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Fish assemblages on the Saba bank (Dutch Caribbean): the effect of habitat, depth and fisheries

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November 2014

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Wageningen, November 2014

Acknowledgements

First of all, I would like to thank Dr. Leo Nagelkerke and Dr. Martin de Graaf for providing me with assistance and support throughout the conduction of this master thesis. Special thanks for the Saba Conservation Foundation (SCF) crew for providing me with the necessary tools and expertise during my fieldwork on Saba. Jimmy van Rijn, you've been more than a colleague and without your help, part of this research was not possible. Many thanks for that! Also, I would like to thank Wouter van Looijengoed who introduced and trained me in the sampling procedure and analysis of the video footage. And of course, Jelmer Pander thank you for sharing your dataset. The research was financed by BO-11-011-05-008.

Contents

Abstract

Many environmental variables may influence fish assemblage structures in terms of abundance, biomass and mean size. The aim of this study is to provide a baseline survey on reef fish assemblages and shark presence covering the whole Saba bank (Dutch Caribbean). Hereby determining the influence of habitat, depth and fishing pressure on the structure of reef fish assemblages and shark presence. Baited Remote Underwater Video (BRUV) survey was used to describe reef fish assemblage structures on the Saba bank. Between 2012-2014, a total of 165 60 min BRUV deployments were conducted on locations varying in habitat complexity (0-4, Polunin and Roberts, 1993), depth (15-40m) and fisheries. The eleven most abundant fish species observed on the Saba bank represented eight families and accounted for nearly 50% of the total number of individual fish observed. *Labridae* was the most abundant fish family observed with a relative abundance of 22%. Most abundant fish species by number of individuals were *Thalassoma bifasciatum* (N=849 (9.8%)) *Stegastus partitus* (N=725 (8.4%)) and *Acanthurus bahianus* (N=430 (5.0%)).

Habitat complexity was positively correlated with species richness (Nsp), fish abundance (MaxN), and mean biomass, and negatively correlated with mean fish length. Strongly developed vertical relief habitats were found to support high numbers of fish species (N=19.1±0.6SE) of relatively low mean lengths (22.4cm±0.3SE), whereas less complex habitats were characterized by low numbers of species (N=8.3±0.8SE) with relatively high mean lengths (24.6cm ±0.81SE). Depth was negatively correlated with Nsp, MaxN and mean biomass and positively correlated with mean fish length. These relationships were all according to expectations based on earlier studies.

A minor part of the variability in the structure of reef fish assemblages was explained by differences in fisheries activity, indicating that no clear fisheries effect was observed in fish assemblages in this study. Furthermore, no significant differences in average size of target species were observed between areas with different fishing pressure. However, the general absence of piscivores such as large snappers and groupers was an indication of the indelible effects of past fisheries on the Saba bank.

A total of 85 shark observations were made with *Ginglymostoma cirratum* as most abundant species (N=41), followed by *Carcharhinus perezii* (N=36), *Galeocerdo cuvier* (N=5) and *Carcharhinus limbatus* (N=3). Relatively high shark abundances (0.20 sharks hour^{-1}) were observed on the Saba bank compared with other Caribbean regions (The Bahamas: 0.14 sharks hour^{-1}, Belize, 0.17 sharks hour^{-1}). Shark abundance (CPUE) was positively correlated with habitat complexity, whereas depth exerted a negative influence on shark abundances. High shark numbers are a good sign for the health of the Saba Bank ecosystem, since sharks are apex predators, making them a prime indicator for ecosystem health.

Besides 'traditional' measures, ecomorphology was presented as an alternative measure in explaining variation in reef fish assemblages. For ecomorphological analysis insight in trophic morphology was obtained by using a Fish Food Model (FFM). The FFM in this study quantitatively related properties of 14 marine food types to morphological characterics of 15 common fish species on the Saba bank and predicted the capacity of utilizing these food types for each species. Strong differences in morphology and little overlap was observed for all different fish species in the FFM-analysis, which was mainly explained by two sets of variables involving predatory and herbivorous lifestyle. By multiplying each species' capacity of using food types with its abundance an ecomorphological profile of each fish assemblage was calculated. On a functional level reef fish assemblages showed less variability than on species composition level, this possibly is an indication for high levels of robustness in niche differentiation in reef fish communities on the Saba bank.

1. Introduction

Reef fish assemblages are driven by complex interactions of many biological and non-biological factors, and therefore are generally highly variable at different spatial scales (Malcolm *et al*., 2011). Environmental influences on individual fish species and reef fish assemblage structure is of central importance in fish ecology in recent years (Anderson and Millar, 2004; Parrish and Boland, 2004; Brokovich *et al*., 2006; Malcolm *et al*., 2010), hereby obtaining valuable insights in conservation and management of the oceans (Chittaro, 2004). One of the most influential factors in shaping reef fish assemblages is habitat type (Ault and Johnson, 1998; Jones and Syms, 1998; Tolimieri, 1998; Chittaro, 2004), with its structural complexity as most important aspect (García-Charton *et al*., 2004). Friendlander and Parrish (1998) described in their research on Hawaiian reef fish assemblages that structural characteristics of habitat may provide shelter from physical stress; modify the availability of resources and their rate of acquisition (Safriel and Ben-Eliahu, 1991) and restrain competitors and predators. This is supported by studies involving artificial reefs with different structural complexity levels, showing that population dynamics in prey fish species is influenced by the availability of vertical relief (Hixon and Beets, 1993; Hackradt *et al*., 2011). On a larger scale, a large quantity of different habitat structures creates barriers which fragment the oceans and provides refuges for many aquatic organisms, resulting in more heterogeneous reef fish assemblages (Sebens, 1991).

Habitat is not the only environmental factor influencing reef fish assemblage structure. A strong correlation of depth with fish assemblage structure was found in many studies (Conell and Lincoln-Smith, 1999; Gaertner *et al*., 1999; Williams and Bax, 2001). Depth may have major impact on the kind of habitat fish encounter, mainly due to changes in light penetration, pressure and temperature (Russ, 1984; Friendlander and Parrish, 1998; Brokovich *et al*. 2008). The percentage of bare rock as habitat substratum increases with depth (Ferreira *et al*., 2001), whereas corals, algae and other photosynthetic organisms are more abundant in shallow water (Friendlander and Parrish, 1998). When research on reef fish assemblages is focussed on shore-less areas without a steep depth gradient, such as an atoll or lagoon, clear differences are found between reef fish assemblages at the centre and near the edge. Fish abundances are consistently lower in the centre of the lagoon compared to its edges (Connel and Kingsford, 1998). The study of Toller *et al*. (2010) in the Southeastern part of the Saba bank (figure 1), a submerged atoll in the Caribbean, shows similar observations. In this study high reef fish abundances at the edges of the Saba bank were found to be higher in number of species and total fish abundances compared to the more centrally located areas. This difference was mainly ascribed by the decrease in structural complexity in habitat towards the center of the Saba bank (Toller *et al*., 2010).

The Saba bank is a completely submerged carbonate platform of approximately 2,200 km^2 and is located about four kilometers southwest of the island of Saba (Netherlands Caribbean) in the Caribbean sea (Macintyre *et al*., 1975). It harbors a diverse range of depth and habitats, including coral reefs, coral patches, sand flats, limestone pavement with algal growth, and sea grass meadows. A wide variety of fish species are found on the Saba bank: 270 species were identified so far and the expected total fish species richness is estimated between 320 and 411 species (Williams *et al*., 2008). The bank also provides residence for many

