases were termed unpolluted, moderately polluted and grossly polluted by Warwick (1986). This can also be equated to unstressed, moderately stressed and heavily stressed habitats/locations. The representative ABC plots of the ABC analysis are presented in Figures 4.10 to 4.18. Further, Table 4.6 shows the pollution levels of the trawl stations. The results indicate that 50% of stations were moderately stressed, 5.56% stressed, 11% heavily stressed (giving a total stress of 66.56%) with 28% unstressed. The degree of stress from the results is inversely related to increasing water depth such that heavily stressed areas fall within shallow depths and vice versa.

Table 4.6 ABC Analysis results of bottom trawl epibenthic data and pollution status.

Trawl Station	Country	Latitude	Longitude	Mean Depth (m)	W-statistics	Pollution Status
*T 02	Nigeria	E2 ⁰ 59.1487	N6 ⁰ 11.9672	64	??	Undetermined
T 04	Nigeria	E2 ⁰ 47.7939	N6 ⁰ 11.5422	61	0.503	unstressed
T 05	Nigeria	E2 ⁰ 26.5627	N6 ⁰ 10.9210	45	0.166	moderately stressed
T 07	Benin	E2 ⁰ 20.5873	N6 ⁰ 14.4042	21	0.104	moderately stresses
T 08	Benin	E2 ⁰ 10.5182	N6 ⁰ 09.7585	54	0.147	moderately stresses
T 10	Benin	E1 ⁰ 42.0839	N6 ⁰ 05.6873	49	0.173	moderately stressed
T 11	Benin	E1 ⁰ 16.5090	N6 ⁰ 04.7729	18	0.173	moderately stressed
T 12	Togo	E1 ⁰ 18°90''	N6 ⁰ 01°56''	13	0.138	moderately stressed
T 13	Togo	E1 ⁰ 21.5790	N5 ⁰ 58.3448	60	0.338	Unstressed
T 14	Togo	E0 ⁰ 52.4986	N5 ⁰ 41.8603	13	-0.02	heavily stressed
T 16	Togo	E0 ⁰ 07.2247	N5 ⁰ 30.6685	56	0.145	moderately stressed
T 17	Ghana	E0 ⁰ 04.5541	N5 ⁰ 33.7917	39	0.248	Unstressed
T 19	Ghana	W0 ⁰ 41.1364	N5 ⁰ 07.6678	28	0.309	Unstressed
T 20	Ghana	W0 ⁰ 22.3600	N5 ⁰ 16.7100	36	0.311	Unstressed
T 22	Ghana	W-1 ⁰ 34.8500	N4 ⁰ 58.1300	16	0.110	moderately stressed
T 24	Ghana	W-1 ⁰ 32.3500	N4 ⁰ 51.2900	32	0.062	Stressed
T 25	Ghana	W-1 ⁰ 25.1300	N4 ⁰ 34.9800	50	0.101	moderately stressed
T 26	Ghana	W-1 ⁰ 08.4700	N4 ⁰ 59.7600	26	-0.189	heavily stressed

**Inadequate data due to high zeroes (97%) for the PRIMER software to analyse for the W-statistics.*

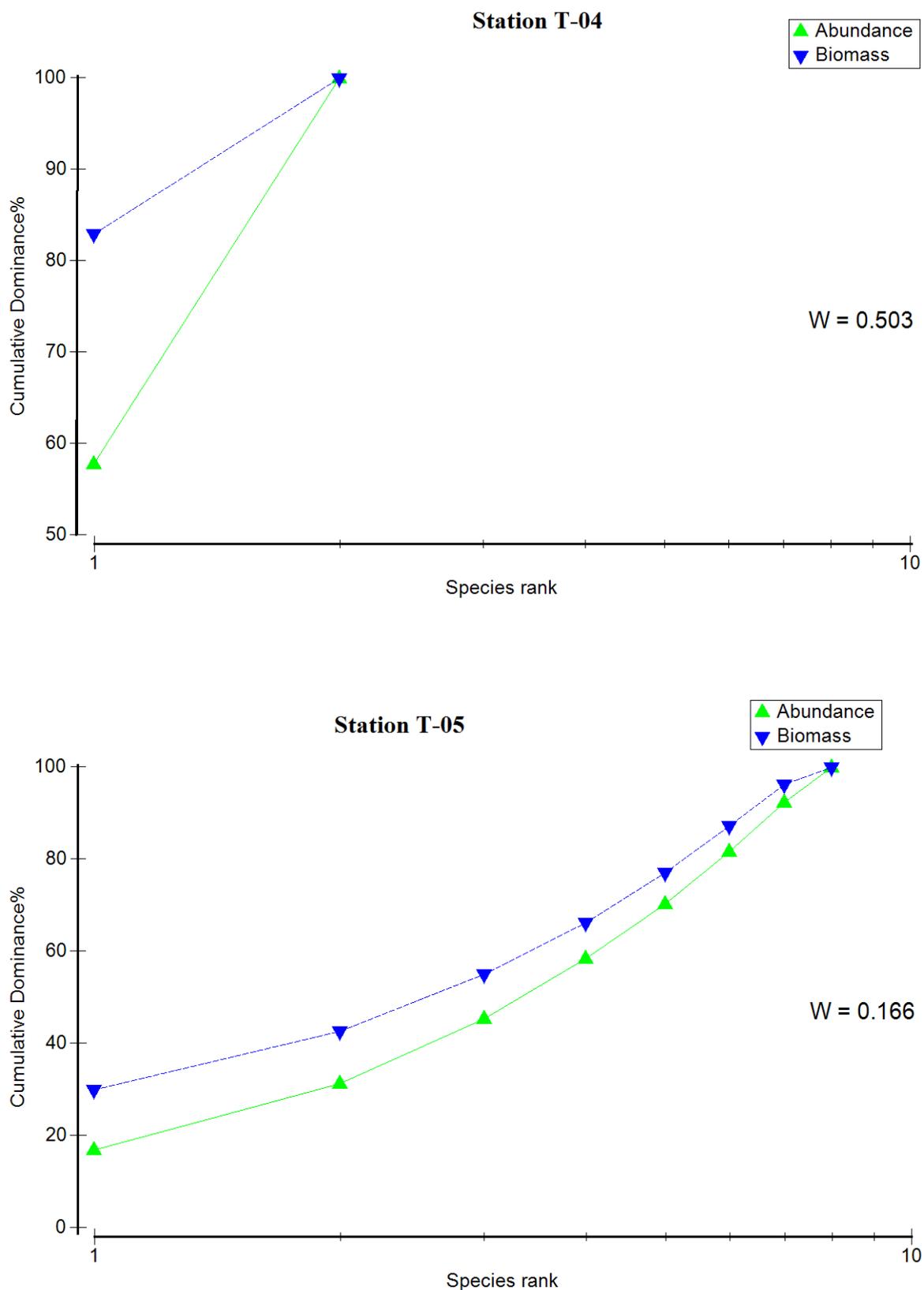


Figure 4.10 ABC plots for stations T-04 (top) and T-05 (bottom) based on epibenthic fauna abundance and biomass data.

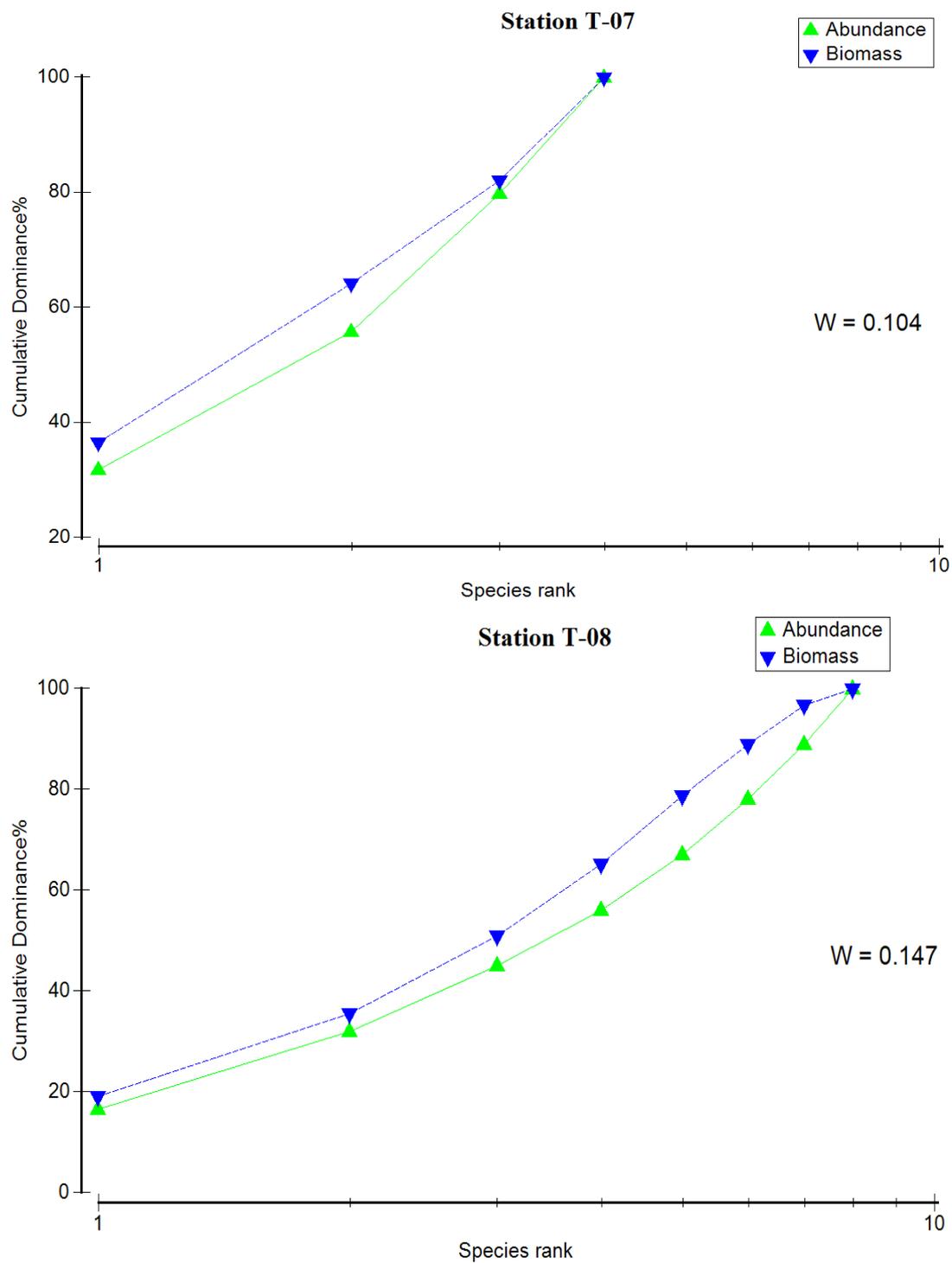


Figure 4.11 ABC plots for stations T-07 (top) and T-08 (bottom) based on epibenthic fauna abundance and biomass data.

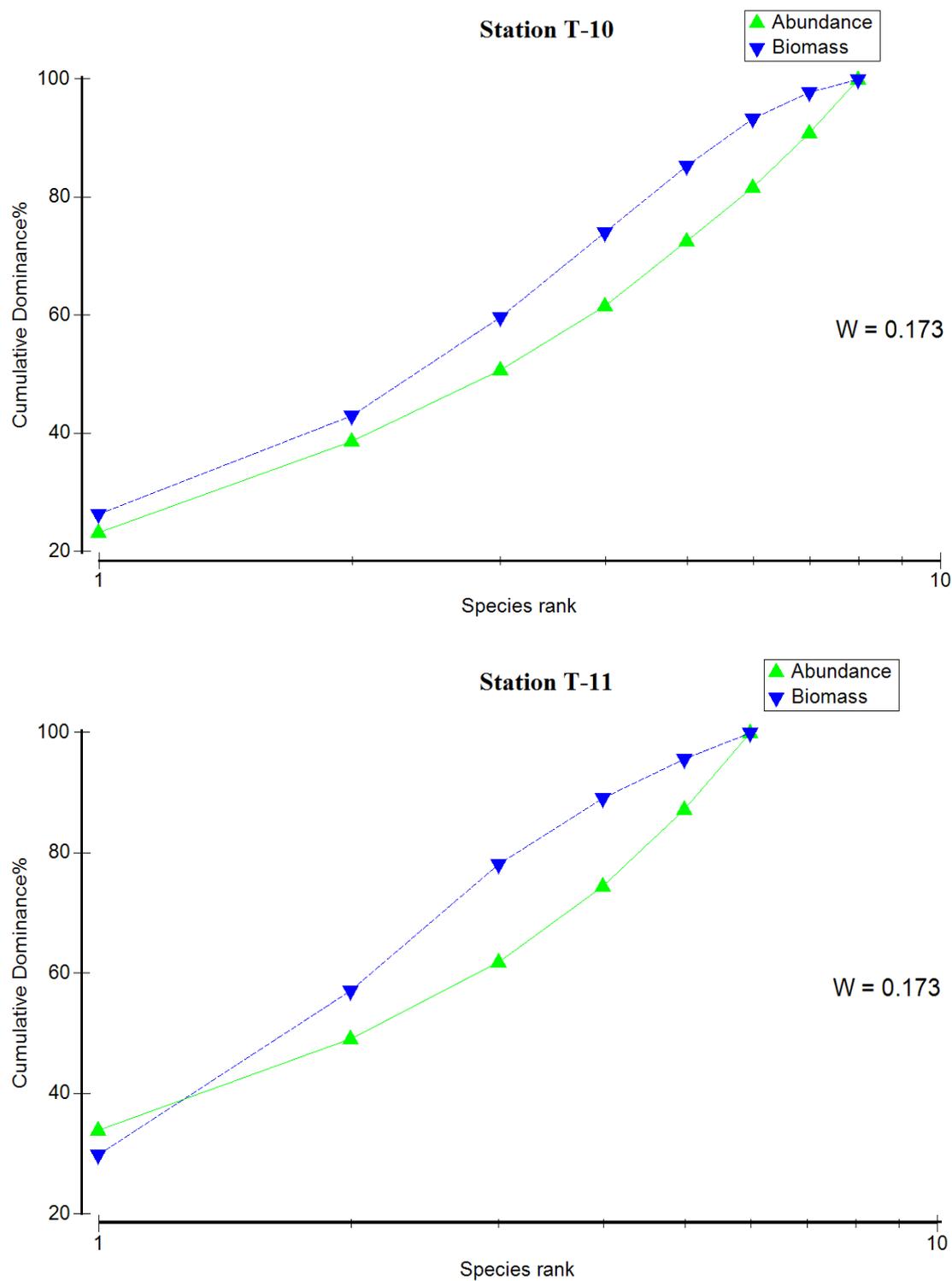


Figure 4.12 ABC plots for stations T-10 (top) and T-11 (bottom) based on epibenthic fauna abundance and biomass data.

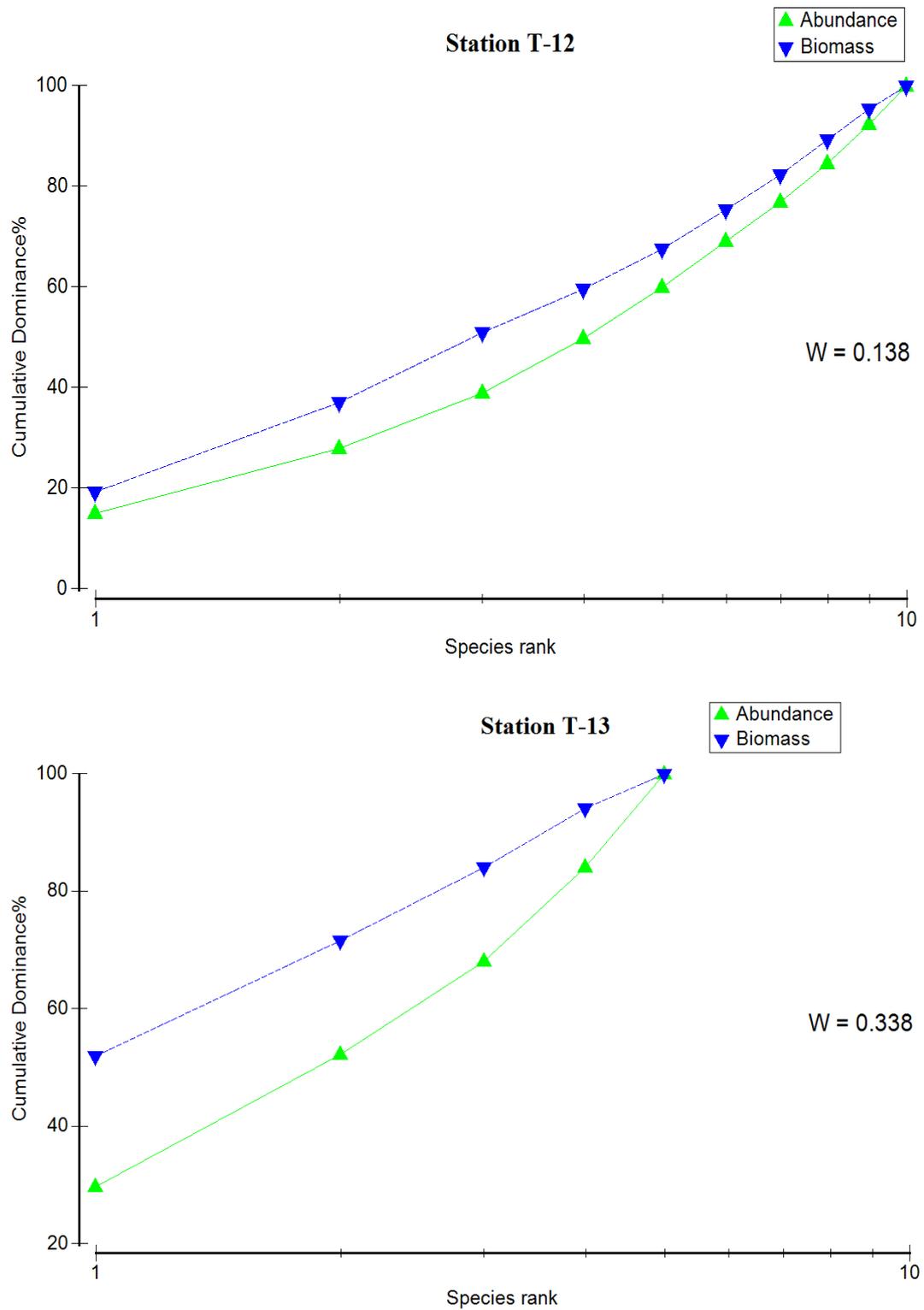


Figure 4.13 ABC plots for stations T-12 (top) and T-13 (bottom) based on epibenthic fauna abundance and biomass data.

