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Changes in polychaete standing stock and diversity on the northern side of Senghor Seamount (NE Atlantic)

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Abstract

Interest in seamount research has gathered momentum over the past five years in an effort to understand the physical, geochemical and biological characteristics as well as the interconnectedness of seamount ecosystems. The majority of biological seamount research has concentrated upon the rich and diverse suspension feeding organisms that dominate the megafauna, such as gorgonians and antipatharian corals; by comparison there have been few studies that have investigated the no less enigmatic, but possibly just as important infauna. To help fill this knowledge gap, the macrofaunal community was sampled from a total of five stations along a northerly transect (capturing water depths from ~ 130 m to ~ 3300 m), on Senghor Seamount (NE Atlantic). The focus of this study is on the polychaete communities. Polychaete abundance peaked at the summit and a mid-slope station (~ 1500 m), a pattern mirrored by the biomass values. The polychaete community along the transect appeared to be particularly diverse, with 135 species nominally identified to putative species from a total of 954 individuals. A diversity maximum was identified on the upper slope at ~ 800 m depth, with species diversity, richness and evenness also all peaking at this station. Depth is likely to be a significant factor in determining levels of similarity between stations.

1 Introduction

Seamounts are defined as topographic features that rise more than ~ 1000 m above the surrounding seafloor. They are therefore significant topographic features of the deep-sea environment; inactive volcanoes which punctuate the often more featureless abyssal plain. It is estimated that at least 33 000 seamounts exist globally and constitute approximately ~ 5 % of the global ocean floor (~ 17 million km²) (Yesson et al., 2011). The high global abundance of seamount ecosystems still represents an immense challenge to scientists, thus it is somewhat unsurprising that < 0.3 % have been sampled biologically in any detail despite significant interest in these features (Ramirez-Llodra et

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al., 2010). Seamounts are often typified by highly rich and diverse communities of predominantly large suspension feeding organisms such as gorgonians and antipatharian corals, which are often the focus of seamount research (Bartsch, 2008; McClain et al., 2009; Clark et al., 2010; McClain, 2010; Rowden et al., 2010; Simpson and Watling, 2010; Bo et al., 2011; Sautya et al., 2011; Tracey et al., 2011). Many studies have also concentrated upon seamount fish populations (Clark, 1999; Matthiesson et al., 2002; Diekmann, 2006; Christiansen et al., 2009; Menezes et al., 2009; Morato et al., 2009; Hirsch and Christiansen, 2010) with relatively few focussed upon the infauna (Gillet and Dauvin, 2000, 2003; Richer De Forges et al., 2000; Koslow et al., 2001; Surugiu et al., 2008).

Deep-sea macrofauna communities are known to be strongly influenced by bathymetric gradients; these shape community assemblage structure, diversity and standing stock (Hessler and Sanders, 1967; Grassle et al., 1979; Rex, 1981; Flach and de Bruin, 1999; Narayanaswamy et al., 2005; 2010a, b). Depth stratification of benthic communities can reflect environmental gradients of temperature, dissolved oxygen concentration and food availability (Clark et al., 2010); these gradients alter faunal composition to such a considerable degree that more faunal change may be witnessed over 1000 m vertically than 1000 km horizontally (Grassle and Maciolek, 1992; Longhurst, 1998; Clark et al., 2010). Consequently depth is thought to be the dominant controlling factor of seamount benthic community composition (Koslow et al., 2001; Schalcher-Hoenlinger et al., 2005; Clark et al., 2010; Rex and Etter, 2010). Whilst the megafauna assemblage structure and abundance variation with depth has been investigated on individual seamounts (McClain, 2010), changes in the macrofauna community in relation to a bathymetric gradient on individual seamounts remains relatively unexplored.

Polychaetes are frequently found to dominate deep-sea environments (Gage and Tyler, 1991; Gage, 2004; Surugiu et al., 2008) including seamount macrofauna communities (Gillet and Dauvin, 2000, 2003; Surugiu et al., 2008). Surugiu et al. (2008) reported that polychaetes represented up to 70 % of the benthic macrofauna

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communities of some of the North-East Atlantic seamounts (e.g. Irving, Plato and Meteor Seamounts). Dominance of deep-sea communities by polychaetes enables this taxon to be used as an indicator of overall changes in population and community structure of deep-sea environments.

5 The aim of this study was to investigate the macro-infauna polychaetes on Senghor Seamount. More specifically we aimed to determine if there were any changes in standing stock, diversity and composition across a transect starting at the summit, capturing the slope and base environments, and ending at a reference station on the neighbouring plain which is not thought to be directly influenced by any intermediate-scale topography.

2 Materials and methods

2.1 Sampling methods

This current study focussed on Senghor Seamount a relatively isolated topographical feature located in the Cape Verde Archipelago ~ 60 nautical miles (nm) north-east of the island of Sal (17.17° N, 21.92° W) (Fig. 1a). Senghor Seamount is fairly circular and symmetrical in shape, with a summit plateau in just ~ 130 m water depth and a northern base located at a depth of ~ 3200–3300 m (Fig. 1b). It is situated in a meso-oligotrophic region of the ocean and thus the food supply to the seafloor is expected to be somewhat reduced (Christiansen et al., 2009).

20 Data presented in this study were derived from samples that were collected from a northerly transect during cruise M79/3 of RV *Meteor* in October 2009. A total of five stations were sampled, four stations on the seamount itself at depths ranging from 133 to 3241 m, and a reference station situated 60 nm to the north (depth 3295 m) (Table 1 and Fig. 1b). The macrofauna were sampled using the German Multicorer (MUC) with a core diameter of 94 mm, equivalent to 69.4 cm² surface area per core. Three deployments were made at each station with a minimum of three cores taken from each

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deployment (i.e. a total of nine cores per station). The upper 5 cm of sediment was sliced for faunal analysis and each sediment sample was placed into a 4 % formaldehyde solution for a minimum of two days to fix the tissues prior to sediment washing and thus to reduce damage to the individuals. The samples were then gently washed on a 250 μm mesh sieve with filtered (20 μm mesh size) seawater and further rinsed in freshwater before being transferred to 70 % ethanol with added 2 % glycol.