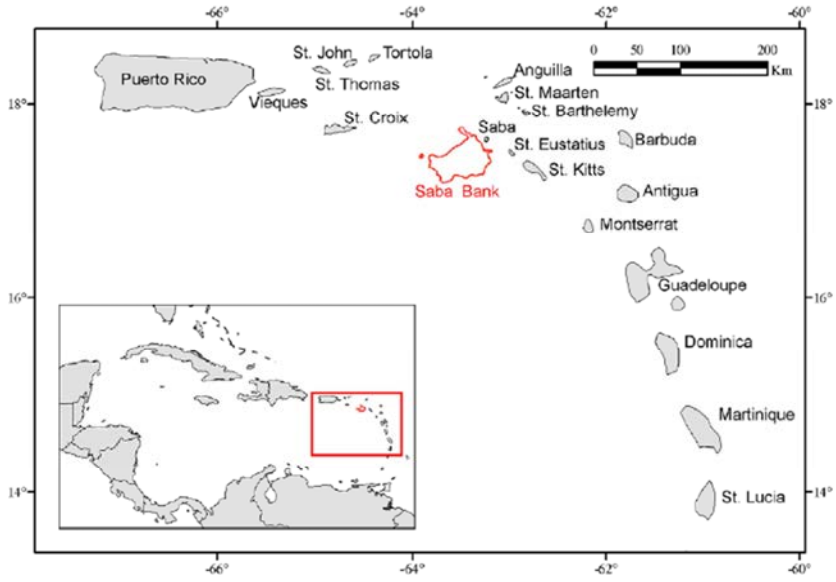

Figure 1. The northeastern part of the greater Caribbean. The Saba bank, study area of this research, is indicated with a red outline. From: Hoetjes & Carpenter (2010)

species of corals (McKenna *et al.,* 2010), sponges (Thacker *et al*., 2010) and macro-algae (Littler *et al*., 2010). Coral reefs are mainly restricted to the shallower edges and the inner lagoon mainly consists of deeper horizontal sand flats and limestone pavement with mainly gorgonians (sea fans) and macro algae. For these reasons a large variability in fish assemblage structures is expected within the banks' ecosystems (Friedlander and Parrish, 1998; Williams *et al*., 2008; Malcolm *et al*., 2011; Toller *et al*., 2010). To protect the Saba bank as a 'biodiversity hotspot' (Lundvall, 2008; Meesters, 2010), it was recognized as a national park in October 2012 by the Dutch government. Hereby banning the anchoring of tankships and allowing sustainable fishery on the Saba bank. Despite recent studies of Toller *et al*. (2010) and Williams *et al*. (2010) on fish assemblages and habitat complexity on parts of the Saba bank, little is known about fish abundances and population structures in general. This information is key for making assessments on whether commercial fisheries on the bank, among other human activities, are sustainable or not.

Besides habitat complexity and depth, fisheries have been shown to, both directly and indirectly, affect fish assemblages and fish species populations (Jennings *et al*., 1995; Bianchi *et al*., 2000; Jennings *et al*., 2009). Direct effects on target fish species include a decline in fish abundance, average size and therefore biomass (Bianchi *et al*., 2000; Jennings *et al*., 2009). This selective fishing also affects the structure of fish assemblages by targeting certain species and therefore causing shifts in assemblage structures (DeMartini *et al*., 2008). Indirect effects of fisheries are the change in fish assemblage structures due to the effect of bycatch (Garcia and Cochrane, 2005) and the change in habitat structure due to destructive fishing methods (Ciappone, 2002). The heavy exploitation of marine resources and associated decline of fish stocks and habitat loss worldwide causes global concern (Pauly *et al*., 2002; Worm *et al.,* 2006; Beddington *et al*., 2007).

The Saba bank is an important fishing location for fishermen of Saba and has been for the fishermen of surrounding islands (Dilrosun, 2000; Toller and Lundvall, 2008). Many foreign vessels used to fish on the Saba bank (Guidicelli and Villegas, 1981; Dilrosun, 2000; Lundvall, 2008; Hoetjes and Carpenter, 2010), but since the implementation of a Dutch fishery law in 1993, the Saba bank is exclusively available for Saban fishermen as part of the Exclusively Economic Zone (EEZ) of Saba. Targeted species by these Saban fishermen are deep water snappers (*Lutjanidae*) and Caribbean spiny lobster (*Panulirus argus*) (Dilrosun, 2000). Lobster fisheries involved bycatch of reef fishes due to the use of size-selective traps. Approximately 15 kg of reef fish is caught every trip, resulting in an estimated 8-10 tonnes of reef fish landed in 2012 (van Gerwen, 2013). Landed reef fish (biomass) consist mainly of grunts (30%: *H. plumieri, H. melanurum and H. album*), queen triggerfish (20%: *B. vetula*) and small groupers (17%: *E. guttatus, C. fulva*). Another estimated 10 tonnes of reef fish was discarded in 2012, consisting mainly of grunts (34%: *H. plumieri, H. melanurum*), boxfishes (19%: *A. polygonia, A. quadricornis*) and surgeonfishes (11%: *A. bahianus, A. coeruleus*) (van Gerwen, 2013). Besides information on landed and discarded fish, little is known about fisheries on the Saba bank and its influence on reef fish assemblages.

So far, research on fisheries and reef fish assemblages on the Saba bank was done by both fisheries-dependent (Dilrosun, 2000) and independent methods (Toller *et al*., 2010; Williams *et al*., 2010). Fisheries-dependent methods used involve trawling and is destructive to benthic communities and size dependent (Williams *et al*., 2010). As fisheries-independent method both the non-destructive SCUBA diving surveys (Toller *et al*., 2010; Williams et al., 2010) and ichtyocide surveys (Williams et al., 2010) were used. With SCUBA a good view on habitat type and fish species assemblages can be obtained. However, SCUBA has its downfalls: it creates a bias towards 'bold species' (Harvey, 2004; Watson *et al*., 2005), has difficulties measuring fish length and abundances, and is limited by time and depth (Watson et al., 2005). To minimize the anthropogenic effects on the study site and to increase the quality of the data, Baited Remote Underwater Video technique (BRUV) was designed. BRUV surveys are non-destructive, cause minimal damage to benthic environment and are not size selective except for the smallest (benthic) fish species (Cappo *et al*. 2006; Watson *et al*. 2007). It is used in many marine studies globally, which range from complete fish assemblages (Malcolm *et al*., 2007; Wraight, 2007) and benthic structures (Harman *et al*., 2003; Westera *et al.,* 2003) in Australia, to abundances and length studies of sharks (Brooks *et al.,* 2011; Bond *et al.,* 2013) in the Caribbean. Also many BRUV studies are done involving sustainable fisheries (Ellis and DeMartini,

1995; Watson *et al.,* 2007; Langlois *et al*., 2012) and marine reserves (Langlois *et al*., 2006; Malcolm *et al*., 2007; Wraight, 2007).

The island of Saba, and therefore the Saba bank as well, is a Dutch overseas public body and is as such part of the country of the Netherlands. The Dutch government is hereby responsible for the protection and management of its biological diversity. For this reason a Nature Policy Plan (NPP) 2013-2017 has been developed. The Plan's objective is to 'ensure that nature on the Caribbean islands is used in a sustainable way so that the island's ecosystems and ecosystem services can be preserved' (MEA, 2013). To adequately preserve the ecosystem of the Saba bank and reach the objectives of the NPP, baseline surveys on its biological diversity are necessary. Both baseline studies for fish assemblages and individuals shark species are mentioned in the Plan and for these studies BRUV surveys were used for its ability to adequately measure individual fish and shark lengths and abundances, and for its cost-efficiency. The Saba bank contains a wide variety of habitat, depth and fishing pressure, and this information is used to study the effects of environmental variables and fisheries on reef fish assemblage structure and the shark population. The objectives of this study are:

1. To conduct a baseline survey on reef fish assemblages covering the whole Saba bank
2. Determine the influence of habitat, depth and fishing pressure on the structure of reef fish assemblages and the influence of fishing pressure on mean fish length of key target species on the Saba bank
3. To conduct a baseline shark survey, involving spatial distribution, species composition, relative abundance, length frequency and the influence of habitat, depth and fishing pressure on the shark population

Changes in reef fish assemblages are quantified by establishing 'traditional' measures such as species richness, fish abundances, mean biomass and trophic level. However, using mean trophic level for determing food source in fish species is a very rough method; it only shows us what a particular fish species eats and tells little about its capacity to eat other food types. Especially in an environment in which the availability of food types constantly changes, a more in-depth method is preferred to describe feeding abilities of a fish assemblage. For this reason also an ecomorphological approach (Food Fish Model) is added to this study. Ecomorphology studies the relationship between form and function to predict feeding strategies and possible competition (overlapping niches) between species. Information on diet (Wainwright, 1989; Ferry-Graham *et al*., 2001a, b; Sibbing and Nagelkerke, 2001; Wainwright and Bellwood, 2002; Choat *et al.,* 2004), lifestyle (Wainwright *et al*., 2002; Collar *et al*., 2008) and trophic interactions (Sibbing and Nagelkerke, 2001) of fish species and complete reef fish assemblages are obtained. The underlying idea is that reef fish assemblages show less variability on a functional level than on species composition level. In other words: a high level of robustness is expected in niche differentiaton of reef fish assemblages.