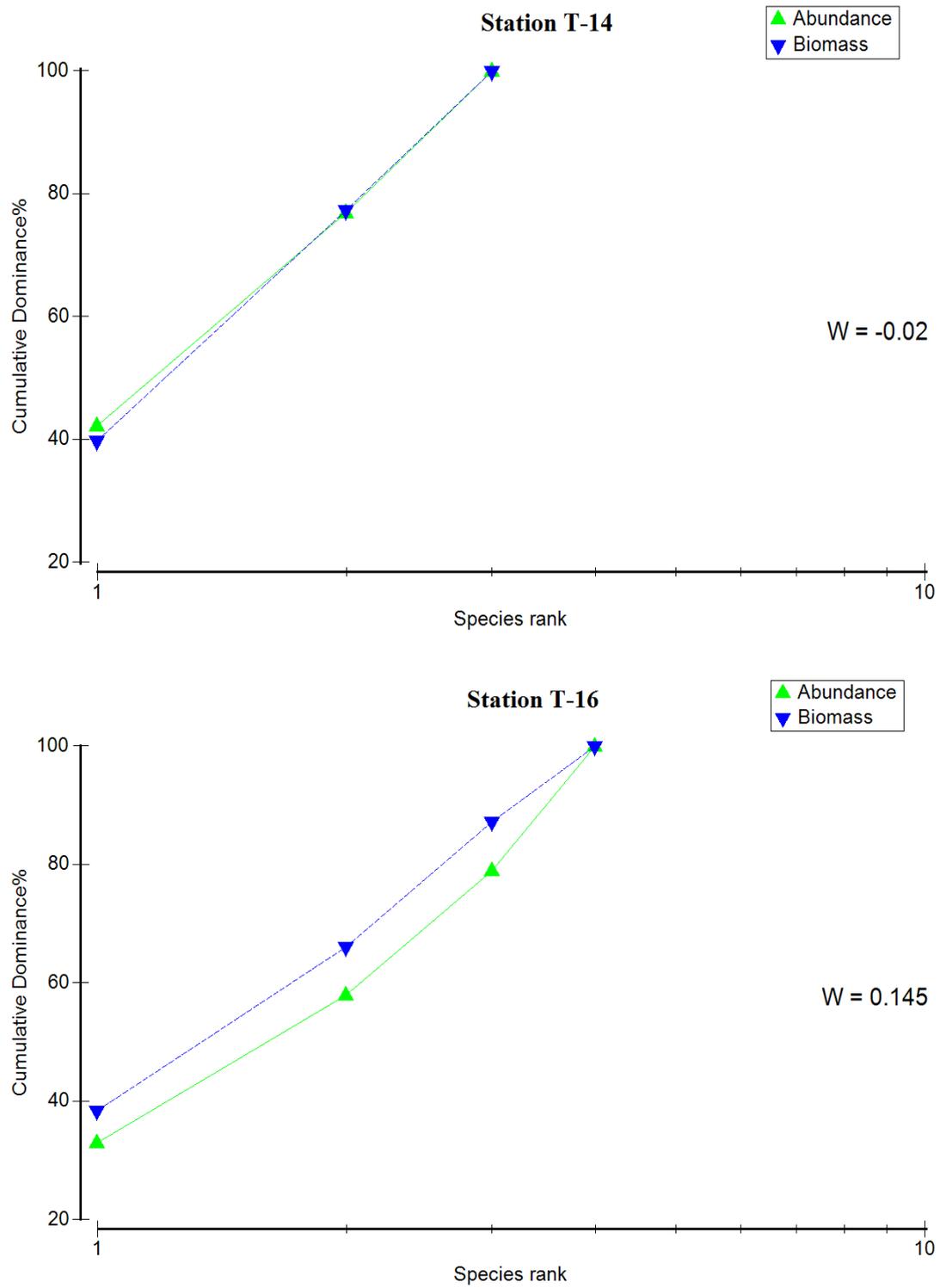


Figure 4.14 ABC plots for stations T-14 (top) and T-16 (bottom) based on epibenthic fauna abundance and biomass data.

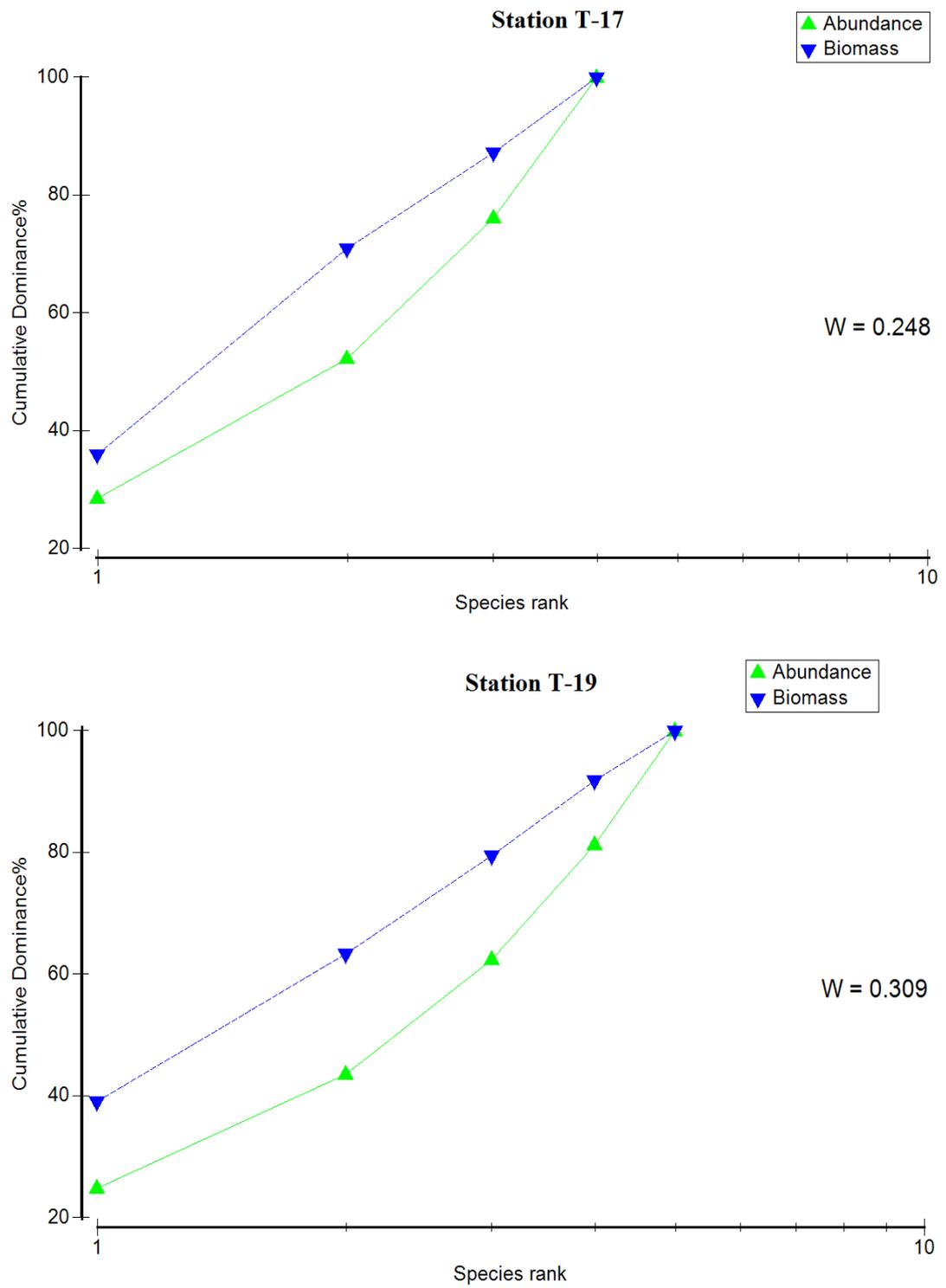


Figure 4.15 ABC plots for stations T-17 (top) and T-19 (bottom) based on epibenthic fauna abundance and biomass data.

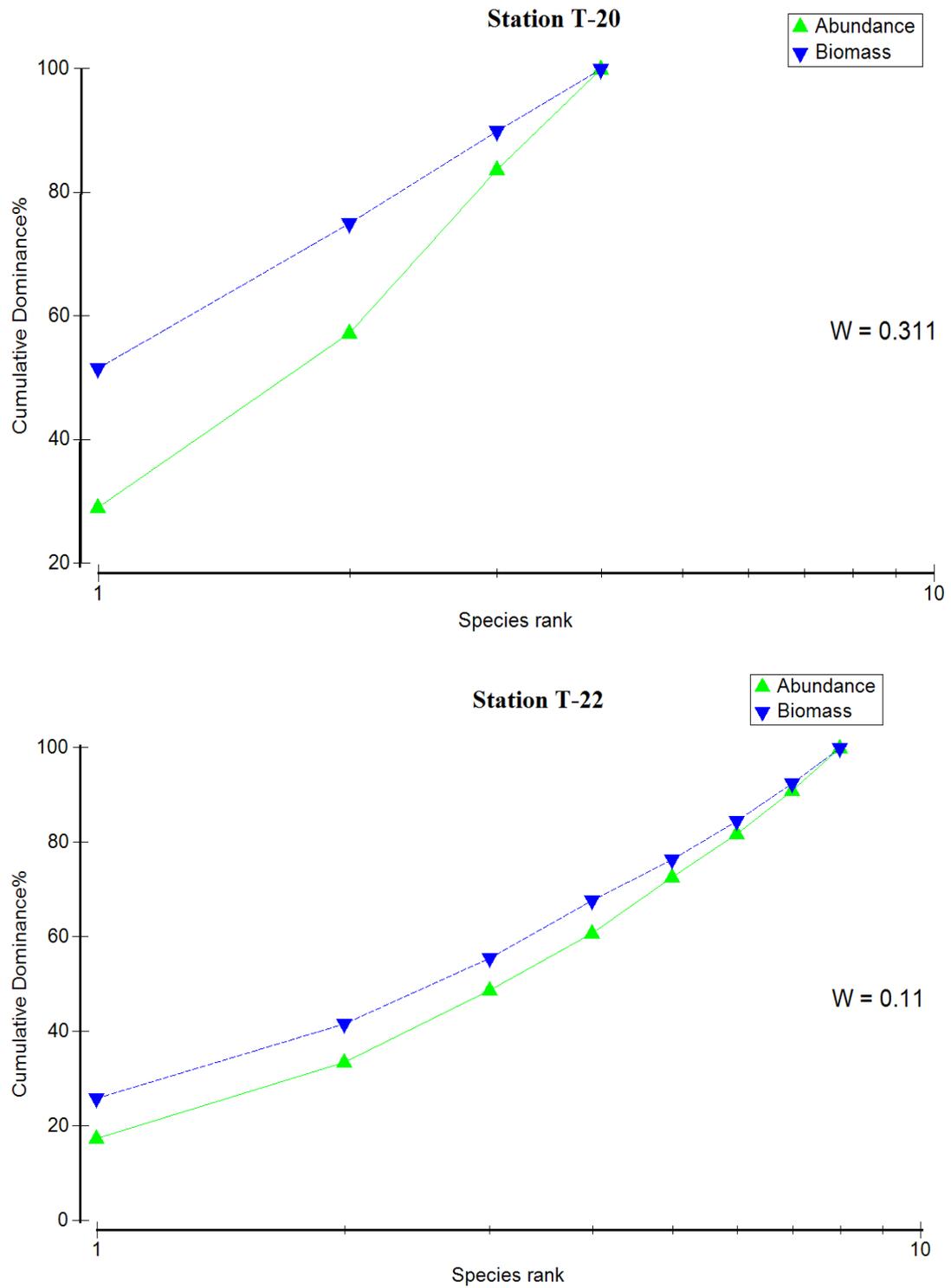


Figure 4.16 ABC plots for stations T-20 (top) and T-22 (bottom) based on epibenthic fauna abundance and biomass data.

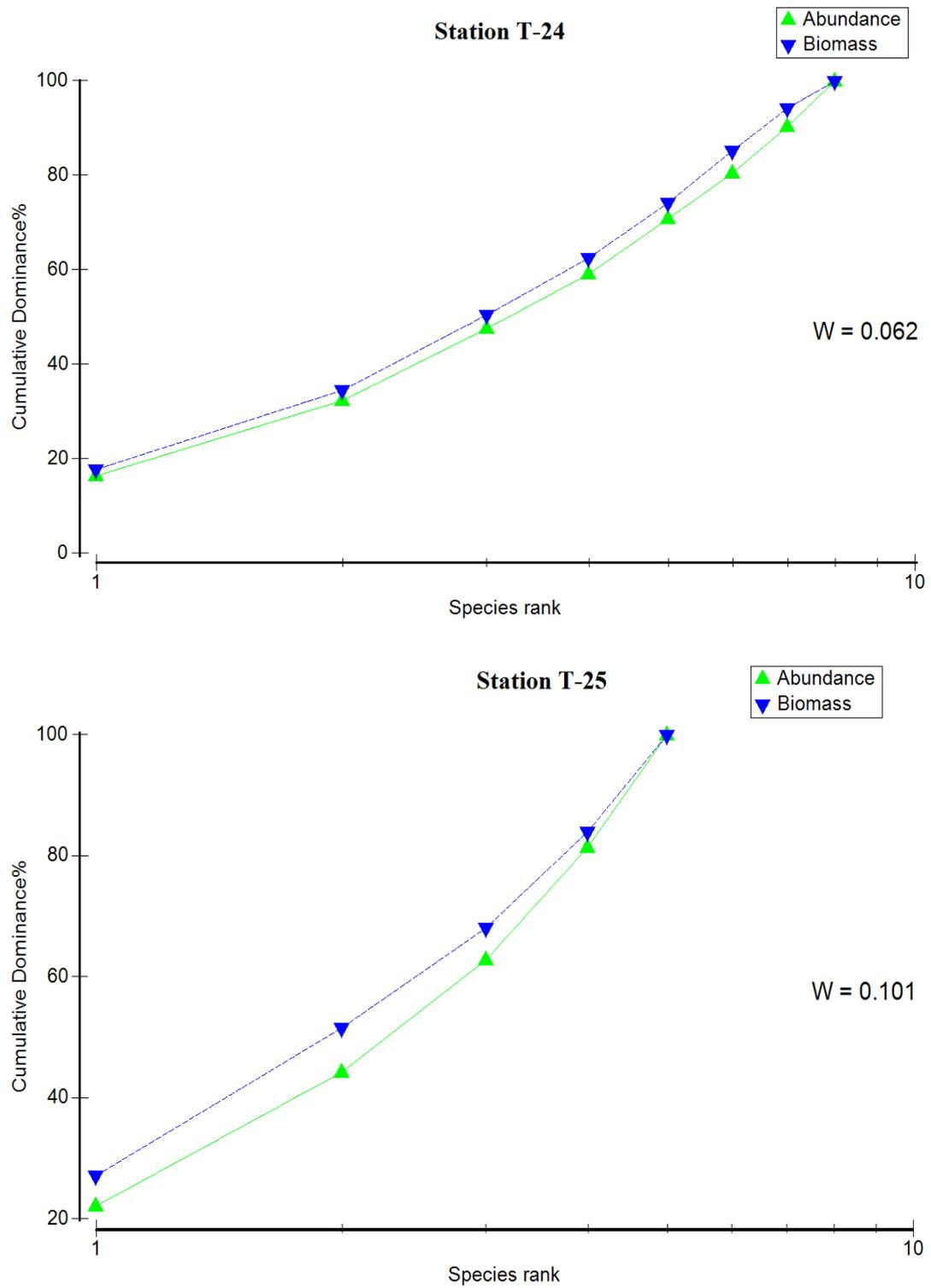


Figure 4.17 ABC plots for stations T-24 (top) and T-25 (bottom) based on epibenthic fauna abundance and biomass data.

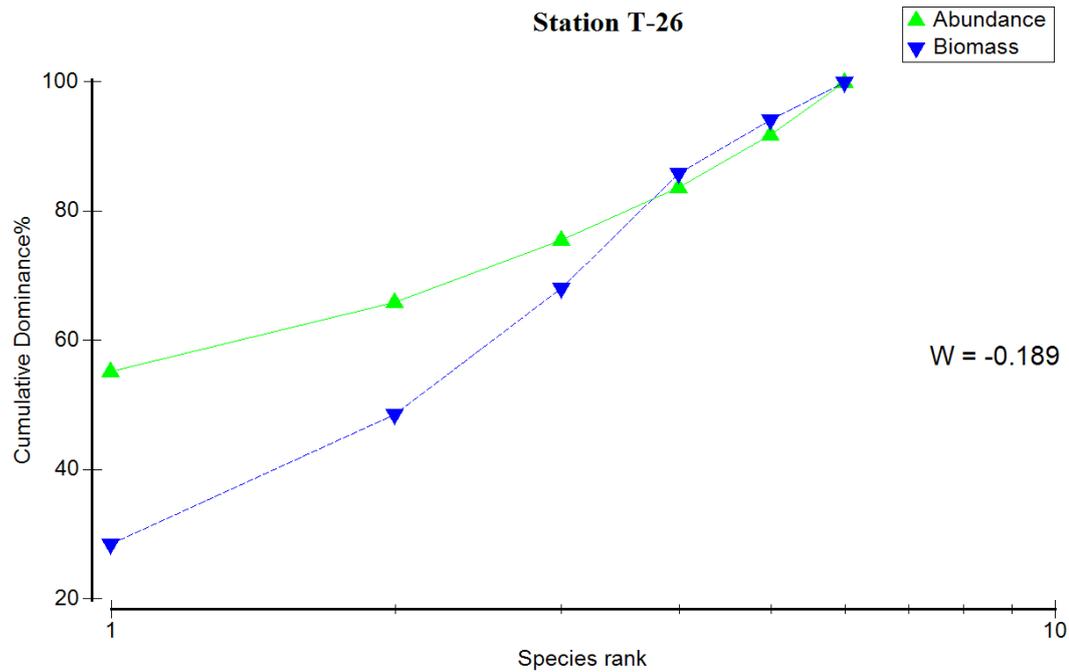


Figure 4.18 ABC plots for station T-26 based on epibenthic fauna abundance and biomass data.

4.4.4 Epifauna Functional Composition

4.4.4.1 Functional Group Diversity

The main benthic feeding types can be divided in two ways: what they feed on and how they feed. Category one can be divided into herbivores, carnivores, and detritivores, and the second into suspension-feeders, filter-feeders, deposit-feeders, scavengers, and predators (Fauchald and Jumars, 1979). Feeding strategy can offer ecologically relevant information on if and how human activities may affect the ecosystem, from the scale of an organism to the community. The Fauchald and Jumars (1979) feeding category was used for the epibenthic functional categorization.

In all, a total of twelve benthic feeding group categories were identified with some organisms sharing more than one feeding group. The result of feeding group composition depicts that carnivores largely contributed to the feeding community with

28% and was followed by filter feeding and predator/scavenging groups with 18% and 12% respectively (Fig. 4.19). The contributions by omnivores, herbivores and opportunists/scavenging were similar. The lowest ranked feeding functional groups were the detritivores, detritivore/carnivore, deposit-feeding, deposit-feeding/herbivores, filter-feeding/omnivores with a contribution of 3% each (Fig. 4.19).

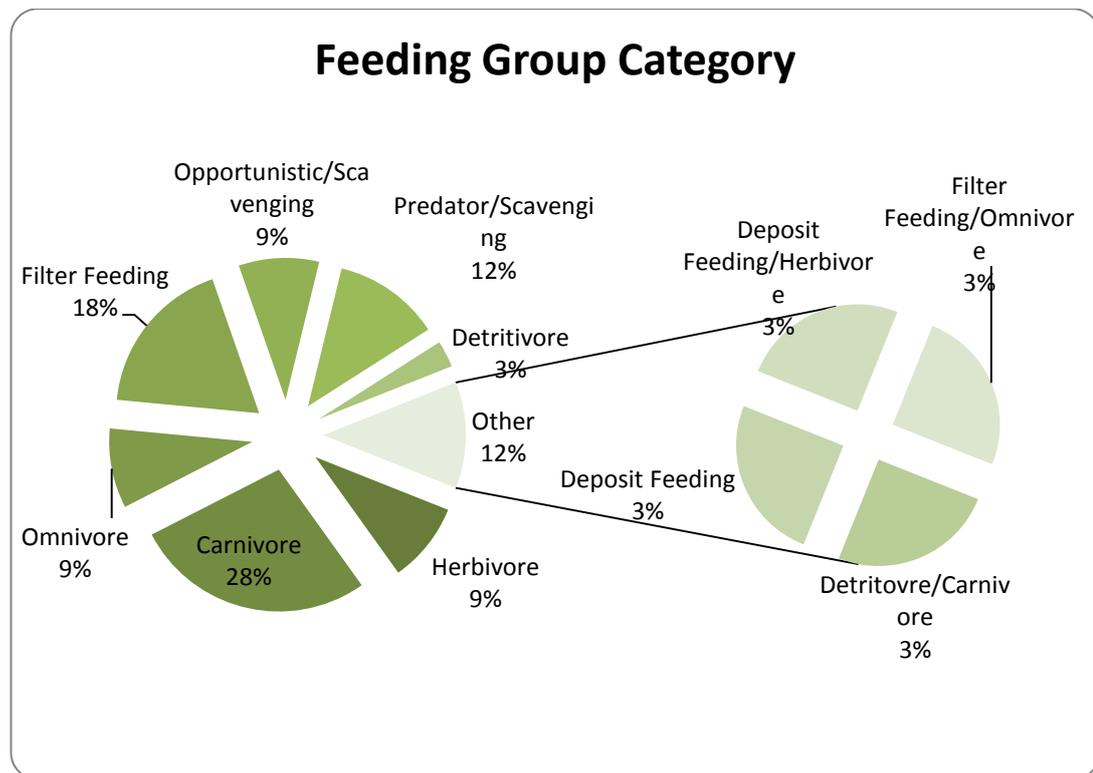


Figure 4.19 Feeding functional group categories for epibenthic fauna from 18 trawl hauls of the Gulf of Guinea.

