Remotely Operated Vehicle exploring ichthyofauna association with habitat from shore-shelf, in an endemism hotspot in South Africa.

Minor dissertation

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Summary

The priority of understanding marine systems increases as expanding pressures are exerted on them. In South Africa, efforts are underway to utilise the ocean to stimulate economic growth which will result in further pressures on marine systems. The aim is to mitigate pressures, largely through proposed offshore marine protected areas (MPAs). One of these proposed MPAs is situated off the Kei river mouth in the Eastern Cape of South Africa.

The area offshore of the Kei river mouth is an endemism hotspot, and a transitional zone between the Subtropical East Coast and the Warm Temperate South Coast. The region was largely unexplored because of its treacherous sea conditions and because it was no longer an area of commercial fishing importance. A remotely operated vehicle (ROV) explored the regions' fish and benthic habitats and investigated their associations.

This study's results provide quantitative information on fish and habitat diversity in the intermediate depths off the Kei river mouth. Observations of rare, commercially important, yet critically endangered charismatic reef fish species were made. These included red steenbras (*Petrus Rupestris*), seventy-four (*Polysteganus undulosus*), red stumpnose (*Chrysoblephus gibbiceps*) and dageraad (*Chrysoblephus cristiceps*). Habitat types, including rhodolith beds, sponges, and deep-water corals were documented.

Maximum predicted fish diversity corresponded with mid-continental shelf, which is incorporated into the regions proposed MPA. The highest fish diversity was 10km within the shelf edge (which had a depth of approximately 100m) and was associated with the most structurally complex habitat biota: Fan Coral. Depth was a fundamental predictor associated with the presence and abundance of species distributions. The results support the location of the proposed MPA and are a step forward in identifying critical habitat to protect diversity

and endangered species, and thus contribute to the regions spatial management and governance.

Introduction

Marine biodiversity

Half of marine species are estimated to be undescribed (Appeltans et al. 2012). Marine species are a critical component of marine ecosystems that provide us with essential resources and services, therefore maintaining their diversity is critical (Worm et al. 2006). High species diversity has been linked to the resilience and the ability of marine ecosystems to adapt to change (Gray 1997) and endure threats such as fishing, ocean mining, habitat loss, invasive species, climate change, and pollution (Dulvy et al. 2003; Duffy et al. 2013). These threats to marine function motivate conservation, as do social and ethical justifications (Duffy et al. 2013). Protection focuses not on species, but on spaces of diversity (Roff & Evans 2002). Thus far, 5% of the global ocean and 13% of coastal and marine areas are protected (UNEP-WCMC & IUCN 2016).

Identifying areas of high diversity

A common strategy to identify marine spaces for protection is to use a randomly stratified survey design to record biodiversity and species as well as factors influencing them. Then, predictive models can be created to determine where diversity is likely to be the highest and species the most abundant (Rodríguez et al. 2007). Studies have found habitat and depth to be key predictors of species abundance and biodiversity, as these two variables are often correlated with a range of physical and biological factors that influence fish abundance (Tittensor et al. 2010; Heyns-Veale et al. 2016).

Intermediate depths

Fish and benthic habitat diversity in the intermediate depths remains largely unexplored. The intermediate depths are here forth defined as the range from 30m to 200m (the shelf break).

These depths include the transition between photic and aphotic zone (Bongaerts et al. 2010). They remain largely unexplored due to the depth limitations of SCUBA and more advanced sampling techniques being expensive and focused on the deep sea (Hinderstein et al. 2010). Their exploration is critical to fully understanding marine diversity and species spatial distributions. An understanding of which is essential for systemic marine conservation (Hinderstein et al. 2010).

Remotely operated vehicles

Remotely Operated Vehicles (ROVs) can uniformly sample vast areas over a range of depths and environmental conditions. ROVs have efficiently and non-destructively collected randomly stratified footage that allows diversity (of both habitats and biota) to be documented. From this documented diversity, habitat and biota distribution maps have been created (Neves et al. 2014; Geldenhuys 2015; Althaus et al. 2015). Protected areas, endangered species, and sensitive habitats can be sampled with ROVs as they are non-destructive, but they have other limitations. For example, taxonomic resolution can be compromised and new species observed not described, since organisms are not retrieved as in trawls and grabs (Stevens & Connolly 2005). Identification and detection can also be challenging as some species actively avoid ROVs while cryptic and small species may go undetected, this can be problematic depending on the objectives of studies (Trenkel et al. 2004; Lorance & Trenkel 2006; Makwela et al. 2016).

The objectives of studies must align with the size of unit area sampled. In marine biodiversity studies, typically resolutions of 10km^2 or finer are used (Stevens & Connolly 2005). Diversity of habitat types is often used as a proxy for marine biodiversity (Agardy et al. 2003; Stevens & Connolly 2005). If sampling occurs at too fine a scale, habitats that are functionally the same can be classified as different habitats based on small physical or biological differences. Alternatively, sampling at too course a scale can mean that small physical or biological differences that are important to habitat functionality will go undocumented (Thrush et al. 1997). The size of unit area sampled impacts protection prioritisation. Too fine scale sampling can result in the detection of an enormous number of unique habitats and habitat compositions that are not necessary functionally different from one another. Such sampling could promote fragmented protection of portions of these unique habitats. On the other hand, sampling at too coarse a scale can prevent important functional habitat from being prioritised for protection because it's functional importance has gone undetected (Armonies 2000).

Marine protected areas

ROV collected fish and habitat data can be mapped to understand the spatial associations between them. This process allows habitats that are essential to fish to be identified and protected. While MPAs may be uniquely designed to meet specific conservation criteria, the general design methodology is to protect areas rich in biodiversity, maximising species' protection (Norse 1993). Effective MPAs have helped some of South Africa's endangered seabreams to recover (Booth & Punt 1998; Kerwath et al. 2013; Mann 2013).

A state of emergency was declared in the line fishery in 2000, as many South African line-caught fishes were severely overexploited. Due to marine spatial planning, mainly in the form of no-take marine protected areas (MPAs), some previously exploited species are recovering. Recovering species include roman (*Chrysoblephus laticeps*), seventy-four (*Polysteganus undulosus*), panga (*Pterogymnus laniarius*), and carpenter (*Argyrozona argyrozona*) (Götz et al. 2008; McCord & Zweig 2011; Mann 2013). To further aid the recovery of previously exploited species and to ensure the sustainability of South Africa’s growing ocean economy, a network of offshore MPAs has been proposed to extend the existing MPAs, which are all coastal (DEA, 2016; Sink, 2016).

One of the new proposed MPAs is an extension of the existing Amathole MPA offshore of the Kei River mouth. The area is relatively unexplored but is an endemism hotspot due to its location (Turpie et al. 2000). Its location is a geographical transition boundary between the subtropical East and warm temperate South Coast (Turpie et al. 2000).

The region contains a diversity of habitats including submarine canyons; rocky reefs; deep water corals; and paleo river beds, dunes, and coastlines (DAFF, unpublished data). The Kei river fluvial fan is thought to be one of a few areas where dusky kob (*Argyrosomus japonicus*) and white steenbras (*Lithognathus lithognathus*) spawn (DAFF, unpublished data). Despite the regions biodiversity significance, it is relatively unexplored due to its treacherous sea conditions and lack of commercial fishing activity. The Agulhas current hugs the narrow continental shelf of the region, often intensifying the nearshore current to speeds that are unsafe for subsurface exploration.

This study provides a quantitative assessment of fish species diversity and relative abundance in relation to depth and habitat type offshore of the Kei river mouth. The aim was to visually explore and describe the benthic habitats and ichthyofauna using a ROV, as well as determine which environmental variables best explain patterns of fish distribution, abundance, and community composition. The outcomes of this study will inform and guide future marine spatial planning and conservation. It will assist in determining if the proposed offshore expansion of the Amathole MPA would protect important fish habitats.

Methods

Study Area

Located in the Eastern Cape of South Africa, off the Kei river mouth is a marine endemism hotspot and important boundary between the subtropical East Coast and warm temperate South Coast (Turpie et al. 2000). As the area has seldom been commercially fished in recent years, data are mostly confined to incidental recreational fishing records. These records suggest that the region contains critical habitat for several formerly commercially important but now endangered sparidae species including red steenbras (*Petrus Rupestris*), seventy-four (*Polysteganus undulosus*), red stumpnose (*Chrysoblephus gibbiceps*) and dageraad (*Chrysoblephus cristiceps*) (DAFF, unpublished data). It potentially contains coelacanths (*Latimeria chalumnae)*. The first live coelacanth was caught in the region in 1938 (Smith 1939; Amemiya et al. 2013). To conserve this sensitive marine ecosystem, and the endangered endemic species that occur there, an offshore marine protected area was proposed under Operation Phakisa (DEA 2016). This proposed MPA will extend the existing inshore Amathole MPA.

Data collection

Locations for ROV transects were selected based on the areas of high recreational fishing activity and information from research surveys, including single and multibeam sonar data.

ROV deployment

Footage from 21 ROV dives was collected between the 30th of January and the 21st of May 2017. Typically, 90 minutes of footage was collected per dive (including descent and ascent). Some dives terminated early due to strong currents and technical difficulties.

The vessel’s on-board GPS tracked each dive transect. The tracks consisted of individual points, ranging between 1 to 17 seconds apart. Each point had position, depth and time data associated with it. The time on the track at which the ROV entered the water and first sighted the sea floor was manually recorded for each dive.

A hydraulic winch was used to deploy the ROV (Sea-Eye Falcon, Saab) and clump weight (300kg) from the vessel. The cable attached the clump weight to the vessel. The tether ran from the vessel along the cable and connected to the ROV (Figure 1). The ROV could move, at most, within a 50m radius around the clump weight. The fast flow of the Agulhas current confined ROV operations to transects in the general direction of the current (in a South-westerly direction parallel to shore and shelf). Transects were conducted in a manner conducive to both assessing fish (diversity and abundance) and surveying benthic habitat, however, speed was variable and largely a function of current speed. During transects the ROV hovered approximately 1m above the seafloor and an effort was made to maintain a slow and steady ROV pace.

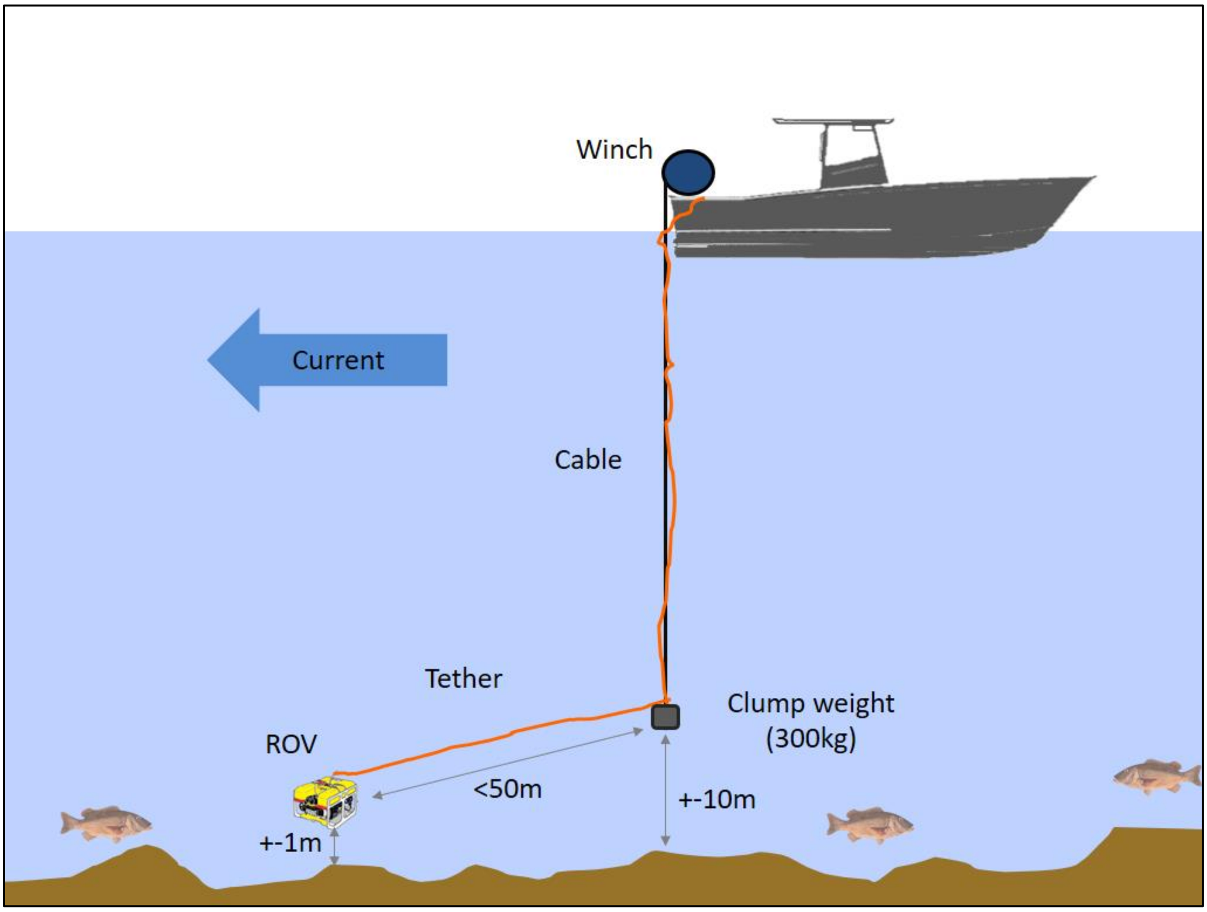

Figure 1: Diagram of remotely operated vehicle (ROV) deployment setup. The ROV was connected to a clump weight by a cable, which was connected to the boat. The clump weight hung directly under the boat, while the ROV flew above the seafloor. Note diagram is not to scale (diagram adjusted from http://www.seaeye.com/rovs.html and Smith & Heemstra (1986)).

The GPS track positions of ROV dives were overlaid with a grid of 464m by 464m (464m = 0.25 nautical miles) cells in ArcMap (ESRI 2011). This was considered the finest feasible resolution given the limited control over the transect direction; the error introduced by the uncertainty over the exact ROV position under the vessel; and the issue of spatial autocorrelation of benthic assemblages at smaller (<100 m) distances (Bernardino et al. 2012).

Data alignment

In ArcMap (ESRI 2011) the time on the GPS track when the ROV entered and exited each grid cell was determined. By aligning the time on the track when the ROV hit the water (which was manually recorded) with the time when it could be seen hitting the water in the footage, the time stamp on the footage (since recording began) was aligned to the vessel GPS data.

Viable grid cells

Grid cells in which the ROV spent less than three minutes were considered to not have collected sufficient data to be representative of the grid cell and were therefore eliminated from further analyses. A total of 58 grid cells were analysed (Figure 2). Distance to shore and shelf (from the centre of the grid cell) were calculated in ArcMap (ESRI 2011), where shelf was defined as the 200m depth contour.