The macrofauna were initially sorted into major taxonomic groups and then counted. The polychaete fauna were then pooled and a wet weight biomass value obtained using a Sartorius BP61S balance. The polychaetes were then further identified to the lowest possible taxonomic level, nominally to putative species level (collectively referred to as species from here on in).

2.2 Data analysis

Polychaete abundance and biomass values per core were pooled as pseudo-replicates to form one replicate per deployment. These standing stock values were then averaged and standardised for each station to either number of individuals per m^2 or grams of wet weight biomass per m^2 . A number of diversity indices were calculated Margalef's Richness (d), Shannon's Diversity (H' loge), Pielou's Evenness (J'), Simpson's Dominance ($1-\lambda$), for each station using PRIMER v6 (Clarke and Warwick, 2001).

Multivariate analysis was undertaken using both cluster analysis and non-metric multi-dimensional scaling (MDS) also using the PRIMER package v6 (Clarke and Warwick, 2001). Square root transformation of the species abundance data was undertaken and a Bray-Curtis similarity matrix generated. A similarity profile test (SIMPROF), was used to determine if the differences seen in the cluster analysis were significant (SIMPROF < 0.05). In addition a similarity percentage test (SIMPER) was undertaken to determine the dissimilarity between stations and which species contributed > 5 % to dissimilarity between stations (Clarke and Warwick, 2001; Clarke and Gorley, 2006). A global ANOSIM test was also conducted to determine if depth was a significant factor in separating deployments.

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3 Results

3.1 Standing stock

On the summit plateau (Station A, 133 m depth) the number of polychaete individuals was very high with $> 10\,000 \text{ ind. m}^{-2}$ (Table 2) and was followed by a noticeable decline on the upper slope (Station B, 834 m depth: $\sim 1150 \text{ ind. m}^{-2}$). The total number of individuals increased slightly at the mid-slope station, (Station C, $\sim 1500 \text{ m}$ depth: $\sim 1750 \text{ ind. m}^{-2}$) before declining again at the base of the seamount (Station D, $\sim 3250 \text{ m}$ depth: $\sim 1250 \text{ ind. m}^{-2}$) and at the reference station (Station E, $\sim 3300 \text{ m}$ depth: $\sim 960 \text{ ind. m}^{-2}$). Polychaete biomass values showed a pattern very similar to that of the abundance values (Table 2), with a primary maximum at the summit (Station A) and a secondary maximum on the mid slope (Station C).

3.2 Polychaete family analysis

In total 34 polychaete families were identified from the 954 polychaete individuals collected. The dominant families (in terms of total individuals) were the Syllidae (34%), Spionidae (10%), Cirratulidae (13%), Chrysopetallidae (7%) and Sabellidae (5%) (Table 3). In terms of total number of species per family, the Syllidae also dominated with 19 species in total, followed by the Spionidae (16), Cirratulidae (11), Paraonidae (9) and the Capitellidae (7). Several families were present at all stations, including the Acrocirridae, Cirratulidae, Nereididae, Paraonidae, Spionidae and the Syllidae, whilst the Arabellidae, Serpulidae, Nephytidae and Ampharetidae were only observed at depths $> 1500 \text{ m}$ (Table 3). The Dorvilleidae, Eunicidae and Lacydoniidae were only found at the summit station. A non-metric MDS plot (Fig. 2) (all cores grouped per deployment) showed that at family level all stations were broadly grouped with a similarity of 27%. The upper slope (834 m) and deeper stations had a 40% similarity in terms of family composition, whilst the base and reference station were 58% similar.

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3.3 Polychaete species diversity

The 954 polychaete individuals collected were nominally separated into 135 species. Changes in polychaete species diversity along the transect are illustrated in Fig. 3. Species diversity, richness and evenness were highest on the upper slope at Station B, whereas evenness and richness were lowest at both the summit station A and the base station on the seamount, Station D. Shannon-Wiener diversity was also noticeably lower at the base station. The reference station had a higher richness value than the base station, but not diversity or dominance and only a slightly higher evenness value.

4 Multivariate analysis

The group-average linked cluster analysis and the SIMPROF permutation test showed a remarkably low level of similarity between stations (Fig. 4) with the summit station, Station A, showing no similarity to the remaining stations ($p < 0.005$). The remaining four stations also showed relatively little similarity to one another (7% similarity). The mid-slope, base and reference stations (Stations C, D and E) displayed a similarity level of $< 10\%$, with the seamount base Station D and the reference Station E showing the greatest similarity at 26% ($p < 0.005$). It is, however, worth noting that this similarity of 26% is still low and it seems that, despite very similar depths, the base and reference stations differ in terms of polychaete species composition. There was no statistical evidence for any other sub-structure within each group (samples connected by dotted lines).

The non-metric MDS plot (species level, all cores grouped per deployment) (Fig. 5) also showed similar groupings of deployments and stations compared with the cluster analysis whereby the three deployments for each station formed one group. The three deployments for the summit plateau (Station A) formed one group at a similarity level of 62%, quite distinct from the other four stations. In addition, the base and reference stations (Stations D and E) were quite similar in their sub-grouping (Station

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D deployment similarity 51 %, Station E deployment similarity 32 %). Using the global ANOSIM test, depth was found to be a significant factor driving deployment clustering at this seamount ($R = 0.75$, $p < 0.001$). However, it appears that, despite very similar depths, the base and reference stations still form two distinct clusters in terms of their polychaete species composition.