The bathymetric distribution of the functional feeding groups of the epibenthic fauna indicated significantly higher numbers of carnivores, herbivores, filter feeders and predatory scavengers at mid-depth than both shallow- and deep-depths, and reflecting in their overall dominance across the feeding groups (Fig. 4.20). Omnivore scavengers and deposit feeders showed significantly ranked higher in deep depths than the mid-depth and shallow areas. As regards, the shallow areas, the opportunistic scavengers and detritivore carnivores significantly dominated (Fig. 4.20)

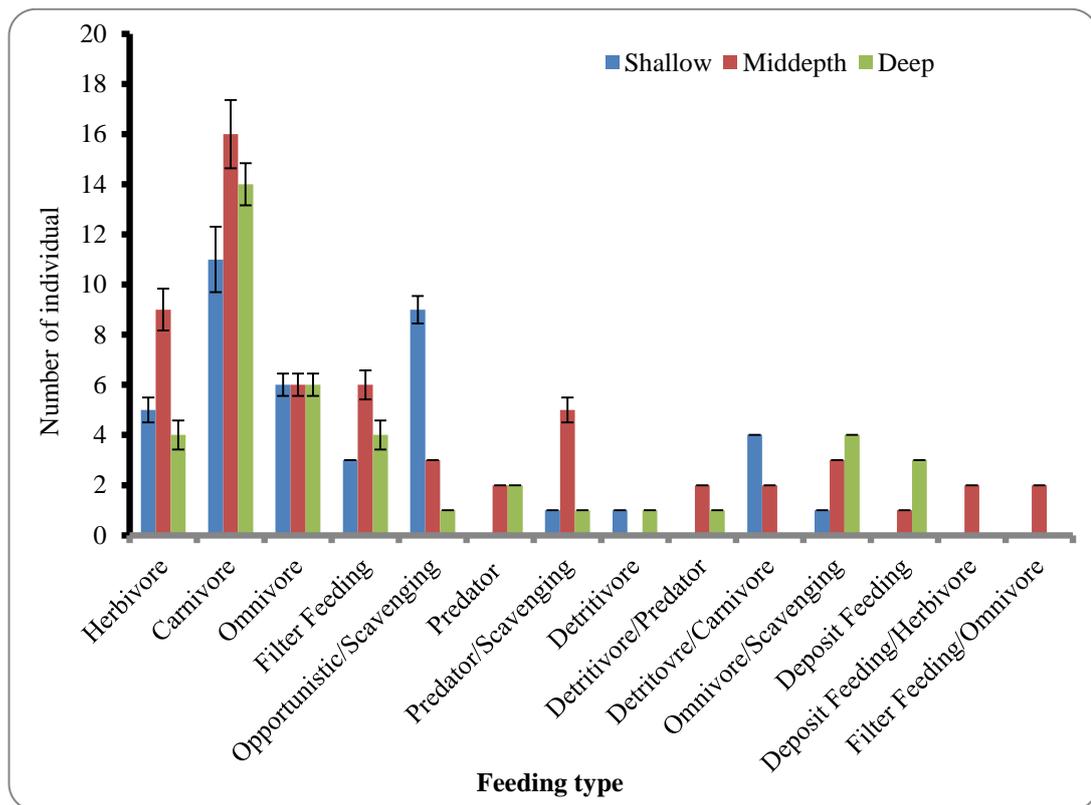


Figure 4.20 Richness of functional feeding groups across bathymetric gradient.

An important component of foraging strategy is motility and motility patterns may be related to feeding. The structure of the feeding apparatus may force the animal to remain sessile while feeding or the use of the feeding apparatus may be independent of, or require locomotion for proper function. Further, the mobility pattern may indicate escape response mechanisms of the organisms from disturbance (e.g., bottom trawling, predation) and may influence the community pattern.

The results of the analysis revealed that approximately 64% of the epibenthic fauna encountered were motile and 12% were sessile with only 3% being sedentary (Fig. 4.21). This high mobility reflects in the dominance of carnivores, herbivores and filter feeders functional groups. These feeding groups require mobility in their foraging

strategies. Sessile organisms throughout their life span do not move sufficiently to feed in an area different from that in which they settled as larvae. Discretely motile organisms are capable of moving between bouts of feeding, while motile species move independently of feeding, or in which efficient use of the feeding apparatus requires locomotion.

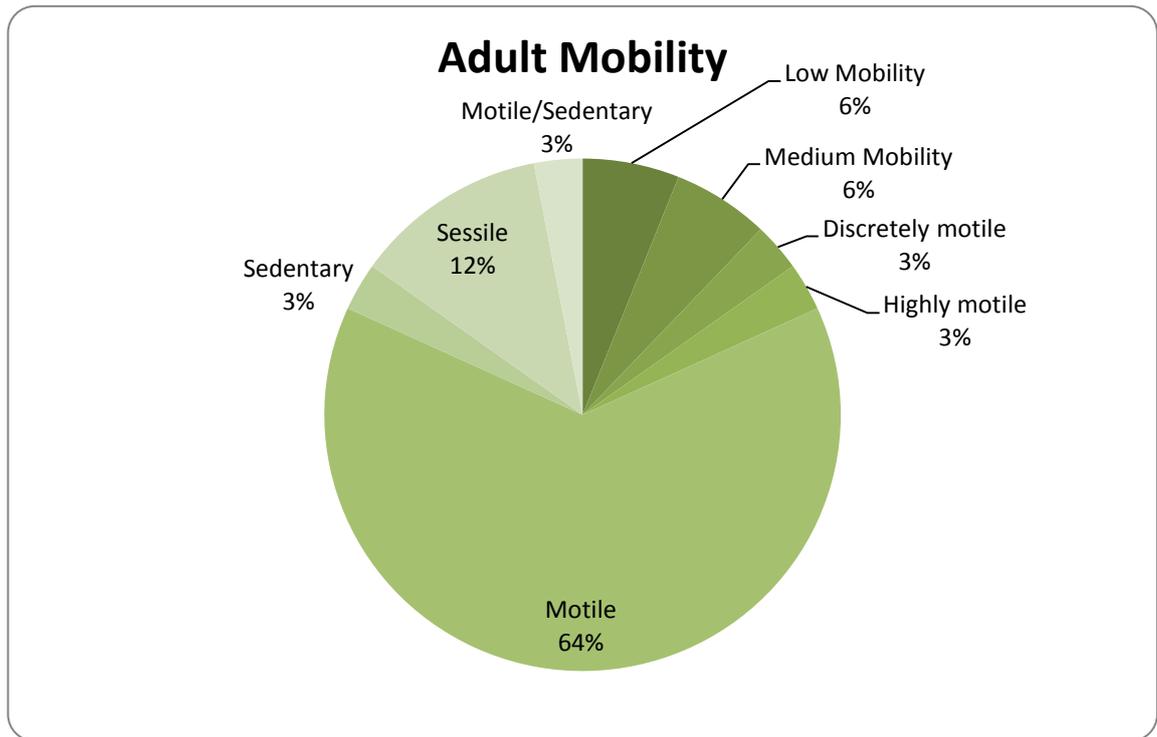


Figure 4.21 The proportion of adult relative mobility of epibenthic fauna from 18 trawl hauls in the Gulf of Guinea.

4.5 Discussion

Typical bottom beam trawling for demersal fishes are very efficient in catching epibenthic invertebrates (Reiss *et al.*, 2006). These epibenthic organisms though often treated as by-catch are a dominant component of the trawl catches. According to Clarke (2000), the direct effect of mortality caused by beam trawling varies from species to species, with 10-40% mortality in gastropods, starfish, crustaceans and annelid worms, from 10-50% for sea urchins to 30-80% for bivalves. However, this study showed that epibenthic invertebrate by-catch was primarily made up of molluscs (82.6% richness and 43.1% numerical abundance), crustaceans (23.1% richness) and echinoderms (15.4% richness) (Table 4.3). These percentages are consistent and compared well with estimated percentage of benthic production that is consumed by fish predators (~45%) (Clarke, 2000).

At the community level, the mortality imposed by the trawl fishery will depend on the level of direct mortality, the trawling frequency and the overlap in spatial distribution between the fishery and the benthic organisms. Studies of the annual direct fishing mortality rates on benthic invertebrates, for example, in the southern North Sea were estimated at between 7 and 45% of the individuals (de Groot and Lindeboom, 1994). The epibenthic faunal organisms often contribute considerably to total benthic biomass (Lampitt *et al.*, 1986) and carbon cycling (Piepenburg *et al.*, 1995) and are supposed to have a strong impact on the micro-scale environment with, for instance, bio-turbation and bio-irrigation (Huettel and Gust, 1992). These important ecosystem services as a result of their functional attributes is potentially eroded by bottom trawling activities, which sweep the seafloor of epibenthic invertebrates that are treated as by-catch. Aside the variation of the severity of impacts from species to species, the impact of the trawling is also spatial dependent as trawling varies from location to location.

The current study revealed significant differences in epibenthic biomass across depth scales. In particular, the biomasses of crustaceans and molluscs decreased with increasing water depth (Fig. 4.8), which confirmed a generally recognized pattern (e.g., Rowe, 1983). Importantly, the epibenthic fauna community of the central sections of the GCLME (Gulf of Guinea) presented a clear defined bathymetric pattern of distribution both in terms of species abundance and functional richness and abundance. The assemblage pattern depicted a significant difference ($p < 0.05$) between shallow-depth and deep-depth suggesting the existence of a unique abiotic factors or conditions structuring the epibenthic species assemblages. At the mid-depth however, both the species richness and diversity of fish and epibenthic fauna assemblages were correlatively higher (Figs. 4.6 and 4.7), which i) suggested a trophic dependence or interactions of fish and epibenthic fauna, and ii) the existence of conducive (or tolerable) abiotic conditions supporting the higher diversity.

Dietary studies have confirmed that large fishes prey on decapods (Polunin *et al.*, 2001) and this was evident in this study with crustaceans numerically dominant at mid-depth (Fig. 4.9). The numerical dominance of echinoderms and species placed in 'Others' category at mid-depth (Fig. 4.9) could further lend credence to the trophic interactions or dependence of fishes on epibenthic fauna. It is reasonable to assume that these epibenthic invertebrates are the dominant food items in the diet of the fishes. Stomach content analyses by several authors have indicated dominance of benthic invertebrates in demersal fishes. For instance, amphipods provide an important food resource to many demersal and benthic fishes (e.g. Gon and Heemstra, 1990; Kock, 1992; Olaso *et al.*, 2000), as well as other benthic invertebrates (McClintock *et al.*, 1994).

The observed higher Margalef's species richness and Shannon-Wiener diversity indices at the mid-depth may have been driven by trophic and physiological adaptation of the communities to the prevailing abiotic conditions. This may be as a result of the existence of multiple micro-habitats serving as, i) refugia (the patchy, diverse and multi-stratified sessile benthos offer a high diversity of potential microhabitats to small vagile invertebrates) and ii) the refugia enhancing foraging strategy (hiding and striking at preys). The assignment of a marine species to a given habitat will depend on the time it spends in that habitat. In other words, it depends on the organism's depth distribution and the resource segment that it feeds upon, as well as on where it has the best chance to avoid being taken as prey in its turn or where it faces less competition for food and space (Sarda *et al.*, 2005).

Some species will likely prefer a certain habitat or move between habitats, as well as gather or disperse, depending on other indirect factors such as vertical migrations under the influence of the photoperiod, annual seasonality, hydrographic conditions of the water masses, or inter and intraspecific relationships (e.g. resource competition, recruitment, sexual maturity, mating, biochemical cues etc.) (Sarda *et al.*, 2005). These factors may have played considerable structuring role in the observed numerically higher epibenthic fauna abundance and biomass as well as fish assemblages in the mid-depth zone by this study. Understandably, the mid-depth zone represents transitional waters of the turbulent shallow-water zone and benign deep-water zone, and probably presented environmentally tolerable conditions that as a consequence supported rich and diverse epibenthic fauna communities such as crustaceans, echinoderms and species in the 'Others' category (Fig. 4.9).

The selection of a given species to particular habitats is driven by the tolerance of the species to the given environment (Lamprey and Armah, 2008). Newell (1970) pointed out that where the tolerance limits for a particular environmental variable have been determined for an organism, the organism's realized distribution is much more restricted than its potential distribution. It is reasonable, therefore, to presume that the relatively large significant bathymetric differences in the taxonomic species and functional assemblages were probably the results of existence of extremes of environmental variables restricting the realized distribution of the species across all bathymetric gradients. In other words, the potential differing abiotic environmental factors (condition and resources) in the shallow-depth and deep-depth ensured that species tolerable to these extreme environmental conditions survived. The declension of species abundance of molluscs with increasing water depth and increased polychaete abundance with increasing water depth (Figs. 4.8 and 4.9) gave further support to the assertion of differing abiotic structuring mechanism along bathymetric gradients.

The distribution pattern of polychaete taxa is indicative that the deep-depth is characteristic of fine-grained soft substrate with potentially high organic matter, which probably was influenced by pelagic productivity. This statement is supported by the observation of dominance of deposit-feeding polychaetes in deep-depth (Fig. 4.20) with low suspension/filter-feeding organisms (e.g. molluscs), emphasizing the theory of trophic group amensalism (Rhoads and Young, 1970). The theory suggested that the physical instability of reworked environment may discourage the settling larvae of suspension feeders, and if settling does occur, early growth stages may be inhibited or killed by the unstable sediment conditions. The inhibitors (deposit-feeders) are unaffected by this relationship, while the amensals (suspension-feeders and sessile epifauna) are either discouraged from settling or are killed during early benthonic stage.

Ostensibly, deep-depth ecosystems have lower energetic turnover than shallow-water or littoral systems and their carrying capacity is expected to be lower (Cartes *et al.*, 2002). Conversely, the high numerical abundance and the correspondingly high biomass of molluscs in shallow-water could mean that there is high current energy, which has trophically favored the molluscan assemblage (or have adapted trophically) due in great part to their active and passive suspension-feeding mechanism. Most molluscs prefer to attach to rock stones and shells (Jorcin, 1996) and thus their abundance in the shallow-waters is a reflection of the nature of the substratum influenced possibly by the current energy.

4.5.1 Functional Group Classification

According to Hamerlynck *et al.* (1993) it will make a great biological sense to base functional and process studies on entities which be can distinguished clearly on the basis of their species-abundance composition. Two methods traditional often used in functional diversity in marine benthic ecosystems are: i) relative taxon composition analysis, which interprets changes in the distribution of taxa in terms of the characteristics they exhibit, and ii) trophic group analysis, which investigates differences in feeding mechanisms between assemblages, although biological trait analysis have been employed recently (Bremner *et al.*, 2008). A more targeted approach proposed for the study of functional diversity focuses specifically on feeding mechanisms, which are generally thought to be one of the central processes structuring marine ecosystems (Pearson and Rosenberg, 1978; 1987). Essentially, functional feeding strategies have been used to explore the mechanims of the adaptations of communties to the

environment in different ecosystem including streams (see Principe *et al.*, 2010), estuaries and marine.

The bathymetric analysis of the functional feeding groups showed significant ($p=0.017$). bathymetric differences between shallow and deep zones, consistent with that of the taxonomic species abundance. This suggests that functional feeding group categorization may give comparable information about community assemblage patterns and possibly the inherent environmental drivers. Bathymetric zonation is reflected in the variations of environmental factors that ensure the selection of species with particular functional trait in which this attribute consequently reflect in the ecosystem functioning of the study locality.

The functional feeding groups contributed differently to the assemblage. For instance, carnivores contributed 28%, filter feeders (18%) and predatory scavengers (12%) and these were dominant at mid-depth. Functional feeding groups is necessary for identification of functional groups partially independent of taxonomic determinations (Cummins, 1974) in order to address important process oriented-ecosystems questions. The concept concerns itself with how a resource or any other ecological component is processed by different species to provide a specific ecosystem service or function (Blondel, 2003). The carnivory was noted as the dominant functional feeding in the epibenthic communities and is a reflection of the nature of the food resources in the habitats level and the morphological and behavioural adaptation that have converged. Feeding strategies are typical traits reflecting the adaptation of species (Statzner *et al.*, 2004). The dominance and distribution of the carnivores could be more closely related to the abundance of their potential preys; the densities of these preys were higher in the mid-depth. Predation can enhance coexistence between species of benthic organisms by

preventing monopolization of space (Parsons *et al.*, 1995). The carnivorous species can facilitate the transport of nutrients retained in the detritivores tissues back in to the mobile pool (Ngai and Srivastava, 2006) and hence renew nutrients for primary producers. The presence of carnivorous species further helped to transfer the nutrients retained in deposit-feeders back into the mobile pool (Sivadas *et al.*, 2013). Thus, the functional diverse macrobenthic community rapidly consumed the organic matter and converted it to benthic biomass which forms the food for organisms at the higher trophic level such as the demersal fish.

The filter-feeders processed organic matter from the water column, while deposit-feeders utilized the sedimented detritus. The numerical dominance of deposit-feeders at the deep-depth is suggestive of the influence of the zone by pelagic resources. The deposit-feeders as consumers of newly sedimented food is related to the production in the water column (Gaston, 1987; Gaston *et al.*, 1988; Josefson and Rasmussen, 2000). Although the present study does not present information on the biological productivity in the area, the Gulf of Guinea (GoG) region is characterized by a coastal upwelling that increases the productivity in the water column (Wiafe, 2002), and part of this production settles forming available food for the benthic community. Filter/suspension feeders need high quality food arriving from surface waters and/or via bottom currents, which also may make them some of the first organisms impacted by changes in pelagic production, high sedimentation, or from pollution to the water column.

The potential food for filter/suspension feeders is mainly phytoplankton, which may be produced in waters far away from their locations and transported to them by currents (Pearson and Rosenberg, 1987). The trophic group mutual exclusion hypothesis postulates that current speed controls community composition, through its effects on

food supply and sedimentary composition. Predators and scavengers on the other hand need a rich community of potential prey in suitable size classes, and may respond positively to enhanced biodiversity, but also to strong disturbances to the seafloor resulting in mortality or exposure of benthic fauna (Kaiser and Spencer, 1996; Ramsay *et al.*, 1998). Food supply is therefore a key factor structuring marine benthic communities (Pearson and Rosenberg, 1978, 1987; Wieking and Kröncke, 2005).

4.5.2 Ecosystem Health and Ecological Status

The ecological status of the marine environment has been assessed using different tools/indices, and these have really focused on the benthos. One of the tools/indices which has successfully been applied to assess the ecological status of the marine benthos is the ABC (Abundance Biomass Curve) proposed by Warwick (1986). The ABC analysis in this study revealed that 11% of the shelf in the Gulf of Guinea (19±9m depth) is heavily stressed due possibly to anthropogenic activities such as fishing and pollution. Five percent (5.56%) (32±8m) of the shelf area is stressed, while 50% (36±18) of the locations were moderately stressed. Adding these areas of stress amounted to a colossal 66.56% of the continental shelf area was stressed although 50% of it is moderately stressed. Nonetheless, this finding presents a worrying picture of the Gulf of Guinea that may exigently necessitate a regional pragmatic effort to arrest the situation. Approximately, 28% (one-third) of the shelf area is unstressed and these areas fall within the average water depth of 45±15m. It is thus evidently striking to note that the degree of stress decrease with increasing water depth. This observation would mean that shallow-depth areas experience intense disturbance possibly from fishing and pollution from land drainages. Many bottom trawlers trawl within shallow-depth due to less advanced technologies and possibly high cost of trawling in deep-depths within the region.