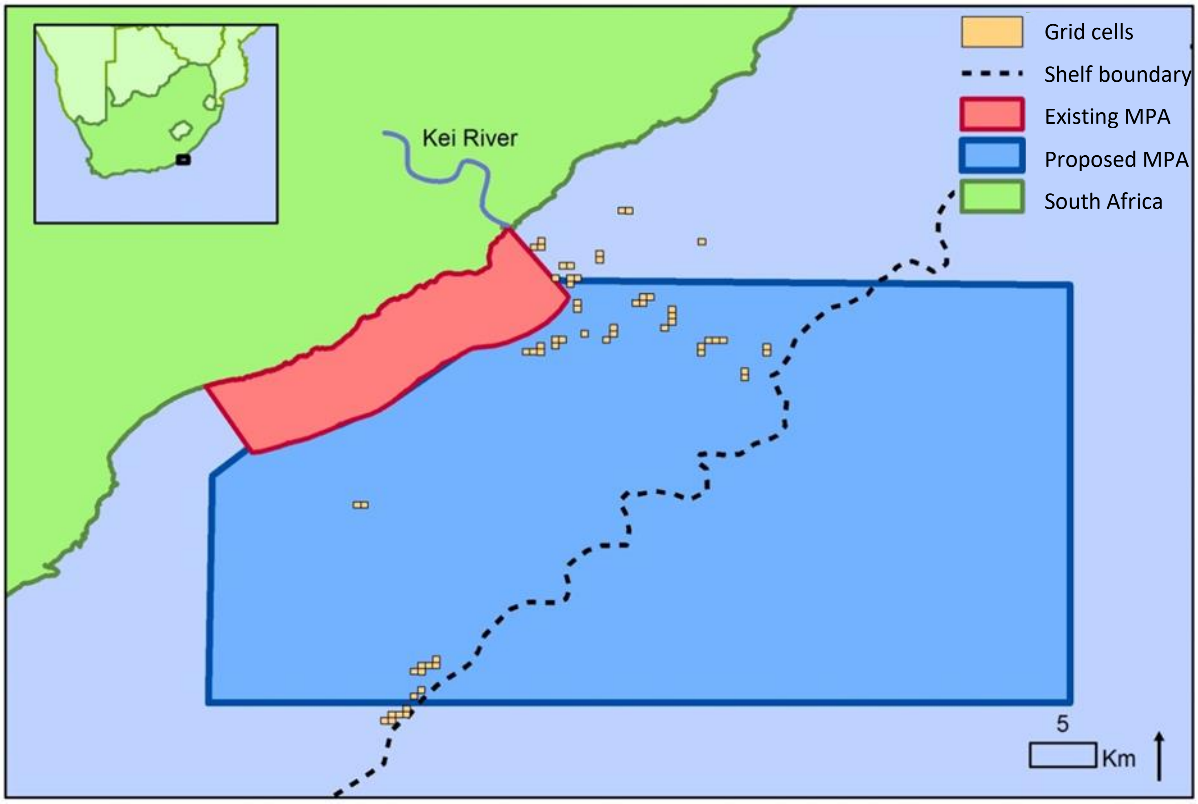

Figure 2: Map of South Africa indicating the study region, the current MPA, and the proposed MPA. Grid cells and continental shelf boundary are indicated.

Sampling environmental factors

As the speed and direction of the transect could not be controlled and varied within and between each dive, a random stratified design was used to sample each grid cell's habitat. Footage of each grid cell was divided into six equal length time segments. The depth and habitat (relief, substrate, and biota) in the last frames of the first five segments were then determined (Figure 3). The depth at the sampling points within each grid cell were determined by matching the time on video to the time on the GPS track and extracting the GPS depth measurement.

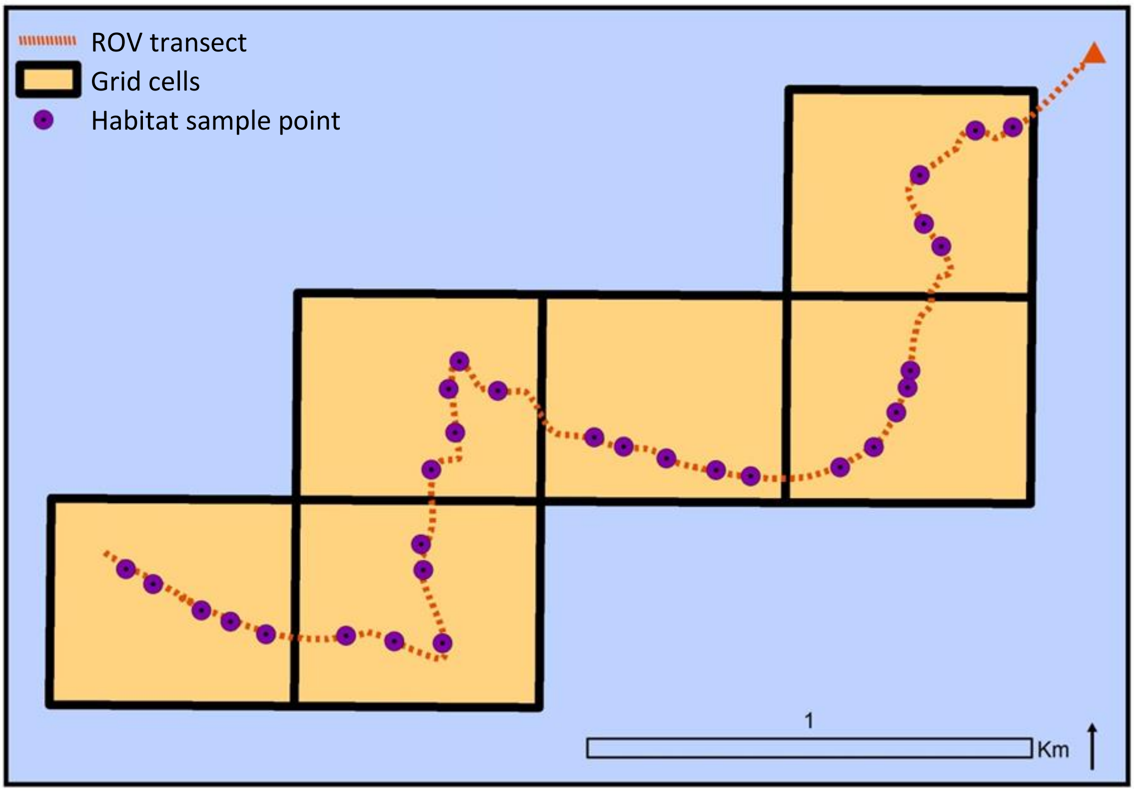

Figure 3: A ROV dive transect and the grid cells it explored. Within each grid, habitat was sampled at five evenly spaced points in time.

Habitat was classified according to the Collaborative and Automated Tools for Analysis of Marine Imagery (CATAMI) classification system (version 1.3) (Althaus et al. 2013). This system was designed to capture the complexity of marine environments from images and videos by categorising physical habitat (substrate, relief, and bedform) and biota. This comprehensive system takes into account that it is not always possible to identify habitat to the lowest classification level, and works on a hierarchical structure to avoid duplication of categories (Althaus et al. 2015) (Figure 4 illustrates the hierarchical classification of substrate, as an example). For substrate and relief, the lowest classification level was consistently reached. For biota it was not possible to ascertain whether fine branching algae was brown or red, thus it was simply classified as fine branching algae. CATAMI bedforms described formations in sand and mud substrate, such as ripples, waves, bioturbation, and no formations. Bedforms data were excluded from analysis because such substrates were largely dominated by no formations. The remaining CATAMI components of biota, substrate, and relief were included.

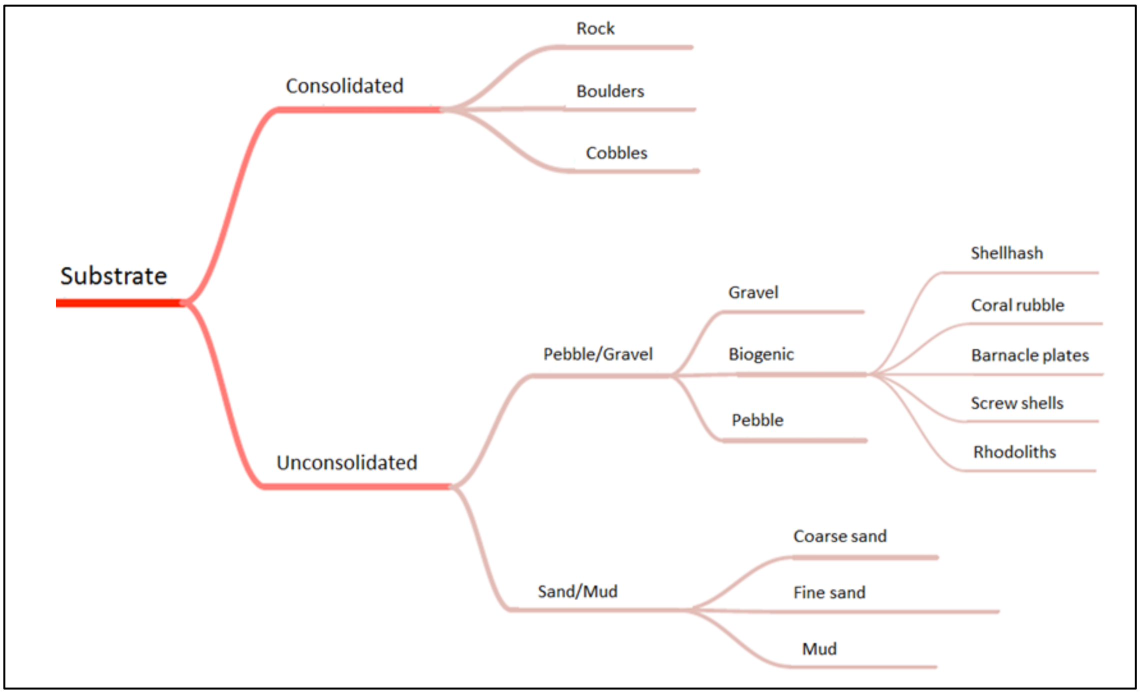

Figure 4: CATAMI classification scheme of physical habitat substrate, used in this study (diagram adapted from Althaus et al. (2013)).

Sampling fish

Fish were identified to species level whenever possible, or alternatively to family level. In each grid cell, the highest number of individuals of each species within one frame (MaxN) was determined for all fish species encountered. MaxN reduces over-estimation by eliminating the possibility of recounting individuals in a grid cell. Thus MaxN is conservative and generally underestimates the abundance of fish present, especially when fish are in dense shoals and visually obstruct one other (Kleczkowski et al. 2008).

Data analysis

Environmental factors

Habitat data collected was clustered to create representative levels of coarse functional habitat. Habitat was documented in terms of the following CATAMI categories: biota, substrate, and relief. CATAMI types rarely encountered (less than five occurrences throughout all grid cells) were removed. Categories were separately and collectively compiled into clusters. Categories in lowercase refer to categories prior to clustering. For example, relief refers to data collected which includes the many types of relief observed (flat, low, moderate, high, and wall). Relief can also simply refer to the change in elevation of the sea floor. While categories' clusters are referred to in uppercase letters and clusters are referred to in italics. The clustered categories of RELIEF include two clusters *high* and *low* (Figure 5).

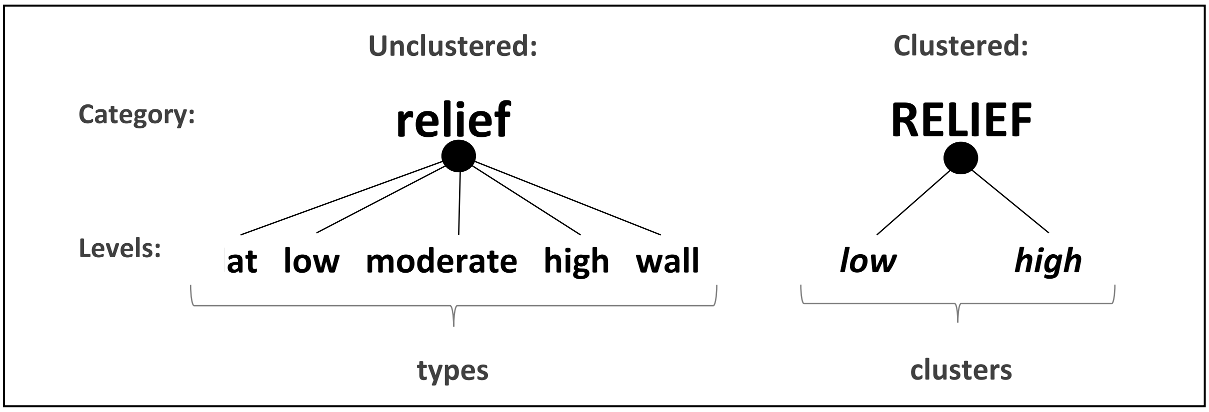

Figure 5: Case and font of the category and levels of clustered and unclustered relief.

The CATAMI categories biota, substrate, and relief, were individually clustered to create new coarse scale habitat variables: BIOTA, SUBSTRATE, and RELIEF. In addition, an overall habitat variable (HABITAT) was derived from collectively clustering the CATAMI biota, substrate, and relief data. Hierarchical cluster analysis was used to create dendrograms of biota, substrate, relief, and habitat. For exploratory purposes each dendrogram was split into between two and seven clusters. The final number of clusters used in analyses going forward for each category was based on the following considerations. Firstly, that the habitat composition of each cluster represented habitats types that were observed in the footage. Secondly, that each cluster was sufficiently explored, i.e. at least five grid cells made up each cluster. Clusters where created using the package Nbclust (Charrad et al. 2015). The resultant cluster groups (BIOTA, SUBSTRATE, RELIEF, and HABITAT) were used as explanatory variables for describing ichthyofauna diversity as well as species abundance.

The median of depths sampled within each grid cell was used to determine grid cell depth. Depth range per grid cell in relation to absolute average depth of the cell was calculated as follows:

$$\frac{(maxium\ depth - minimum\ depth)}{median\ depth}$$

Dividing the depth range by the median accounts for changes in depth having different effects for shallow and deep water; for instance, small changes in depth when in shallow water will have greater impacts on environmental factors such as light, tidal surge, etc, than in deep water.

Fish and environmental factors

Sampling effort

A species accumulation curve, species richness sampled per unit effort (grid cell), was constructed to assess whether the entire sampling effort had been sufficient. This was constructed using iNEXT (Hsieh et al. 2016). If more than 75% of species where predicted to have been sampled, sampling was considered sufficient.

Habitat factors associated with ichthyofaunal composition

Relations between ichthyofaunal composition and environmental explanatory variables were explored by creating a Multivariate Regression Tree (MRT). This approach tolerates non-linear relationships and higher order interactions between environmental explanatory variables and multivariate response variables. In this approach, grid cells were clustered into groups according to species similarity by means of binary recursive portioning of the data. Data portioning was created through a series of binary splits of the environmental explanatory variables, while the highest within-group species similarity was achieved by minimizing the sum of square Euclidean distance within each resultant group (De'ath 2002; Parker 2015).

For the MRT analysis the ichthyofaunal composition (MaxN per species per grid cell) data was square root transformed, to give weight to rare species. The species composition of each cell was related to the spatial variables depth, RELIEF, SUBSTRATE, and BIOTA with the purpose of objectively grouping cells into units of high species similarity. The percentage contribution of each species (>5% frequency of occurrence) to the ichthyofaunal composition of each terminal group of the MRT was calculated (Parker 2015). All MRT analyses were carried out with the mvpart library (De'ath 2002).

Species richness and individual species associations with habitat factors

Generalised additive models (GAMs) were used to investigate the effects of environmental variables on fish species richness and individual species abundance. A range of categorical and continuous explanatory variables were considered in each GAM. The categorical variables were created from the cluster data, they consisted of: BIOTA; SUBSTRATE; RELIEF; and HABITAT. The continuous explanatory variables included: distance to shore; distance to shelf; depth; and variation in depth (which were smoothed with k=5) (Table 1).

Table 1: Summary of variables investigated during generalised additive model selection.

Variable	Continuous				Categorical			
	Depth	Distance to shore	Distance to shelf	Variation in depth	BIOTA	SUBSTRATE	RELIEF	HABITAT
d.f.	1	1	1	1	5	4	2	5
Spline	k=5	k=5	k=5	k=5	-	-	-	-

The GAMs were run in two general forms. The first general forms' response variables were species richness per grid cell and individual fish species MaxN (only of fish that were not observed in dense shoals) per grid cell. These individual species included barred fingerfin (*Cheilodactylus pixi*), twotone fingerfin (*Chirodactylus brachydactylus*), spottail coris (*Coris caudimacula*), cape gurnard (*Chelidonichthys capensis*), fransmadam (*Boopsoidea inornata*), and comber (*Serranus cabrilla*). In this first form a Poisson distribution was used.

The second general form used a binomial error structure. It accommodated data from species observed only occasionally but in dense shoals (zero-inflation probability). Abundance data for these species were converted to presence-absence data and a binomial error structure was used. These species include seventy-four, and blue hottentot (*Pachymetopon aeneum*).

Two models structures, A and B, were used for each response variable. The explanatory variable HABITAT was the basis for model structure A, while BIOTA, SUBSTRATE, and RELIEF were the basis of model structure B. HABITAT could not be included as a term in any model that included BIOTA, SUBSTRATE, or RELIEF, because the datasets used to create BIOTA, SUBSTRATE, and RELIEF clusters were combined to create HABITAT clusters, and are thus innately correlated. Variation in depth was added as an explanatory variable to both the models structures A and B.