2. Literature review - Habitat influences on reef fish assemblages

Many environmental variables may be of influence on both individual fish species and fish assemblages. The aim of the literature review is to provide an overview of the environmental variables that are known for their influence on reef fish assemblage structure. In addition, their rate of influence based on the literature found is summarized in a compact table. Environmental variables that are expected to be most explanatory for changes in reef fish assemblages are further analyzed in this study.

2.1 Introduction

Habitat defined as 'the place where an organism lives' (Hudson *et al*., 1992) is probably one of the most simplified definitions in biological science. The relationship between habitat and its inhabitants is not as straightforward as this definition implies. Peters and Cross (1991) described habitat for fish as 'the structural component of the environment that attracts organisms and serves as a centre of biological activity', which emphasizes more on the interactions of habitat with its inhabitants. Environmental influences on fish, and especially reef fish assemblages, is of central importance in fish ecology in recent years (Anderson and Millar, 2004; Parrish and Boland, 2004; Brokovich *et al*., 2006; Malcolm *et al*., 2010). Research on what factors account for the variation of reef fish community structure across space, can provide valuable insights for conservation and management of the oceans (Chittaro, 2004).

Structural complexity of habitat is an important factor in the life history of many aquatic organisms and therefore for complete reef fish assemblages (Mora *et al*. 2003; Anderson and Millar, 2004). Friendlander and Parrish (1998) described in their research on Hawaiian reef fish assemblages that structural characteristics of habitat may provide shelter from physical stress; modify the availability of resources and their rate of acquisition (Safriel and Ben-Eliahu, 1991) and restrain competitors and predators. The large quantity of different habitat structures creates barriers which fragment the oceans and provides refuges for many aquatic organisms, resulting in more heterogeneous reef fish assemblages (Sebens, 1991). Other studies focus more on biological factors influencing fish assemblages, such as: predation (Willis and Anderson, 2003), resource availability (Wellenreuther and Cornell, 2002), ontogenic shifts and sex distributions (McCormick, 1989) and inter/intra-specific behavioural interactions (Levin *et al*., 2000).

Reef fish assemblages are driven by complex interactions of many biological and non-biological factors, and therefore are generally highly variable at different spatial scales. Hence, it is important to focus on the factors that have been shown to have an influence. This literature review focussed on five key factors important in determining habitat type: (1) depth, (2) distance from shore, (3) reef type, (4) dominant benthos and (5) latitude, each with its own influence on reef fish assemblages (Malcolm *et al*., 2011).

2.2 Depth

In most marine ecology studies, depth is seen as an important habitat variable in explaining variances in distribution and abundance of reef fish assemblages (Friendlander and Parrish, 1998). Connel and Lincoln-Smith (1999) revealed a strong gradient in assemblage structure from shallow to deeper water. The structure of those assemblages also changed among locations and sampling time, but those factors explained not as much of the variation as depth (Conell and Lincoln-Smith, 1999).

Change of depth may have major impact on the kind of habitat fish encounter, mainly due to changes in light penetration, pressure and temperature. The percentage of bare rock as habitat substratum increases with depth (Ferreira *et al*., 2001), whereas corals, algae and other photosynthetic organisms are more abundant in shallow waters. Therefore, herbivores are generally more abundant in shallow water reef habitat. This assumption is supported by research in both the Great Barrier Reef (Russ, 1984) and the Hawaiian island Hanaley (Friendlander and Parrish, 1998). Whereas the depth range of suitable habitat types for herbivores seems to be rather small, (mobile) invertebrate feeders occupy can be found over a much broader depth range. Planktivores are mostly found near the deep reef slopes. They are distributed by size, with the smaller species more abundant near the reef, whereas larger species tend to be more numerous

towards the edge of deeper water or drop-off (Friendlander and Parrish, 1998). It has been suggested that to occurrence of larger, mostly diurnal, planktivorous fish along the reef slopes is due to the fact that their major prey are most accessible here (Hobson and Chess, 1978).

Because reef fish communities usually consist of fish species belonging to many trophic guilds, such patterns on a larger scale are more complicated, but still exist in many fish community studies. The strong correlation of depth with fish assemblage structure is found by many research groups (Conell and Lincoln-Smith, 1999; Gaertner *et al*., 1999; Williams and Bax, 2001). Other studies off the Southwest coast of the Australian continent found significant differences in the species composition of fish faunas between near-shore depths (~2m) and further offshore (5-15m and 20-35m) (Hyndes *et al*., 1999). Some fish species were far more abundant in depths of 5-15m, whereas other species were mainly occurring in deeper waters, hereby explaining the differences in species composition found in this study. Similar patterns were found is assemblages further offshore by Gray and Otway (1994), in which fish assemblages in 30-60m depth range differed from the structures at 100m depth. Williams and Bax (2001) stated that depth-related patterns continue to a depth of at least 200m, whereas Zintzen *et al.* (2011) found that species richness does not stabilize down to an average depth of 700 to 1200m. These patterns are seen in both soft-sediment and reef/rock substrata, but also in fish assemblages within the same habitat complexity level (Curley *et al*., 2002). Depth also co-varies with other factors such as, habitat (Bouchon-Navaro *et al*., 2005), distance to shore (Malcolm *et al*., 2011) and food availability (Ferreira *et al*., 2001). Therefore it is difficult to address differences in reef fish assemblages completely to the change in depth.

2.3 Distance from shore

Malcolm *et al*. (2010) found that depth range greatly co-varied with distance from shore, and stated that therefore both the effect of distance from shore and depth on reef fish assemblages is difficult to determine. The study found little effect of the factors reef type and dominant benthic communities, whereas the same factors were closely related to fish assemblages in research done by Chittaro (2004) and Williams *et al.* (2008). Malcolm *et al*. (2011) concluded that the strong influence of distance to shore as a factor could mask the patterns created by other factors. When research is focussed on habitat types without a shore or real depth gradient, such as an atoll or lagoon, clear differences are found between fish assemblages at the centre and near the edge. Fish abundances were consistently lower in the centre of the lagoon, compared to its edges (Connel and Kingsford, 1998). Research of Toller *et al*. (2010) on the Saba bank, a submerged atoll in the Caribbean, shows also high reef fish abundances at the edges of the bank, when compared to the lagoon. This difference is mainly ascribed to the decrease is habitat complexity towards the centre of the atoll (figure 2), which is less suitable for supporting large reef fish assemblages (Toller *et al*., 2010).

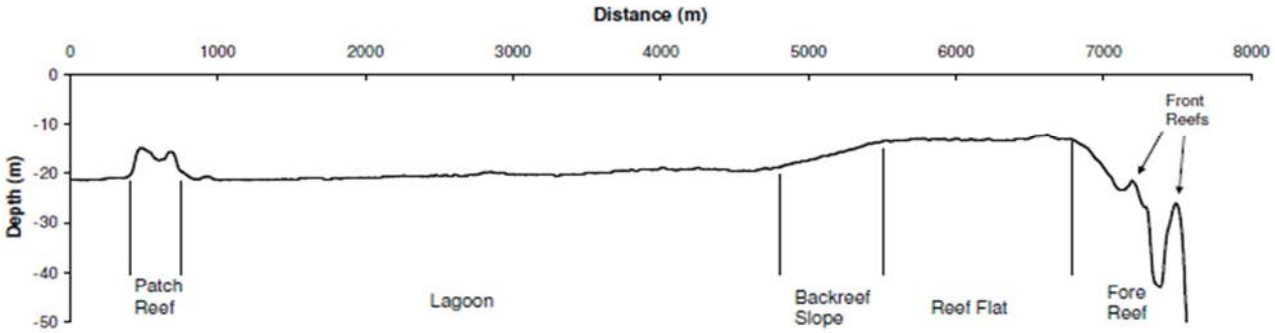

Figure 2. Depth profile across the Saba bank, a submerged atoll in the Netherlands Caribbean. Different depths and associated habitat types can be found on the Saba bank from open ocean and the beginning of the atoll in the East (right) towards the center of the atoll (left). From: Toller (2008)

2.4 Reef type

Many studies show that reef fish assemblages, fish species and individual fish are closely correlated with habitat complexity (Jones and Syms, 1998; Chittaro, 2004), habitat richness (Ault and Johnson, 1998) and habitat abundance (Tolimieri, 1998). Habitat complexity can be simplified and divided into two categories: soft (sand) and hard (rock) substratum. Soft sediments are the most abundant marine habitat around the

world, yet their flora and fauna receive far less attention in ecological research than animals and plants associated with hard substrata (Gray and Otway, 1994). One explanation is that a large part of the world's soft sediment is inaccessible for human research, whereas hard substratum is found in proximity of human resources. Also scientists believe and have concluded that sand habitat and soft sediment is characterized by a general absence of fish species (Williams *et al*., 2008). Fish assemblage structure has been studied intensively on coral and rocky reefs along the shores in shallow water (Williams and Hatcher, 1983; Choat and Ayling, 1987; Lincoln-Smith *et al*., 1991; Connel and Kingsford, 1998), whereas fish assemblages on soft sediments in deeper water are relatively unknown (Connel and Lincoln-Smith, 1999).