The ecological health of marine ecosystem has been a concern and global efforts are being made to ensure ‘good’ ecological statuses in marine ecosystems. For example, the Marine Strategy Directive Framework (European Commission, 2008), viewed the ecological status as the integration of structure, function and processes of the marine ecosystem with anthropogenic impacts. These require background scientific works to fully understand the dynamics that will ensure that any intervention is not bereft with adequate scientific information. The background works identified by the European Commission to define the good ecological status has been grouped under various task descriptors namely biodiversity (Cochrane *et al.*, 2010); non-indigenous species (Olenin *et al.*, 2010); exploited fish (Piet *et al.*, 2010); food-webs (Rogers *et al.*, 2010); human-induced eutrophication (Ferreira *et al.*, 2010); seafloor integrity (Rice *et al.*, 2010); contaminants (Law *et al.*, 2010); litter (Galgani *et al.*, 2010); noise (Tasker *et al.*, 2010) and hydrographical conditions. This holistic initiative of the European Commission could be harmonized within the Guinea Current Large Marine Ecosystem (GCLME) Programme backed by sound management for implementing the tasks’ findings in order to stem the tide of the ecosystem deterioration, which if continued will lead to the breakdown of its resilience with very devastating consequences.

CHAPTER FIVE

GENERAL CONCLUSION AND RECOMMENDATIONS

5.1 Conclusion

The study has demonstrated that functional traits of soft-bottom macrobenthic assemblage patterns represented a direct and complex response to environmental factors notably sedimentary nitrate, calcium, magnesium, organic carbon and sediment grain-size fraction (silt & clay), which are in turn influenced by their interactions with other variables to drive functional and species diversity and assemblages. The study revealed that the dominant functional traits (i.e., small adult size, solitary, burrow-dwelling & deposit-feeding) potentially control the assemblage patterns and thus exert the strongest influence on ecosystem processes such as biogeochemical function (nutrient mineralization) contributing immensely to the productivity of the ecosystem. The dominance and distribution of these key eco-functional traits are direct responses to tolerance and trophic, morphological, behavioral adaptations to a highly dynamic and unstable ecosystem.

The functional traits analysis, which is first its kind in the GCLME region, has demonstrated that the BTA not only preserve taxonomic information, but also provide important ecological information. These ecological information included the nature of the ecosystem, the ecological status, potential ecosystem processes/functions, and importantly discrimination between habitats/locations, with the latter creating biodiversity zonation in the GCLME. These zones are i) central GCLME, (biodiversity rich), ii) western GCLME (moderately rich biodiversity), and iii) eastern GCLME (poor biodiversity). This habitat zonation may have significant implications not only for

resources management but monitoring of ecosystem health for conservation purposes in the GCLME, which is experiencing some degree of ecological stress.

The empirically derived inferences of mechanistic effects of functional biodiversity on ecosystem processes from this study provide important demonstration of relationship between functional diversity and ecosystem functions in natural marine ecosystem. This is against the backdrop of little effort in the scientific literature to demonstrate and substantiate biodiversity-functional relations using data from the real world according to Solan *et al.* (2008).

The key inferential findings of the study were:

- The small body size dominant functional trait provided strongest evidence of habitat instability, high productivity and low-biomass supported ecosystem (i.e., GCLME)
- The habitat instability may be attributable to anthropogenic activities (i.e., fishing and pollution) creating a stressful condition that affect the ecological health of the GCLME as evidenced by the inverse relations between habitat stress and increasing water depth. Most marine fishing activities are concentrated on shallow waters.
- The ecological disturbances through fishing and/or pollution play interactive and structuring roles in epibenthic fauna distribution patterns especially along bathymetric gradient.
- Benthic species adaptations to the unstable, dynamic, stressful and productive GCLME environment are corroboratively through combined mechanism/strategies notably feeding, lifestyle, anatomical and morphological.

- The identified dominant traits provided an indication of a productive ecosystem primarily influenced by ecosystem process/functions (i.e., nutrient mineralization through biogeochemical functions by burrow dwelling deposit-feeders) and thus providing the strongest empirical evidence of ecosystem function. This is further corroborated by the identification of nitrate and organic carbon as key drivers of functional and species richness.
- The structuring effects of abiotic parameters (e.g., calcium, magnesium) on functional and species diversities suggest climate change factors in the GCLME and thus climate change factors are potential surrogates of abiotic drivers of benthic community and functional structure.
- Results indicated evidence of trophic/feeding dependence (or interactions) of demersal fishes on (between) epibenthic fauna (notably crustaceans, echinoderms and species in 'others' category), but this occurred in the most benign conditions or within environmental tolerable areas.

5.2 Recommendations

- The use of functional traits notably adult body size, feeding habit, sociability and mobility for environmental monitoring of the ecosystem health and to understand ecosystem processes in the GCLME should be given a highest priority.
- Concurrent investigations of marine benthos and demersal fisheries should be important focus in any GCLME fisheries survey in order to understand the effects of bottom trawling on the benthos with associated ecosystem services, as well as trophic interactions.

- Influence of Benguella and Canary currents on primary productivity or carbon input in the GCLME should be investigated to elucidate the impact they have on benthic community assemblages.
- It is imperative for a long-term monitoring of rate of accumulation or dissolution of CaCO_3 and MgCO_3 in marine organisms (benthic and planktonic) and also quantification of shifts in calcification rate in order to understand and delineate the effects of climate change mechanisms in the GCLME.

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APPENDIX I

Functional trait data base for the benthic macrofauna biodiversity in the GCLME

Species	Feeding Habit	Feeding Structure	Adult Mobility	Sociability	Adult Body Size	Adult Body Form
POLYCHAETA						
<i>Amaeana trilobata</i>	Filter feeder	Tentacles	Peristaltic crawling	Solitary	20mm	Trefoil-shaped
<i>Ampharete acutifrons</i>	Deposit feeder	Tentacles	Burrow/sessile	Solitary	80mm	Cylindrical and tapers towards tail
<i>Ampharete sp</i>	Deposit feeder	Tentacles	Burrow/sessile	Solitary	80mm	Cylindrical and tapers towards tail
<i>Ampharete agulhaensis</i>	Deposit feeder	Tentacles	Burrow/sessile	Solitary	15mm	Cylindrical and tapers towards tail
<i>Amphictes gunneri</i>	Deposit feeder	Buccal tentacles	Burrow	Solitary	60mm	Cylindrical and tapers towards tail
<i>Ampithoie rubricata</i>	Carnivore/detritivore	Maxillipeds	Burrow	Solitary	2.5-7mm	Laterally flattened
<i>Ancistrosyllis rubosta</i>	Carnivore/omnivore	Proboscis/Papillose	Creep	Solitary	54mm	Elongate and flattened
<i>Aphrodita alba</i>	Carnivore	Jaw	Crawl	Solitary	30mm	Oval
<i>Aphrodita sp</i>	Carnivore	Jaw	Crawl	Solitary	30mm	Oval
<i>Arenicola sp.</i>	Deposit feeder	Proboscis/Papillose	Burrow	Solitary	100-400mm	Elongate
<i>Arabella irricolor</i>	Carnivore	Proboscis	Burrow	Solitary	80mm	Vermiform and iridescent
<i>Aricidea capensis</i>	Deposit feeder	Proboscis	Burrow	Solitary	10mm	Vermiform and tapering
<i>Aricidea curvata</i>	Deposit feeder	Proboscis	Burrow	Solitary	20mm	Vermiform and tapering
<i>Aricidea fauveli</i>	Deposit feeder	Proboscis	Burrow	Solitary	20mm	Vermiform and tapering
<i>Aricidea fragilis</i>	Deposit feeder	Proboscis	Burrow	Solitary	20mm	Vermiform and tapering
<i>Aricidea jeffreysi</i>	Deposit feeder	Proboscis	Burrow	Solitary	15mm	Vermiform and tapering
<i>Aricidea longobranchiata</i>	Deposit feeder	Proboscis	Burrow	Solitary	20mm	Vermiform and tapering
<i>Aricidea sp</i>	Deposit feeder	Proboscis	Burrow	Solitary	20mm	Vermiform and tapering
<i>Armandia cf. melanura</i>	Deposit feeder	Proboscis	Burrow	Solitary	30mm	Long and round
<i>Armandia intermedia</i>	Deposit feeder	Proboscis	Burrow	Solitary	12mm	Long and round
<i>Armandia sp.</i>	Deposit feeder	Proboscis	Burrow	Solitary	12-30mm	Long and round
<i>Asychis atlantideus</i>	Deposit feeder	Proboscis/Papillose	Burrow	Solitary	100mm	Cylindrical
<i>Asychis dorsofilis</i>	Deposit feeder	Proboscis/Papillose	Burrow	Solitary	100mm	Cylindrical
<i>Axiothella jarli</i>	Deposit feeder	Proboscis/Papillose	Burrow	Solitary	35mm	Cylindrical
<i>Capitella capitata</i>	Deposit	Papillose	Burrow	Solitary	30mm-40mm	Thread-like

	feeder/detritivore					
Capitellid sp	Deposit feeder/detritivore	Papillose	Burrow	Solitary	30mm-40mm	Thread-like
<i>Caulleriella acicula</i>	Deposit feeder	Feeding palps/tentacular cirri	Burrow	Solitary	20mm	Thread-like
<i>Caulleriella capensis</i>	Deposit feeder	Feeding palps/tentacular cirri	Burrow	Solitary	20mm-30mm	Thread-like
<i>Caulleriella</i> sp	Deposit feeder	Feeding palps/tentacular cirri	Burrow	Solitary	25mm-40mm	Thread-like
<i>Ceratonereis</i> sp.	Omnivore	Mandibles and maxillae/jaws	Burrow	Solitary	30mm	Slender
<i>Chloeia</i> sp.	Carnivore	Pharynx	Burrow	Solitary	20mm-70mm	Depressed and oval
<i>Cirratulus filliformis</i>	Deposit feeder	Tentacles	Burrow/Sessile	Solitary	50mm	Slender
<i>Cirratulus</i> sp	Deposit feeder	Tentacles	Burrow/Sessile	Solitary	25mm-50mm	Slender/thread-like
<i>Cirriformia punctata</i>	Deposit feeder	Pharynx/ feeding palps	Burrow/Sessile	Solitary	40mm	Fairly broad
<i>Cirriformia tentacula</i>	Deposit feeder	Pharynx/ feeding palps	Burrow/Sessile	Solitary	200mm	Fairly broad
<i>Clymene</i> sp	Detritivore	Papillose proboscis	Burrow	Solitary	40mm-138mm	Cylindrical
<i>Clymenura tenuis</i>	Detritivore	Papillose proboscis	Burrow	Solitary	120mm	Cylindrical
<i>Cossura costa</i>	Deposit feeder	Pharynx	Burrow	Solitary	15mm	Thread-like and round
<i>Diopatra cf. monroi</i>	Carnivore	Mandibles and maxillae/jaws	Burrow	Solitary	100mm-150mm	Tube sausage-like
<i>Diopatra cf. musseraensis</i>	Carnivore	Mandibles and maxillae/jaws	Burrow	Solitary	50mm	Tube sausage-like
<i>Diopatra cuprea cuprea</i>	Carnivore	Mandibles and maxillae/jaws	Burrow	Solitary	120mm	Tube sausage-like
<i>Diopatra monroi</i>	Carnivore	Mandibles and maxillae/jaws	Burrow	Solitary	100mm-150mm	Tube sausage-like
<i>Diopatra neopolitana</i>	Carnivore	Mandibles and maxillae/jaws	Burrow	Solitary	300mm	Tube sausage-like
<i>Diopatra neapolitana cuprea</i>	Carnivore	Mandibles and maxillae/jaws	Burrow	Solitary	120mm	Tube sausage-like
<i>Dorvillea rubrovittata</i>	Carnivore	Mandibles and maxillae/jaws	Crawl	Solitary	15mm-30mm	Vermiform and elongate
<i>Dorvillea rudolphi</i>	Carnivore	Mandibles and maxillae/jaws	Crawl	Solitary	15mm	Vermiform and elongate
<i>Dorvillea</i> sp	Carnivore	Mandibles and maxillae/jaws	Crawl	Solitary	10mm-30mm	Vermiform and elongate
<i>Drilonereis falcata</i>	Carnivore	Mandibles and	Burrow	Solitary	100mm	Slender and round

		maxillae/jaws				
<i>Drilonereis monroi</i>	Carnivore	Mandibles and maxillae/jaws	Burrow	Solitary	100mm	Slender and round
<i>Drilonereis sp</i>	Carnivore	Mandibles and maxillae/jaws	Burrow	Solitary	100mm	Slender and round
<i>Epidiopatra gilchristi</i>	Deposit feeder/carnivore	Tentacles	Burrow	Solitary	60mm	Slender
<i>Epidiopatra hupferiana</i>	Deposit feeder/carnivore	Tentacles	Burrow	Solitary	30mm	Slender
<i>Epidiopatra hupferiana monroi</i>	Deposit feeder/carnivore	Tentacles	Burrow	Solitary	35mm	Slender
<i>Epidiopatra sp</i>	Deposit feeder/carnivore	Tentacles	Burrow	Solitary	30mm-60mm	Slender
<i>Eteone foliosa</i>	Deposit feeder	Proboscis	Burrow	Solitary	120mm	Tapered
<i>Eteone ornata</i>	Deposit feeder	Proboscis	Burrow	Solitary	120mm	Enlongate and tapered
<i>Eteone (Mysta) siphodonta</i>	Deposit feeder	Proboscis	Burrow	Solitary	200mm	Elongate and flatten
<i>Euclymene luderitziana</i>	Detritivore	Papillose proboscis	Burrow	Solitary	40mm	Long and broad
<i>Euclymene lumbricoides</i>	Detritivore	Papillose proboscis	Burrow	Solitary	150mm	Long and broad
<i>Euclymene oerstedii</i>	Detritivore	Papillose proboscis	Burrow	Solitary	100mm	Slender
<i>Euclymene sp</i>	Detritivore	Papillose proboscis	Burrow	Solitary	40mm-150mm	Slender
<i>Eunice antennata</i>	Carnivore/predator	Mandibles and maxillae/pharynx	Burrow	Solitary	50mm-100mm	Round top, flattened bottom
<i>Eunice indica</i>	Carnivore/predator	Mandibles and maxillae/pharynx	Burrow	Solitary	50mm	Cylindrical top, flattened bottom
<i>Eunice sp</i>	Carnivore/predator	Mandibles and maxillae/pharynx	Burrow	Solitary	50mm-100mm	Cylindrical top, flattened bottom
<i>Eunice vittata</i>	Carnivore/predator	Mandibles and maxillae/pharynx	Burrow	Solitary	50mm	Cylindrical top, flattened bottom
<i>Eurythoe complanata</i>	Carnivore	Mandibles and maxillae/jaws	Burrow/sessile	Solitary	140mm	Elongate and flattened
<i>Eurythoe sp.</i>	Carnivore	Mandibles and maxillae/jaws	Burrow/sessile	Solitary	140mm-220mm	Elongate and flattened
<i>Glycera convoluta</i>	Carnivore/detritivore	Pharynges/papillose proboscis	Burrow	Solitary	120mm	Elongate, rounded and tapered at ends
<i>Glycera longipinnis</i>	Carnivore/detritivore	Pharynges/papillose proboscis	Burrow	Solitary	100mm	Elongate, rounded and tapered at ends
<i>Glycera sp.</i>	Carnivore/detritivore	Pharynges/papillose	Burrow	Solitary	20mm-100mm	Elongate, rounded and

		proboscis				tapered at ends
<i>Glycera unicornis</i>	Carnivore/detritivore	Pharynges/papillose proboscis	Burrow	Solitary	350mm	Elongate, rounded and tapered at ends
<i>Glycinde sp</i>	Carnivore	Papillose proboscis/macrognath	Burrow	Solitary	30mm-40mm	Elongate and tapered at both ends
<i>Goniada sp</i>	Carnivore	Pharynges	Burrow	Solitary	50mm-150mm	Elongate and tapered at both ends
<i>Gravirella sp.</i>	Carnivore/detritivore	Papillose proboscis	Burrow	Solitary	80mm	Slender and elongate
<i>Harmothoe corralophilla</i>	Carnivore	Pharynx	Burrow/sessile	Commensal/solitary	15mm	Broad
<i>Harmothoe goreensis</i>	Carnivore	Pharynx	Burrow/sessile	Commensal/solitary	10mm	Small, short and flattened
<i>Harmothoe sp</i>	Carnivore	Pharynx	Burrow/sessile	Commensal/solitary	10mm-35mm	Short and flattened
<i>Hyalinoecia sp</i>	Carnivore/omnivore	Mandibles and maxillae/jaws	Crawl	Solitary	60mm-120mm	Quill-like tube
<i>Hyalinoecia tubicola</i>	Carnivore/omnivore	Mandibles and maxillae/jaws	Crawl	Solitary	60mm-120mm	Quill-like tube
<i>Isolda pulchella</i>	Deposit feeder	Tentacles	Tube-dwelling	Solitary	45mm	Tapered
<i>Isolda whydahaensis</i>	Deposit feeder	Tentacles	Tube-dwelling	Solitary	5mm	Tapered
<i>Jasmineira elegans</i>	Filter feeder	Radioles/palps	Creep/tube-dwelling	Solitary	20mm	Small and elongated
<i>Laonice cirrata</i>	Deposit feeder	feeding palps	Sessile	Solitary	100mm	Vermiform and flattened
<i>Lumbriclymene sp.</i>	Detritivore	Papillose proboscis	Burrow	Solitary	120mm	Long, cylindrical and slender
<i>Lumbrineris gracilis</i>	Carnivore	Mandibles and maxillae/jaws	Burrow	Commensal	20mm	Slender and elongate
<i>Lumbrineris aberrans</i>	Carnivore	Mandibles and maxillae/jaws	Burrow	Commensal	10mm	Slender and elongate
<i>Lumbrineris cf. cavifrons</i>	Carnivore	Mandibles and maxillae/jaws	Burrow	Commensal	25mm-65mm	Slender and elongate
<i>Lumbrineris coccinea</i>	Carnivore	Mandibles and maxillae/jaws	Burrow	Commensal	40mm	Slender and elongate
<i>Lumbrineris hartimani</i>	Carnivore	Mandibles and maxillae/jaws	Burrow	Commensal	100mm	Slender and elongate
<i>Lumbrineris cf. magalhaensis</i>	Carnivore	Mandibles and maxillae/jaws	Burrow	Commensal	100mm	Slender and elongate
<i>Lumbrineris heteropoda</i>	Carnivore	Mandibles and maxillae/jaws	Burrow	Commensal	120mm	Slender and elongate
<i>Lumbrineris latreilli</i>	Carnivore	Mandibles and maxillae/jaws	Burrow	Commensal	20mm	Slender and elongate