Depth, distance to shore, and distance to shelf were collinear, and therefore only one of these environmental variables could be retained - collinearity was concluded as the variables variance inflation factor (VIF) was greater than 3 (Zuur 2009). Selection for one of the collinear variables was performed as follows: the collinear explanatory variables were individually added to null models, and these model results were compared. Depth was excluded from subsequent models only if it explained 10% less deviance than either of the other explanatory variables. This bias was applied because depth was considered to more directly impact environmental variables than the other collinear variables and be more reliable and useful in predicting species distributions. In cases where depth was excluded, the remaining explanatory variable that explained the highest deviance was retained in both the models structures A and B.

Final models for both structures A and B were constructed using a backward elimination procedure, dropping the least significant term in the subsequent model, until only terms with a significance of greater than 10% were retained in the final model. If by this rule no terms were retained in the model, the last term left in the model was retained.

The most appropriate overall final model between the two final model structures (A or B) was determined as that with the highest deviance explained. The final models were tested for over dispersion, which was classified as a dispersion parameter greater than 1.3 using the following formula:

$$dispersion\, parameter = \sum \frac{(model\, residuals)^2}{(degrees\ of\ freedom\ of\ model\ residuals)}$$

If over dispersion was detected model selection was repeated using Quasi-Poisson (for originally Poisson models) or negative binomial distribution (for originally binomial models) (Zuur 2009).

Explanatory variables retained in the final models were isolated and their influence on their response variables explored. The impact of explanatory variables for a reference set of standard conditions was predicted for each response variable. The reference set was chosen by fixing categorical explanatory variables to their most common value and the continuous variables to their mode. The results therefore represent the predicted values of a chosen response variable's range while the remaining variables were fixed at predefined values. This aided the interpretation of models. Analysis was performed using the mgcv library (Wood & Augustin 2002).

Results

Environmental factors

Biota

Observed biota were dominated by algae, corals, and sponges (see Figure 6). Algae biota consisted primarily of erect fine algae; corals mainly by fan corals; sponges by erect sponges; and the other biota category was dominated by brittle stars (see Figure 6 & Figure 7). The maximum depth at which algae biota was observed was 90m.

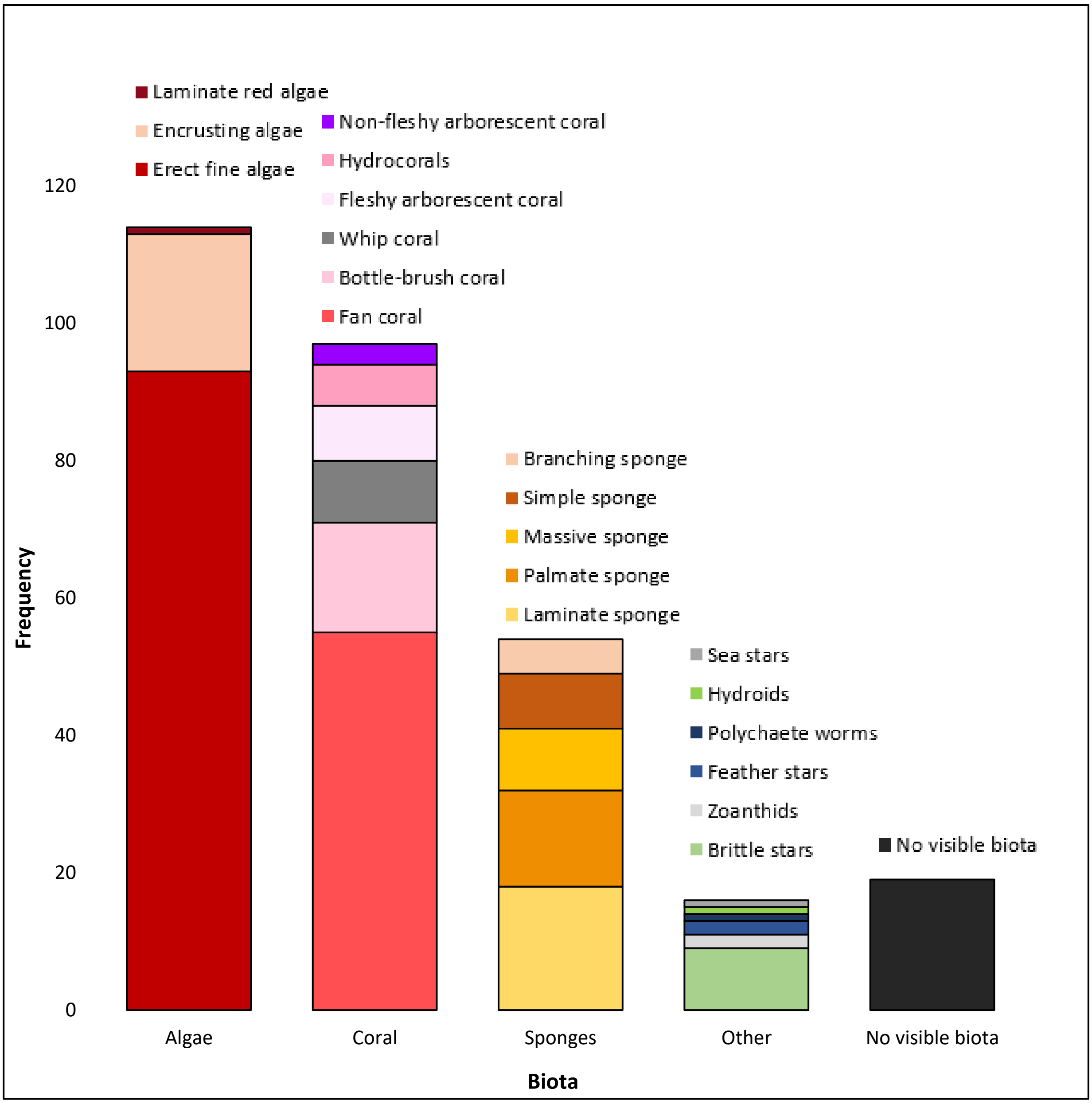

Figure 6: Frequency of benthic marine habitat biota sampled at 5 points within each of the 58 sampling grid cells off the Kei river mouth in the Eastern Cape, South Africa.

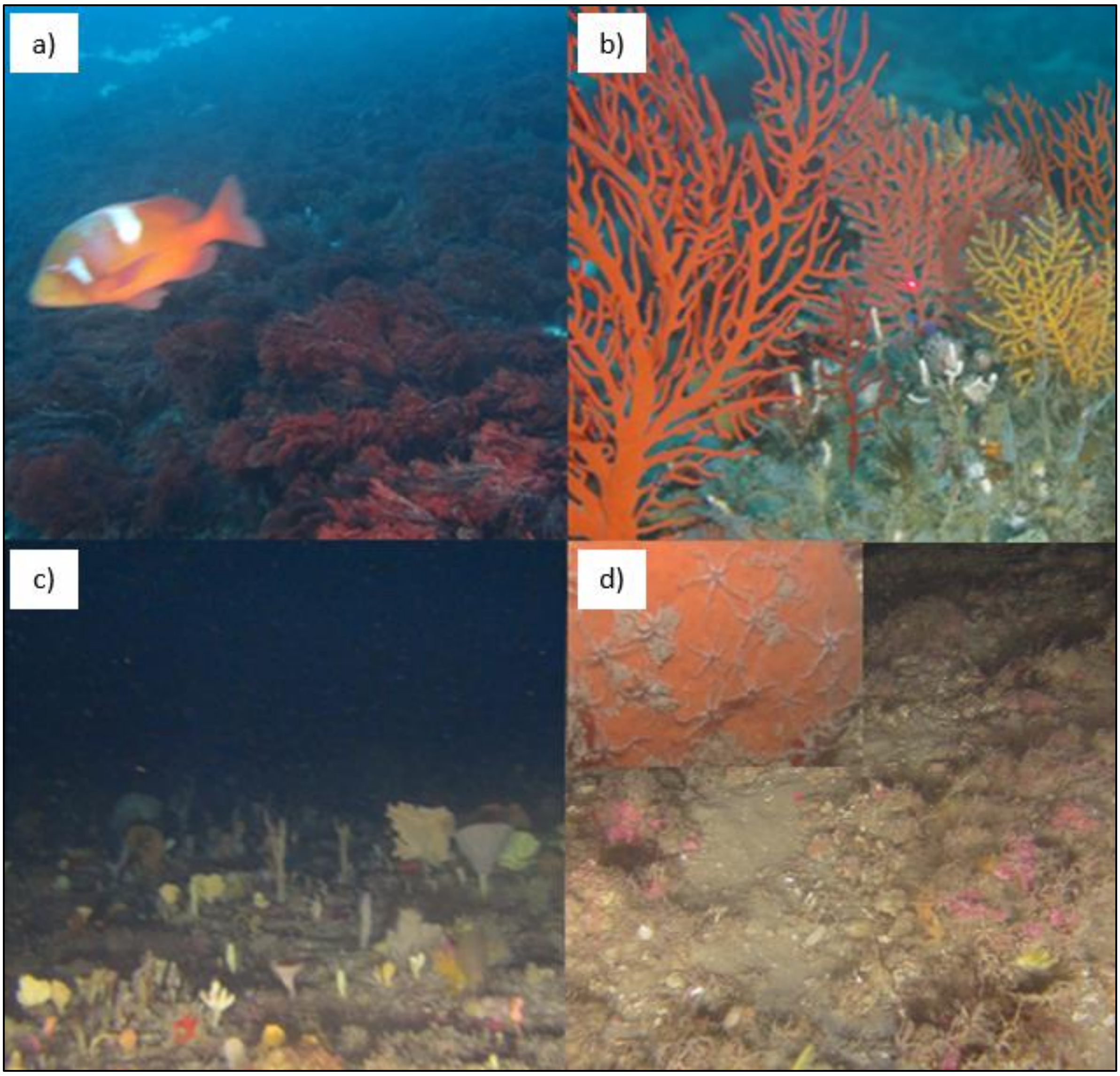

Figure 7: Benthic habitat biota that dominated each habitat biota category. Algae was dominated by a) erect fine algae, coral by b) fan coral, sponges by c) erect sponges, and other by d) brittle stars.

Biota in grids clustered into 5 groups: *Erect and encrusting algae*; *Erect algae*; *Fan coral*; *No visible biota*; and *Sponges and coral* (Figure 8). The *Sponges and coral* cluster had the highest diversity of biota and greatest number of grids sampled. The BIOTA of *Erect and encrusting algae* represents the biota associated with the substrate type rhodolith beds.

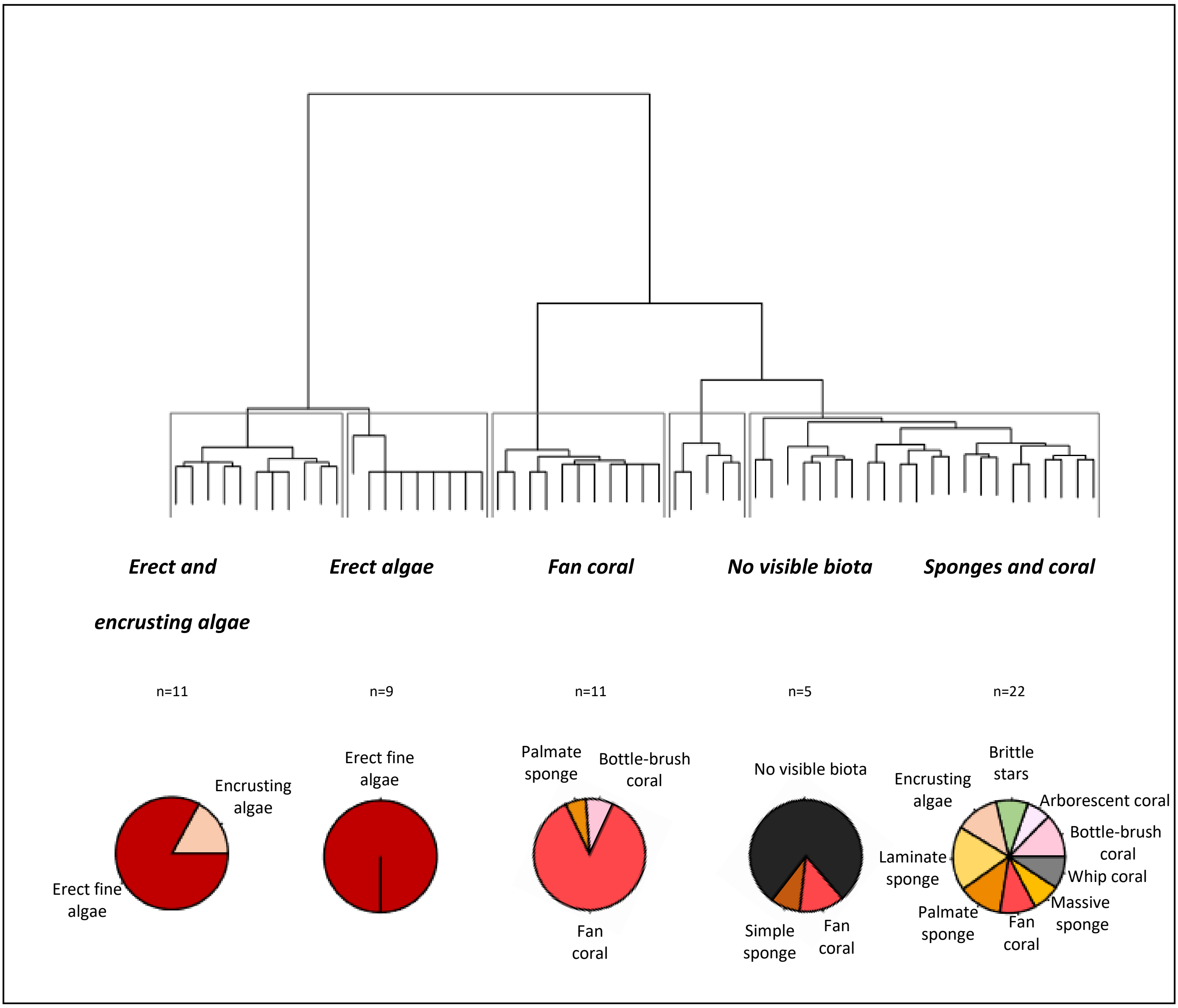

Figure 8: BIOTA cluster dendrogram with final clusters indicated; clusters descriptive names; number of grids each cluster contains (n); and the contribution of each biota (>5% frequency of occurrence) to each cluster.

Substrate

Substrate broadly consisted of consolidated and unconsolidated substrate. Consolidated substrate was largely dominated by rock, however unconsolidated substrate was more abundant, and consisted of primarily coarse sand, rhodoliths, and coral rubble (see Figure 9 and Figure 10). Rhodoliths are unattached orbs of non-geniculate coralline algae. They remain unattached because currents and waves continuously move them, preventing them from attaching to the sea floor. Large numbers of rhodoliths form rhodolith beds, which create a unique substrate (Foster 2001) (Figure 10 c).