Using SIMPER, the dissimilarity between stations based on the contribution of different species was calculated (Table 4). Dissimilarity between the summit plateau (Station A) and other stations was particularly high (> 99 %) and was the result, predominantly of a single syllid species (sp. 909) which contributed > 7.5 % to the total dissimilarity. Whilst sp. 977 of the family Spionidae contributed 12.6 % to the dissimilarity between Stations B and C, it was also found to be important in contributing to the differences between Stations C and D and between Stations C and E.

5 Discussion

5.1 Changes in polychaete standing stock with depth

Extremely high levels of polychaete abundance which corresponded with high biomass levels were observed on the summit of Senghor Seamount, Station A (10 000 ind. m⁻²) (Table 2). However, this was not unexpected as the summit of the seamount at ~ 130 m water depth lies at the bottom of the surface ocean layer from which significant amounts of organic carbon are exported into deeper waters. Therefore, this station is likely to be influenced by higher supply of freshly produced food which is likely to sustain higher macrofauna (polychaete) abundances. On the upper slope (Station B) there was a significant decrease in polychaete standing stock, followed by a noticeable increase on the mid slope (Station C) which was somewhat unexpected. In many deep-sea environments, macrofaunal abundance is observed to decrease exponentially or linearly with depth (Etter and Rex, 1990; Cosson-Sarradin et al., 1998), however on the northern transect at Senghor Seamount, this does not appear to hold true. An oxygen minimum

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zone has been detected within the Senghor Seamount area (Christiansen et al., 2009), with the lowest oxygen % saturation detected at ~ 400 m water depth. Low oxygen levels are still observed on the upper slope (Station B) and do not return to a higher level until 1500 m water depth. This is likely to reduce the observed standing stock values from the upper slope station (Station B).

It is well known that macrofauna standing stock may be influenced by an array of abiotic and biotic factors that operate at local and regional scales, influencing biodiversity and community composition (Consalvey et al., 2010). Many researchers have suggested that the benthic community structure is strongly influenced by depth, and altered abiotic and biotic conditions induced by a bathymetric gradient (Gage and Tyler, 1991; O'Hara, 2007; Naraynaswamy et al., 2005, 2010a, b; Lundsten et al., 2009). On seamounts, local hydrodynamics and changes in flow patterns may be induced by seamount topography and hence have an influence on both macrofaunal abundance and community composition by impacting upon sediment properties and composition (Turnewitsch et al., 2004), nutrient and larval dispersal, entrainment and retention (Lavelle and Mohn, 2010) and potentially enhancing secondary productivity by exporting organic material from surrounding environments (Consalvey et al., 2010). In this context it is important to note that, even for perfectly axisymmetric seamounts, combined flow fields of tidal and quasi-steady background flows around the seamount would be asymmetric (e.g. Chapman and Haidvogel, 1992; Goldner and Chapman, 1997; Holloway and Merrifield, 1999; Munroe and Lamb, 2005). This implies that, on a given side of the seamount, any direct or indirect depth-related effects may be superimposed by the effects of horizontal asymmetries in the flow field around the seamount. Or, in other words, any depth dependences one finds may well look different depending on the side of the seamount one looks at. Consequently, it should not be assumed that any depth dependences of the biological parameters this study finds for the northern side of the seamount can be applied directly to the other sides of the seamount: on the other sides of the seamount the depth-dependences may well be of a different nature as compared to the northern side.

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5.2 Changes in polychaete family diversity and composition

Seamount macrofauna research in the North Atlantic has predominantly focused upon seamounts and banks in the Azores and Madeira-Canary Island regions. Gillet and Dauvin (2000, 2003) investigated seamounts in the Southern Azores (Atlantis, Hyeres, Irving, Meteor and Plato), whilst Surugiu et al. (2008), looked at Ampere, Goringe, Josephine and Seine Seamounts/Banks in the same region. It is difficult to draw direct comparisons with the research of Gillet and Dauvin (2000, 2003) and Surugiu et al. (2008) as they used a variety of qualitative sampling techniques to sample the investigated seamounts e.g. Warren Dredges (mesh size 2 mm), Epibenthic Dredges and Beam Trawls (mesh size 5 mm). In addition to markedly different sampling strategies the seamounts have variable summit depths ranging from ~25–600 m water depth, and also widely variable heights above the surrounding abyssal seafloor. The sampling depth range was also smaller than that of Senghor Seamount, ~150–2000 m compared to ~130–3300 m at Senghor.

At Senghor Seamount a total of 34 polychaete families were identified from 954 individuals, this value is higher than identified on Atlantis (403 ind.; 18 fam.) and Hyeres (346 ind.; 13 fam.) seamounts. If the ratio of polychaete families/total individuals collected is compared from the different seamounts there are in fact clear similarities between Senghor Seamount ($34/954 = 0.036$), and Atlantis ($18/403 = 0.045$) and Hyeres ($13/346 = 0.038$) Seamounts. Five families dominate the polychaete fauna at Senghor, contributing > 95 % of the total polychaete abundance (see Table 3). Surugiu et al. (2008) also identified a number of dominant polychaete families e.g. the Onuphidae (~28 %, 1053 indiv.), Syllidae (~18 %, 699 ind.), Eunicidae (~16 %, 600 ind.), Amphinomidae (~12 %, 439 ind.) and the Nereididae (~5 %, 215 ind.); in total 10 families were identified which represented > 90 % of the total fauna collected.