<i>Lumbrinereis paradoxa</i>	Carnivore	Mandibles and maxillae/jaws	Burrow	Commensal	20mm	Slender and elongate
<i>Magelona cincta</i>	Deposit feeder	Feeding palaps/proboscis	Burrow	Solitary	30mm	Slender
<i>Magelona papillicornis</i>	Deposit feeder	Feeding palaps/proboscis	Burrow	Solitary	170mm	Slender
<i>Magelona capensis</i>	Deposit feeder	Feeding palaps/proboscis	Burrow	Solitary	35mm	Slender
<i>Malacoceros indica</i>	Deposit feeder	Tentacles/feeding palps	Burrow	Solitary	60mm	Vermiform and flattened
Malacoceros sp	Deposit feeder	Tentacles/feeding palps	Burrow	Solitary	60mm	Vermiform and flattened
<i>Magelona sp</i>	Deposit feeder	Feeding palps	Burrow	Solitary	20mm-170mm	Slender
<i>Maldane decorata</i>	Detritivore	Pharynx	Burrow	Solitary	100mm	Sausage-like mud tube
<i>Maldane sarsi</i>	Detritivore	Pharynx	Burrow	Solitary	100mm	Sausage-like mud tube
Maldanella sp	Detritivore	Pharynx	Burrow	Solitary	45mm-70mm	Cylindrical and elongate
<i>Marphysa adenensis</i>	Omnivore/detritivore	Mandibles and maxillae/pharynx	Burrow	Solitary	70mm	Slender and rounded
<i>Marphysa cf. mossambica</i>	Omnivore/detritivore	Mandibles and maxillae/pharynx	Burrow	Solitary	350mm	Slender and flattened
<i>Marphysa sanguinea</i>	Omnivore/detritivore	Mandibles and maxillae/pharynx	Burrow	Solitary	250mm	Long and oval
<i>Marphysa sp.</i>	Omnivore/detritivore	Mandibles and maxillae/pharynx	Burrow	Solitary	30mm-250mm	Slender, rounded /flattened
<i>Magelomma vesiculosum</i>	Filter feeder	Tentacular crown	Sessile	Solitary	100mm	Slightly tapered
<i>Megalomma sp</i>	Filter feeder	Tentacular crown	Sessile	Solitary	20mm-100mm	Slightly tapered
<i>Mesochaetopterus minutes</i>	Detritivore	Grooved palps	Burrow	Solitary	15mm	Elongate
<i>Naineris laevigata</i>	Detritivore/carnivore	Proboscis	Burrow	Solitary	40mm	Vermiform and flattened
<i>Nematonereis unicornis</i>	Detritivore/carnivore	Mandibles and maxillae	Burrow	Solitary	150mm-200mm	Slender
<i>Nephtys capensis</i>	Carnivore	Pharynges/papillose proboscis	Burrow	Solitary	60mm	Elongate and depressed
<i>Nephtys (aglaophamus) dibranchis</i>	Carnivore	Pharynges/papillose proboscis	Burrow	Solitary	25mm	Elongate and depressed
<i>Nephtys (aglaophamus) lyrochaeta</i>	Carnivore	Pharynges/papillose proboscis	Burrow	Solitary	30mm	Elongate and depressed
<i>Nephtys hombergi</i>	Carnivore	Pharynges/papillose proboscis	Burrow	Solitary	200mm	Elongate and depressed
<i>Nephtys macrousa</i>	Carnivore	Pharynges/papillose	Burrow	Solitary	150mm	Elongate and depressed

		proboscis				
<i>Nephtys sp.</i>	Carnivore	Pharynges/papillose proboscis	Burrow	Solitary	6.5mm-200mm	Elongate and depressed
<i>Nephtys sphaerocirrata</i>	Carnivore	Pharynges/papillose proboscis	Burrow	Solitary	25mm	Elongate and depressed
<i>Neries sp.</i>	Omnivore/filter feeder/deposit feeder	Papillose proboscis	Burrow/creep	Solitary/commensal	15mm-120mm	Elongate
<i>Neridines gilchristi</i>	Deposit feeder	Tentacles/palps	Burrow	Solitary	25mm	Vermiform and flattened
<i>Nicolea sp.</i>	Deposit feeder	Buccal tentacles	Sessile	Solitary	50mm-100mm	Elongate and tapered
<i>Nicomache sp.</i>	Deposit feeder	Jaws/keel	Burrow/sessile	Solitary	160mm-240mm	Cylindrical
<i>Notomastus aberrans</i>	Deposit feeder	Jaws	Burrow	Solitary	60mm	Elongate and round
<i>Notomastus fauvelii</i>	Deposit feeder	Jaws	Burrow	Solitary	90mm	Elongate and round
<i>Notomastus latriceus</i>	Deposit feeder	Jaws	Burrow	Solitary	300mm	Elongate and round
<i>Notomastus sp.</i>	Deposit feeder	Jaws	Burrow	Solitary	60mm-300mm	Elongate and round
<i>Onuphis (Nothria) conchylega</i>	Omnivore	Jaws	Sessile	Solitary	40mm-150mm	Elongate and vermiform
<i>Onuphis eremita</i>	Omnivore	Jaws	Sessile	Solitary	80mm-120mm	Elongate and vermiform
<i>Onuphis geophiliformis</i>	Omnivore	Jaws	Sessile	Solitary	30mm	Elongate and vermiform
<i>Onuphis holobranchiata</i>	Omnivore	Jaws	Sessile	Solitary	60mm	depressed
<i>Onuphis sp.</i>	Omnivore	Jaws	Sessile	Solitary	40mm-350mm	Elongate and vermiform
<i>Ophelina sp.</i>	Deposit feeder	Proboscis	Burrow	Solitary	50mm	Vermiform
<i>Ophiodromus cf. berrisfordi</i>	Carnivore	Proboscis	Burrow	Solitary	28mm	Flattened and tapered
<i>Ophiodromus sp.</i>	Carnivore	Proboscis	Burrow	Solitary	8mm-28mm	Flattened and tapered
<i>Orbinia curvieri</i>	Deposit feeder	Pharynges	Burrow	Solitary	300mm	Vermiform
<i>Oriopsis neglecta</i>	Suspension feeder	Branchial crown/radioles/palps	Creep	Solitary	3mm-4mm	Fairly stout
<i>Paralacydonia paradoxa</i>	Omnivore/carnivore	Pharynx/papillose	Burrow/swim	Solitary	20mm-30mm	Elongate and rectangular
<i>Paraonides sp.</i>	Deposit feeder/surface feeder	Pharynges	Burrow	Solitary	10mm-20mm	Thread-like
<i>Paraonides lyra capensis</i>	Deposit feeder/surface feeder	Pharynges	Burrow	Solitary	10mm	Thread-like
<i>Pareulepis sp.</i>	Deposit feeder/carnivore	Jaws	Burrow	Solitary/commensal	35mm	Oblong
<i>Paronuphis antarctica</i>	Carnivore	Mandibles and maxillae/pharynx	Burrow	Solitary	20mm-30mm	Vermiform and elongate
<i>Paronuphis sp.</i>	Carnivore	Mandibles and	Burrow	Solitary	20mm-30mm	Vermiform and elongate

		maxillae/pharynx				
<i>Pectinaria koreni</i> cirrata	Deposit feeder	Tentacles	Burrow/sessile	Solitary	10mm	Tapered
<i>Pherusa</i> sp	Detritivore	Grooved palps/papillose	Burrow	Solitary	30mm	Cylindrical and narrowed posteriorly
<i>Pholoe minuta</i>	Carnivore	Jaws	Creep/crawl	Solitary	10mm	Small and oblong
<i>Phyllocomus</i> sp	Deposit feeder	Buccal tentacles	Burrow	Solitary	50mm	Tapered
<i>Phyllodoce (anatides) madarensis</i>	Carnivore	Pharynx	Burrow	Solitary	100mm	Long and tapered
<i>Phyllodoce malmgreni</i>	Carnivore	Pharynx	Burrow	Solitary	70mm	Long and slender
<i>Phyllodoce scharmadai</i>	Carnivore	Pharynx	Burrow	Solitary	30mm	Long and slender
<i>Phyllodoce</i> sp	Carnivore	Pharynx	Burrow	Solitary	25mm	Long and slender
<i>Phylo foetida linguistica</i>	Deposit feeder	Proboscis	Burrow	Solitary	50mm	Vermiform and flattened
<i>Pistia costata</i>	Filter feeder	Tentacles	Peristaltic crawling	Solitary	25mm	Tapered
<i>Pista cristata</i>	Filter feeder	Tentacles	Peristaltic crawling	Solitary	60mm	Tapered
<i>Pista</i> sp	Filter feeder	Tentacles	Peristaltic crawling	Solitary	10mm	Tapered
<i>Piromis</i> sp	Detritivore	Jaws	Burrow/creep	Solitary	90mm	Tapered posteriorly
<i>Polycirrus</i> sp	Deposit feeder	Buccal tentacles	Burrow	Solitary	15mm	Evenly tapered
<i>Potamilla linguicollris</i>	Filter feeder	Branchial crown	Burrow	Solitary	60mm	Slender
<i>Polyopphthalamus</i> sp	Deposit feeders	Proboscis	Burrow	Solitary	25mm	Short and slender
<i>Polyodontes melanontus</i>	Carnivore/omnivore	Pharynx	Burrow	Solitary	300mm	Stout anterior and flattened posterior
<i>Praxillela</i> cf. affinis	Deposit feeder/detritivore	Proboscis	Burrow	Solitary	100mm	Cylindrical
<i>Praxillela</i> sp	Deposit feeder/detritivore	Proboscis	Burrow	Solitary	100mm	Cylindrical
<i>Prionospio cirrifera</i>	Deposit feeder	Proboscis	Burrow	Solitary	30mm	Vermiform and flattened
<i>Prionospio cirrobranchiata</i>	Deposit feeder	Proboscis	Burrow	Solitary	15mm	Small and thread-like
<i>Prionospio elhersii</i>	Deposit feeder	Proboscis	Burrow	Solitary	20mm	Vermiform and flattened
<i>Prionospio malmgreni</i>	Deposit feeder	Proboscis	Burrow	Solitary	25mm	Thread-like
<i>Prionospio pinnata</i>	Deposit feeder	Proboscis	Burrow	Solitary	60mm	Vermiform and flattened
<i>Prionospio saldanha</i>	Deposit feeder	Proboscis	Burrow	Solitary	25mm	Thread-like
<i>Prionospio sexoculata</i>	Deposit feeder	Proboscis	Burrow	Solitary	10mm-20mm	Vermiform and flattened
<i>Prionospio</i> sp	Deposit feeder	Proboscis	Burrow	Solitary	10mm-60mm	Vermiform and flattened
<i>Sabellides octocirrata</i>	Filter feeder	Tentacles	Burrow	Solitary	10mm	Tapered
<i>Scalistosus fragilis</i>	Deposit feeder	Proboscis/jaws	Burrow	Solitary	15mm	Short and depressed
<i>Schroederella</i> sp.	Deposit feeder	Proboscis	Burrow	Solitary	3mm-4mm	Vermiform, flattened and minute

<i>Scolelepis squamata</i>	Deposit feeder	palps	Burrow	Solitary	80mm	Vermiform and flattened
<i>Scolaricia dubia</i>	Detritivore	Proboscis	Burrow	Solitary	35mm	Vermiform and flattened
<i>Scoloplos madagascariensis</i>	Carnivore	Tentacles	Burrow	Solitary	120mm	Vermiform and flattened
<i>Scoloplos</i> sp.	Carnivore	Tentacles	Burrow	Solitary		Vermiform and flattened
<i>Scyphoproctus</i> sp.	Deposit feeder	Probocsis/papillose	Burrow	Solitary	23mm-30mm	Slender and cylindrical
<i>Sigalion</i> spp.	Carnivore	Jaws	Burrow	Solitary	30mm-300mm	Depressed and square in section
<i>Spiohanes</i> sp.	Deposit feeder	Palps	Burrow	Solitary	25mm-60mm	Vermiform and flattened
<i>Spio filicornis</i>	Deposit feeder	Palps	Burrow	Solitary	30mm	Vermiform and flattened
<i>Spiohanes bombyx</i>	Deposit feeder	Palps	Burrow	Solitary	60mm	Vermiform and flattened
<i>Spio multiculata</i>	Deposit feeder	Palps	Burrow	Solitary		Vermiform and flattened
<i>Spio</i> sp.	Deposit feeder	Palps	Burrow	Solitary		Vermiform and flattened
<i>Sternapsis scutata</i>	Deposit feeder/detritivore	Papillose	Burrow	Solitary	20mm-30mm	Dumb-bell shaped and swollen
<i>Sthenelais limicola</i>	Deposit feeder/detritivore	Papillose	Burrow	Solitary	80mm	Elongate and flattened
<i>Sthenolepis tetragona</i>	Deposit feeder/detritivore	Papillose	Burrow	Solitary	80mm	Elongate and flattened
<i>Sthenolepis</i> sp.	Deposit feeder/detritivore	Papillose	Burrow	Solitary	50mm	Elongate and flattened
<i>Strenaspsis persica</i>	Deposit feeder/detritivore	Papillose	Burrow	Solitary	20mm-30mm	Dumb-bell shaped and swollen
<i>Syllis benguellana</i>	Carnivore	Pharyngeal tooth/proventricle	Burrow	Solitary	9mm	Thread-like
<i>Syllis (syllis) gracilis</i>	Carnivore	Pharyngeal tooth/proventricle	Burrow	Solitary	35mm	Slender
<i>Syllis hyalina</i>	Carnivore	Pharyngeal tooth/proventricle	Burrow	Solitary	35mm	Slender
<i>Syllis</i> sp	Carnivore	Pharyngeal tooth/proventricle	Burrow	Solitary	8mm-40mm	Thread-like/slender
<i>Syllis spongida</i>	Carnivore	Pharyngeal tooth/proventricle	Burrow	Solitary	25mm	Thread-like/slender
<i>Terebella pterochaeta</i>	Deposit feeder	Tentacles/ mouth	Burrow	Solitary/colony	100mm	Slender and evenly tapered
<i>Terebellids</i> sp.	Deposit feeder	Tentacles	Burrow	Solitary/colony	70mm	Uniformly tapered
<i>Terebellides stroemi</i>	Deposit feeder	Tentacles	Burrow	Solitary/colony	70mm	Uniformly tapered
<i>Thalenessa oculata</i>	Detritivore	Jaws	Burrow	Solitary	200mm	Elongate and flattened
<i>Tharynx</i>	Deposit feeder	Pharynx/feeding palps	Burrow	Solitary	35mm	Thread-like

<i>dorsobranchialis</i>						
<i>Tharyx filibranchia</i>	Deposit feeder	Pharynx/feeding palps	Burrow	Solitary	20mm	Cylindrical and elongate
<i>Tharyx sp</i>	Deposit feeder	Pharynx/feeding palps	Burrow	Solitary	20mm-100mm	Cylindrical and elongate
CRUSTACEA						
<i>Alpheus sp.</i>	Deposit feeder/detritivore	Rostrum	Burrow/swim	Solitary	50mm	Laterally-compressed
<i>Ampelisca sp.</i>	Detritivore	Mandibular palps	Swim	Solitary	5mm	Laterally-flattened/hunchbacked
<i>Ampithoe sp.</i>	Detritivore/scavengers	Rostrum/gills	Crawl/Burrow	Solitary	15mm	Laterally-flattened/hunchbacked
<i>Anthura sp.</i>	Carnivore/predator	Mandibular palps/maxillipeds	Crawl/Burrow/swim	Solitary	8mm-20mm	Elongate, worm-like body/dorso-ventrally compressed
<i>Aorid sp</i>	Filter feeder	Mandibular palps	Crawl/Burrow/swim	Solitary	2.5mm-6mm	Laterally-flattened/hunchbacked
<i>Apeudes latreille</i>	Filter feeder/detritivore	Mandibular palps/maxillipeds	Creep	Solitary	2mm-12mm	Elongate, cylindrical/dorso-ventrally flattened
<i>Apeudes sp.</i>	Filter feeder/detritivore	Mandibular palps/maxillipeds	Creep	Solitary	2mm-6mm	Elongate, cylindrical/dorso-ventrally flattened
<i>Callianassa sp. A</i>	Detritivore	Maxillipeds	Burrow	Solitary	40mm-50mm	Laterally-compressed
<i>Caridea sp.</i>	Scavenger/detritivore	Rostrum/teeth	Swim	Solitary	12mm-70mm	Laterally-compressed
<i>Cirolana sp.</i>	Omnivore	Mandibles, maxillae and maxillipeds	Runs/Burrow	Solitary	10mm-15mm	Dorso-ventrally compressed
<i>Eurydice</i>	Omnivore	Mandibles, maxillae and maxillipeds	Runs/Burrow	Solitary	10mm	Dorso-ventrally compressed
<i>Excirolana sp.</i>	Scavenger	Mandibular palps/maxillipedes	Swim/Burrow	Solitary	10mm	Dorso-ventrally compressed
<i>Galathea sp..</i>	Omnivore	Rostrum/teeth	Burrow/creep	Solitary	7mm	Lobster-like, hard body with fan shaped tail
<i>Hermit crab</i>	Detritivore/ filter feeding	Claws/third maxillipedes	Crawl	Solitary	20mm-40mm	Occupys hard spiralled gastropod shell
<i>Hyalé pontica</i>	Herbivore/omnivore	Mandibular palps/ maxillipeds	Swim/Burrow	Solitary	10mm	Laterally flattened
<i>Iphinoe brevipes</i>	Carnivore	Mandibles and maxillae	Burrow/swim	Solitary	10mm-20mm	Oval, flattened and compact
<i>Iphinoe sp</i>	Carnivore	Mandibles and maxillae	Burrow/swim	Solitary	10mm-20mm	Oval, flattened and compact
<i>Ischyrocerus sp</i>	Herbivore/omnivore	Mandibular palps/maxillipeds	Burrow/crawl	Solitary	1.5mm-6mm	Laterally flattened
<i>Leucothoe sp</i>	Filter feeder	Pumped through	Burrow/swim	Commensal	10mm	Laterally flattened

		sponge				
<i>Ligia olfersi</i>	Scavengers	Mandibles,maxillae and maxillipeds	Runs/Burrow	Solitary	15mm-25mm	Broad, flattened and smooth
<i>Liljeborgia</i> sp.	Carnivore	Mandibular palp/maxillipeds	Burrow	Commensal/solitary	1.5mm-5mm	Latterally flattened
<i>Mysid</i>	Omnivore/herbivore	Mandibles, maxillae and maxillipeds	Swim/Burrow	Solitary	40mm-50mm	Latterally compressed
<i>Palinurus</i> sp	Omnivore	Rostrum/teeth	Burrow	Solitary	250mm	Elongate, semi-circular with fan-like telson
<i>Penaeid shrimp</i>	Scavenger/detritivore	Rostrum/teeth	Swim	Solitary	60mm	Cylindrical and latterally compressed
<i>Perioculodes</i> sp.	Omnivore	Rostrum/teeth	Burrow/swim	Solitary	2mm-5mm	Larrerally flattened
<i>Portumnus</i> sp.	Carnivores /detritivore	Maxilliped, mandibular, cheliped	Swim	Solitary	33-170mm width, 23-76mm length	Dorso-ventrally flattened
<i>Tanaids</i>	Filter feeder	Mandibles, maxillipeds and chela	Burrow	Solitary	2mm-6mm	Elongate body, cylindrical/dorsoventrally flattened
<i>Uca tangerii</i>	Detritivore	buccal frame,chelae	Burrow	Solitary	14-30mm width, 8-17mm length	Dorso-ventrally flattened
<i>Upogebia</i> sp.	Filter feeder	Maxillipeds/mandibular palps	Burrow	Solitary	40mm	Elongate,semi-circular withfan-like telson
<i>Urothoe</i> sp.	Detritivore	Maxillipeds/mandibles	Burrow	Solitary	2mm-5mm	Latterally flattened
Xanthid crab	Detritivore	Buccal frame, chelae	Burrow	Solitary/commensal	15mm-25mm	Dorso-ventrally flattened with broad carapace
MOLLUSCS						
<i>Arca subglobosa</i>	Filter feeder	Siphon/gills	Burrow/sessile	Solitary	12mm-25mm	Almost square,rounded anterior, pointed posterior
<i>Asterina</i> sp.	Carnivore	Tube feet/ stomach	Burrow/sessile	Solitary	20mm	Flattened body with short rounded arms
<i>Cardium</i> sp	Filter feeder	Siphon/gills	Burrow/sessile	Solitary	15-100mm	Circular
<i>Corbula</i> sp	Filter feeder	Siphon/gills	Burrow	Solitary	200mm	Oval to triangular
<i>Chiton canariensis</i>	Omnivore	Radula	Creep/sessile	Colony	20mm-35mm	Oval and flattened
<i>Diplodonta</i> sp.	Filter feeder	Siphon/gills	Burrow/ creep	Solitary	15mm-25mm	Circular
<i>Donax oweni</i>	Filter feeder	Siphon/gills	Burrow/sessile	Colony	10mm-20mm	Triangular
<i>Dosinia</i> sp.	Filter feeder	Siphon/gills	Burrow	Colony	15mm-30mm	Circular /triangular
<i>Glycemeris scripta</i>	Filter feeder	Siphon/gills	Burrow	Solitary	50mm	Slightly rounded