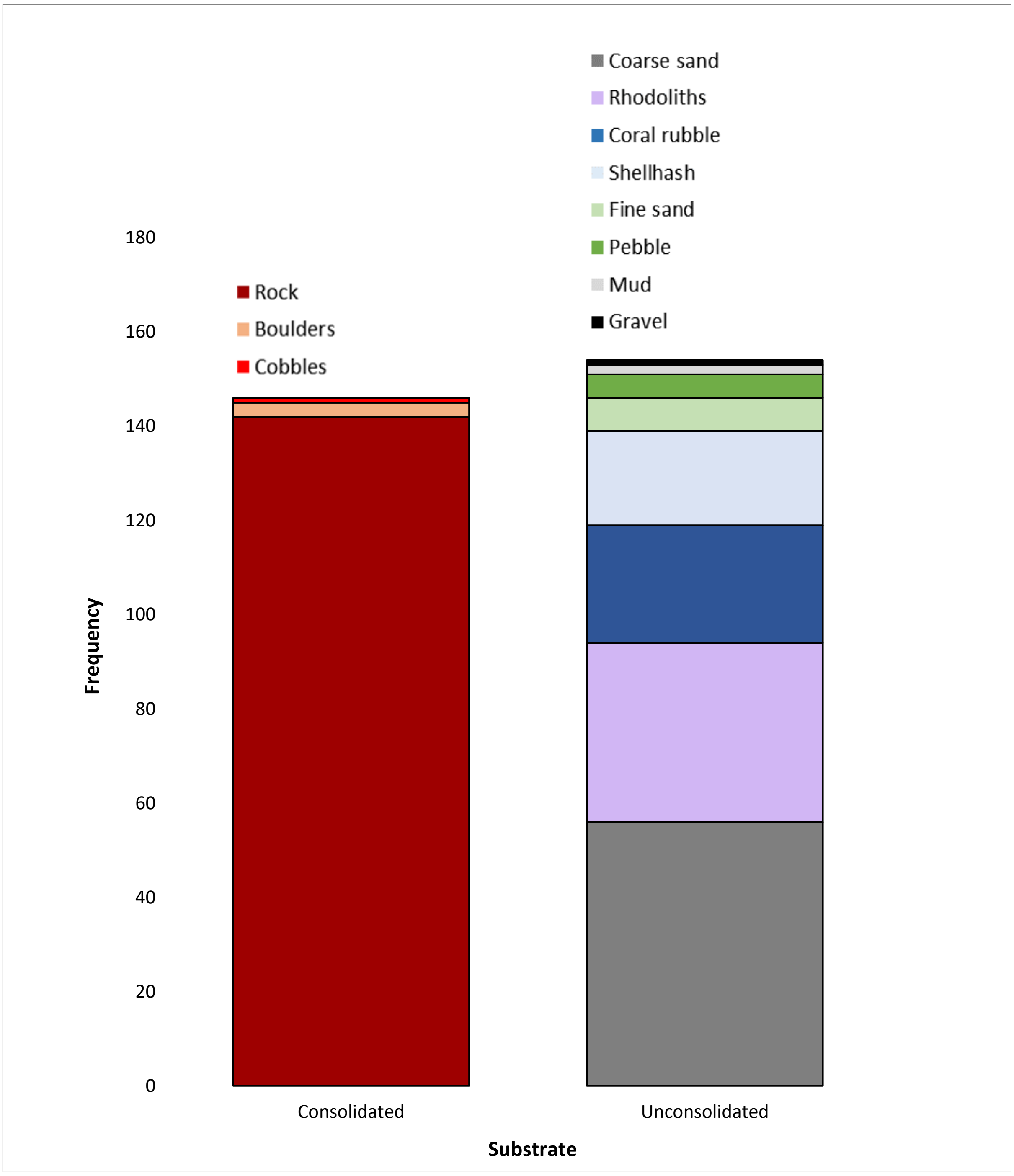

Figure 9: Frequency of marine benthic substrate sampled at 5 points within each of the 58 sampling grid cells off the Kei river mouth in the Eastern Cape, South Africa.

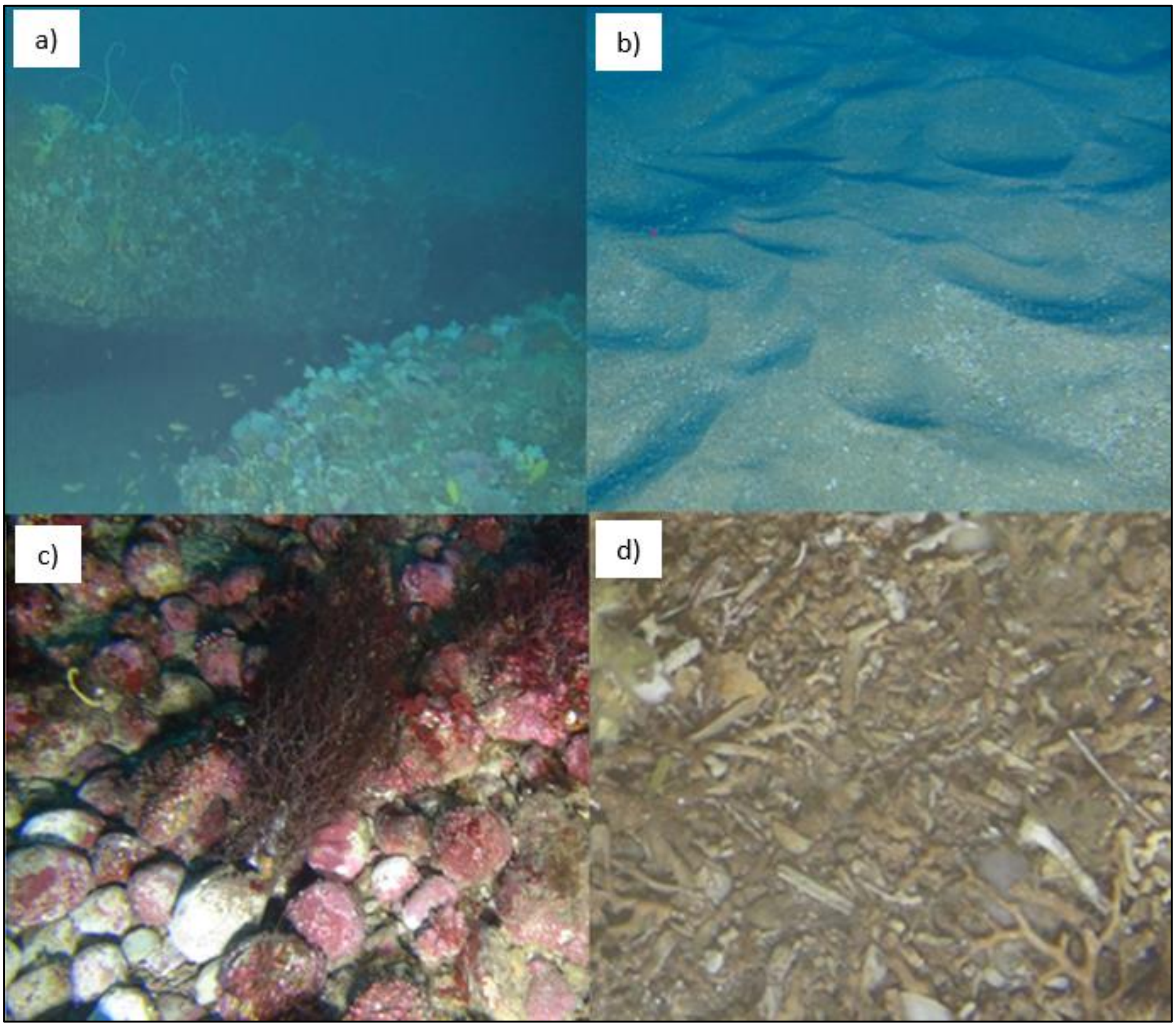

Figure 10: The substrate consolidated category was dominated by a) rocks, while the unconsolidated category comprised mainly of b) coarse sand, c) rhodoliths, and d) coral rubble.

Substrate in grids clustered into 4 groups: *Rock*; *Coarse sand*; *Rhodoliths*; and *Coral rubble* (Figure 11). The cluster *Rock* characterised most of the grids sampled (n=31). While *Rhodoliths* characterised the least (n=10).

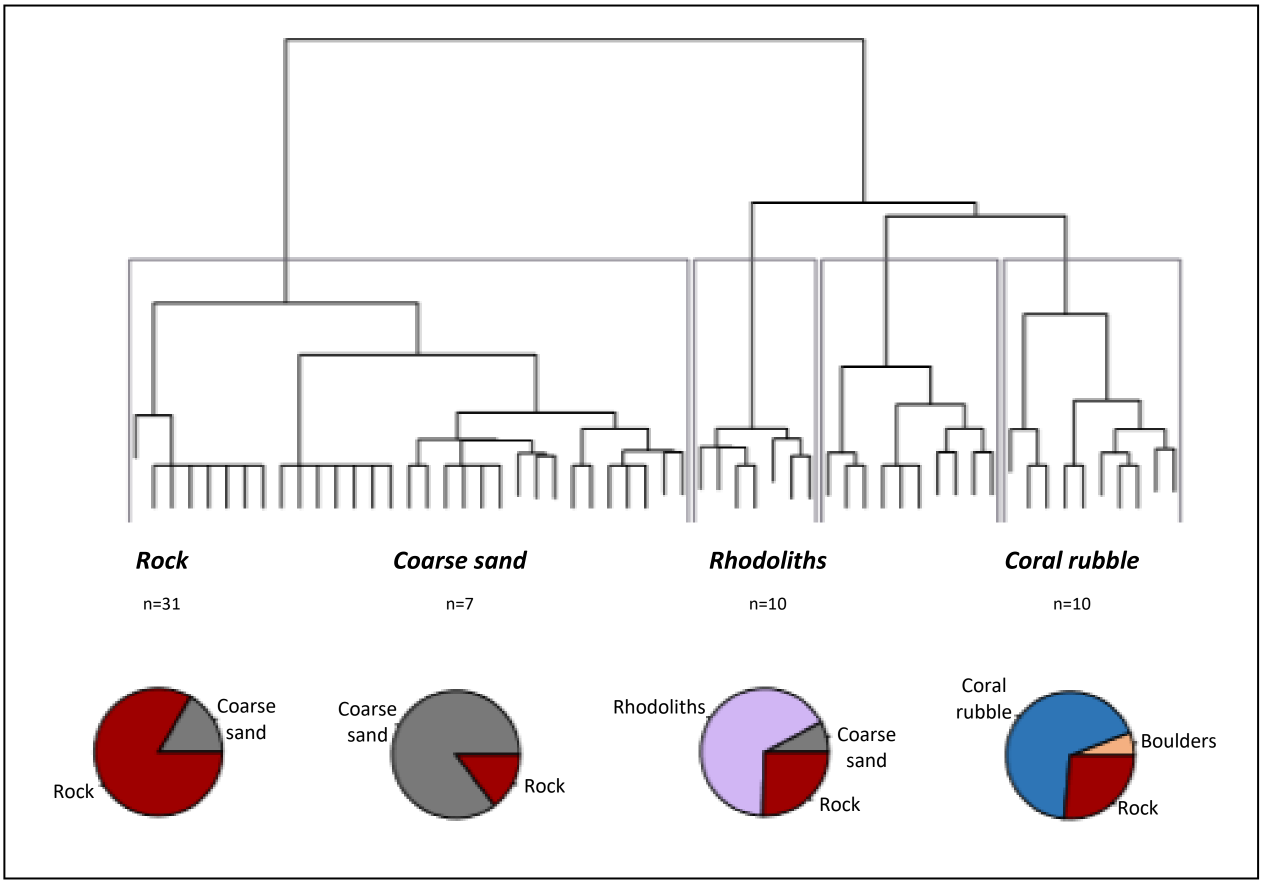

Figure 11: Substrate cluster dendrogram with final SUBSTRATE clusters indicated; clusters descriptive names; number of grids each cluster contains (n); and the contribution of each substrate (>5% frequency of occurrence) to each cluster.

Relief

Reliefs of below 1m were surveyed more extensively than others. The most frequently sampled habitat relief was flat followed closely by low (<1m), moderate (1-3m), and then high (>3m) (see Figure 12 and Figure 13).

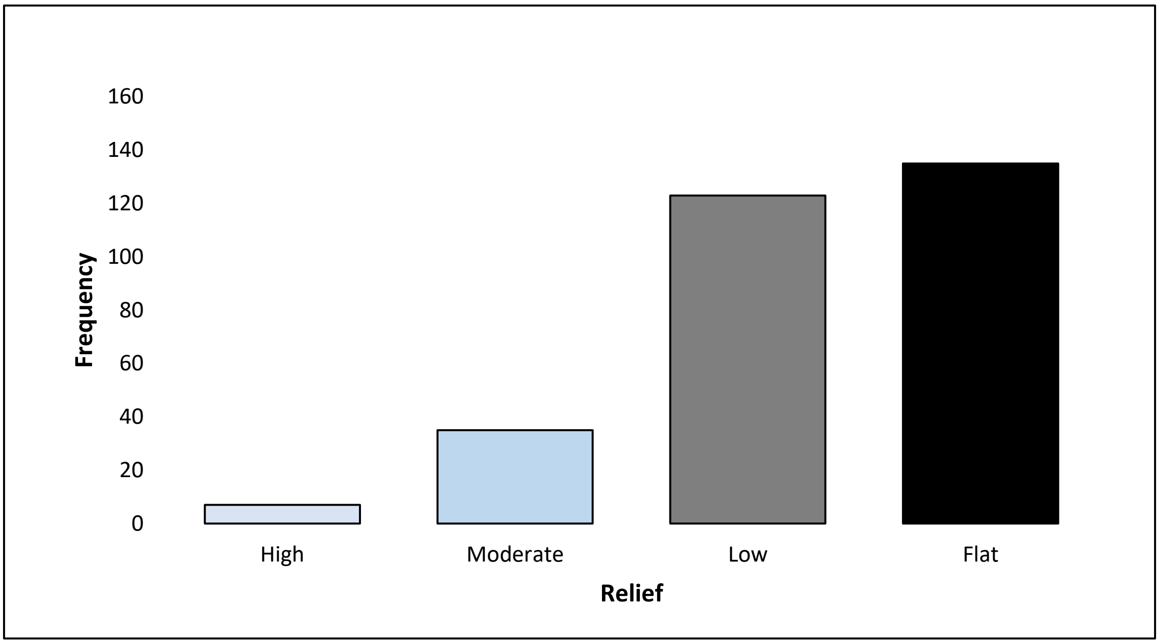

Figure 12: Frequency of marine benthic habitats relief sampled at 5 points within each of the 58 sampling grid cells off the Kei river mouth in the Eastern Cape, South Africa.

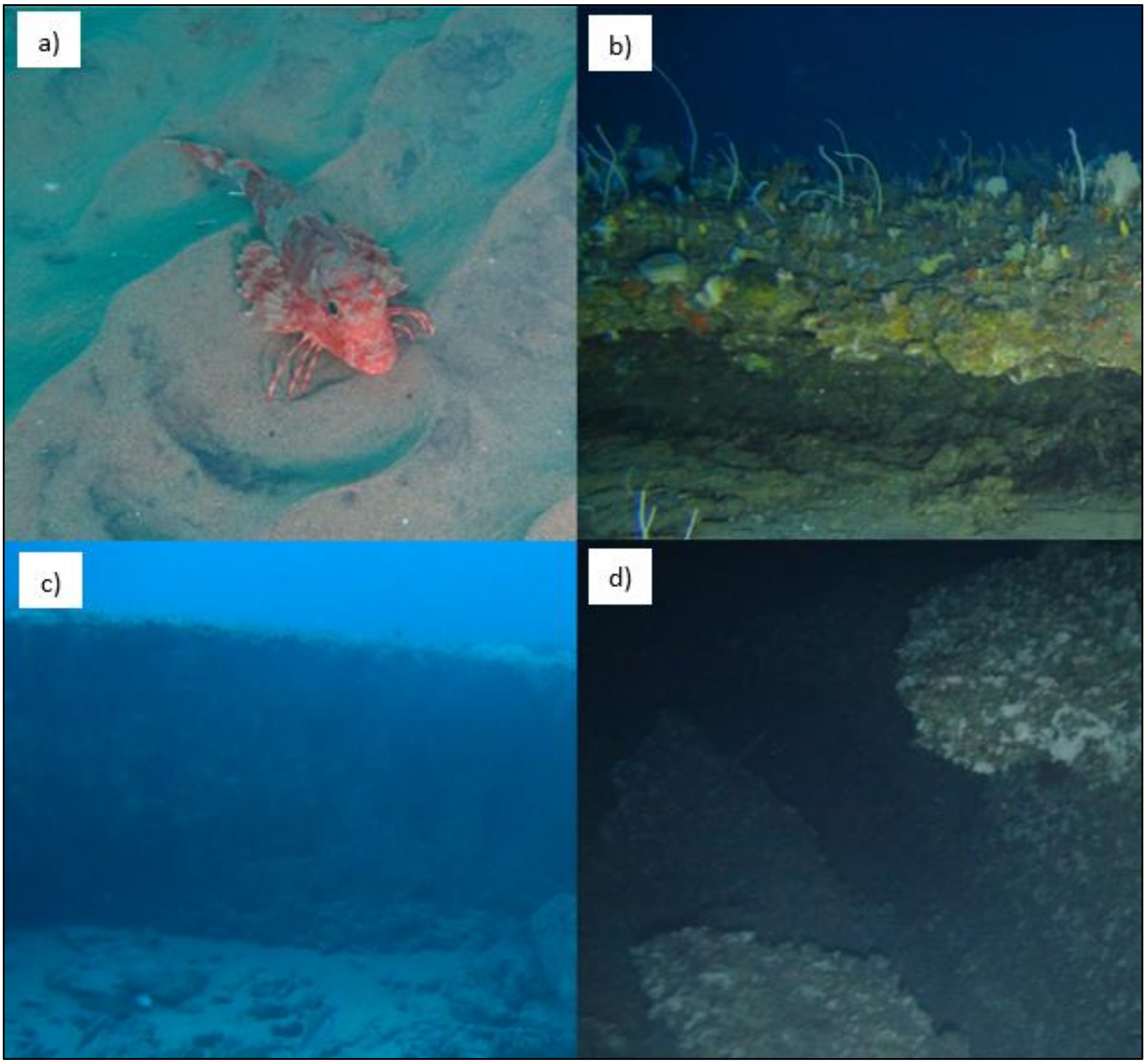

Figure 13: Habitat relief categories included a) flat, b) low (<1m), c) moderate (1-3m), and d) high(>3m).