The main difference between hard and soft substrate is characterized by substratum complexity, which is an important structural component for fish within their habitat (Williams and Bax, 2001). Food and shelter from predators is provided by vertical relief, together with high rugosity of substratum at certain locations of the reef (Jones, 1988; Hixon and Beets, 1993; Auster *et al*., 1995). A strong linear relationship is found by Friedlander and Parrish (1998) between mean volume of cavities and mean fish length, indicating the importance of shelter possibilities for reef fish assemblages. When artificial reefs are equipped with cavities of various sizes, also clear relationships can be found between cavity size and size and numbers of fish in close proximity of these cavities. Matching cavities to body size is apparently a measure for reef fish to minimize the predation risk. (Hixon and Beets, 1989) This could be a reason why more site attached, smaller, fish, are more abundant at locations with lots of sheltering possibilities (Ferreira *et al*., 2001). Furthermore, Friendlander and Parrish (1998) found in their study that herbivorous fish abundance and biomass could also be explained by roughness of sediment. The same holds for mobile invertebrate feeders, which abundance is also negatively related to depth. Another important structural component of reef fish habitat is the hydrodynamic climate, small-scale interactions with substratum composition and relief and thus influencing local food supplies (Williams and Bax, 2001).

Many piscivores (larger jacks, snappers and sharks) do not have close affinity with a particular kind of substratum, mostly because they forage close to reef edges and are less dependent on certain habitat structures for safety. They are mainly found in deeper waters without a substantial macroalgal cover (Friendlander and Parrish, 1998). However, when hunting for food these fish are mainly active in the habitat structure in which their prey is most abundant and therefore more easily caught. For this reason many piscivores are associated with high relief habitats (Hobson, 1974; Parrish, 1987).

At the reef fish assemblage level, more structurally and topographically complex reef substratum exerts a positive effect on structure and composition of reef fish assemblages. Moreover, if those complex habitat types are located more towards the reef edge, especially near a drop-off, an even more positive effect on reef fish assemblages was found (Friendlander and Parrish, 1998). La Mesa *et al*. (2011) found a clear relationship between fish assemblages and habitat type. This relationship was also found by other studies, in both coral reef fish assemblages (Roberts and Ormond, 1987; Holbrook *et al*., 2000; McClanahan and Arthur, 2001) and rocky reef systems (Guidetti, 2000; Garcia-Charton and Perez-Ruzafa, 2001; Letourneur *et al*., 2003) at small spatial scales. Fish assemblages near seagrass beds and rocky reefs show high similarity on species level, and little overlap with fish assemblages in sandy habitat was found. On rocky reefs and seagrass meadows assemblages mostly contained high number of species and individuals, compared with the ones in a sandy habitat (La Mesa *et al*., 2011). Before these reef fish assemblages can be managed effectively, they are in need to be monitored and examined with a more subtle range of habitat types (Polunin and Roberts, 1993) to allow changes in reef fish assemblage structures to be detected (Williams *et al*., 2008).

2.5 Dominant Benthos

An important ecological function of benthic communities is the regulation of the flow of materials and energy trough food webs (Minshall *et al*., 2014). As prey item, predator and substratum they influence reef fish communities in various ways. Sessile invertebrates also provide hiding and housing possibilities for many small and juvenile fish (Hixon, 1991; Munda, 1992). In temperate regions, kelp and other large algae species provide an additional dimension to fish habitat, by creating refuges and enhancing local food availability (Holbrook *et al*., 1990; Ebeling and Hixon, 1991).

The distribution of many reef fish is dependent on the availability of their main food source. Obligatory corralivore fish species feed on coral, and therefore the availability of coral reefs largely determines the abundance and distribution of these fish species (Reese, 1981; Bouchon-Navaro et al., 1985; Houtigan *et al*., 1988). Coral reefs form complex networks which provide refuges and microhabitats for many organisms. The presence of those small organisms in coral reef systems attracts many non-corallivore fish species as well, creating one of the most diverse reef fish systems on our planet (Chabanet *et al*., 1997). Planktivores are also more abundant in close proximity of their food source; when the percentage drift material in the form of macroplankton increases due to a large influx of water, an increase in abundance and number of planktivorous species was observed (Ferreira *et al*., 2001). Ferreira *et al*. (2001) also found in their study at the rocky shore of the Brazilian southeastern coast an increase of omnivorous fish species at locations with large diversity of benthic organisms, mainly sessile invertebrates.

Seagrass meadows and seaweed beds in other tropical regions are found to have a positive influence on fish abundance and diversity (Carr, 1989; Jenkins and Wheatly, 1998; Ornellas and Coutinho, 1998). Research by Curley *et al*. (2002) shows that when sites have a different diversity of benthic organisms, they are able to support different reef fish assemblages. If reef fish communities of five near shore benthic habitats (sponge flats, algal turf, sand, shallow kelp and deep kelp) are compared, significant differences are observed between all benthic habitat types (Williams *et al*., 2008). Generally, an increase of reef fish diversity from sand to sponge to algal turf to kelp habitat can be observed. Reef type and dominant benthos are not treated as different factors in this study, therefore it is difficult to address their influences as main cause for differences in fish assemblages. The structure of reef fish assemblages is dependent on type of benthic communities, with food sources of this benthic environment as major explanatory factor for species diversity in the fish community (Chabanet *et al*., 1997; Ferreira *et al*., 2001; Curley *et al*., 2002).

2.6 Latitude

Latitude as a factor involved in affecting structure of reef fish assemblages is poorly documented. It is assumed that fish assemblages of northern and southern hemisphere show significant differences. Even a small difference in latitude can have a large influence on fish assemblage composition, whereas some fish species are more 'homebound' than others for different reasons (Ferreira *et al*., 2004). Mora *et al*. (2003) mentioned in their study on the Indonesian and Philippine region (IPR) the Centre-of-Origin hypothesis (Darwin, 1859). It suggests that there is an major centre of speciation, in their study the IPR, from which species disperse to other locations (Boyet *et al*., 2002; Kleine *et al*., 2002), hereby creating a non-random species distribution. Both the IPR and the Greater Caribbean (GC) are considered to be major centres of endemism for fish and other taxa (Mora *et al*., 2003; Rocha *et al*., 2008).