<i>Fusus</i> sp.	Herbivore	Radula	Burrow /sessile	Solitary	70mm	Slender shell
<i>Mactra</i> sp.	Filter feeder	Siphon/gills	Burrow	Colony	30-55mm	Triangular
<i>Dentalium coarti</i>	Omnivore	Tentacles/captacula	Burrow/creep	Solitary	40mm	Tusk-shaped
<i>Dentalium maltzani</i>	Omnivore	Tentacles/captacula	Burrow/creep	Solitary	40mm	Tusk-shaped
<i>Mactra stultorum</i>	Filter feeder	Siphon/gills	Burrow	Colony	30-50mm	Triangular
<i>Pitaria cf. tumens</i>	Filter feeder	Siphon/gills	Burrow/sessile	Solitary	20mm-50mm	Triangular and rounded
<i>Dentalium</i> spp.	Filter feeder	Tentacles/feeding chamber	Burrow/creep	Solitary	32mm	Tusk-shaped
<i>Tellina hyalina</i>	Filter feeder	Siphon/gills	Burrow/sessile	Colony	25-40mm	Triangular and rounded
<i>Tellina</i> sp.	Filter feeder	Siphon/gills	Burrow/sessile	Colony	25-40mm	Triangular and rounded
<i>Tivela</i> sp.	Filter feeder	Siphon/gills	Burrow	Solitary	15-30mm	Triangular
ECHINODERMA						
<i>Amphioplus archeri</i>	Suspension feeder/ deposit feeder	Tube feet	Crawl	Solitary	10mm	Flat,circular body with five thin arms
<i>Amphioplus aurensis</i>	Suspension feeder/ deposit feeder	Tube feet	Crawl	Solitary	10mm	Flat,circular body with five thin arms
<i>Amphiura</i> sp	Suspension feeder/ deposit feeder	Tube feet	Crawl	Solitary	25mm	Flat,circular body with five thin arms
<i>Sand dollar</i>	Suspension feeder	Aristotle's lantern	Burrow	Solitary	38mm-40mm	Oval/ circular and flattened
<i>Ophiura africana</i>	Deposit feeder	Aristotle's lantern	Burrow	Solitary	25mm	Star-like and flattened
<i>Ophiotrix</i> sp.	Detritivore	Aristotle's lantern/tube feet	Crawl	Solitary	50mm	Flat,circular body with five thin arms
<i>Diadema</i> sp.	Detritivore/herbivore	Aristotle's lantern/tube feet	Burrow	Solitary	70mm	Oval, heart-shaped, circular and flattened
OTHERS						
<i>Cavolinia</i> sp.	Herbivore/detritivore	Radula	Swim	Solitary	3mm	Bubble-like shell with three stubby horns
<i>Echiura</i>	Deposit feeder/filter feeder	Proboscis	Burrow	Solitary	30mm-40mm	Sausage-shaped trunk with flaccid proboscis
Hermit crab	Omnivore/detritivore	Mandibles,maxillae and chela	Creep/burrow	Solitary		Occupys spiralled gastropod shell
<i>Hirudinea</i> sp.	Carnivore/blood sucking	Proboscis/suckers	Wiggle	Solitary	12mm-30mm	Dorso-ventrally flattened
<i>Hydrozoa</i>	Carnivore	Gastrozoid	Sessile	Solitary/colony	10mm-200mm	Tree-like or feather-like
<i>Nemertean worm</i>	Carnivore/scavenger	Proboscis/mouth	Glide/crawl/swim	Solitary	20mm-300mm	Thin and elongate
<i>Sea cucumber</i>	Scavenger/commensal	Tentacles	Crawl	Solitary	30mm-240mm	Elongate or sausage-saped
<i>Sipuncula</i> sp.	Suspension feeder/ deposit feeder	Introvert/tentacles	Burrow	Solitary	2mm-720mm	Cylindrical/sac-like body

Hydroid	Carnivore	Tentacles	Sessile	Colony	10mm-200mm	Tree-like or feather-like
Oligochate sp.	Detritivore/omnivore	Mouth	Burrow	Solitary	10mm	Long, cylindrical, tapered at ends
Ophiroid sp.	Detritivore/herbivore	Tube feet/toothed jaw	Crawl	Solitary	45mm-100mm	Flat, circular body with five thin arms
Ostracod	Herbivore	Mandibles, maxillae	Burrow	Solitary	1mm-4mm	Short head and oval body
<i>Pagurus</i> sp.	Filter feeder	Mandibles, maxillae and chela	Burrow	Solitary	8mm	Occupys spiralled gastropod shell
<i>Sipunculid</i> sp.	Detritivore	Tentacles	Burrow	Solitary	10mm-50mm	Short bulbous body and elongate tubular introvert
<i>Virgularia</i> sp.	Carnivore	Tentacles, pharynx and siphonoglyph	Sessile	Colony	70mm	Feather-shaped, fan-like body

FEEDING STRUCTURE	GB-01	GB-02	GB-03	GB-04	GU-01	GU-02	GU-03	GU-04	SL-01	SL-02	SL-03	SL-04	LI-01	LI-02	LI-03	LI-04
Tentacles	0	6	2	0	4	2	2	1	0	0	3	2	3	0	2	0
Buccal tentacles	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Maxillipeds	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proboscis/Papillose	0	0	0	0	1	0	0	0	0	0	1	1	0	1	0	0
Jaws	0	0	0	0	1	2	0	2	0	1	2	1	0	1	0	2
Proboscis	2	4	2	2	7	9	6	6	0	2	4	0	1	1	0	1
Papillose	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Feeding palps/Tentacular cirri	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0
Mandibles/Maxillae/Jaws	0	3	0	0	4	0	3	4	2	0	6	5	3	3	1	4
Pharynx	1	2	0	0	1	1	2	2	0	1	1	0	0	0	1	0
Pharynx/ Feeding palps	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Pharynges/Papillose	0	2	0	0	3	1	1	2	1	0	0	2	1	1	1	2
Papillose Proboscis/Macrogath	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Pharynges	0	0	0	0	1	0	0	1	0	0	0	0	1	0	0	1
Radioles/palps	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Feeding palps	0	0	0	0	0	0	0	0	0	0	1	0	0	1	0	0
Feeding palps/Branchial crown	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Feeding palps/Proboscis	0	1	0	0	0	0	0	0	0	0	2	0	0	1	0	0
Tentacles/Feeding palps	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Tentacular crown	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Grooved Palps	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Mandibles and Maxillae	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0
Tentacles/palps	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Jaws/Keel	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0
Branchial crown/Radioles/palps	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Pharynx/Papillose	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0
Pharynges/Papillose	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Grooved palps/Papillose	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0
Branchial Crown	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proboscis/jaws	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0

Mandibles/maxillipedes	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Tentacles/Pharynx/Siphonoglyph	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
RELATIVE ADULT MOBILITY	GB-01	GB-02	GB-03	GB-04	GU-01	GU-02	GU-03	GU-04	SL-01	SL-02	SL-03	SL-04	LI-01	LI-02	LI-03	LI-04
Peristaltic crawling	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Burrowing/Sessile	1	2	1	0	1	1	1	2	1	0	1	2	0	0	0	0
Burrowing	5	19	7	5	22	17	16	23	4	6	20	10	7	8	7	8
Creeping	0	0	0	0	0	1	0	1	0	0	0	0	0	0	0	0
Crawling	0	1	0	0	2	0	1	0	1	1	3	0	2	1	2	2
Sessile	0	0	0	0	1	3	0	1	0	0	2	0	0	1	0	2
Sessile/Creep	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Burrow/Creep	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Tube-dwelling	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Creep/Tube-dwelling	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Burrow/Swim	0	1	3	0	2	2	2	2	2	0	0	0	1	2	0	0
Creep/Crawl	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Swim	0	1	1	1	1	1	1	3	1	0	1	1	1	1	1	1
Crawl/Burrow	0	0	0	0	0	2	0	2	0	0	0	0	0	0	0	0
Crawl/Burrow/Swim	0	0	0	0	0	1	1	1	0	0	0	0	0	0	0	0
Run/Burrow	0	0	0	0	0	1	1	0	0	0	0	0	0	0	0	0
Wiggle	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Glide/Crawl/Swim	0	1	0	0	0	1	0	0	0	0	0	0	0	0	0	0
SOCIABILITY	GB-01	GB-02	GB-03	GB-04	GU-01	GU-02	GU-03	GU-04	SL-01	SL-02	SL-03	SL-04	LI-01	LI-02	LI-03	LI-04
Solitary	5	24	10	6	27	28	22	28	6	7	25	11	9	12	8	11
Commensal	0	1	1	0	2	0	0	3	2	0	1	2	1	2	0	2
Commensal/Solitary	0	1	0	0	0	1	1	2	0	0	0	0	0	0	0	0
Solitary/Colony	0	0	0	0	0	1	0	2	0	0	1	0	1	0	1	0
Colony	1	0	1	0	0	0	0	0	1	0	0	0	0	0	1	0
ADULT BODY SIZE	GB-01	GB-02	GB-03	GB-04	GU-01	GU-02	GU-03	GU-04	SL-01	SL-02	SL-03	SL-04	LI-01	LI-02	LI-03	LI-04
0.5-20mm	1	7	9	4	7	12	6	11	6	4	7	2	3	3	4	5
20.5-40mm	4	4	1	0	3	4	7	6	1	1	4	2	2	6	2	1

Elongate/ Sausage-saped	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0
Cylindrical/Sac-like	0	0	0	0	0	1	0	0	1	0	0	1	0	0	0	1	1
Short Head & Oval Body	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
FEEDING HABIT	CD-01	CD-02	CD-03	CD-04	GH-01	GH-02	GH-03	GH-04	TG-01	TG-02	TG-03	TG-04	BN-01	BN-02	BN-03	BN-04	
Herbivore	0	0	0	0	0	0	0	0	1	1	2	0	1	1	1	2	
Carnivore	5	3	4	2	5	1	6	3	10	12	13	11	11	16	12	12	
Omnivore	0	0	0	0	2	1	0	0	4	0	2	3	3	4	1	1	
Filter Feeding	0	0	0	0	6	0	4	1	3	2	4	2	1	6	1	6	
Deposit Feeding	3	3	6	4	7	9	5	5	14	13	31	16	7	13	4	13	
Detritivore	0	0	0	0	2	1	0	1	6	3	6	5	3	7	6	5	
Scavenging	0	0	0	0	2	1	0	1	0	0	0	0	0	0	1	0	
Suspension Feeding	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	
Carnivore/Omnivore	1	1	1	0	1	0	2	1	1	0	0	0	0	0	1	0	
Herbivore/Omnivore	0	0	1	0	0	0	1	0	2	1	1	2	0	1	1	0	
Carnivore/Detritivore	0	1	0	0	2	1	2	1	5	1	3	0	2	2	1	2	
Detritivore/Deposit Feeding	0	0	1	0	2	0	1	2	3	0	3	2	3	3	2	4	
Carnivore/Deposit Feeding	0	0	0	0	0	0	0	0	1	0	1	1	0	1	1	1	
Carnivore/Predator	0	1	0	0	1	0	1	1	1	2	2	1	1	0	1	2	
Omnivore/Detritivore	1	2	0	0	0	0	0	1	1	0	0	1	0	1	0	2	
Detritivore/Filter Feeding	0	1	0	0	2	0	1	0	1	0	1	0	1	0	0	0	
Detritivore/Scavenging	0	0	0	0	0	0	0	0	0	1	0	0	1	0	0	1	
Herbivore/Scavenging	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	
Herbivore/Detritivore	0	0	0	0	0	0	0	0	2	0	0	2	2	0	0	2	
Carnivore/Scavenging	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	
Scavenging/Commensal	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
Carnivore/Blood Sucking	0	0	0	0	0	0	0	1	0	0	0	1	0	0	0	0	
Deposit Feeding/Filter Feeding	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
Deposit Feeding/Surface Feeding	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	
Deposit Feeding/Suspension Feeding	0	1	2	1	3	1	0	2	0	0	0	0	0	0	0	0	
Autotroph/Carnivore/Filter Feeding	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
Omnivore/Filter Feeding/Deposit Feeding	0	0	0	0	0	0	0	0	1	1	0	0	0	1	0	0	
FEEDING STRUCTURE	CD-01	CD-02	CD-03	CD-04	GH-01	GH-02	GH-03	GH-04	TG-01	TG-02	TG-03	TG-04	BN-01	BN-02	BN-03	BN-04	
Tentacles	0	0	0	0	2	3	0	0	3	3	10	6	4	7	2	0	

Buccal tentacles	0	0	0	0	1	0	0	0	2	1	3	0	0	0	0	1
Maxillipeds	0	0	0	0	2	0	0	0	0	0	0	1	0	0	0	0
Proboscis/Papillose	0	0	1	0	0	1	0	0	4	2	3	3	0	6	3	1
Jaws	0	0	1	0	2	1	1	1	6	3	8	4	3	4	2	2
Proboscis	3	3	2	1	4	2	2	3	4	6	8	5	3	5	4	7
Papillose	0	0	0	0	0	0	0	0	3	0	2	0	1	2	1	3
Feeding palps/Tentacular cirri	0	0	0	0	0	0	0	0	0	0	1	2	0	0	0	0
Mandibles/Maxillae/Jaws	5	5	1	1	3	1	5	4	6	7	3	7	7	7	5	7
Pharynx	1	0	1	1	1	0	1	0	2	2	0	1	2	2	2	0
Pharynx/ Feeding palps	0	0	0	1	0	1	0	1	2	1	3	1	2	1	0	2
Pharynges/Papillose	1	2	1	0	1	1	0	1	3	0	2	3	0	6	2	4
Papillose Proboscis/Macrognath	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Pharynges	0	0	0	1	0	0	0	0	0	1	0	0	0	0	0	1
Radioles/palps	0	0	0	0	0	0	0	0	0	1	1	0	0	0	0	0
Feeding palps	0	0	0	0	2	0	0	1	0	1	0	0	0	1	0	0
Feeding palps/Branchial crown	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
Feeding palps/Proboscis	0	0	0	0	0	1	1	1	0	0	1	0	0	1	0	0
Tentacles/Feeding palps	0	0	0	0	0	0	0	0	0	0	1	1	0	0	0	0
Tentacular crown	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Grooved Palps	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0
Mandibles and Maxillae	0	0	1	0	0	0	1	0	2	1	1	0	0	1	1	2
Tentacles/palps	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0
Jaws/Keel	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Branchial crown/Radioles/palps	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0
Pharynx/Papillose	0	0	1	0	1	0	1	1	0	0	0	0	0	0	0	0
Pharynges/Papillose	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Grooved palps/Papillose	0	0	0	0	0	0	0	0	1	0	1	1	0	0	0	1
Branchial Crown	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0
Proboscis/jaws	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Pumped through sponge	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0
Palps	0	0	3	1	0	0	1	0	1	0	2	0	0	0	1	0
Pharyngeal tooth/proventricle	0	0	0	0	0	0	0	0	4	1	2	1	0	0	2	0
Tentacles/ mouth	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0
Rostrum	0	0	0	0	1	0	1	1	0	0	1	1	1	0	0	1
Mandibular palps	0	0	0	0	0	1	0	0	1	1	1	1	1	2	2	1

Rostrum/gills	0	0	0	0	0	0	0	0	0	1	0	0	1	0	0	1
Mandibular palps/Maxillipeds	0	0	0	0	3	1	3	1	3	0	1	1	2	0	2	1
Rostrum/Teeth	0	0	0	0	0	0	0	0	0	0	1	2	1	2	0	0
Mandibles/Maxillae/Maxillipeds	0	0	1	0	1	1	0	0	1	1	1	1	0	1	1	0
Mandibles	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Mandibles and Maxillipeds	0	0	0	0	0	0	0	0	1	0	0	0	0	0	1	0
Claws/Third maxillipedes	0	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0
Maxilliped, Mandibular, Cheliped	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0
Mandibles, Maxillipeds/ Chela	0	0	0	0	1	0	1	0	1	0	0	0	0	0	0	1
Buccal Frame/Chelae	0	0	0	0	1	0	0	0	0	0	0	0	0	0	1	0
Siphon/Gills	0	0	0	0	4	0	3	1	2	1	1	2	0	5	0	3
Tube feet/ Stomach	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0
Radula	0	0	0	0	0	0	0	0	0	0	2	0	2	0	0	2
Tentacles/Captacula	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Tentacles/Feeding chamber	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Tube feet	0	0	1	0	2	0	0	1	0	0	0	0	0	0	0	0
Aristotle's lantern	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Aristotle's lantern/Tube feet	0	0	0	0	0	0	0	0	1	0	0	1	0	0	0	0
Gastrozoid/Tentacles	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proboscis/suckers	0	0	0	0	1	0	0	1	0	0	0	1	0	0	0	0
Gastrozoid	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proboscis/mouth	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0
Introvert/tentacles	0	1	1	1	1	1	0	1	0	0	0	0	0	0	0	0
Ostia/Pinacocytes	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Beak/radula/tentacles	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0
Mouth	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	1
Tube feet/Toothed jaw	0	0	0	0	0	0	0	0	1	0	0	1	1	0	0	1
Mandibles/maxillipedes	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0
Tentacles/Pharynx/Siphonoglyph	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
RELATIVE ADULT MOBILITY	CD-01	CD-02	CD-03	CD-04	GH-01	GH-02	GH-03	GH-04	TG-01	TG-02	TG-03	TG-04	BN-01	BN-02	BN-03	BN-04
Peristaltic crawling	0	0	0	0	1	0	0	0	0	0	2	0	0	0	0	1
Burrowing/Sessile	0	0	1	2	4	2	3	1	1	2	5	5	3	4	1	4
Burrowing	9	11	9	5	20	7	13	12	40	24	45	30	21	38	26	34
Creeping	0	0	0	0	1	0	1	0	2	0	3	0	1	0	1	0