Relief in grids clustered into 2 groups: *Low* and *Flat* (Figure 14). Functional habitat justified the single split between predominately low (<1m) and flat relief. *Flat* characterised the majority of grids (n=35), while *Low* the minority (n=23). Due to the scale and method of sampling, moderate and high relief did not result in high enough proportions within grids to meaningfully reflect in the clustering or have an impact at the scale being accessed in this study.

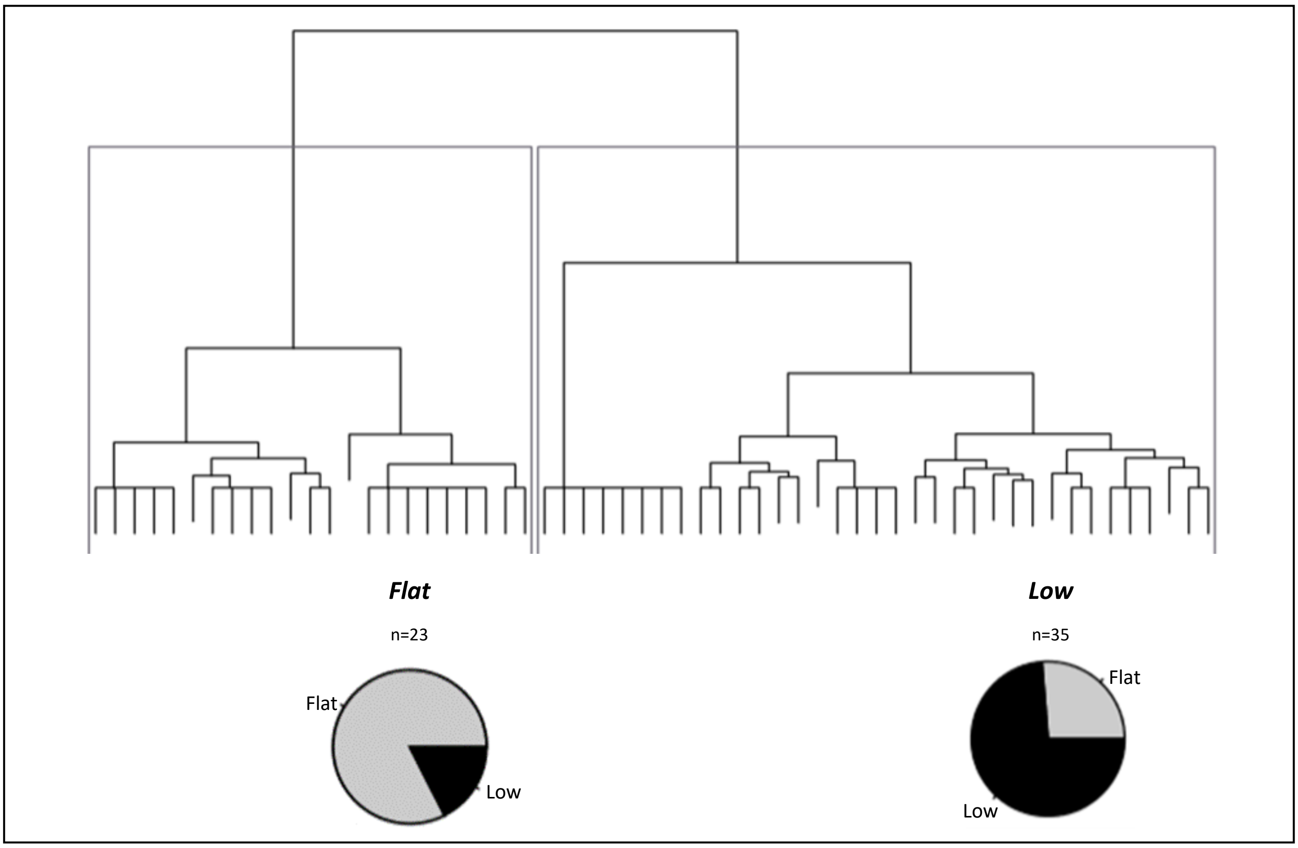

Figure14: Reliefs cluster dendrogram with RELIEF clusters indicated; clusters descriptive names; number of grids each cluster contains (n); and the contribution of each relief (>5% frequency of occurrence) to each cluster.

Habitat

Five habitat clusters were obtained by clustering biota, substrate, and relief data. The five clusters included: *Sponges and Coral on Rock; Fan coral on rock*; *Erect algae on rock*; *Rhodolith beds*; and *Course sand with No visible biota* (Figure 15). *Rhodolith beds* incorporated the smallest number of grids (n=6), while *Sponges and coral on rock* incorporated the highest (n=16).

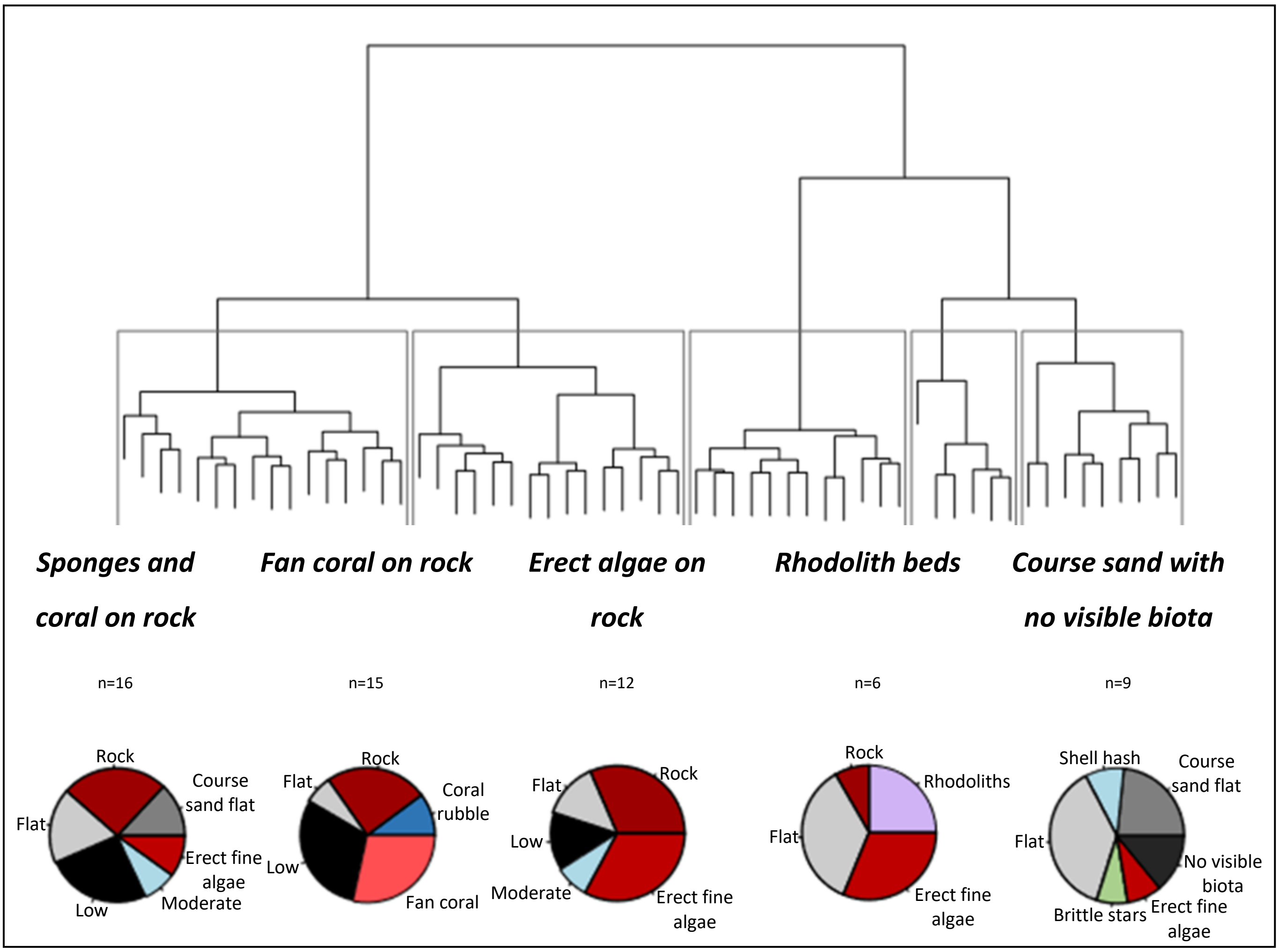

Figure 15: Habitat cluster dendrogram with final clusters HABITAT indicated; clusters descriptive names; number of grids each cluster contains (n); and the contribution of each biota, substrate, and relief (>5% frequency of occurrence) to each cluster.

Depth, variation in depth, and distance to shore and shelf

Grids were sampled at a range of depths (30-162m), variance in depth (0-0.18), as well as distances to shore (2-25km) and shelf (0-18km). Depths shallower than 100m were more extensively sampled than deeper than 100m. The majority of grid cells contained very little relative variation in depth. Most grids sampled where situated between 5-9km from shore, and between 10-14km and 0-4 km from the continental shelf (200m depth contour) (Figure 16 a-d).

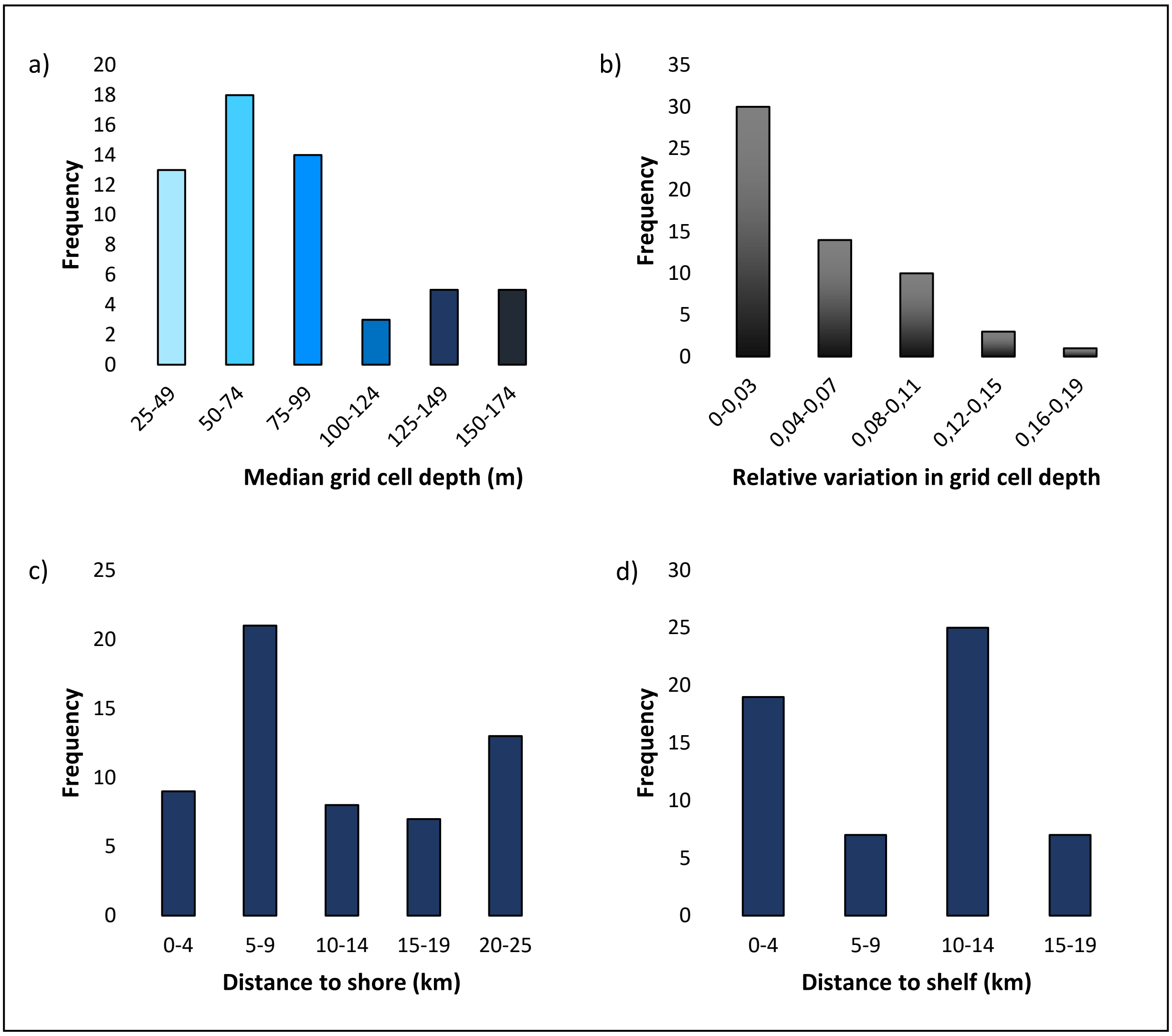

Figure 16: Frequency of a) median depth, b) variation in depth, c) distance to shore, and d) distance to shelf sampled at 5 points within each of the 58 sampling grid cells off the Kei river mouth.

Fish

From shore to continental shelf off the Kei river mouth 46 species of fish from 24 families were observed. Of all the species observed, barred fingerfin, spottail coris, twotone fingerfin, and blue hottentot were the most frequently sampled per grid (Table 2, Figure 16, and Figure 17). Blue hottentot, striped grunter (*Pomadasys striatus*), and wreckfish (*Polyprion americanus*) had the highest MaxN (Table 2, Figure 16, and Figure 17). The critically endangered endemic reef fish seventy-four and dageraad were observed. Endangered species observed included miss lucy (*Chrysoblephus* gibbiceps), red steenbras, and yellowbelly rockcod (*Epinephelus marginatus*) (Table 2, Figure 16, and Figure 17).

The South African Sustainable Seafood Initiative (SASSI) has lists that denote the sustainability of seafood species using three colours; green, orange and red. Green is considered the most sustainable fish to purchase, while red is the least sustainable. Seven species observed in this study were on the red list and five were orange list, while another was red or orange depending on the method of capture (Table 2).

This study collected footage of a living speckled guitarfish (*Rhinobatos ocellatus*) and wreckfish (*Rhinobatos ocellatus*) schooling. Little is known about these species and both are listed as data deficient by the IUCN red list (IUCN 2017) (Table 2, Figure 16, Figure 17, and for more information on these other species sampled see Appendix 1).

Table 2: Species sampled on the continental shelf off the Kei river mouth in the Eastern Cape that were common, of conservation concern, or rare. The species common name, family, South African Sustainable Seafood Intuitive (SASSI) status, International Union for Conservation of Nature (IUCN) status, percentage of grids cells it was sampled in, median MaxN, and maximum MaxN are presented.