Gillet and Dauvin (2000, 2003) noted the Eunicidae, Onuphidae and Amphinomidae as dominant families both in terms of individuals and species number at Atlantis and Hyeres Seamounts. The Syllidae, Nereidae and Pholoidae were the dominant families

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on Josephine and Meteor and the Eunicidae, Onuphidae and Amphinomidae were dominant on Irving and Plato Seamounts, whilst at Senghor the dominant families in terms of total taxa number appeared to be the Syllidae, Spionidae and the Cirratulidae. A number of families were represented by only one species at Senghor Seamount, these included e.g. the Arabellidae, Eunicidae, Fauvelliopsidae and Glyceridae (Table 3).

Gillet and Dauvin (2000, 2003) observed two main bathymetric zones at Atlantis and Hyeres Seamounts, the first from the summits to 600 m and the second from the slope > 600 m. They identified a number of families which were restricted to the deeper section of the slope, including the Ampharetidae, Hesionidae, Terebellidae and Sabellidae. Surugiu et al. (2008) also identified eight families which were only observed at deeper sites, these included the Hesionidae and the Sabellidae and a number of shallow-dwelling families living on the summit of the seamount e.g. Amphinomidae, Eunicidae and Syllidae. At Senghor the Dorvilleidae, Eunicidae and Lacydoniidae were found to be shallow dwelling families, only collected from the summit station, with a number of deeper dwelling families from > 1500 m also observed e.g. Ampharetidae, Arabellidae and Glyceridae (Table 3).

Few similarities were observed between Senghor Seamount and the Azores and Madeira-Canary Island seamounts. Many more families were identified at Senghor Seamount, although this may be the result of the higher number of individuals collected, it may also be a result of different sampling gear and mesh size used in this study to collect families with a smaller than average individual body size. The dominant families were also very different, the only similarity appearing to be the family Syllidae which dominated on Josephine and Meteor seamounts (Gillet and Daumvin, 2000, 2003). On Senghor Seamount there does not appear to be such a distinct bathymetric zonation of families, with a relatively high degree of similarity between stations in terms of family similarity (Fig. 2). A number of families were only observed on the summit of Senghor or below 1500 m, which contrasts with the families observed in the bathymetric zones identified by Gillet and Dauvin (2000, 2003). In addition to this, six families were

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widespread and found at all depths on Senghor Seamount i.e. Acrocirridae, Cirratulidae, Nereididae, Paraonidae, Spionidae and Syllidae, and therefore were not restricted to any bathymetric zone.

There are many differences between our findings on Senghor Seamount and those of Gillet and Dauvin (2000, 2003) and Surugiu et al. (2008), which may be attributed to a number of factors, including differences in sampling regimes, sampling gear, mesh sizes and the depth range sampled. In addition variable ecological and physical conditions (water chemistry, hydrodynamic regime and the possibility of sampling of different sectors of the asymmetric flow fields surrounding seamounts (see Sect. 4.1), oxygen concentrations and food availability) may also account for differences between the seamounts. It is particularly interesting to note that the majority of families, with an often lower than average individual body size were found in lower numbers at the Azores and Madeira-Canary Island sites, a difference likely to be attributable to the larger mesh size (2 mm–5 mm) used for these studies. There are also clear advantages of identifying the fauna to the lowest possible taxonomic level, i.e. (putative) species compared to family, as we found in our study that differences between the stations were much more pronounced when identified to (putative) species level (Figs. 2 and 5).

5.3 Changes in polychaete species diversity and composition

At the summit and deeper stations on Senghor Seamount, species richness and evenness were both relatively low, with what appears to be a uni-modal relationship between species diversity and depth, with a peak observed at the upper-slope station (Station B, 834 m depth). However, this peak in diversity was found at a shallower depth compared to many other deep-sea polychaete studies where the observed diversity maxima occurred at 1400–1800 m along the Hebridean Slope (Paterson and Lamshead, 1995) whereas in the tropical NE Atlantic, Cosson-Sarradin et al. (1998) found that polychaete diversity peaked at ~2000 m. In the Faroe-Shetland Channel polychaete species- and genus- level diversity occurred at depths between 450–550 m (Bett, 2001; Narayanaswamy et al., 2005, 2010a, b). In addition, others have found

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different patterns with other taxa for example, amphipods collected to the south of Iceland showed an increase in diversity with increasing depth, whilst in the Norwegian Sea, over the same depth range no discernible trend could be elucidated (Weissshappel and Svavarsson, 1998). When investigating the whole macrofauna community, Gage et al. (2000) observed a diversity maximum at 1400 m along the Scottish continental slope.

If the summit station values from Senghor seamount are removed a different pattern emerges; polychaete diversity appears to show a gradual and almost linear decrease in diversity with increasing depth across the remaining seamount stations. The base and reference station also have no discernible difference in diversity (Fig. 3c). In terms of species composition, the base and reference station displayed the highest between-station similarity (> 25%); however, as mentioned above, overall this is still a relatively low degree of similarity, suggesting quite different community compositions at each site, despite very similar depths.

At the species level the polychaete communities along the northern transect of Senghor seamount were found to be significantly different from one another ($p < 0.005$), with the shallow summit station (Station A) showing very low similarity (< 1%) to the remaining four stations (Figs. 4 and 5). It is not surprising that the polychaete community at Station A is so different from the other stations considering it is at only 133 m and very close to the main source of food supply. As mentioned above, the base and reference stations (Stations D and E at ~3200–3300 m depth) did not have a high level of similarity (< 30%) even though they were both at similar depths. The dominant species found at the base station (sp. 981) and the reference station (sp. 970) both belonged to the same family, Spionidae, however; sp. 981 was absent from the reference station and sp. 970 was absent from the base station, thus contributing ~15% to the dissimilarity between the stations.