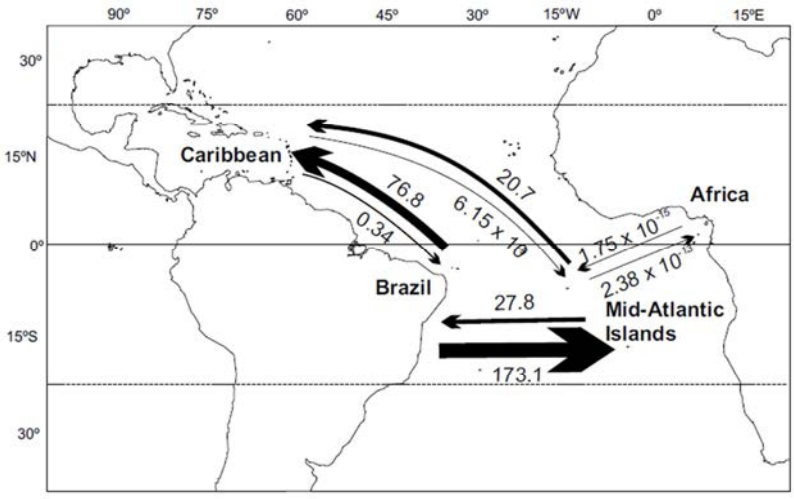

Figure 3. Migration routes of the brown chromis (*chromis multilineata*) Migration between different populations in the Tropical Atlantic biogeographic provinces, based on the program MIGRATE. Arrow direction and thickness is respectively direction and amount of migration. From: Rocha *et al*. (2008)

The GC can be stated as a centre of origin of fish and other marine taxa, in which species richness decreases in latitudinal axis. Rocha *et al*. (2008) studied multiple Caribbean fish species, including the brown chromis (*chromis multilineata*). Migration routes from *chromis multilineata* presented in figure 3 shows how migration between different populations occurs in this species. These migration routes are consistent with the general ocean surface currents, which is highest from the mid-Atlantic islands to Brasil and from the South Atlantic

to the Caribbean (Rocha *et al*., 2008). Latitudinal changes in species distribution and species richness are associated with evolutionary processes regulating these patterns. The processes of dispersal, speciation and extinction are of major importance in determining the species structure of local fish assemblages (Mora *et al*., 2003).

2.7 Conclusion

In many studies both number of individuals and biomass of reef fish assemblages were highest in complex back reef systems in shallow water (Friedlander and Parrish, 1998; Williams *et al*., 2008; Malcolm *et al*., 2010; Toller *et al*., 2010). Limited shelter and low spatial relief habitats are associated with fish assemblages with low species richness, low biomass and low number of individuals. Apparently, fish are more attracted to sites with high spatial relief (Friedlander and Parrish, 1998; Toller *et al*., 2010). Fish biomass and numbers of individuals can be predicted with 'cavity volume' and other three-dimensional structures, which are variables associated with high spatial relief sites. These variables play an important role in the sheltering and housing of many reef fish species.

The expected effects, based on this literature review, of five environmental variables on reef fish assemblage structures mentioned in this literature review are shown in table 1. Some factors are expected to play a larger role in structuring fish assemblages on the Saba bank than others. Depth, reef type and dominant benthos are the three environmental factors that are believed to have the highest influence on reef fish assemblages and are shown in bold. Expected effect in fish assemblage characteristics is shown with *increase* or *decrease*. An increase in depth is expected to have a negative influence on fish abundance, species richness and biomass, whereas a positive effect is expected for mean trophic level and fish length. The same holds for distance to shore, which is directly related with depth. Reef type and dominant benthos are habitat characteristics based on habitat structure and substrate and therefore similar influence on reef fish assemblages is expected. With an increase of dominant benthos availability and reef type complexity, an increase is fish abundance, species richness and mean biomass is expected. Whereas a decrease in mean fish length and trophic level is expected with a change in these environmental variables. The influence of latitude of fish assemblages is poorly documented, therefore only its influence on species richness is given.

Table 1. The expected effect of five different environmental variables on reef fish assemblage structures, based on literature review. Reef fish assemblages are characterized by fish abundance, species richness, mean fish length, mean biomass and mean trophic level

Fish assemblage characteristic	Expected effect on				
	Depth	**Reef type**	**Dominant benthos**	Distance to shore	Latitude
Abundance	Decrease	Increase	Increase	Decrease	NA
Species richness	Decrease	Increase	Increase	Decrease	Decrease
Mean length	Increase	Decrease	Decrease	Increase	NA
Mean biomass	Decrease	Increase	Increase	Decrease	NA
Mean trophic level	Increase	Decrease	Decrease	Increase	NA

Realistically, many interactions and complex linkages exist between a great number of habitat (Curley *et al*., 2002), ecological (Tolimieri *et al*., 1998; Shima, 2001) and environmental (Williams and Bax, 2001) variables. All these factors have influence on reef fish structures. A multi-factor study is required to address the amount of influence on reef fish assemblages to every factor involved. Such a study should include habitat as one categorical variable and measurements of all environmental parameters involved (Williams *et al*., 2008).

3. Material and Methods

3.1 Study area

This study was conducted between October 2012 and February 2014 on the Saba bank in the Caribbean Sea (figure 1). The Saba bank (17˚25N, 63˚30W) is a completely submerged carbonate platform of approximately 2,200 km^2 and is located about four kilometers southwest of the Caribbean island of Saba (Dutch Caribbean islands) (Macintyre *et al*., 1975). Actively growing coral reefs are situated at the edges of the platform, with highest coral abundances on the eastern and southern edges, surrounding a central lagoon. The bank rises about 1,000 m above the surrounding seafloor and is not directly connected to any land (Lundvall, 2008). It harbors a diverse range of habitats, including coral reefs, coral patches, sand flats, limestone pavement with algal growth, and sea grass meadows. These habitats are situated at depths between approximately 11-100m (Toller *et al*., 2010).

3.2 Fishing pressure

In order to quantitatively relate reef fish communities to different levels of fishing pressure the Saba bank was divided into twenty evenly-sized quadrants with variable fishing pressure. Table 2 shows fisheries activity as a percentage of total fisheries activity of recent years. When more than 10 percent of the fishing trips takes place to a particular quadrant, it was classified as 'high' fishing activity quadrant. This quadrant was then marked red in the map in figure 4. Quadrants marked as 'medium' fisheries activity (fisheries activity between 2 and 10 percent) were indicated in orange, whereas 'low' (<2 percent) fishing quadrants were marked green. Fisheries activity was mainly situated close to Saba and decreases with distance to shore (Saba). The lobster fishery was mainly restricted to the more shallow quadrants on the South and Eastern part of the bank.

Table 2 Fisheries activity per quadrant. Activity is shown as percentage of total fisheries activity of recent years. When percentage >10, fisheries type 2 (Category High) is given to the quadrant. Fisheries activity between 2 and 10 percent are categorized as fisheries type 1 (Medium) and when percentage is below 2 the quadrant is considered as fisheries category 0 (Low). Data obtained from Van Rijn (pers. comm.)

Quadrant	Fisheries Activity (%)	Fisheries	Category
A3	0.0	0	Low
A4	0.0	0	Low
A5	0.0	0	Low
B3	2.1	1	Medium
B4	21.3	2	High
B5	21.6	2	High
C1	0.0	0	Low
C2	0.5	0	Low
C3	1.8	0	Low
C4	14.7	2	High
C5	19.7	2	High
D2	0.5	0	Low
D3	6.4	1	Medium
D4	7.5	1	Medium
D5	3.8	1	Medium

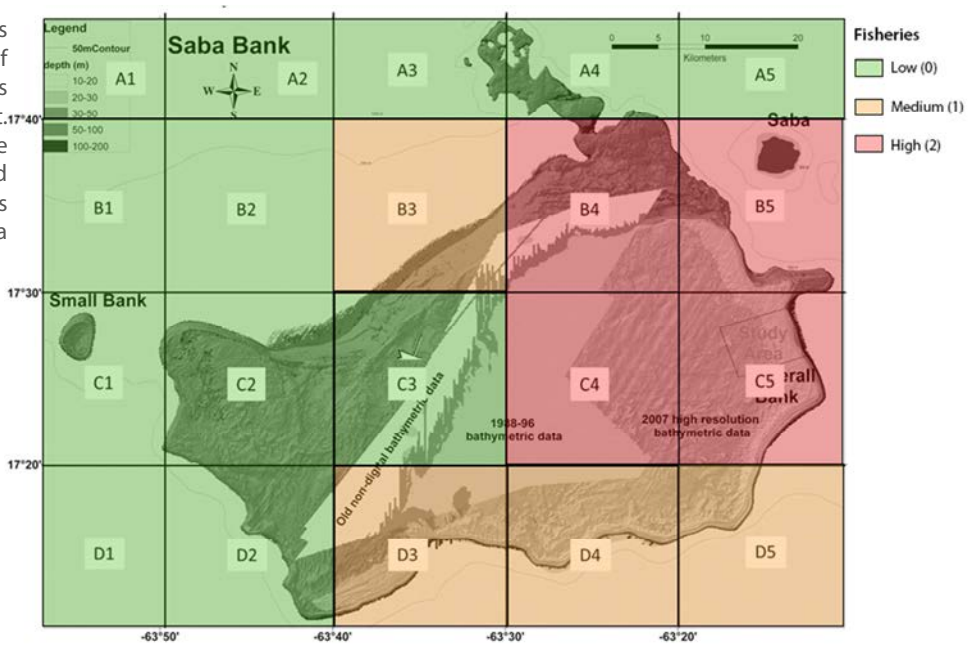

Figure 4 Fisheries activity per quadrant on the Saba bank. Activity is shown as different colors for percentage ranges of total fisheries activity in recent years. High (red), medium (orange) and low (green) are categories used indicating fisheries activity.