Common Name	**Family**	**SASSI status**	**IUCN status**	**% of grids**	**Median MaxN**	**Maximum MaxN**
Barred fingerfin	Cheilodactylidae	-	-	67%	1	5
Spottail coris	labridae	-	-	45%	1	3
Twotone fingerfin	Cheilodactylidae	-	-	38%	1	4
Blue hottentot	Sparidae	Green	Least concern	34%	7	100
Panga	Sparidae	Orange	Least concern	34%	2	7
Cape gurnard	Triglidae	Orange	-	29%	1	2
Seventy-four	Sparidae	Red	Critically endangered	28%	2	11
Carpenter	Sparidae	Orange/green	-	16%	2	9
Miss Lucy	Sparidae	Red	Endangered	14%	1	2
Cape knifejaw	Oplegnathidae	Red	-	12%	1	1
Jacopever	Scorpenidae	Red	-	10%	1	1
Roman	Sparidae	Orange	Near threatened	9%	1	5
Dageraad	Sparidae	Red	Critically endangered	7%	1	1
Englishman	Sparidae	Orange	-	7%	1	2
Red steenbras	Sparidae	Red	Endangered	7%	1	1
John Brown	Sparidae	Red	Least concern	5%	1	1
Smoothhound shark	Triakidae	Red/orange	Vulnerable	3%	1	1
Striped grunter	Haemulidaea	-	-	3%	30	54
Wreckfish	Polyprionidae	-	Data deficient	3%	10	19
Yellowbelly rockcod	Epinephelinae	Orange	Endangered	3%	1	1
Speckled guitarfsh	Rhinobatoidei	-	-	2%	1	1

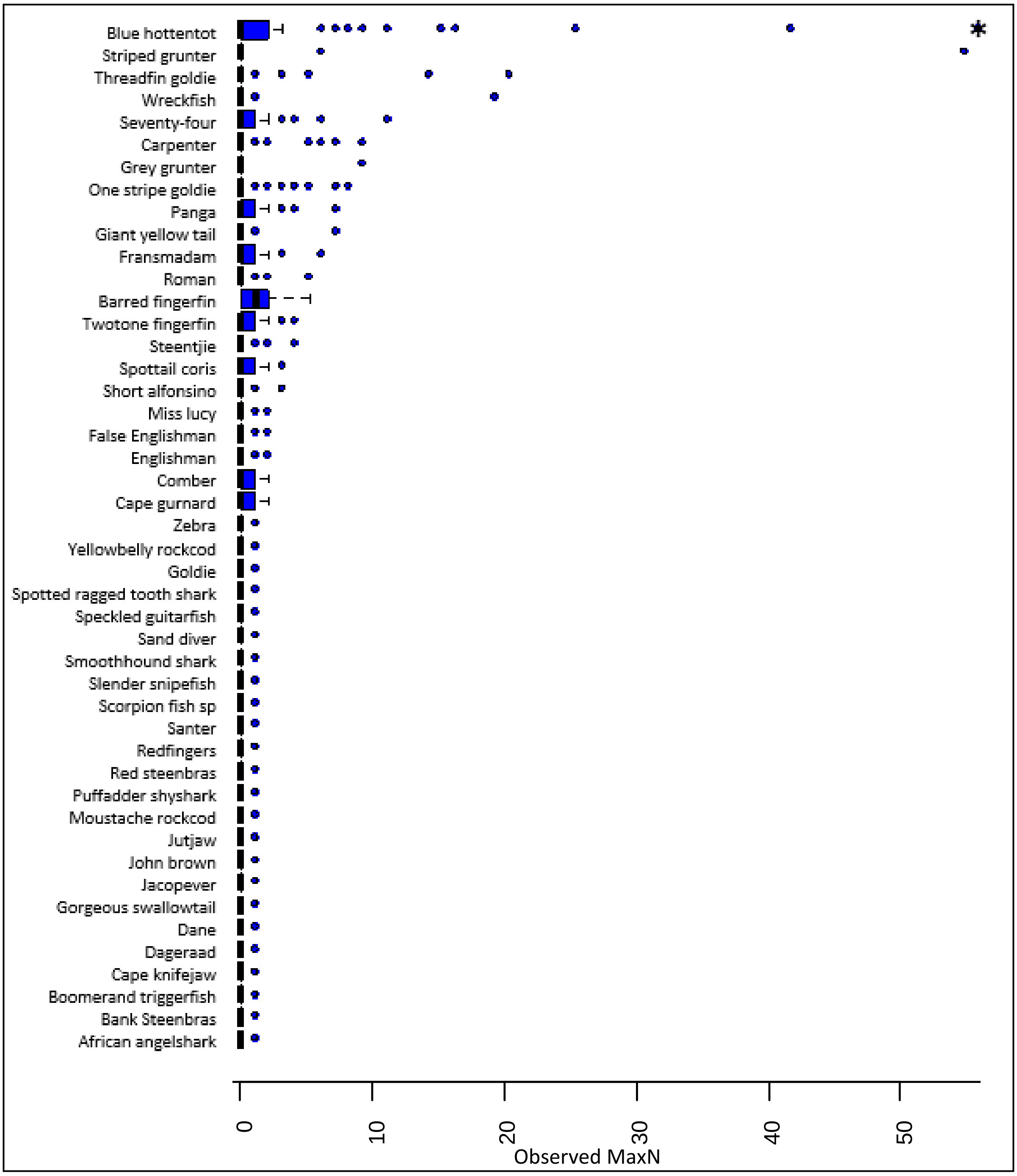

Figure 16: Observed MaxN (highest number of individuals of each species within one frame of the footage in each grid) for each species. Asterisk denotes that not all MaxN values for blue hottentot are displayed, observed values of 80, 100 and 186 were omitted. Where there is narrow entirely black box present, all quartiles (including median) are zero and only outliers are displayed as dots.

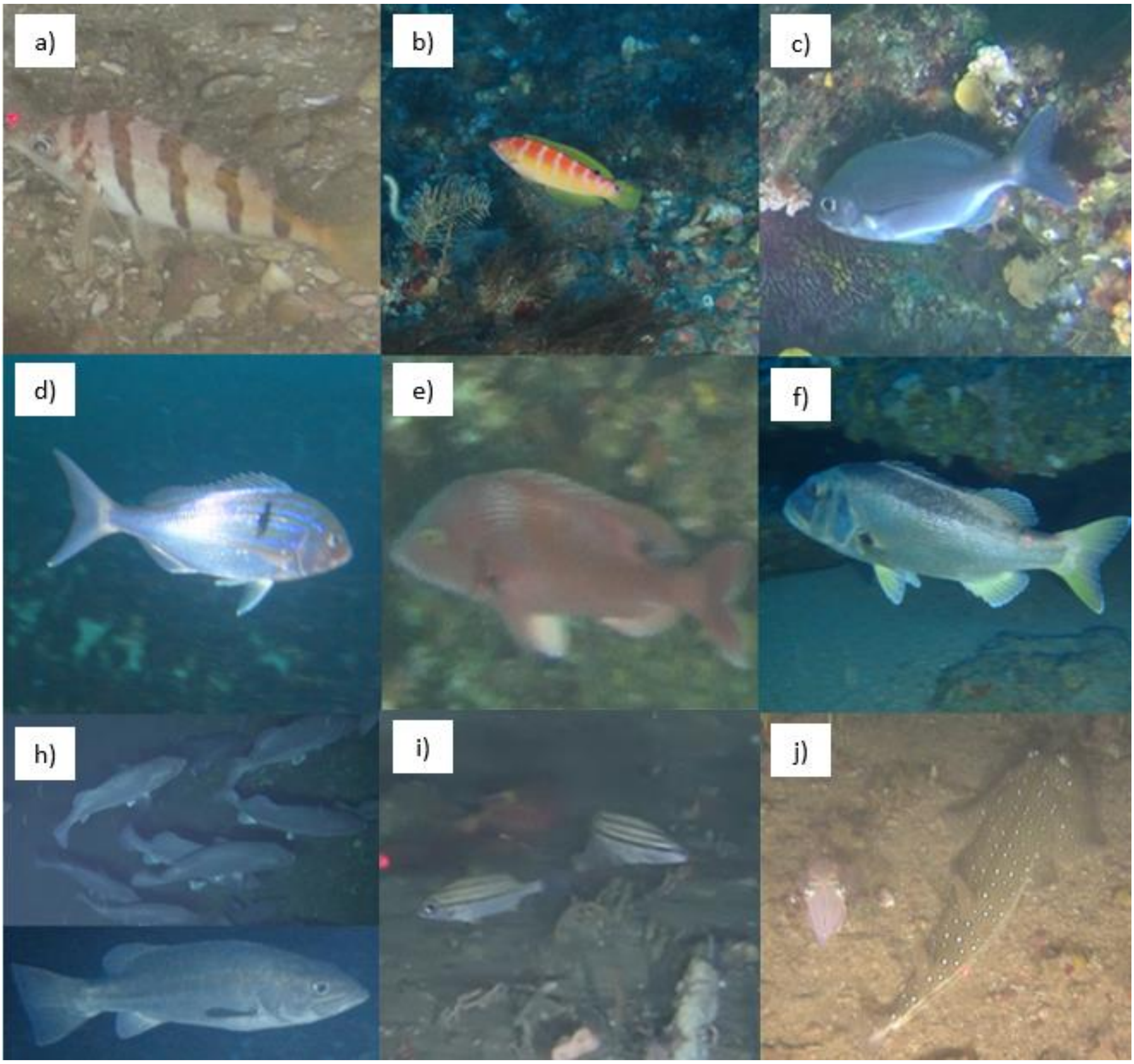

Figure 17: Species occurring in the most number of grid cells a) barred fingerfin (*Cheilodactylus pixi*), b) spottail coris (*Coris caudimacula*), and c) blue hottentot (*Pachymetopon aeneum*). Endangered endemic sparidae species observed a) seventy-four (*Polysteganus undulosus*), dageraad (*Chrysoblephus cristiceps*), and red steenbras (*Petrus rupestris*). Species with the highest number of individuals per frame (MaxN) included c) blue hottentot, h) wreckfish (*Polyprion americanus*), and i) striped grunter (*Pomadasys striatus*). This study was the first to record: a living j) speckled guitarfish (*Rhinobatos ocellatus*) and h) wreckfish schooling.

Fish and environmental factors

Sampling effort

Each ROV transect explored between one and seven grid cells. The accumulation of species diversity per grid cell sampled predicted that more than 95% of the species detectable had been sampled (Figure 18).

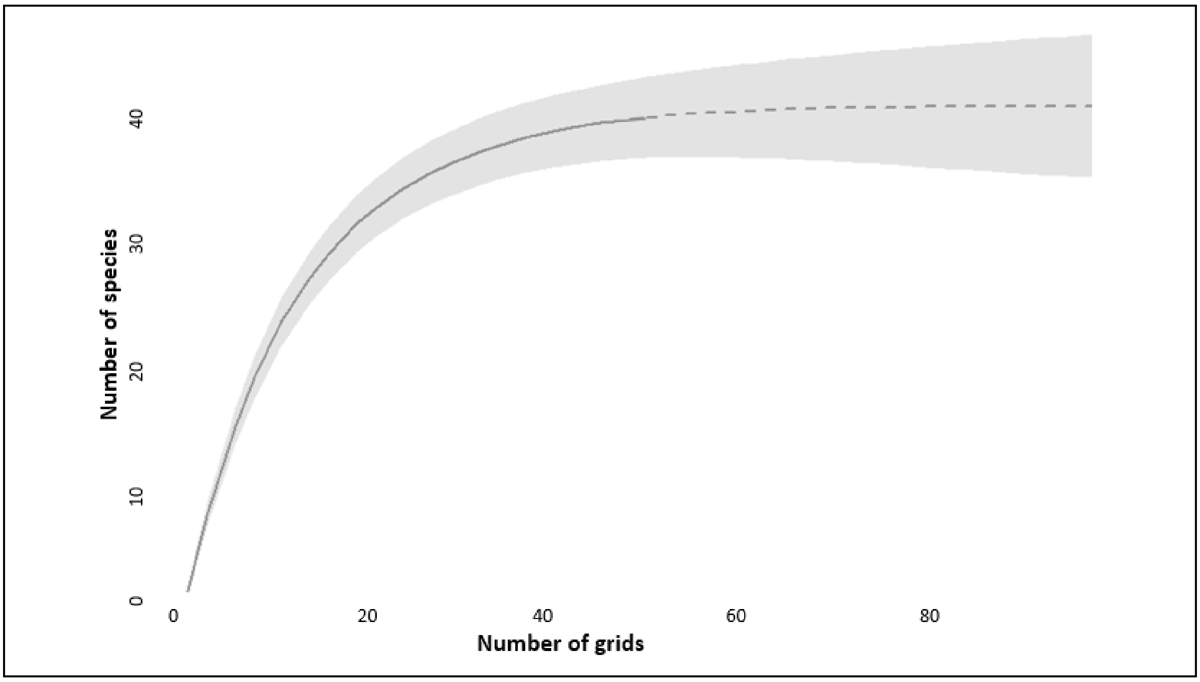

Figure 18: The accumulation of species diversity as the number of grids cells sampled offshore of the Kei river mouth in the Eastern Cape increases, with 95% confidence intervals (shaded areas). The interpolation and extrapolation are indicated by solid and dashed line indicate respectively.

Environmental factors association with ichthyofaunal composition

Species composition was mainly explained by depth and the MRT revealed that the ichthyofaunal composition was first split by depth at 111 metres. The species composition below 111m was dominated by blue hottentot and one stripe goldie. The species composition above 111m was dominated by threadfin goldie and wreckfish. The shallower than 111m branch split further according to SUBSTRATE. One branch was characterised by *Coral rubble* and *Coarse sand* contained mainly sedentary fish species such as spottail coris, comber, cape gurnard, and barred fingerfin, but also panga and blue hottentot. The remaining branch was characterised by *Rhodoliths* and *Rocks* and dominated by blue hottentot (Figure 19).

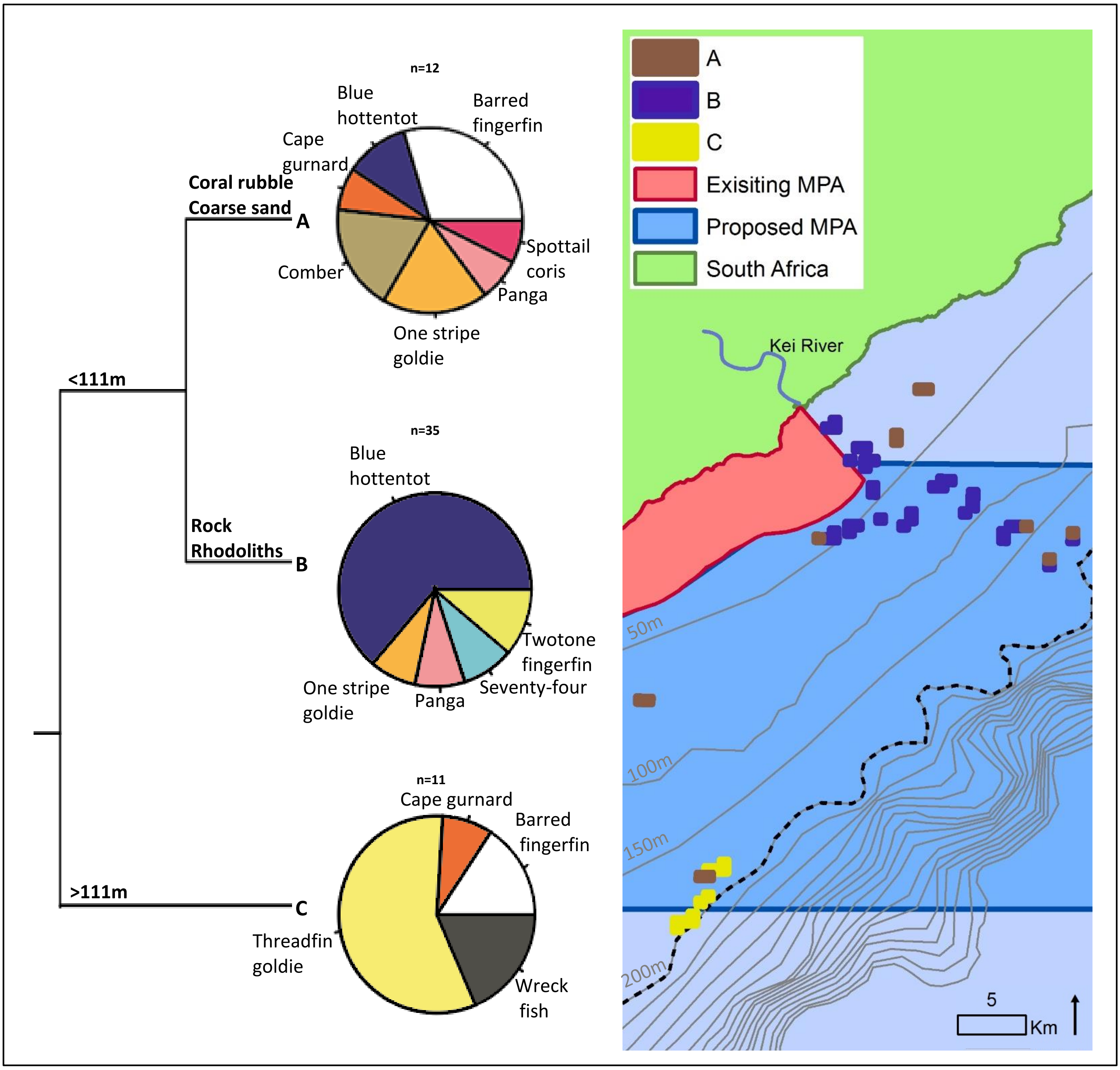

Figure 19: Multivariate regression tree of ichthyofaunal composition and environmental explanatory variables; number of grids each node contains (n); the contribution of each species (>5% frequency of occurrence) to each node; as well as a map indicating the node each grid cell is included in.