It has been suggested that seamounts may act as biodiversity “hotspots” with elevated species richness (Samadi et al., 2006). Seamounts were also thought to act as “biogeographic islands” enabling many species to co-exist over a wide bathymetric

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range, creating a distinct, individual and complex environment with a suite of environmental and evolutionary factors (seamount geomorphology, geological origin, local hydrodynamic regime, light levels, oxygen concentration and water chemistry) acting in concert to shape community diversity (Clark et al., 2010). Koslow et al. (2001) found that most seamount species were distributed over a wide depth range on a Southern Tasmanian Seamount whereas at Senghor Seamount each station appeared to have very different species compositions. However, the results here do support the theory proposed by Longhurst (1998), that more change may be witnessed over 1000 m vertically than 1000 km horizontally. In addition the findings of McClain (2010) indicate that substantial change in assemblage structure may be observed over vertical scales, often as much as a 50 % change over a vertical distance of only 1500 m, which supports our findings. Depth is a significant factor driving the clustering of deployments at Senghor Seamount (Global ANOSIM, $R = 0.75$, $p < 0.001$), with depth often correlated to changes in environmental conditions (Grassle et al., 1979; Clark et al., 2010). It appears that at Senghor Seamount this effect is more pronounced, with a more marked change in community composition observed between stations, in as little as a vertical distance of 700 m. However, as emphasised above, although depth is very likely to be a direct and/or indirect driver of biodiversity and community composition, the effect of asymmetric flow fields around the seamount as a potential additional driver that is superimposed on the depth effect also needs to be kept in mind.

5.4 Seamount research

Although abundance, biomass and diversity of benthic macro and megafauna seamount communities remain relatively unknown, the communities themselves are of great interest due to the potential ecological importance of seamounts. Seamounts may form “oases of productivity” (Rowden et al., 2010) and biodiversity hotspots which contain a high proportion of endemic species (Richer De Forges et al., 2000). A lack of biological seamount studies however means such theories remain widely untested.

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Seamount ecosystems are understudied and poorly understood, they remain under-protected and commercial seamount focused fisheries remain widely unregulated. Additional evolving threats such as deep-sea mineral and metal extraction place further potential pressures upon seamount environments (Guinotte et al., 2006). It is important to continue interdisciplinary research to address the significant gaps in global seamount sampling (Consalvey et al., 2010) and gain a heightened awareness of these vulnerable, complex and intriguing habitats. In this context, it seems crucial to aim at a much improved mechanistic understanding of how interactions between the different flow components and the topography are translated into ecosystem patterns and processes.

Although the macro infauna of the deep North Atlantic is relatively well known, there are still habitats that remain unexplored and potentially new species to be discovered. Interest in the seamounts of the North Atlantic has grown over the past decade with more studies being undertaken both nationally and internationally (Gillet and Dauvin, 2000, 2003; Surugiu et al., 2008) and within a more integrated, interdisciplinary context (e.g. the OASIS, Topodeep and HERMIONE projects).

An increase in fishing for deep-water fish has raised concerns regarding the impact of trawling on the benthic community. On some seamounts/banks, e.g. Hatton, Rockall and Stanton banks, trawling for deep-sea fish is now prohibited (JNCC, 2011) with further protected deep-sea Special Areas of Conservation (SACs) planned as the scale of the damage is so great. In addition, interest in offshore energy development or oil and gas licensing has increased in deeper waters requiring initial baseline studies to be conducted (Narayanaswamy et al., 2005) in order to understand the biological communities present in these areas and to determine the potential impact upon the environment. Often these concerns are focussed on the larger sessile and motile megafauna and there have been few studies that have investigated the macro-infauna of seamounts (Gillet and Dauvin, 2000, 2003; Richer De Forges et al., 2000; Koslow et al., 2001; Surugiu et al., 2008), which is important when seeking to gain an integrated understanding of seamount ecosystem processes. Senghor Seamount is an important

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fishing area for Cape Verdean and also foreign fishing vessels and is fished for tuna (a species highly prized by Cape Verdean fishermen) and tuna-like fishes (Christiansen et al., 2009) in particular. A holistic study of this and other seamounts is therefore important when seeking to provide adequate information, to enable effective protection and management of these poorly understood, poorly protected and vulnerable deep-sea habitats.

Acknowledgements. The authors would like to thank the crew of the *RV Meteor*, the chief scientist Dr Bernd Christiansen and all scientific personnel of research cruise M79-3. We further thank Dr Gordon Paterson for assistance with polychaete identification, Dr Kai George and Ms Lena Albers of the Senckenberg Institute, Wilhelmshaven, for providing additional sediment samples for the research and for hosting AC for a month long visit to the Senckenberg institute in June 2011. Also thanks go to Dr Natalia Serpetti for assistance with polychaete identification and statistical analysis and to Miss Rosalind Barnes for support with the sorting of sediment samples.

The research leading to these results has received funding from the Natural Environment Research Council (grant awarded to RT and BN) (NE/G006415/1) and the European Community's Seventh Framework Programme (FP7/2007-2013) under the HERMIONE project, grant agreement n° 226354 (awarded to BN). AC was jointly funded through a PhD studentship by the Natural Environment Research Council and from the MASTS pooling initiative (The Marine Alliance for Science and Technology for Scotland) and their support is gratefully acknowledged. MASTS is funded by the Scottish Funding Council (grant reference HR09011) and contributing institutions.

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Table 1. Depth and position of stations sampled on and near Senghor Seamount.

Station	Depth (m)	Latitude (N)	Longitude (W)
A (summit plateau)	133	17°12.30′	21°57.70′
B (upper slope)	834	17°13.80′	21°57.29′
C (mid slope)	1534	17°15.57′	21°59.97′
D (base)	3241	17°21.75′	21°57.90′
E (reference)	3295	18°05.00′	22°00.20′

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Table 2. Total abundance (ind. m⁻²) and biomass values (g m⁻²) per depth station (Standard error values included).