3.3 Sampling technique

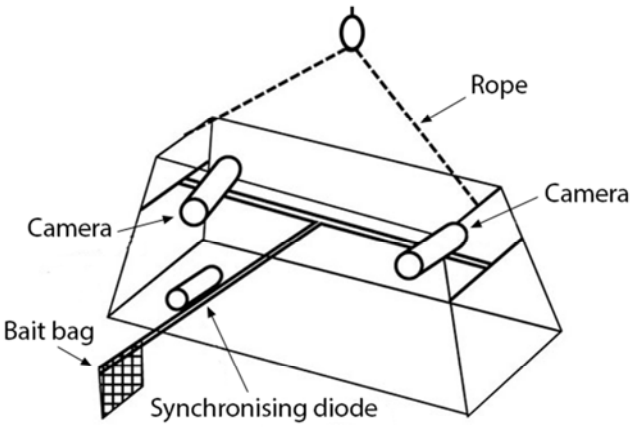

Figure 5. Set-up of baited remote underwater stereo-video (stereo-BRUV). After Langlois *et al*. (2010)

Three stereo-BRUV systems were used to obtain video footage of reef fish assemblages. Specific information on design and calibration of the stereo-BRUVs can be found in Harvey and Shortis (1995, 1998). To provide accurate length measurements during video analysis, all BRUV systems were calibrated for in a swimming pool, prior to use (Harvey *et al*. 2003, Shortis *et al*. 2007). Video footage of these calibration sessions was analyzed with SeaGIS CAL V2.10 software (http://www.seagis.com.au). Each BRUV system consisted of two video cameras (Canon Legria HFG10) which were mounted in high-density PVC housings. The cameras were attached to an aluminum frame, orientated along a horizontal plane relative to the sea-floor. Mooring rope was attached to the BRUV system with at the end a buoy for retrieval. A bait bag containing ca. 800 grams of pilchards (*Sardinops sp*.) was mounted on a pole and placed at 1.5m from the lens. Complete set-up of the BRUV system can be seen in figure 5. The three BRUV units were used concurrently at a minimum distance of 500 m apart to reduce overlap of bait odor plumes (Willis & Babcock, 2000, Harvey *et al.*, 2007, Heagney *et al*., 2007). One hour recordings were made per location. After deployment, the boat drove away from the sampling area.

3.4 Sampling design

A total of 165 samples were taken between October 2012 and February 2014 on the Saba bank (figure 6), 52 by Jelmer Pander and 113 by Twan Stoffers. Study sites were deployed over different habitat types along three different depth layers (15, 25 and 40m) to conduct a comprehensive baseline survey on the whole Saba bank. However, sampling was not completely random due to time restrictions and large surface of the bank (2,200 km^2). Therefore relatively more samples were taken in the shallow areas (<20m) of the bank (East and South), where range of habitat types is expected to be widest (Harvey *et al,*. 2007, Toller *et al*., 2010). Study sites were characterized by type of habitat complexity (see habitat characteristics), depth range and fisheries activity (figure 6 and Appendix II). In total 66 samples were taken in 15m depth (<20m), 52 samples in 25m depth (20-35m) and the 40m depth layer (>35m) was 47 times sampled. These depth categories were chosen because recent studies (Hyndes *et al*., 1999; Williams and Bax, 2001; Curley *et al*., 2002) have shown that fish assemblages can differ

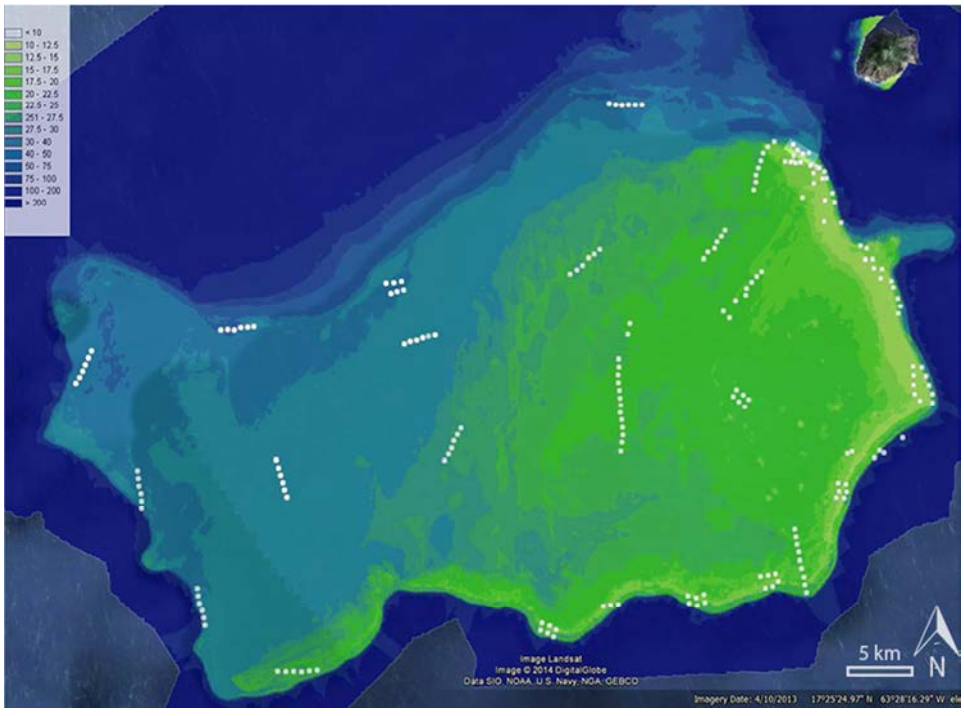

Figure 6. Sampling design in Google Earth. Sample locations are evenly distributed over Saba bank and different habitat types. Therefore relatively more sampling took place in the shallower areas on the eastern and southern site, where range of habitat types is widest.

greatly within these depths layers at other locations. An overview of all sites sampled can be found in Appendix III.

For habitat quantification the 6-point scale of Polunin and Roberts (1993) was used. This scale (figure 7) is divided into: (0) bare substratum, (1) low and sparse relief, (2) low but widespread relief, (3) moderate complexity, (4) high complexity and (5) extreme complexity. The latter category (5) was not found in the data set of the Saba bank and therefore left out in this study. Habitat type classification and characteristics of each sample can be found in Appendix I and II.

Figure 7. The 6-point scale of Polunin and Roberts (1993) used in this study to quantify habitat. It is divided into: (0) bare substratum, (1) low and sparse relief, (2) low but widespread relief, (3) moderate complexity, (4) high complexity and (5) extreme complexity. The latter category (5) was not found in the sampling data of the Saba bank and therefore left out in this study.

3.5 Image analysis

Seagis Eventmeasure software (http://www.seagis.com.au/event.html) was used to analyze fish assemblages on the video footage. Each fish was manually classified to species level and for each species the maximum number seen together in any one time (MaxN) on the whole tape (1 hour) was recorded. MaxN is considered a conservative estimator of the relative abundance of a species (Willis *et al*., 2000) and its use has been reviewed in detail by Cappo *et al*. (2003, 2004). Fork length of all individual fish of a species at the time of MaxN was measured afterwards. Rays were an exception, since their length was measured with disk width. A ~8m distance range was used in MaxN and length measurements for consistency among samples (Cappo *et al*., 2004; Harvey *et al*. , 2007). Screenshots of image analysis and calibration software can be found in Appendix IV.