Fish species associations with environmental variables

The GAM for species richness was able to explain 48% of the null deviance in the data. The variables distance to shelf, SUBSTRATE, and BIOTA significantly explained species richness. Species richness peaked at 10 km from the shelf. The SUBSTRATE *Coarse sand* was associated with the lowest species count and the highest species count was characterised by *Rhodoliths*. The *Fan coral* BIOTA was associated with the highest species richness, and *No* *visible biota* was associated with the lowest species richness (Table 3, Figure 20, and Figure 21).

GAMs predicted the abundance for the six most commonly sampled solitary species. The GAM for barred fingerfin was able to explain 10% of the null deviance in the data, depth was retained in the model. The abundance of barred fingerfin troughed at 75m deep. The GAM for twotone fingerfin explained 29% of the null deviance, depth was retained in the model. Abundance peaked at 20m deep. The GAM for spottail coris was able to explain 45% of the null deviance in the data, depth was retained in the model. Abundance peaked at 75m deep. The GAM for cape gurnard explained 34% of the null deviance in the data, depth was retained in the model. Abundance troughed weakly at 90m deep. The GAM for fransmadam explained 13% of the null deviance, depth was retained in the model. Abundance peaked at 20m deep. The GAM for comber explained 92% of the deviance, depth was retained in the model. Abundance peaked at 90m deep (Table 3 and Figure 22).

The GAM predicted the presence of two schooling species. The GAM for seventy-four explained 27% of the null deviance in the data, depth was retained in the model. The presence of seventy-four peaked at 60m deep. The GAM for blue hottentot explained 28% of the null deviance, depth and *relief* were retained in the model. The presence of blue hottentot peaked at 60m deep and on the SUBSTRATE group *Low* (Table 3 and Figure 23).

Table 3: Response variables distributions; selected explanatory variables; associated degrees of freedom or estimated degrees of freedom; and adjusted r-squared values indicated. Asterisks denote significant explanatory variables and for all response variables sample size (n) equals 58.

Response variables	**Distribution**	**Explanatory variables**	**P value**	**Deviance explained**	**Degrees of freedom**	**Estimated degrees of freedom**	**R-squared value (adjusted)**
Species count	Quasi-Poisson	Distance to shelf	0.004*	47.8%	-	2.08	0.36
		BIOTA	0.04*	-	4	-	
		SUBSTRATE	0.03*	-	3	-	
Barred fingerfin	Poisson	Depth	0.123	10.1%	-	2.21	0.07
Twotone fingerfin	Poisson	Depth	0.260	29%	-	2.13	0.2
Spottail coris	Poisson	Depth	0.233	44.7%	-	2,78	0.36
Cape gurnard	Poisson	Depth	0.259	34%	-	2.15	0.24
Fransmadam	Poisson	Depth	0.261	12.8%	-	1.88	0.07
Comber	Poisson	Depth	0.417	92.2%	-	1.92	0.874
Seventy-four	Binomial	Depth	0.203	27.2%	-	2.12	0,24
Blue hottentot	Binomial	Depth	0.1	28.4%	-	2.14	0.26
		RELIEF	0.084		1	-	

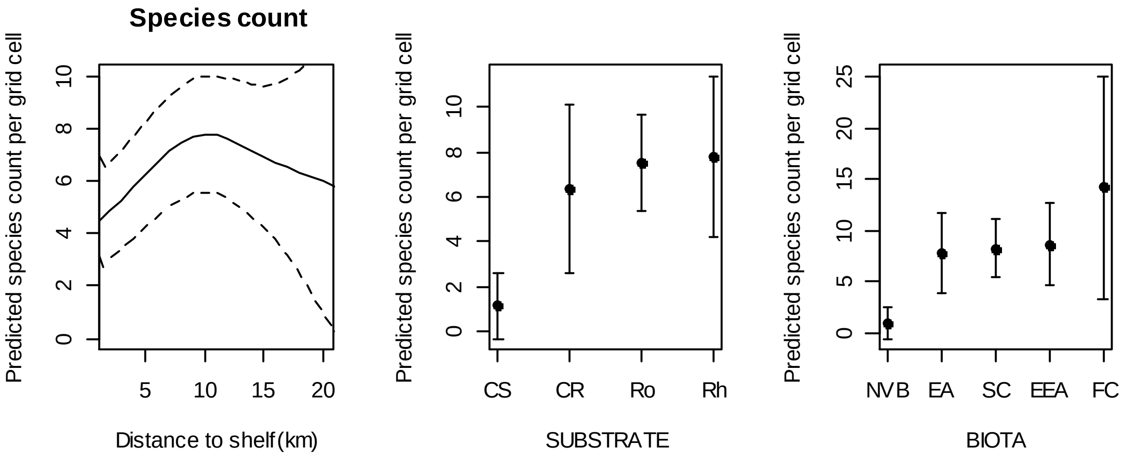

Figure 20: Predicted species richness in relation to its selected explanatory variables: distance to shelf, SUBSTRATE, and BIOTA. In the distance to shelf line graph solid lines represent the predicted species count per grid cell, dashed lines illustrate 95% confidence intervals. In both the SUBSTRATE and BIOTA plots dots represent the predicted species count per grid cell and whiskers illustrate 95% confidence intervals. The SUBSTRATE groups consist of *Coarse sand* (CS), *Coral rubble* (CR), *Rock* (Ro), and *Rhodoliths* (Rh). The BIOTA groups consist of *No visible biota* (NVB), *Erect algae* (EA), *Sponges and coral* (SC), *Erect and encrusting algae* (EEA), and *Fan coral* (FC).

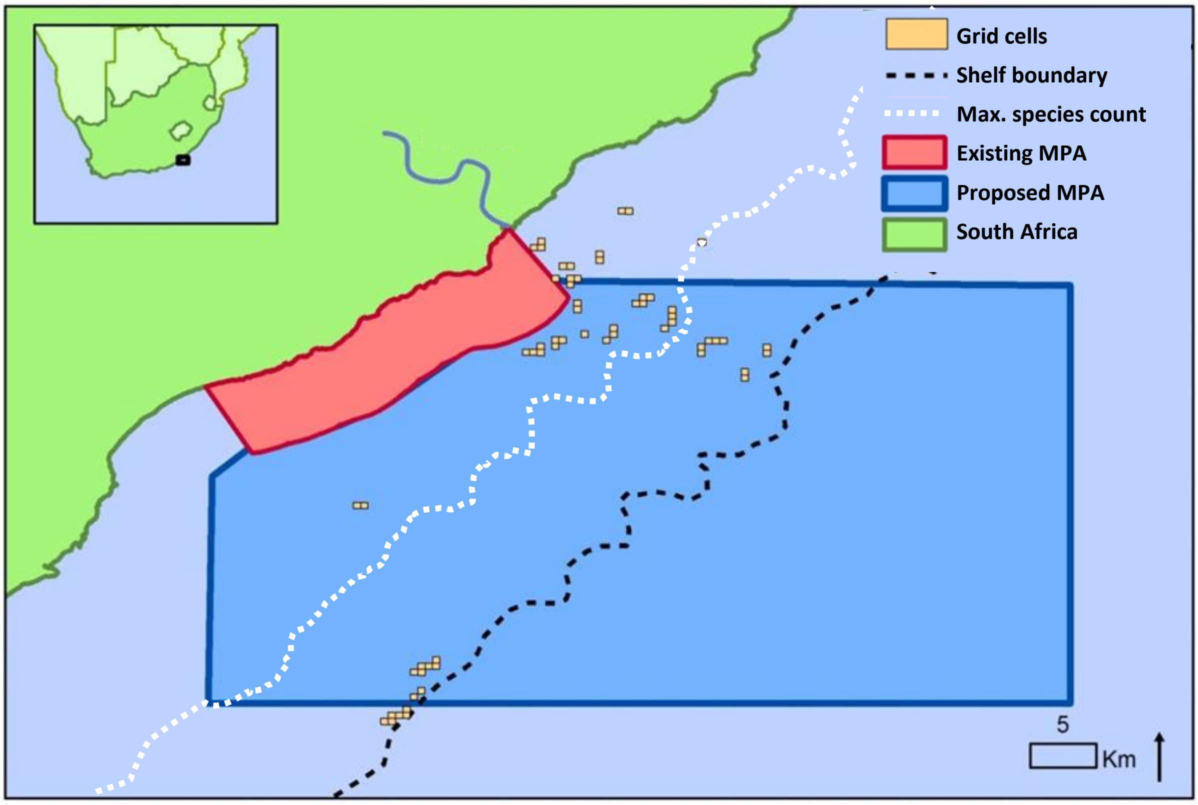

Figure 21: Map of South Africa indicating the study region, the current MPA, and the proposed MPA. Grid cells sampled, continental shelf boundary, and predicted position of maximum species count (10km from shelf boundary) indicated.

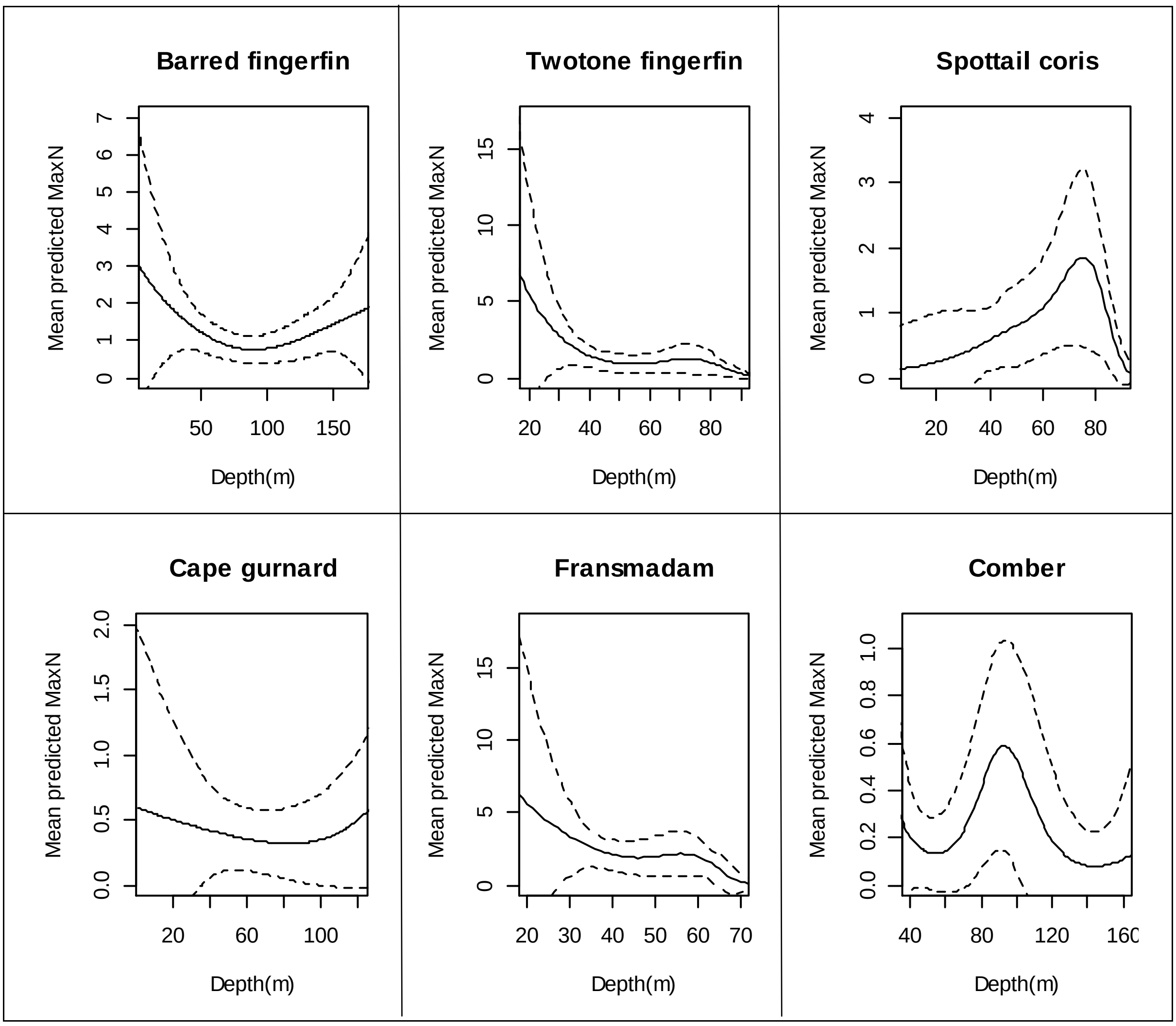

Figure 22: Species mean predicted MaxN in relation to their selected explanatory variables. Solid lines represent the species mean predicted MaxN, dashed lines illustrate 95% confidence intervals.

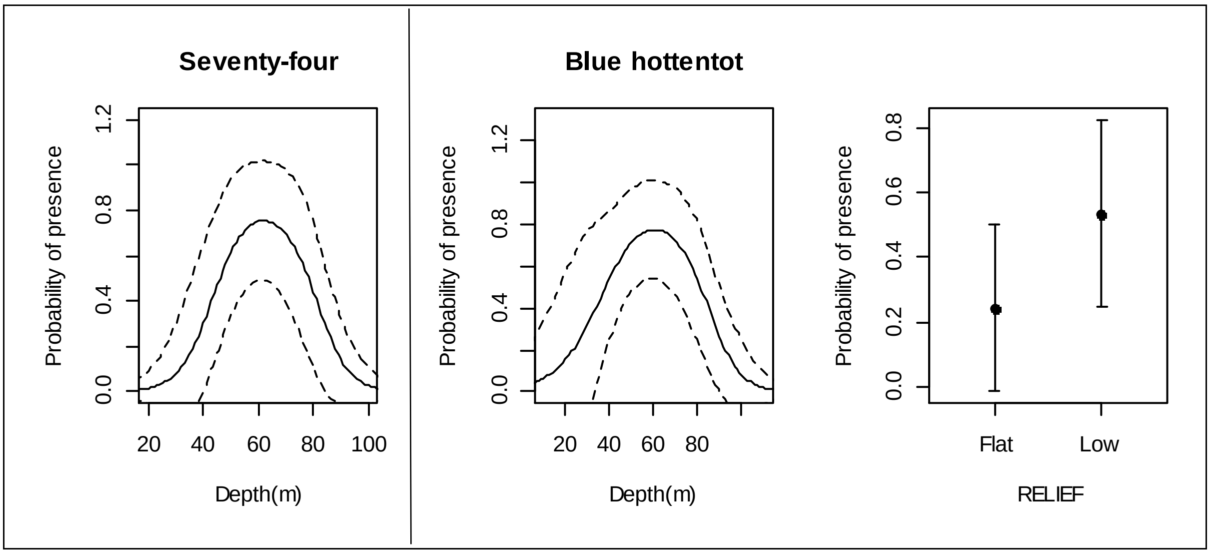

Figure 23: Species predicted probability of presence in relation to their selected explanatory variables. In line graphs solid lines represent the species probability of presence per grid cell, and dashed lines illustrate 95% confidence intervals. In the RELIEF plot dots represent the blue hottentot predicted probability of presence and whiskers illustrate 95% confidence intervals.