Station	Depth (m)	Abundance (ind. m ⁻²)	SE Abundance (ind. m ⁻²)	Biomass (g m ⁻²)	SE Biomass (g m ⁻²)
A (summit plateau)	133	10160	1943	2.97	0.63
B (upper slope)	834	1136	232	0.48	0.14
C (mid slope)	1534	1744	251	1.22	0.30
D (base)	3241	1264	122	0.25	0.05
E (reference)	3295	960	269	0.33	0.12

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Table 3. Polychaete family analysis (total No. of species, total No. of individuals, presence (Y) /absence (–), according to depth). Five most dominant families in terms of total individuals also highlighted.

Polychaete family	Total No. of sp.	Total No. of ind.	133 m Stat. A	834 m Stat. B	1534 m Stat. C	3241 m Stat. D	3295 m Stat. E
Acrocirridae	5	24	Y	Y	Y	Y	Y
Ampharetidae	2	9	–	–	Y	–	–
Amphinomidae	3	6	Y	Y	Y	–	Y
Apistobrachidae	3	7	–	Y	–	–	–
Arabellidae	1	1	–	–	–	Y	–
Capitellidae	7	24	Y	Y	Y	–	–
Chrysopetalidae	3	62	Y	Y	Y	Y	–
Cirratulidae	11	123	Y	Y	Y	Y	Y
Dorvilleidae	2	6	Y	–	–	–	–
Eunicidae	1	30	Y	–	–	–	–
Flabelligeridae	2	3	Y	–	–	–	Y
Fauveliopsidae	1	9	–	Y	–	–	–
Glyceridae	1	1	–	–	–	Y	–
Hesionidae	5	40	Y	–	Y	–	Y
Lacydoniidae	2	2	Y	–	–	–	–
Lumbrineridae	2	6	–	–	–	–	–
Magelonidae	1	1	–	–	–	Y	–
Maldanidae	6	12	Y	–	Y	–	Y
Nephtyidae	1	1	–	–	Y	–	–
Nereididae	3	11	Y	Y	Y	Y	Y
Onuphidae	2	9	Y	–	–	–	Y
Opheliidae	4	17	–	Y	Y	Y	Y
Paraonidae	9	37	Y	Y	Y	Y	Y
Pholoidae	4	6	Y	Y	–	–	–
Phyllodocidae	1	1	–	–	–	–	Y
Pilargidae	2	2	–	Y	–	–	Y
Poecilochaetidae	1	1	–	–	Y	–	–
Sabellidae	3	47	Y	–	–	Y	Y
Serpulidae	3	3	–	–	–	Y	Y
Sigalionidae	5	7	–	Y	–	Y	Y
Sphaerodoridae	1	2	–	–	Y	–	–
Spionidae	16	97	Y	Y	Y	Y	Y
Syllidae	19	324	Y	Y	Y	Y	Y
Terebellidae	3	23	Y	Y	Y	–	Y

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Table 4. Cluster dissimilarity percentages as identified by similarity percentages (SIMPER). The number of species contributing to total dissimilarity between stations. Species contributing to > 5% dissimilarity included.

Stations	% Dissimilarity	No. sp. contributing dissimilarity	Sp. contributing to > 5% dissimilarity		
			Family	Species	% Contribution
A–B	99.5%	42	Syllidae	sp. 909	8.3
			Cirratulidae	sp. 997	6.2
			Chrysopetallidae	sp. 900	6.0
A–C	99.5%	44	Syllidae	sp. 907	5.6
			Syllidae	sp. 909	7.6
			Cirratulidae	sp. 997	5.7
A–D	99.9%	37	Syllidae	sp. 907	5.2
			Spionidae	sp. 977	5.0
			Syllidae	sp. 909	8.0
A–E	100.0%	41	Cirratulidae	sp. 997	6.0
			Chrysopetallidae	sp. 900	5.7
			Syllidae	sp. 907	5.5
B–C	97.2%	41	Syllidae	sp. 909	8.4
			Cirratulidae	sp. 997	6.2
			Chrysopetallidae	sp. 900	6.0
B–D	97.1%	37	Syllidae	sp. 907	5.6
			Spionidae	sp. 977	12.6
			Cirratulidae	sp. 1000	5.1
B–E	98.7%	42	Paraonidae	sp. 991	11.8
			Cirratulidae	sp. 1002	10.1
			Sabellidae	sp. 968	6.7
C–D	91.6%	34	Spionidae	sp. 970	8.2
			Cirratulidae	sp. 1002	6.2
			Spionidae	sp. 977	10.8
C–E	97.6%	40	Spionidae	sp. 981	10.5
			Cirratulidae	sp. 1002	8.9
			Sabellidae	sp. 968	5.9
D–E	82.4%	33	Cirratulidae	sp. 1000	5.0
			Spionidae	sp. 977	13.5
			Spionidae	sp. 970	6.9
			Cirratulidae	sp. 1000	5.7
			Cirratulidae	sp. 1002	5.2
			Spionidae	sp. 981	15.1
			Spionidae	sp. 970	9.1
			Sabellidae	sp. 968	7.5
			Cirratulidae	sp. 1002	7.1