3.6 Ecomorphological analysis

3.6.1 Fish Food Model (FFM)

In order to obtain a more in depth view on feeding performance of fish species and eventually reef fish assemblages, ecomorphological analysis was done. For this a Fish Food Model (FFM) was used as described by Sibbing and Nagelkerke (2001). The FFM quantitatively relates how morphological traits of fish species

can be used to deal with traits of prey species, based on experimental evidence. The steps involved in this were obtaining individual fish of a set of species representative of the Saba bank; measuring morphological traits of these fish species; relate these morphological traits to traits of food sources and eventually create a 'suitability-list' per fish species for eating the different food types. A standardized set of morphological traits of the fish species was related to food source traits with a 'specialist dataset' (table 3), which contains values that indicate 'optimal' fish characteristics for each food type. By comparing the set of morphological fish traits with de specialist dataset, a new set of values was obtained, which said something about the suitability of a fish species for eating a particular food item.

Table 3. The specialist dataset. These values indicate 'optimal' fish characteristics(rows) for each food type (columns). These values were compared with morphological traits of individuals of fish species (not shown). With these comparisons most suited food types per fish species were predicted. Derived from Sibbing and Nagelkerke (2001)

	Phytoplankton - townet	Phytoplankton - pump	Algae - scraping	Algae - biting	Detritus - particulate	Microcrustaceans - townet	Microcrustaceans - pump	Crustaceans - diverse	Larvae / worms - particulate	Molluscs - particulate	Fish - pursuit	Fish - ambush
Ba	0	0	0	0	2	0	0	0	2	0	0	0
MBD	-1	0	0	0	1	-1	0	0	1	1	-2	0
CPD	-1	0	0	0	0	-1	0	0	0	0	-2	2
HL	1	1	-1	-1	0	1	1	0	0	0	1	2
ED	0	0	0	0	0	0	1	0	0	0	0	0
Pr	0	0	0	-2	2	0	0	1	2	1	0	2
OGAx	-1	-1	0	0	1	-1	-1	0	1	0	-1	0
GL	1	1	1	0.5	2	0	0	0	0	0	0	0
LJL	0	0	-1	-2	0	0	0	0	0	0	2	2
TOT1	1	1	1	1	0	1	1	1	0	1	0	0
TOT2	1	1	1	1	0	1	1	1	0	1	0	0
TOT3	0	0	0	1	0	0	0	1	1	1	1	1
TOT4	0	0	0	1	1	0	0	0	0	0	1	1
RL	2	2	1	0	1	2	2	0	0	0	-2	-2
GiRD	-2	-2	-1	0	-1	0	-2	0	0	0	1	1
PLOW	0	0	0	1	0	0	0	1	0	0.5	2	2
TPT_1	1	1	1	1	0	1	1	1	0	1	0	0
TPT_2	1	1	1	1	0	1	1	1	0	1	0	0
TPT_3	0	0	0	1	1	0	0	1	1	1	1	1
TPT_4	0	0	0	1	1	0	0	0	0	0	1	1
RBD	1	0	0	0	0	1	1	0	0	0	0	0
LJFEiC	0	0	1	2	0	0	0	0	0	0.5	-2	-2
VCOp	0	1	0	0	0	0	0	0	0	0	1	2
OpAr	0	1	0	0	0	0	0	0	0	0	0	2
GiAr	2	2	0	0	0	2	2	0	0	0	-2	-1
RGA	1	0	0	0	0	1	1	0	0	0	1	0
HyJsR	0	0	0	0	0	0	0	0	0	0	0	1
HyL	0	0	0	0	0	0	0	0	0	0	0	1

Twelve food types were categorized on properties such as size, shape, immobility, toughness and shell presence. Also mechanical and chemical properties were important for categorizing these food types. Because many different food type characteristics are involved in the FFM, the link between a fish variable and certain food type comprises the complete process of prey consumption, from detecting to defecating. Among the processes involved are detecting, approaching, grabbing, swallowing and digesting of the prey item. Because the FFM-model was designed for freshwater systems, small modifications were made to use this model for the marine environment. Those modifications involved the conversion of the food types to marine food types: the removal of seeds and insects and the change of plants into algae (biting). The following food types were used in this analysis: phytoplankton (both pump- and townet mechanism), algae (both scraping and biting), detritus (particulate), micro-crustaceans (both pump- and townet mechanism), crustaceans, larvae/worms, mollusks and fish (both pursuit and ambush method). (Sibbing and Nagelkerke, 2001)

All 47 feeding variables used in Sibbing and Nagelkerke (2001) are shown below with a short explanation. Some variables were adapted to accommodate for the marine fish species used in this study. Adaptations were indicated as such and all other variables were directly taken from Sibbing and Nagelkerke (2001) and the MSc thesis of Eline van Onselen (2013), who executed a similar study on fish species in Dutch waters.

1. **Barbels (Ba)** – Barbels present yes (1) or no (0). This is an adaptation from Sibbing and Nagelkerke (2001) in which the barbel length is measured. However as most species in this study do not have barbels, a decision was made to only use the absence or presence of barbels. Barbels are important for detecting benthic prey in the substratum, giving the species with barbels an advantage over species without (Sibbing and Nagelkerke, 2001).
2. **Maximum body depth (MBD)** – in mm. Measured as the deepest part of the fish, in the vertical plane, 90° against the body axis (figure 8). The shape of the fish is related to its swimming capability. For example, a streamlined body will allow speed, while a more rounded body will allow maneuverability. This swimming capacity is in turn related to the feeding strategy of the fish, as speed is needed to hunt certain types of prey while maneuverability is needed for others (Webb, 1984).
3. **Caudal Peduncle Depth (CPD)** – in mm. Measured as the smallest body depth between the anal fin and the caudal fin (figure 8). A narrow caudal peduncle reduces drag while swimming whereas a large caudal peduncle increases thrust in an attack. Subsequently this can indicate swimming and hunting habits of the fish as certain prey types require endurance while swimming while others require a fast ambush attack (Sibbing and Nagelkerke, 2001).

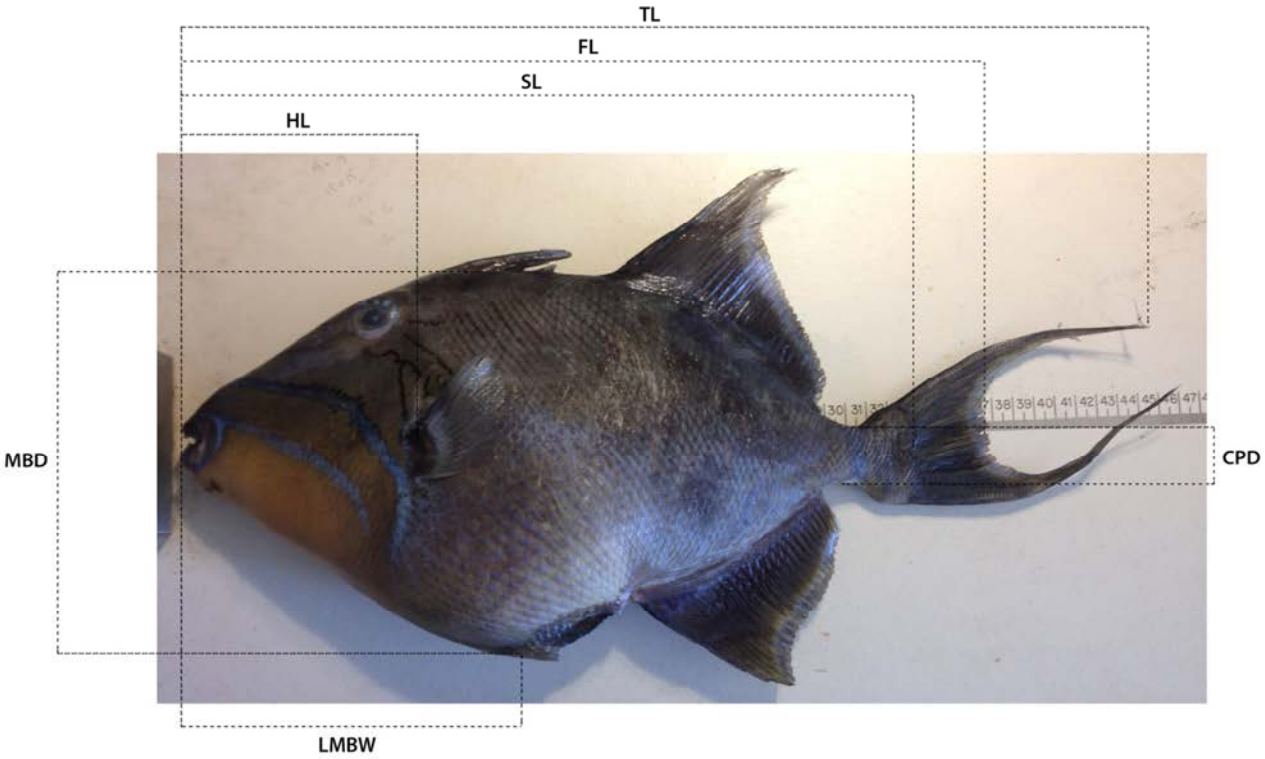

Figure 8. Morphological measurements on the common Caribbean fish *Balistes vetula* (queen triggerfish). Total length (TL), Standard length (SL), Fork length (FL), Head length (HL), Maximum body depth (MBD), Length at maximum body depth (LMBD) and Caudal peduncle depth (CPD) are indicated.