Crawling	1	1	1	0	3	1	1	1	1	1	2	2	1	1	0	2
Sessile	0	0	0	0	1	0	0	1	5	1	1	1	2	3	1	2
Sessile/Creep	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
Burrow/Creep	0	0	0	0	1	0	0	0	1	2	2	1	1	4	0	1
Tube-dwelling	0	0	0	0	0	1	0	0	2	2	2	2	1	2	0	2
Creep/Tube-dwelling	0	0	0	0	0	0	0	0	0	1	1	0	0	0	0	0
Burrow/Swim	0	1	3	0	3	1	5	3	1	2	2	3	0	1	2	1
Creep/Crawl	0	0	0	0	0	0	0	1	0	1	1	0	0	1	0	0
Swim	0	0	0	0	0	1	0	0	1	1	3	1	3	1	1	3
Crawl/Burrow	0	0	0	0	0	0	0	0	1	1	0	1	1	0	0	1
Crawl/Burrow/Swim	0	0	0	0	0	0	0	0	1	0	0	0	1	1	1	1
Run/Burrow	0	0	0	0	1	1	0	0	0	0	0	0	0	0	0	0
Wiggle	0	0	0	0	1	0	0	1	0	0	0	1	0	0	0	0
Glide/Crawl/Swim	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0
SOCIABILITY	CD-01	CD-02	CD-03	CD-04	GH-01	GH-02	GH-03	GH-04	TG-01	TG-02	TG-03	TG-04	BN-01	BN-02	BN-03	BN-04
Solitary	8	12	13	5	31	15	19	17	50	34	66	42	34	47	28	46
Commensal	2	1	0	1	1	0	1	2	2	3	2	3	2	4	3	3
Commensal/Solitary	0	0	2	1	2	0	0	0	1	2	0	1	0	2	2	0
Solitary/Colony	0	0	0	0	0	0	0	0	1	0	2	0	0	1	0	1
Colony	0	0	0	0	2	0	2	1	2	0	1	1	0	1	0	3
ADULT BODY SIZE	CD-01	CD-02	CD-03	CD-04	GH-01	GH-02	GH-03	GH-04	TG-01	TG-02	TG-03	TG-04	BN-01	BN-02	BN-03	BN-04
0.5-20mm	3	4	4	3	15	6	8	8	12	12	18	8	10	18	12	13
20.5-40mm	2	3	3	0	7	4	4	4	13	7	20	15	7	11	5	13
40.5-60mm	2	1	3	1	4	2	5	3	12	6	13	8	5	3	7	10
60.5-80mm	1	0	0	0	1	1	0	0	6	2	4	3	3	5	1	4
80.5-100mm	1	1	1	0	4	1	3	3	6	8	4	6	5	10	6	3
100.5-120mm	0	1	0	0	1	0	2	0	1	1	4	2	2	3	1	2
>120mm	1	3	2	3	4	1	1	2	6	1	7	4	4	6	1	8
ADULT BODY FORM	CD-01	CD-02	CD-03	CD-04	GH-01	GH-02	GH-03	GH-04	TG-01	TG-02	TG-03	TG-04	BN-01	BN-02	BN-03	BN-04
Vermiform and Flattened	2	2	4	1	2	1	1	3	2	4	7	3	2	5	5	4
Slender and Elongate	2	1	1	1	1	0	1	2	2	2	2	3	2	4	3	3
Slender	0	0	0	0	3	2	1	1	3	2	3	3	1	2	2	3
Trefoil-shaped	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0

oval	0	0	0	0	0	0	0	0	0	1	1	1	0	0	0	0
Cylindrical & Tapered Posterior	0	0	0	0	1	1	0	0	1	2	3	2	2	1	0	1
Elongate	0	0	0	0	0	0	0	0	1	1	1	0	0	1	1	0
Vermiform & Iridescent	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0
Vermiform and Tapering	0	0	0	0	2	1	2	0	0	0	2	0	0	0	0	0
Long and Round	0	0	0	0	0	0	0	0	1	1	1	0	0	0	0	1
Cylindrical	0	0	2	0	1	1	0	1	1	0	1	2	1	5	3	0
Thread-like	1	0	0	0	0	1	0	1	3	2	3	4	0	1	1	4
Depressed and Oval	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Broad	0	0	0	1	0	0	0	0	0	1	1	0	0	0	0	1
Thread-like & Round	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Sausage-like	1	1	0	0	1	0	1	0	1	1	2	2	2	1	1	1
Vermiform and Elongate	0	0	0	0	1	0	0	0	4	0	2	1	3	2	0	2
Tapered	0	0	0	0	1	1	0	0	2	2	5	3	1	2	0	3
Elongate and Tapered	0	0	0	0	0	0	0	0	2	1	1	1	1	0	0	1
Long and Broad	0	0	0	0	0	0	0	0	1	0	0	0	0	2	0	1
Round top/Flattened bottom	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0
Cylindrical top/Flattened bottom	0	1	0	0	0	0	1	1	1	2	2	1	0	0	1	1
Elongate/Rounded & Tapered at ends	0	1	0	0	1	1	1	1	2	1	2	0	2	2	1	1
Elongate & Tapered at ends	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0
Small/Short & Flattened	0	0	1	1	1	0	0	0	0	0	0	1	0	0	1	0
Quill-like tube	1	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0
Small & Elongated	0	0	0	0	0	0	0	0	0	1	1	0	0	0	0	0
Long, Cylindrical & Slender	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Cylindrical & Elongate	0	0	0	0	0	0	0	0	2	0	1	0	2	1	0	0
Slender & Rounded	0	0	0	0	1	0	0	0	1	3	0	0	1	1	1	1
Slender & Flattened	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Long & Slender	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Slender & Rectangular	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Long & Oval	1	1	0	0	0	0	0	1	1	0	0	1	0	0	0	0
Slender, Rounded & Flattened	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
Slightly tapered	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Elongate & Depressed	1	1	1	0	0	0	1	0	1	2	0	3	2	4	1	3
Elongate & Flattened	0	0	0	0	0	0	1	0	3	0	0	0	3	0	1	3
Elongate & Round	0	0	1	0	0	1	1	0	1	1	3	2	0	1	0	0

Depressed	0	0	0	0	0	0	0	0	1	0	1	0	1	0	1	1
Vermiform	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0
Flattened & tapered	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Fairly Stout	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Elongate & Rectangular	0	1	1	0	1	0	1	1	0	0	0	0	0	0	0	0
Oblong	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0
Cylindrical & Narrow Posteriorly	0	0	0	0	0	0	0	0	1	0	1	1	0	0	0	1
Small & Oblong	0	0	0	0	0	0	0	1	0	1	1	0	0	1	0	0
Long & Slender	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Tapered Posteriorly	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	1
Evenly Tapered	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0
Short & Slender	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Stout Anterior & Flattened Posterior	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Small & Thread-like	0	1	0	1	0	0	0	0	1	0	0	0	0	0	0	1
Short & Depressed	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Vermiform/flattened & Minute	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Slender & Cylindrical	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Depressed & Square in Section	0	0	0	0	0	0	0	0	0	0	1	0	0	0	1	0
Dumb-bell shaped and Swollen	0	0	0	0	0	0	0	0	0	0	2	0	0	1	1	0
Thread-like/Slender	0	0	0	0	0	0	0	0	2	0	2	1	0	0	0	0
Slender & Evenly tapered	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0
Uniformly Tapered	0	0	0	0	0	0	0	0	1	0	1	0	0	1	0	1
Laterally-compressed	0	0	1	0	2	0	1	1	1	1	2	3	1	1	1	1
Laterally-flattened	0	0	0	0	0	1	0	0	1	2	1	1	2	2	2	2
Elongate, Worm-like & Dorso-ventrally Compressed	0	0	0	0	0	0	0	0	1	0	0	0	1	0	0	1
Elongate, Cylindrical/Dorso-ventrally Flattened	0	0	0	0	2	0	2	0	2	0	1	0	1	0	0	0
Dorso-ventrally compressed	0	0	0	0	1	2	0	1	0	0	0	0	0	0	1	0
Lobster-like, Hard body with Fan shaped tail	0	0	0	0	0	0	0	0	0	0	1	0	1	1	0	0
Hard spiralled Shell	0	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0
Latterally Flattened	0	0	0	0	2	0	1	1	1	1	0	2	0	0	0	0
Oval, Flattened & Compact	0	0	1	0	0	0	1	0	0	0	0	0	0	0	0	0
Broad, Flattened & Smooth	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0
Elongate, Semi-circular with fan-like telson	0	0	0	0	0	0	0	0	0	0	0	1	0	1	0	0
Cylindrical & Latterally Compressed	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Dorso-ventrally flattened	0	0	0	0	2	0	0	1	0	0	1	1	0	0	0	0

Dorso-ventrally flattened with broad carapace	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0
Square, Rounded anterior, Pointed posterior	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0
Flattened & Short Rounded Arms	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0
Circular	0	0	0	0	1	0	0	0	0	1	0	0	0	1	0	0
Oval to triangular	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0
Oval & Flattened	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Triangular	0	0	0	0	1	0	2	1	2	0	0	0	0	0	0	1
Slightly Rounded	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Slender shell	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Tusk-shaped	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Triangular and Rounded	0	0	0	0	2	0	0	0	0	0	1	1	0	0	0	1
Flat, Circular & Five thin arms	0	0	1	0	2	0	0	1	1	0	0	1	1	0	0	1
Oval/ Circular and flattened	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Star-like & Flattened	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Oval, Heart-shaped, Circular & Flattened	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0
Bubble-like shell & Three Stubby Horns	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	1
Sausage-shaped trunk & Flaccid Proboscis	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Tree-like or Feather-like	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Thin and Elongate	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0
Elongate/ Sausage-saped	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Cylindrical/Sac-like	0	1	1	1	1	1	0	1	0	0	0	0	0	0	0	0
Short Head & Oval Body	0	0	0	0	0	0	0	0	1	1	1	0	0	1	1	1

FEEDING HABIT	NG-01	NG-02	NG-03	NG-04	CR-01	CR-02	CR-03	CR-04	GA-01	GA-02	GA-03	GA-04
Herbivore	1	0	0	0	0	0	0	0	0	0	0	0
Carnivore	6	3	4	1	0	0	2	0	0	2	0	1
Omnivore	1	0	1	0	0	0	0	0	0	1	0	0
Filter Feeding	2	1	2	1	1	1	0	0	0	1	1	0
Deposit Feeding	5	1	6	1	1	0	0	0	0	2	1	1
Detritivore	0	2	0	0	0	0	1	1	0	1	0	1
Scavenging	0	0	0	0	0	0	0	0	0	0	0	0
Suspension Feeding	0	0	0	0	0	0	0	0	0	0	0	0
Carnivore/Omnivore	0	0	0	0	1	0	1	0	0	0	0	0

Thread-like	1	0	0	0	0	0	0	0	0	0	0	1
Depressed and Oval	0	0	0	0	0	0	0	0	0	0	0	0
Broad	0	0	0	0	0	0	0	0	0	0	0	0
Thread-like & Round	0	0	0	0	0	0	0	0	0	0	0	0
Sausage-like	0	0	0	0	0	0	0	0	0	1	0	0
Vermiform and Elongate	0	0	0	0	0	0	0	0	0	0	0	0
Tapered	0	0	1	0	0	0	0	0	0	0	0	0
Elongate and Tapered	0	0	0	0	0	0	0	0	0	0	0	0
Long and Broad	0	0	0	0	0	0	0	0	0	0	0	0
Round top/Flattened bottom	0	0	0	0	0	0	0	0	0	0	0	0
Cylindrical top/Flattened bottom	0	0	0	0	0	0	0	1	0	0	0	0
Elongate/Rounded & Tapered at ends	1	1	0	0	1	0	1	1	0	0	0	0
Elongate & Tapered at ends	0	0	0	0	0	0	0	0	0	0	0	0
Small/Short & Flattened	0	0	0	0	0	0	0	0	0	0	0	0
Quill-like tube	0	0	0	0	0	0	0	0	0	0	0	0
Small & Elongated	0	0	0	0	0	0	0	0	0	0	0	0
Long, Cylindrical & Slender	0	1	0	0	0	0	0	0	0	0	0	0
Cylindrical & Elongate	1	0	0	0	0	0	0	0	0	0	1	0
Slender & Rounded	1	1	0	0	0	0	0	0	0	0	0	0
Slender & Flattened	0	0	0	0	0	0	0	0	0	0	0	0
Long & Slender	0	0	0	0	0	0	0	0	0	0	0	0
Slender & Rectangular	0	0	0	0	0	0	0	0	0	0	0	0
Long & Oval	0	0	0	0	1	0	0	0	0	0	0	0
Slender, Rounded & Flattened	0	0	1	0	0	0	0	0	0	0	0	0
Slightly tapered	0	0	0	0	0	0	0	0	0	1	0	0
Elongate & Depressed	3	1	2	1	0	0	1	0	0	0	0	0
Elongate & Flattened	0	1	1	0	0	0	0	0	0	0	0	0
Elongate & Round	0	0	0	0	0	0	0	0	0	0	0	0
Depressed	0	0	0	0	0	0	0	0	0	0	0	0
Vermiform	0	0	0	0	0	0	0	0	0	0	0	0
Flattened & tapered	0	0	0	0	0	0	0	0	0	0	0	0
Fairly Stout	0	0	0	0	0	0	0	0	0	0	0	0
Elongate & Rectangular	0	0	0	0	1	0	0	0	0	0	0	0

Appendix III

Carbon-nitrate ratio (nitrate used as a proxy for total nitrogen) indicating sources of organic carbon and corresponding organisms according to Bordowskiy, 1965ab). Phyto=phytoplankton, Zoo=zooplankton, Orga=organisms.

Station Code	C:N	Source	Source Organism
GB-01	0.11	Autochthonous	Phyto/Zoo
GB-02	1.20	Autochthonous	Phyto/Zoo
GB-03	1.04	Autochthonous	Phyto/Zoo
GB-04	1.24	Autochthonous	Phyto/Zoo
GU-01	3.66	Autochthonous	Phyto/Zoo
GU-02	1.72	Autochthonous	Phyto/Zoo
GU-03	4.62	Autochthonous	Phyto/Zoo
GU-04	16.63	Allochthonous	Terrestrial
SL-01	25.80	Allochthonous	Terrestrial
SL-02	14.60	Allochthonous	Terrestrial
SL-03	38.80	Allochthonous	Terrestrial
SL-04	14.54	Allochthonous	Terrestrial
LI-01	12.15	Allochthonous	Terrestrial
LI-02	15.30	Allochthonous	Terrestrial
LI-03	25.12	Allochthonous	Terrestrial
LI-04	12.85	Allochthonous	Terrestrial
CD-01	4.62	Autochthonous	Phyto/Zoo
CD-02	10.40	Autochthonous	Terrestrial
CD-03	4.40	Autochthonous	Phyto/Zoo
CD-04	12.30	Allochthonous	Terrestrial
GH-01	8.85	Autochthonous	Planktonic orga
GH-02	71.06	Allochthonous	Terrestrial

Station Code	C:N	Source	Source Organism
GH-03	22.46	Allochthonous	Terrestrial
GH-04	33.04	Allochthonous	Terrestrial
TG-01	12.78	Allochthonous	Terrestrial
TG-02	15.40	Allochthonous	Terrestrial
TG-03	4.83	Autochthonous	Phyto/Zoo
TG-04	8.11	Autochthonous	Planktonic orga
BN-01	11.60	Autochthonous	Terrestrial
BN-02	14.60	Allochthonous	Terrestrial
BN-03	3.30	Autochthonous	Phyto/Zoo
BN-04	5.68	Autochthonous	Phyto/Zoo
NG-01	1.87	Autochthonous	Phyto/Zoo
NG-02	7.47	Autochthonous	Planktonic orga
NG-03	1.61	Autochthonous	Phyto/Zoo
NG-04	2.86	Autochthonous	Phyto/Zoo
CR-01	1.92	Autochthonous	Phyto/Zoo
CR-02	2.08	Autochthonous	Phyto/Zoo
CR-03	3.63	Autochthonous	Phyto/Zoo
CR-04	3.88	Autochthonous	Phyto/Zoo
GA-01	1.44	Autochthonous	Phyto/Zoo
GA-02	1.57	Autochthonous	Phyto/Zoo
GA-03	1.80	Autochthonous	Phyto/Zoo
GA-04	4.75	Autochthonous	Phyto/Zoo

APPENDIX IV**Sediment physical and chemical analytical results**

Parameter	Guinea Bissau	Guinea Conakry	Sierra Leone	Liberia	Cote d'Ivoire	Ghana	Togo	Benin	Nigeria	Cameroun	Gabon
Sand	92.65	92.53	83.05	61.83	79.07	33.77	56.00	59.25	71.41	29.23	87.74
Silt	3.56	3.53	6.13	20.48	5.63	3.11	16.50	13.25	4.12	21.77	1.38
Clay	3.81	3.87	10.75	17.68	15.30	63.13	27.25	27.50	24.47	48.99	10.88
Phosphate	0.73	0.21	0.41	0.91	0.49	1.51	2.53	1.04	0.43	0.66	0.74
Nitrate	1.23	0.50	0.23	0.25	0.15	0.20	0.14	0.11	0.73	0.83	0.80
Org. Carbon	0.50	2.01	4.73	3.91	1.02	6.12	1.15	1.01	2.48	2.18	1.83
Potassium	2.50	1.04	0.65	2.26	1.80	3.03	2.02	3.16	2.73	2.18	4.20
Sodium	2.53	1.93	1.64	5.33	3.12	7.48	3.64	3.25	1.89	3.08	3.95
Calcium	21.90	24.58	42.09	23.19	15.39	23.50	7.57	7.00	10.81	25.67	29.47
Magnesium	0.04	0.04	0.04	0.03	0.03	0.04	0.02	0.01	0.02	0.03	0.01

APPENDIX V

Water depth of sampling locations

Station Code	Country	Depth (m)
GB-01	Guinea Bissau	53.0
GB-02	Guinea Bissau	125.0
GB-03	Guinea Bissau	153.0
GB-04	Guinea Bissau	28.0
GU-01	Guinea	26.0
GU-02	Guinea	94.0
GU-03	Guinea	43.0
GU-04	Guinea	27.0
SL-01	Sierra Leone	52.0
SL-02	Sierra Leone	34.0
SL-03	Sierra Leone	27.0
SL-04	Sierra Leone	49.0
LI-01	Liberia	34.0
LI-02	Liberia	54.0
LI-03	Liberia	54.0
LI-04	Liberia	24.0
CD-01	Cote d'Ivoire	63.0
CD-02	Cote d'Ivoire	102.0
CD-03	Cote d'Ivoire	49.0
CD-04	Cote d'Ivoire	24.0
GH-01	Ghana	100.0
GH-02	Ghana	76.0
GH-03	Ghana	60.0
GH-04	Ghana	29.0
TG-01	Togo	59.0
TG-02	Togo	20.0
TG-03	Togo	35.0
TG-04	Togo	17.0
BN-01	Benin	28.0
BN-02	Benin	18.0
BN-03	Benin	16.0
BN-04	Benin	23.0
NG-01	Nigeria	87.0
NG-02	Nigeria	37.0
NG-03	Nigeria	67.9
NG-04	Nigeria	41.0

CR-01	Cameroon	64.0
CR-02	Cameroon	22.0
CR-03	Cameroon	98.0
CR-04	Cameroon	22.0
GA-01	Gabon	101.0
GA-02	Gabon	111.0
GA-03	Gabon	55.0
GA-04	Gabon	104.0

APPENDIX VI

Results of Statistical Analyses

**** Correlation matrix ****

SPEC AX1	1.0000								
SPEC AX2	0.0397	1.0000							
SPEC AX3	-0.0884	-0.1315	1.0000						
SPEC AX4	0.2604	0.3002	-0.3847	1.0000					
ENVI AX1	0.7154	0.0000	0.0000	0.0000	1.0000				
ENVI AX2	0.0000	0.5430	0.0000	0.0000	0.0000	1.0000			
ENVI AX3	0.0000	0.0000	0.3341	0.0000	0.0000	0.0000	1.0000		
ENVI AX4	0.0000	0.0000	0.0000	0.3758	0.0000	0.0000	0.0000	1.0000	
Sand	-0.1046	0.1404	-0.1130	-0.2462	-0.1463	0.2586	-0.3382	-0.6551	
Silt	0.2215	-0.3952	0.0276	0.0038	0.3096	-0.7278	0.0828	0.0100	
Clay	0.0907	-0.0843	0.1104	0.2520	0.1267	-0.1553	0.3305	0.6704	
Phosphat	0.1583	0.0108	0.0876	-0.0192	0.2213	0.0199	0.2623	-0.0510	
Nitrate	-0.4643	-0.0913	-0.1377	0.0646	-0.6490	-0.1682	-0.4121	0.1718	
Org. Car	-0.2870	0.0004	0.2060	0.0005	-0.4012	0.0007	0.6164	0.0012	
Potassiu	-0.0568	-0.2624	0.1513	0.0886	-0.0793	-0.4832	0.4528	0.2358	
Sodium	0.1026	-0.0481	0.1737	0.1528	0.1434	-0.0885	0.5200	0.4066	
Cacium	-0.4293	0.1058	0.0310	-0.0773	-0.6001	0.1948	0.0928	-0.2056	
Magnesium	-0.2293	0.1703	0.0588	-0.0478	-0.3205	0.3136	0.1761	-0.1273	

	SPEC AX1	SPEC AX2	SPEC AX3	SPEC AX4	ENVI AX1			
	ENVI AX2	ENVI AX3	ENVI AX4					
Sand	1.0000							
Silt	-0.4671	1.0000						
Clay	-0.7186	0.3780	1.0000					
Phosphat	-0.2046	0.2195	0.1927	1.0000				
Nitrate	0.0407	-0.3212	-0.3087	-0.0834	1.0000			
Org. Car	-0.2867	0.0628	0.2316	0.0918	-0.1097	1.0000		
Potassiu	-0.2505	0.1582	0.3073	0.0652	0.1390	-0.1379	1.0000	
Sodium	-0.4369	0.2863	0.2541	0.4441	-0.1296	0.1394	0.4245	1.0000
Cacium	0.0061	-0.0704	-0.1324	-0.0635	0.2256	0.4136	-0.1225	-0.0256
Magnesium	-0.1364	0.0131	-0.0513	-0.0676	-0.0345	0.0491	-0.0365	0.1565

	Sand	Silt	Clay	Phosphat	Nitrate	Org. Car	Potassiu	Sodium
Calcium		1.0000						
Magnesium		0.5109	1.0000					

Calcium Magnesium

N	name	(weighted) mean	stand. dev.	inflation factor
1	SPEC AX1	0.0000		1.3977
2	SPEC AX2	0.0000		1.8415
3	SPEC AX3	0.0000		2.9931
4	SPEC AX4	0.0000		2.6610
5	ENVI AX1	0.0000		1.0000
6	ENVI AX2	0.0000		1.0000
7	ENVI AX3	0.0000		1.0000
8	ENVI AX4	0.0000		1.0000
1	Sand	4.0720	0.6833	3.7842

2	Silt	1.7245	1.1168	1.5808
3	Clay	2.7123	1.0868	3.2564
4	Phosphat	0.5261	0.3880	1.3763
5	Nitrate	0.3393	0.2721	1.9401
6	Org. Car	1.0889	0.5260	1.7068
7	Potassiu	1.0741	0.5030	1.7059
8	Sodium	1.3009	0.6342	2.1259
9	Cacium	2.8634	0.7507	2.2074
10	Magnesi	0.0286	0.0175	1.7838

**** Summary ****

Axes	1	2	3	4	Total variance
Eigenvalues :	0.495	0.004	0.002	0.001	1.000
Trait-environment correlations :	0.715	0.543	0.334	0.376	
Cumulative percentage variance					
of Trait data :	49.5	49.9	50.0	50.1	
of Trait-environment relation:	98.7	99.5	99.8	100.0	
Sum of all eigenvalues					1.000
Sum of all canonical eigenvalues					0.501

All four eigenvalues reported above are canonical and correspond to axes that are constrained by the environmental variables.