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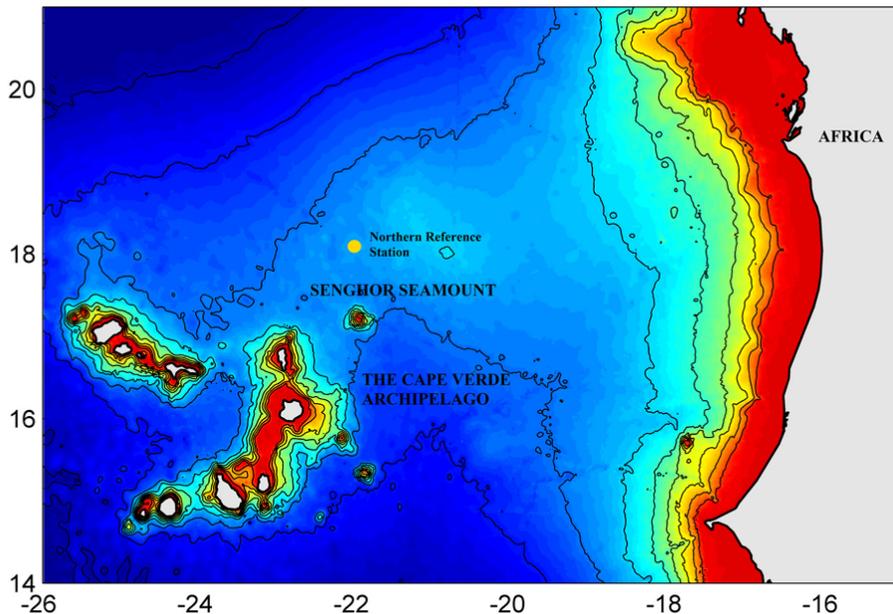


Fig. 1a. Senghor seamount, located in the Cape Verde Archipelago, 60 nm northeast of the island of Sal and ~ 550 km from the African mainland. Northern reference station also displayed. Data extracted from Smith and Sandwell (1997) dataset, created by A. Dale (SAMS).

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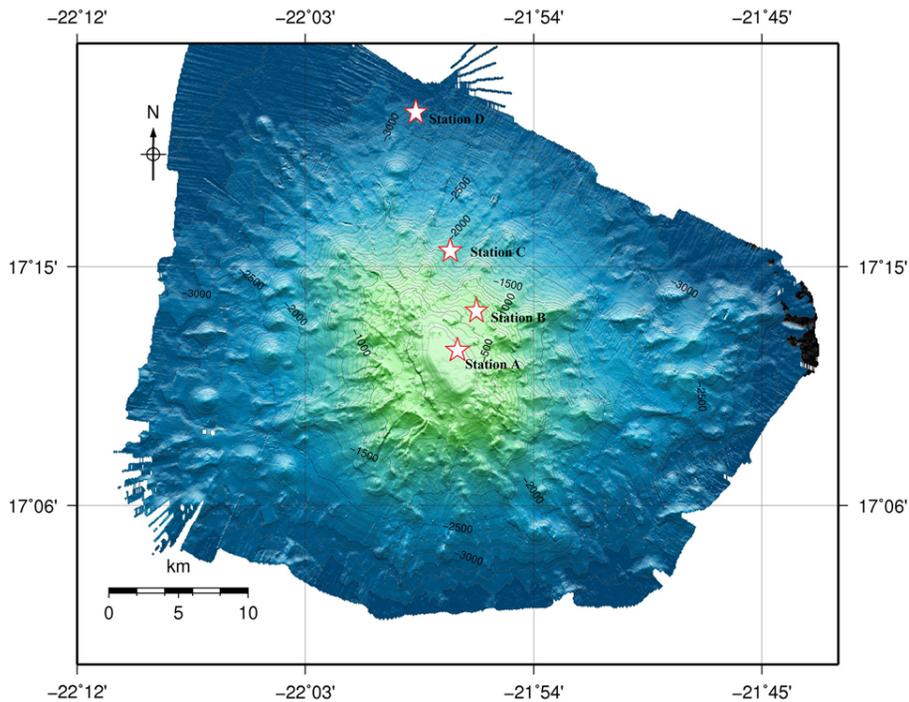


Fig. 1b. Senghor Seamount and the four on seamount north transect sampling stations (summit plateau depth ~ 130 m, base depth ~ 3200–3300 m). Adapted by A. Chivers, original data and map created by Dr. Thor Hansteen and Alexander Schmidt, GEOMAR.

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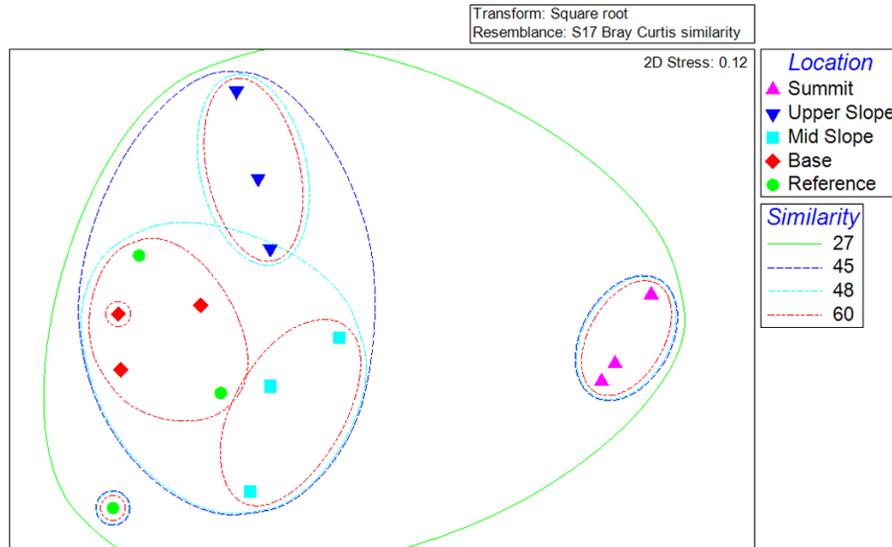


Fig. 2. Non-metric multi-dimensional scaling (MDS) ordination of the polychaete families along the Northern transect on Senghor Seamount (27%, 40%, 48%, 58%) similarity levels defined by Cluster analysis).