Discussion

This study visually explored in the intermediate depths offshore of the Kei river mouth and discovered a vast diversity of habitats and ichthyofauna. The rare habitats, endangered species, and predicted location of maximum species richness are in support of the establishment of the proposed Amathole MPA expansion.

Exploratory observations

Habitats

This study documented a diverse matrix of a wide variety of habitats. Within habitat biota, various algal forms and a large diversity of coral and delicate sponge forms were observed. Habitat substrate included rhodoliths which are unattached orbs of encrusting coralline algae. This study adds to what little is known about South Africa's habitat diversity offshore on the continental shelf (Sink et al. 2006).

Ichthyofauna

A diversity of fish that were rare and/or of conservation concern where documented, as well as rare behaviour for a species. This study collected footage of a speckled guitarfish. A species for which three specimen records exist, despite their habitat being well-sampled and their distinctive appearance (Smith & Heemstra 1986; Compagno et al. 1989). Though little is known about Speckled guitarfish biology, such as other species in the Rhinobatoidei family, they are likely targeted for the high value of their fins and are vulnerable to depletion due to limiting life history characteristics (IUCN 2017).

Many species that are currently unsustainably fished (according to SASSI), as well as critically endangered and endangered (according to the IUCN) were observed. Wreckfish are listed as data deficient by the IUCN and are thought to be impacted by overfishing. They are illegal to catch in South Africa (Heemstra & Heemstra 2004). This species was observed shoaling in this study, a behaviour rarely captured. It is known that wreckfish spawning aggregations occur at specific locations deeper than 300m around the coast of Brazil and it is thought possible that pairs or small aggregations of wreckfish might also spawn along the continental slope of Brazil (Peres & Klippel 2003). Typically a solitary species only known to aggregate to breed (Peres & Klippel 2003), the shoaling of wreckfish on South Africa's continental shelf suggests that the area constitutes as a spawning habitat for the species.

Analyses of habitats

Habitat

To create coarse functional habitat types from the observed habitats, some of which were extremely patchy, habitat observations were compressed into clusters. The method and scale employed resulted in influential micro habitat patches observed being classified as the larger homogenous habitats they were nested within (Parry et al. 2003). The presence of influential fine scale rocky outcrops in vast expanses of coarse sand or coral rubble was clustered into *Coarse sand* and *Coral rubble* respectively. Potentially influential micro habitat detail was therefore lost, however if habitat had been documented on a finer scale it may have hindered efforts to extract habitat associations with fish species, as fish are motile and the boundaries between the environments they inhabit vague and potentially dynamic.

Ichthyofuana

Community

Ichthyofauna community structure was primarily split by depth (111m). Marine communities are often structured by depth, as depth is linked to changes in environmental factors such as temperature, light which influences productivity, abiotic stress (such as pressure and tides), and habitat type (Smith & Brown 2002; Heyns-Veale et al. 2016). The primary ichthyofauna community split at 111m likely denotes the split between the photic and aphotic communities. The boundary between the photic and aphotic zone was at a depth of near 90m (as beyond this depth algae was absent).

Most of the dominant species that characterised the *Coral rubble* and *Coarse sand* habitats exhibited high site-fidelity (barred fingerfin, comber, and spottail coris). These species were consistently observed near the small patches of rock within their coarse scale habitat type. The detail of the fine scale rock habitats within coarse sand and coral rubble dominated grids was lost due to the compression of habitat into coarse habitat types. These species likely remain near fine scale rocky habitats within *coral rubble* and *coarse sand* grids because of the higher structural complexity of rock and it associated biota. As higher structurally complex habitats are typically richer in resources (such as food and shelter) (Crowder & Cooper 1982; Heyns-Veale et al. 2016; Ferrari et al. 2017).

Most of the dominant species that were associated with the more continuous highly structurally complex substrates of *Rhodoliths* and *Rock* were observed to be more mobile. These species included blue hottentot, twotone fingerfin, and panga. These species were not observed displaying site-fidelity.

Species richness

Species richness peaked mid shelf, on the substrate group *Rhodoliths*, and on the biota group *Fan coral*. The biota group *No visible biota* and substrate group *Coarse sand* were associated with low species richness. Species richness has been shown to be largely determined by substrate (Kostylev et al. 2001). Substrate types can provide shelter and surfaces for attachment and is influenced by the strength of flows of tides and currents.

Substrate can influence the longevity and size of biota, specifically of biogenic structures (Reise 2002). *No visible biota* is likely associated with *Coarse sand*, which is highly unconsolidated which poses challenges for biota to grow. *Coarse sand* and *No visible biota* had low structural habitat complexity which is typically associated with scarce resources (such as food and shelter from predation). The scarceness of resources attracts relatively fewer species (Crowder & Cooper 1982; Heyns-Veale et al. 2016; Ferrari et al. 2017). The remaining substrate and biota groups contained greater species richness which could have resulted from their greater habitat structural complexity providing resources (Crowder & Cooper 1982).

The mid shelf peak in species richness supports the mid-domain effect (MDE) hypothesis and is likely a product of high overlap between shallow and deep ichthyofaunal communities on the mid shelf. The MDE states that without environmental gradients, if species ranges were random within a bounded geographical area overlap between ranges would increase towards the middle of the area (Colwell & Lees 2000; Colwell et al. 2004). Thus, the species richness peak can be explained by its location in the middle of the geographic range of the continental shelf which is bounded by the shelf edge and the shore. Though the shelf is not without environmental gradients, which is one on the assumption of the MDE (Colwell et al. 2004).

Species richness mid shelf peak could also be as a result of the overlap between photic and aphotic fish communities. The strongest ichthyofauna community splitting factor we detected on the shelf was depth at 111m. This depth is near the lower limit of the photic zone (90m). The community split likely delimits the photic and aphotic ichthyofauna communities. The maximum species count at approximately 100m deep (10km from the continental shelf) is a result of the presence of both photic and aphotic species present near the boundary between the zones.

Species

Depth was the only explanatory variable retained in the species abundance and presence models, except for blue hottentot. Depth is known to be an important factor for predicting fish distributions. Depth is closely related to physical properties of light, oxygen, nutrients, temperature, and thermocline position (Heyns-Veale et al. 2016). Depth and relief both were important explanatory variables for blue hottentot presence, with greater relief (more habitat complexity) resulting in the presence of blue hottentot shoals. This is to be expected as greater structural habitat complexity is commonly associated with a greater abundance of species because it provides more resources (Ferrari et al. 2017). Blue hottentot are also known to be associated with high profile reefs (Mann 2013).

The lack of habitat explanatory variables being retained in models that explained species abundance and presence could imply that habitat type is less important for predicting individual species distributions. It could also be as a result of representative habitat (formed from clustering habitat data) not representing functional habitat types utilised by individual species (Thrush et al. 1997; Parry et al. 2003). Habitat could have been analysed at the incorrect scale or the diverse composition of habitats in close proximity could negate individual habitats from impacting species distributions. The lack of interaction terms included in models as explanatory variables could have impacted the lack of habitat variables retained. Interaction terms were not included in the models because of the lack of data to pick up these relationships.

Conservation implications

The outcomes of this exploratory study have revealed that the proposed MPA site encompasses a wide variety of habitats, a number of fish species of conservation concern, and rare fish species. Habitat diversity is often used as a proxy for marine diversity when prioritising areas for protection (Agardy et al. 2003; Stevens & Connolly 2005), thus the diversity of habitats off the Kei river mouth provide support for the spatial protection. The distance from the continental shelf at which species richness is predicted to peak (10km) falls just outside of the existing MPA but within the proposed MPA, providing further support for the proposed MPA. The establishment of this proposed offshore MPA would play a part in providing systematic conservation for critical habitat for commercial species and species of conservation concern. MPAs and other protection measures helped many target species in the commercial line-fishery (including some observed in this study namely panga, carpenter, seventy-four, and roman) recover from over exploitation (Booth & Punt 1998; Kerwath et al. 2013; Mann 2013). All existing MPAs in South Africa are coastal and provide protection to half of fish species that are directly impacted by exploitation (Solano-Fernández et al. 2012). Offshore MPAs, such as the one proposed off the Kei river mouth will afford more protection to large, sexually mature individuals, that contribute greatly to the sustainability of fish populations (Hixon et al. 2014; Heyns-Veale et al. 2016). The protection of this offshore area will thus accelerate the recovery of over exploited species and help sustain harvested populations.

Deep water corals provide nurseries and spawning grounds for many species (Baillon et al. 2012). The observation of schooling wreckfish above deep-water corals within the proposed MPA suggest that the area might be a spawning ground for wreckfish too. This adds more support for the proposed MPA.

This study's footage and dataset can act as baseline information for the region. If the proposed MPA is established, its impact on species diversity and abundance can be monitored through time by repeating this study. However, if this study is repeated for monitoring purposes, it is important its limitations are noted and understood.

Limitations

This study was explorative and had limitations. Sampling across the entire area was not randomly stratified and not all imposed habitats types and environmental gradients were equally sampled. Sampling points were chosen based on known recreational fishing locations and areas of high structural complexity identified via sonar. A random design of equal sampling effort within each imposed habitat type throughout the proposed MPA could result in more accurate predictions of species distributions and species count in the region.

The patterns observed in this study may change seasonally, as a result of pulse recruitment, or be as a result of historic fishing pressure (Hyndes et al. 1999). Recording fish size could help monitor some of these patterns, rough measurement estimates of fish can be made from footage from this study. Though, ideally footage from stereo cameras should be used in conjunction with software to calculate accurate fish size (Amin et al. 2017). Fish size can be used as a proxy for age and maturity, which is useful in determining the viability of populations and monitoring recruitment trends (Dunbrack 2006; Langlois et al. 2012).

The strong current and the depths sampled made the ROV an efficient choice of semi quantitatively sampling fish and habitat simultaneously over a large area. The ROV was able to adequately capture habitats and species but, the strong current, sometimes exceeding 3 knots, often hindered the ROVs ability to stop and examine points of interest. This made the identification of cryptic species challenging, and some species could only be identified to family level. A few species were noticeably deterred by the ROVs presence, such species included dageraad and dane. Other studies have also documented that ROVs deter certain species (Makwela et al. 2016).

Conclusion

The presence of a diversity of habitats and fish species, including many species of conservation concern, and maximum species richness falling outside of the existing MPA and within the proposed MPA suggest support for the position of the proposed MPA. This study is a step forward in identifying critical habitat to protect diversity and endangered species, and thus contributes to marine spatial management and governance of the region. Going forward a habitat map of the region will be created from a bathymetric map and benthic habitats documented by this study. This map will be used to create predictive maps of fish species distributions and diversity.

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Appendix 1

For each species, the percentage of cells it occurs in as well as MaxN (maximum number of fish observed in a single video frame) median, average, and maximum for each cell.

Common Name	**Family**	**Genus**	**Species**	**% of grids**	**Median MaxN**	**Average MaxN**	**Maximum MaxN**
Barred fingerfin	Cheilodactylidae	*Cheilodactylus*	*pixi*	67%	1	1,6	5
Spottail coris	labridae	*Coris*	*caudimacula*	45%	1	1,2	3
Twotone fingerfin	Cheilodactylidae	*Chirodactylus*	*brachydactylus*	38%	1	1,5	4
Blue hottentot	Sparidae	*Pachymetopon*	*aeneum*	34%	7	17,3	100
Panga	Sparidae	*Pterogymnus*	*laniarius*	34%	2	2,4	7
Cape gurnard	Triglidae	*Chelidonichthys*	*capensis*	29%	1	1,2	2
Fransmadam	Sparidae	*Boopsoidea*	*inornata*	29%	2	1,9	6
Seventy-four	Sparidae	*Polysteganus*	*undulosus*	28%	2	3	11
Comber	Serranidae	*Serranus*	*knysnaensis*	26%	1	1,1	2
One stripe goldie	Serranidae	*Pseudanthias*	*gibbosus*	24%	3,5	3,5	8
Carpenter	Sparidae	*Argyrozona*	*argyrozona*	16%	2	3,8	9
Steentjie	Sparidae	*Spondyliosoma*	*emarginatum*	16%	2	2	4
Threadfin goldie	Serranidae	*Nemanthias*	*carberryi*	16%	3	6,9	20
Miss Lucy	Sparidae	*Chrysoblephus*	*gibbiceps*	14%	1	1,3	2
Cape knifejaw	Oplegnathidae	*Oplegnathus*	*conwayi*	12%	1	1	1
Jacopever	Scorpenidae	*Helicolenus*	*dactylopterus*	10%	1	1	1
Redfingers	Carangidae	*Cheilodactylus*	*fasciatus*	10%	1	1	1
Roman	Sparidae	*Chrysoblephus*	*laticeps*	9%	1	2	5
Dageraad	Sparidae	*Chrysoblephus*	*cristiceps*	7%	1	1	1
Englishman	Sparidae	*Chrysoblephus*	*anglicus*	7%	1	1,3	2
Red steenbras	Sparidae	*Petrus*	*rupestris*	7%	1	1	1
Sand diver	Pinguipedidae	*Parapercis*	*maritzi*	7%	1	1	1
Bank steenbras	Cheilodactylidae	*Chirodactylus*	*grandis*	5%	1	1	1
Dane	Sparidae	*Porcostoma*	*dentata*	5%	1	1	1
False englishman	Sparidae	*Chrysoblephus*	*lophus*	5%	1	1,3	2
John Brown	Sparidae	*Gymnocrotaphus*	*curvidens*	5%	1	1	1
Jutjaw	Parascorpididae	*Parascorpis*	*typus*	5%	1	1	1
Slender snipefish	Centriscidae	*Macroramphosus*	*scolopax*	5%	1	1	1
African angelshark	Squatinidae	*Squatina*	*africana*	3%	1	1	1
Giant yellowtail	Carangidae	*Seriola*	*lalandi*	3%	4	4	7
Gorgeous swallowtail	Serranidae	*Meganthias*	*natalensis*	3%	1	1	1
Santer	Sparidae	*Cheimerius*	*nufar*	3%	1	1	1
Short alfonsino	Berycidae	*Centroberyx*	*spinosus*	3%	2	2	3
Smoothhound shark	Triakidae	*Mustelus*	*mustelus*	3%	1	1	1
Striped grunter	Haemulidaea	*Pomadasys*	*striatus*	3%	30	30	54
Wreckfish	Polyprionidae	*Polyprion*	*americanus*	3%	10	10	19
Yellowbelly rockcod	Epinephelinae	*Epinephelus*	*marginatus*	3%	1	1	1
Grey grunter	Haemulidae	*Pomadasys*	*furcatum*	2%	9	9	9
Boomerang triggerfish	Balistidae	*Sufflamen*	*bursa*	2%	1	1	1
Moustache rockcod	Epinephelinae	*Epinephelus*	*chabaudi*	2%	1	1	1
Puffadder Shyshark	Scyliorhinidae	*Haploblepharus*	*edwardsii*	2%	1	1	1
Scorpian fish species	Scorpaenidae			2%	1	1	1
Speckled guitarfish	Rhinobatoidei	*Rhinobatos*	*ocellatus*	2%	1	1	1
Spotted ragged-tooth shark	Odontaspididae	*Carcharias*	*taurus*	2%	1	1	1
Goldie	Callanthiidae	*Callanthias*	*legras*	2%	1	1	1
Zebra	Sparidae	*Diplodus*	*cervinus*	2%	1	1	1