*** Unrestricted permutation ***

Seeds: 23239 945

**** Summary of Monte Carlo test ****

Test of significance of first canonical axis: eigenvalue = 0.495

F-ratio = 32.322

P-value = 0.0050

Test of significance of all canonical axes : Trace = 0.501

F-ratio = 3.316

P-value = 0.0050

(199 permutations under reduced model)

Canonical Correspondence Analysis

Program CANOCO Version 4.54 October 2005 - written by Cajo J.F. Ter Braak
 (C) 1988-2005 Biometris - quantitative methods in the life and earth sciences
 Plant Research International, Wageningen University and Research Centre
 Box 100, 6700 AC Wageningen, the Netherlands
 CANOCO performs (partial) (detrended) (canonical) correspondence analysis,
 principal components analysis and redundancy analysis.
 CANOCO is an extension of Cornell Ecology program DECORANA (Hill,1979)

For explanation of the input/output see the manual or
 Ter Braak, C.J.F. (1995) Ordination. Chapter 5 in:
 Data Analysis in Community and Landscape Ecology
 (Jongman, R.H.G., Ter Braak, C.J.F. and Van Tongeren, O.F.R., Eds)
 Cambridge University Press, Cambridge, UK, 91-173 pp.

*** Type of analysis ***

Model Gradient analysis
 indirect direct hybrid
 linear 1=PCA 2= RDA 3
 unimodal 4= CA 5= CCA 6
 ,, 7=DCA 8=DCCA 9
 10=non-standard analysis

Type analysis number

Answer = 5

*** Data files ***

Species data : C:\Users\user 1\Desktop\Functional Traits_Infauna\BioAbunDOM
 Covariable data :
 Environmental data : C:\Users\user 1\Desktop\Functional Traits_Infauna\EnvDataTrasformed
 Initialization file:

Forward selection of envi. variables = 1

Scaling of ordination scores = 2

Diagnostics = 3

File : C:\Users\user 1\Desktop\Functional Traits_Infauna\BioAbunDOM

Title : WCanoImp produced data file

Format : (I5,I1X,10F4.0)

No. of couplets of species number and abundance per line : 0

No samples omitted

Number of samples 44

Number of species 10

Number of occurrences 150

File : C:\Users\user 1\Desktop\Functional Traits_Infauna\EnvDataTrasformed

Title : WCanoImp produced data file

Format : (I5,I1X,10F6.2)

No. of environmental variables : 10

No interaction terms defined

No transformation of species data
 No species-weights specified
 No sample-weights specified
 No downweighting of rare species

No. of active samples: 43
 No. of passive samples: 0
 No. of active species: 10

Total inertia in species data=
 Sum of all eigenvalues of CA = 2.62242

***** Check on influence in covariable/environment data *****

The following sample(s) have extreme values

Sample Environmental Covariable + Environment space
 variable Influence influence influence

2			8.5x
2	1	5.1x	
2	6	8.1x	
2	7	7.8x	
2	10	15.1x	
2			3.1x
5			4.7x
5	3	13.7x	
5	5	20.2x	
5	10	6.8x	
5			3.4x
24	4	5.7x	
24	6	5.6x	
25	1	16.2x	
25	2	8.3x	
26	4	18.4x	
26			3.1x
27			4.2x
27	7	8.9x	
27	8	6.1x	
27	9	7.2x	
27	10	6.1x	

***** End of check *****

**** Start of forward selection of variables ****

*** Unrestricted permutation ***

Seeds: 23239 945

N Name Extra fit

4	Phosphat	0.0555
3	Clay	0.0846
1	Sand	0.1124
2	Silt	0.1324
8	Sodium	0.1609

5 Nitrate 0.1793
 7 Potassiu 0.1800
 9 Cacium 0.1899
 6 Org. Car 0.3290
 10 Magnesiu 0.3542
 Environmental variable 10 tested
 Number of permutations= 199

*** Permutation under reduced model ***

P-value 0.0050 (variable 10; F-ratio= 6.40; number of permutations= 199)

Environmental variable 10 added to model
 Variance explained by the variables selected: 0.35
 " " " all variables : 1.33

N	Name	Extra fit
7	Potassiu	0.0303
4	Phosphat	0.0555
3	Clay	0.0962
1	Sand	0.1125
8	Sodium	0.1147
2	Silt	0.1388
5	Nitrate	0.1788
9	Cacium	0.2008
6	Org. Car	0.3066

Environmental variable 6 tested
 Number of permutations= 199

*** Permutation under reduced model ***

P-value 0.0050 (variable 6; F-ratio= 6.25; number of permutations= 199)

Environmental variable 6 added to model
 Variance explained by the variables selected: 0.66
 " " " all variables : 1.33

N	Name	Extra fit
7	Potassiu	0.0341
4	Phosphat	0.0486
8	Sodium	0.0890
9	Cacium	0.0912
3	Clay	0.0963
2	Silt	0.1080
1	Sand	0.1216
5	Nitrate	0.1826

Environmental variable 5 tested
 Number of permutations= 199

*** Permutation under reduced model ***

P-value 0.0050 (variable 5; F-ratio= 4.00; number of permutations= 199)

Environmental variable 5 added to model
 Variance explained by the variables selected: 0.84
 " " " all variables : 1.33

N Name Extra fit

9 Calcium 0.0231
 4 Phosphat 0.0266
 7 Potassiu 0.0352
 3 Clay 0.0362
 2 Silt 0.0660
 8 Sodium 0.0824
 1 Sand 0.1170

Environmental variable 1 tested
 Number of permutations= 199

*** Permutation under reduced model ***

P-value 0.0250 (variable 1; F-ratio= 2.67; number of permutations= 199)

Environmental variable 1 added to model
 Variance explained by the variables selected: 0.96
 " " " all variables : 1.33

N Name Extra fit

9 Calcium 0.0323
 4 Phosphat 0.0378
 3 Clay 0.0712
 2 Silt 0.0741
 7 Potassiu 0.0951
 8 Sodium 0.1302

Environmental variable 8 tested
 Number of permutations= 199

*** Permutation under reduced model ***

P-value 0.0050 (variable 8; F-ratio= 3.15; number of permutations= 199)

Environmental variable 8 added to model
 Variance explained by the variables selected: 1.09
 " " " all variables : 1.33

N Name Extra fit

9 Calcium 0.0233
 4 Phosphat 0.0283
 7 Potassiu 0.0526
 3 Clay 0.0709
 2 Silt 0.0871

Environmental variable 2 tested

Number of permutations= 199

*** Permutation under reduced model ***

P-value 0.0150 (variable 2; F-ratio= 2.17; number of permutations= 199)

Environmental variable 2 added to model

Variance explained by the variables selected: 1.18

" " " all variables : 1.33

N Name Extra fit

4 Phosphat 0.0127

9 Cadium 0.0233

7 Potassiu 0.0533

3 Clay 0.0718

Environmental variable 3 tested

Number of permutations= 199

*** Permutation under reduced model ***

P-value 0.0700 (variable 3; F-ratio= 1.83; number of permutations= 199)

Environmental variable 3 added to model

Variance explained by the variables selected: 1.25

" " " all variables : 1.33

N Name Extra fit

4 Phosphat 0.0189

9 Cadium 0.0252

7 Potassiu 0.0439

Environmental variable 7 tested

Number of permutations= 199

*** Permutation under reduced model ***

P-value 0.3750 (variable 7; F-ratio= 1.12; number of permutations= 199)

Environmental variable 7 added to model

Variance explained by the variables selected: 1.29

" " " all variables : 1.33

N Name Extra fit

4 Phosphat 0.0148

9 Cadium 0.0201

Environmental variable 9 tested

Number of permutations= 199

*** Permutation under reduced model ***

P-value 0.8700 (variable 9; F-ratio= 0.51; number of permutations= 199)

Environmental variable 9 added to model

Variance explained by the variables selected: 1.31

" " " all variables : 1.33

N Name Extra fit

4 Phosphat 0.0165

Environmental variable 4 tested

Number of permutations= 199

*** Permutation under reduced model ***

P-value 0.9450 (variable 4; F-ratio= 0.41; number of permutations= 199)

Environmental variable 4 added to model

Variance explained by the variables selected: 1.33

" " " all variables : 1.33

No more variables to improve fit

*** End of selection ***

N	name	(weighted) mean	stand. dev.	inflation factor
1	SPEC AX1	0.0000		1.1269
2	SPEC AX2	0.0000		1.1788
3	SPEC AX3	0.0000		1.3312
4	SPEC AX4	0.0000		1.3985
5	ENVI AX1	0.0000		1.0000
6	ENVI AX2	0.0000		1.0000
7	ENVI AX3	0.0000		1.0000
8	ENVI AX4	0.0000		1.0000
1	Sand	4.1891	0.6514	5.7573
2	Silt	1.7114	0.9086	2.2318
3	Clay	2.2340	1.2095	6.3910
4	Phosphat	0.5846	0.5301	3.1719
5	Nitrate	0.2762	0.1965	3.9020
6	Org. Car	0.9869	0.6192	3.6998
7	Potassiu	1.0260	0.5739	2.8325
8	Sodium	1.3836	0.5999	4.3227
9	Cacium	2.7635	0.6408	6.2848
10	Magnesi	0.0292	0.0221	3.9462

**** Summary ****

Axes	1	2	3	4	Total inertia	
Eigenvalues	:	0.502	0.378	0.202	0.141	2.622
Species-environment correlations	:	0.887	0.848	0.751	0.715	
Cumulative percentage variance of species data	:	19.2	33.6	41.3	46.7	

of species-environment relation:	37.8	66.2	81.4	92.0
Sum of all eigenvalues				2.622
Sum of all canonical eigenvalues				1.330

All four eigenvalues reported above are canonical and correspond to axes that are constrained by the environmental variables.

Program CANOCO Version 4.54 October 2005 - written by Cajo J.F. Ter Braak
(C) 1988-2005 Biometris - quantitative methods in the life and earth sciences
Plant Research International, Wageningen University and Research Centre
Box 100, 6700 AC Wageningen, the Netherlands
CANOCO performs (partial) (detrended) (canonical) correspondence analysis,
principal components analysis and redundancy analysis.
CANOCO is an extension of Cornell Ecology program DECORANA (Hill,1979)

For explanation of the input/output see the manual or
Ter Braak, C.J.F. (1995) Ordination. Chapter 5 in:
Data Analysis in Community and Landscape Ecology
(Jongman, R.H.G., Ter Braak, C.J.F. and Van Tongeren, O.F.R., Eds)
Cambridge University Press, Cambridge, UK, 91-173 pp.

*** Type of analysis ***

Model	Gradient analysis			
	indirect	direct	hybrid	
linear	1=PCA	2= RDA	3	
unimodal	4= CA	5= CCA	6	
„	7=DCA	8=DCCA	9	
	10=non-standard analysis			

Type analysis number

Answer = 5

*** Data files ***

Species data : C:\Users\user 1\Desktop\Functional Traits_Infauna\BioAbunD0m

Covariable data :

Environmental data : C:\Users\user 1\Desktop\Functional Traits_Infauna\EnvDataTrasformed

Initialization file:

Forward selection of envi. variables = 0

Scaling of ordination scores = 2

Diagnostics = 3

File : C:\Users\user 1\Desktop\Functional Traits_Infauna\BioAbunD0m

Title : WCanoImp produced data file

Format : (I5,I1X,10F4.0)

No. of couplets of species number and abundance per line : 0

No samples omitted

Number of samples 44

Number of species 10

Number of occurrences 150

File : C:\Users\user 1\Desktop\Functional Traits_Infauna\EnvDataTrasformed

Title : WCanoImp produced data file

Format : (I5,1X,10F6.2)

No. of environmental variables : 10

No interaction terms defined

No transformation of species data

No species-weights specified

No sample-weights specified

No downweighting of rare species

No. of active samples: 43

No. of passive samples: 0

No. of active species: 10

Total inertia in species data=

Sum of all eigenvalues of CA = 2.62242

***** Check on influence in covariable/environment data *****

The following sample(s) have extreme values

Sample Environmental Covariable + Environment space

variable Influence influence influence

2			8.5x		
2	1	5.1x			
2	6	8.1x			
2	7	7.8x			
2	10	15.1x			
2				3.1x	
5			4.7x		
5	3	13.7x			
5	5	20.2x			
5	10	6.8x			
5				3.4x	
24	4	5.7x			
24	6	5.6x			
25	1	16.2x			
25	2	8.3x			
26	4	18.4x			
26				3.1x	
27			4.2x		
27	7	8.9x			
27	8	6.1x			
27	9	7.2x			
27	10	6.1x			

***** End of check *****

1

**** Weighted correlation matrix (weight = sample total) ****

SPEC AX1	1.0000					
SPEC AX2	-0.0724	1.0000				
SPEC AX3	0.0013	-0.1029	1.0000			
SPEC AX4	-0.0836	-0.0953	0.2112	1.0000		
ENVI AX1	0.8874	0.0000	0.0000	0.0000	1.0000	
ENVI AX2	0.0000	0.8483	0.0000	0.0000	0.0000	1.0000

ENVI AX3	0.0000	0.0000	0.7512	0.0000	0.0000	0.0000	1.0000	
ENVI AX4	0.0000	0.0000	0.0000	0.7151	0.0000	0.0000	0.0000	1.0000
Sand	0.2289	0.1846	-0.0941	0.4429	0.2580	0.2176	-0.1253	0.6194
Silt	0.0386	-0.3665	-0.3735	-0.1228	0.0435	-0.4321	-0.4972	-0.1718
Clay	-0.1690	-0.1322	-0.2686	-0.2799	-0.1905	-0.1559	-0.3576	-0.3914
Phosphat	-0.0687	0.1560	-0.2377	-0.2141	-0.0774	0.1839	-0.3164	-0.2994
Nitrate	0.1353	0.1526	0.5922	0.3063	0.1525	0.1799	0.7883	0.4284
Org. Car	-0.5006	0.5331	0.1823	-0.0446	-0.5641	0.6284	0.2427	-0.0624
Potassiu	0.4647	0.2475	-0.0949	-0.1157	0.5237	0.2918	-0.1263	-0.1618
Sodium	0.2304	0.3594	-0.0471	-0.4534	0.2597	0.4236	-0.0627	-0.6341
Cacium	0.1658	0.4644	0.3263	0.1389	0.1869	0.5474	0.4343	0.1942
Magnesi	0.7038	0.2184	-0.0174	-0.0654	0.7931	0.2575	-0.0231	-0.0915

SPEC AX1	SPEC AX2	SPEC AX3	SPEC AX4	ENVI AX1
ENVI AX2	ENVI AX3	ENVI AX4		

Sand	1.0000							
Silt	-0.5015	1.0000						
Clay	-0.7623	0.5064	1.0000					
Phosphat	-0.3234	0.4245	0.4265	1.0000				
Nitrate	0.2746	-0.4072	-0.6518	-0.3158	1.0000			
Org. Car	-0.2197	-0.1818	-0.0173	0.2024	0.1984	1.0000		
Potassiu	-0.2797	0.3311	0.2699	0.0966	0.0202	-0.1134	1.0000	
Sodium	-0.4988	0.3289	0.3958	0.6086	-0.1137	0.2253	0.5769	1.0000
Calcium	0.1433	-0.2895	-0.3131	-0.1014	0.5123	0.5523	0.1636	0.2041
Magnesium	-0.0005	0.0846	0.0622	-0.0003	0.0038	-0.0879	0.5539	0.4005

Sand	Silt	Clay	Phosphat	Nitrate	Org. Car	Potassiu	Sodium
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Cacium	1.0000		
Magnesi	0.5281	1.0000	

Calcium	Magnesi
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N	name	(weighted) mean	stand. dev.	inflation factor
1	SPEC AX1	0.0000		1.1269
2	SPEC AX2	0.0000		1.1788
3	SPEC AX3	0.0000		1.3312
4	SPEC AX4	0.0000		1.3985
5	ENVI AX1	0.0000		1.0000
6	ENVI AX2	0.0000		1.0000
7	ENVI AX3	0.0000		1.0000
8	ENVI AX4	0.0000		1.0000
1	Sand	4.1891	0.6514	5.7573
2	Silt	1.7114	0.9086	2.2318
3	Clay	2.2340	1.2095	6.3910
4	Phosphat	0.5846	0.5301	3.1719
5	Nitrate	0.2762	0.1965	3.9020
6	Org. Car	0.9869	0.6192	3.6998
7	Potassiu	1.0260	0.5739	2.8325
8	Sodium	1.3836	0.5999	4.3227
9	Calcium	2.7635	0.6408	6.2848
10	Magnesi	0.0292	0.0221	3.9462

**** Summary ****

Axes	1	2	3	4	Total inertia
Eigenvalues :	0.502	0.378	0.202	0.141	2.622
Species-environment correlations :	0.887	0.848	0.751	0.715	
Cumulative percentage variance					
of species data :	19.2	33.6	41.3	46.7	
of species-environment relation:	37.8	66.2	81.4	92.0	
Sum of all eigenvalues					2.622
Sum of all canonical eigenvalues					1.330

All four eigenvalues reported above are canonical and correspond to axes that are constrained by the environmental variables.

*** Unrestricted permutation ***

Seeds: 23239 945

**** Summary of Monte Carlo test ****

Test of significance of first canonical axis: eigenvalue = 0.502

F-ratio = 7.585

P-value = 0.0100

Test of significance of all canonical axes : Trace = 1.330

F-ratio = 3.293

P-value = 0.0050

(199 permutations under reduced model)



Ampipod



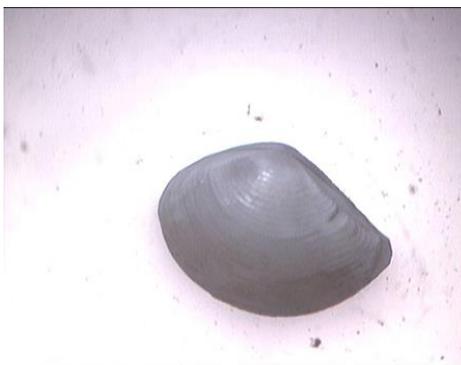
Capitellid sp.



Tanaid sp.



Nephtys sp.



Tellina sp.



Sipuncula sp. (Sipunculidae)



Glycera spp. (Glyceridae)



Marphysa sp. (Eunicidae)



Nephtys sp. (Nephtyidae)



Maldane sp. (Maldanidae)