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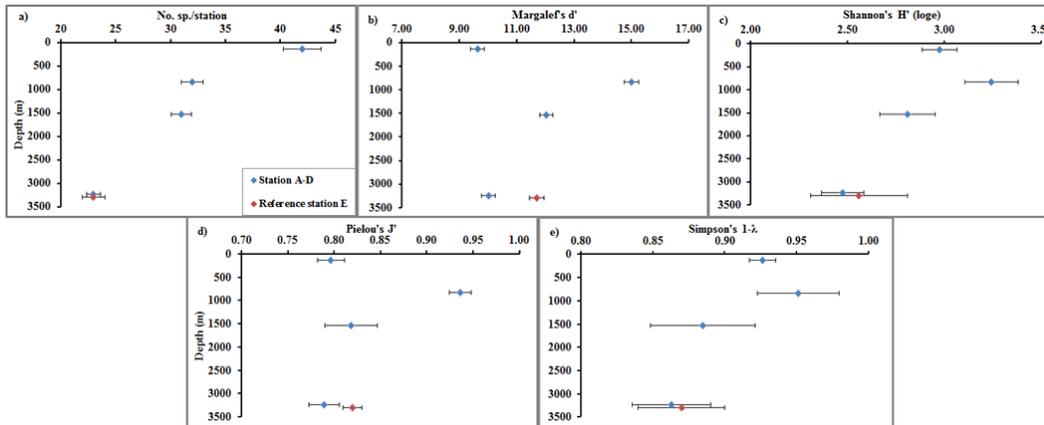


Fig. 3. Diversity of the macrobenthic polychaetes along the North transect; **(a)** No. sp./station, **(a)** Margalef's d' , **(a)** Shannon's H' (loge), **(a)** Pielou's J' , **(a)** Simpson's $(1-\lambda)$.

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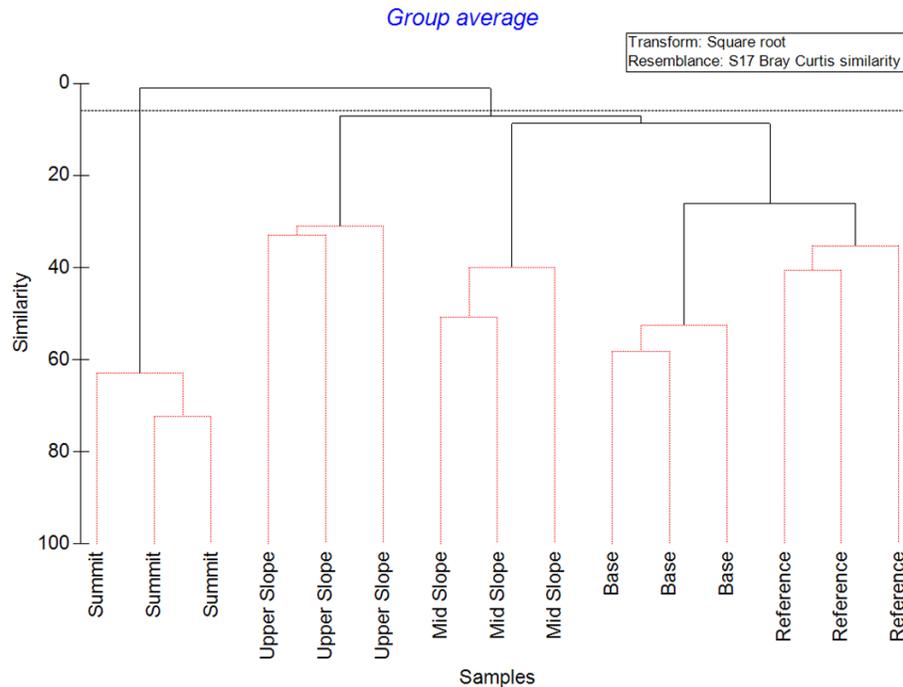


Fig. 4. Hierarchical, group-average linkage Cluster analysis on deployment replicate resemblance. The similarity profile (SIMPROF) test ($p < 0.05$) defines non-random clusters in the analysis.

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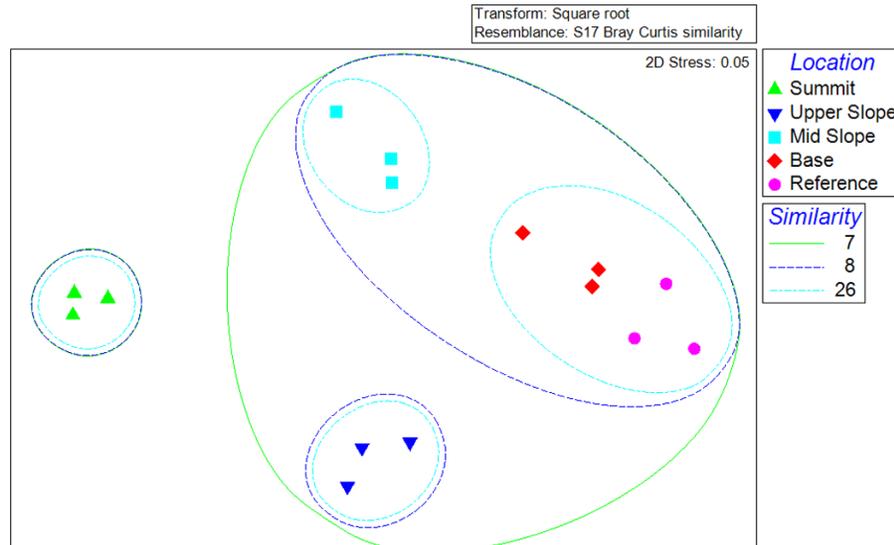


Fig. 5. Non-metric multi-dimensional scaling (MDS) ordination of the polychaete species along the Northern transect on Senghor Seamount (7%, 8%, 26% similarity levels defined by Cluster analysis).

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