4. **Head Length (HL)** – in mm. Measured from the most anterior point of the head to the most posterior point of the opercular bone, excluding spines and the gill membrane (figure 8) (Holčik, 1989). Relative to the body length, the head length can give information on the suction capacity of the fish; a larger head will increase this capability (Sibbing and Nagelkerke, 2001). Also the volume capacity will increase as head size increases, giving the fish the opportunity for larger prey when in combination with a large gape size.
5. **Eye diameter (ED)** – in mm. In detecting prey, a relatively larger eye compared to body length can give an advantage in murky or dark circumstances, as visual sensitivity and acuity can increase with eye size (Sibbing and Nagelkerke, 2001).
6. **Protrusion (Pr)** – in mm. Measured as the difference of protrusion between opened and closed mouth, from most anterior point of the skull to the tip of the upper jaw. A larger protrusion (relative to body length) increases the grasping range of the bite and also increases the velocity of catching the prey when used in combination with swimming. It can also increase suction forces and bend the mouth in the direction of the prey (Motta, 1984).

7. **Oral gape axis (OGAx)** – in degrees. The angle the mouth makes in comparison to the body axis when fully opened. This can indicate the preferred food position and thus the location of the food (Sibbing and Nagelkerke, 2001).
8. **Gut length (GL)** – in mm. The relative gut length is inversely correlated with diet quality, because low-quality food such as plant material is needed in larger quantities than for example muscle tissue (Griffen and Mosblack, 2011).
9. **Lower jaw length (LJL)** – in mm. Measured from anterior tip to posterior joint. The jaw length is directly related to the size of the mouth and thus the prey size capability (Sibbing and Nagelkerke, 2001).
10. **Oral tooth type 1 (TOT1)** - present yes (1) or no (0). This, together with 11, 12 and 13, is a new variable, as the model was based on fish without oral teeth. It is based on the pharyngeal teeth functions, in combination with a suitable form. Type 1 is Papilliform (figure 9), which is suitable to grind or crush the food (Sibbing, 1991 and Sibbing and Nagelkerke, 2001).
11. **Oral tooth type 2 (TOT2)** - present yes (1) or no (0). Type 2 is Molariform (figure 9), which is suitable to grind or crush the food (Sibbing, 1991 and Sibbing and Nagelkerke, 2001).
12. **Oral tooth type 3 (TOT3)** - present yes (1) or no (0). Type 3 is Caniniform (figure 9), which is suitable to lacerate, cut, pierce or split the food (Sibbing, 1991 and Sibbing and Nagelkerke, 2001).

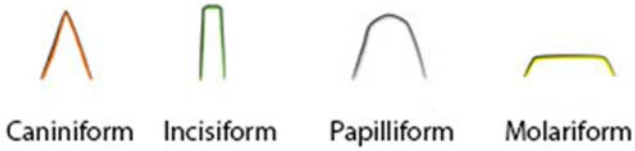

Figure 9. Simplified representation of different oral teeth types in marine fish. Caniniform (lacerate, cut, pierce and split food), Incisiform (shear food), papilliform (grind and crush food) and molariform (grind and crush food) are the types of teeth found in this study.

13. **Bony gill raker length (RL)** – in mm. Measured as an average of 10 rakers (or as many as the gill arch holds), lateral on the second arch. Short gill rakers with a smooth profile give a smoother water outlet and reduce internal drag, which is advantageous for hunters (Sibbing and Nagelkerke, 2001).
14. **Gill inter-raker distance (GiRD) –** in mm. Measured on the second arch as an average of at least three inter-raker distances. Widely spaced gill rakers decrease the branchial arch resistance, while gill rakers placed close together retain more particles (Sibbing and Nagelkerke, 2001).
15. **Postlingual organ width (PLOW)** – in mm. Measured as the distance of the oral floor between the left and right second gill-arch. This indicates the size of prey which can enter (Sibbing and Nagelkerke, 2001).
16. **Pharyngeal tooth type 1 (TPT_1)** - present yes (1) or no (0). Adapted from Sibbing and Nagelkerke (2001), together with 18, 19 and 20. It is based on the pharyngeal teeth functions, in combination with a suitable form. Type 1 is Papilliform (figure 9), which is suitable to grind or crush the food (Sibbing, 1991 and Sibbing and Nagelkerke, 2001).
17. **Pharyngeal tooth type 2 (TPT_2) -** present yes (1) or no (0). Type 2 is Molariform (figure 9), which is suitable to grind or crush the food and thus directly correlated to the preferred food type (Sibbing, 1991; Sibbing and Nagelkerke, 2001).
18. **Pharyngeal tooth type 3 (TPT_3) -** present yes (1) or no (0). Type 3 is Caniniform (figure 9), which is suitable to lacerate, cut, pierce or split the food (Sibbing, 1991; Sibbing and Nagelkerke, 2001).
19. **Relative Body Depth (RBD) –** this is a ratio; MBD / MBW. Like variable 2, this is about the shape of the fish, which is correlated to its swimming- and thus feeding-capabilities.
    a. **Maximum body width (MBW)** – in mm. Measured as the widest part of the fish in the horizontal plane, 90° as opposed to the body axis.
20. **Lower jaw force efficiency in closing (LJFEiC) –** this is a ratio; Ljin / LJout**.** Depending on the food source a higher force in closing the mouth may be necessary (Sibbing and Nagelkerke, 2001).
    a. **Lower jaw in-lever (LJin) -** The in-lever is measured from the centre of the joint between the quadrate and articular to most dorsal point of the dentary in mm. (Wainwright and Richard, 1995).
    b. **Lower jaw out-lever (LJout) -** The out-lever is measured from the centre of the joint between the quadrate and articular to the tip of the anterior-most row of teeth on the dentary in mm. (Wainwright and Richard, 1995).
21. **Volume capacity operculum (VCOp) –** This is a ratio; POrL / OpD. It represents the volume displacement of one unit of operculum area (Sibbing and Nagelkerke, 2001).
    a. **Postorbital length (POrL)** - in mm. Measured as the greatest distance between the posterior margin of the orbit and the most posterior tip of the opercular bone, excluding the spines and the opercular membrane (Holčik, 1989).

b. **Operculum depth (OpD)** – in mm. Measured from the top of the operculum to most ventral point of operculum.

22. **Relative operculum area (OpAr)** – calculated as (POrL ∗ OpD) / SL2. The operculum area gives an indication of the ability to let water out of the mouth area; a bigger operculum area could mean a higher capacity and a higher flow.
    a. **Standard length (SL)** – in mm. Measured from most anterior point of the head to the beginning of the caudal fin.
23. **Gill arch resistance (GiAR) –** This is a ratio; RL / GiRD. Widely spaced gill rakers decrease the branchial arch resistance, while gill rakers placed close together retain more particles (Sibbing and Nagelkerke, 2001).
24. **Relative gape area (RGA)** – This is a ratio; OGA / FBA. This ratio indicates the ability of the mouth to open in comparison to the body shape. A larger gape area could indicate the ability to take in larger prey or larger volumes of water.
    a. **Oral gape area (OGA)** – calculated as (OGH ∗ OGW) / SL2 (Sibbing and Nagelkerke, 2001).
    b. **Oral gape height (OGH)** – in mm. Measured when mouth is fully opened.
    c. **Oral gape width (OGW)** – in mm. Measured when mouth is fully opened.
    d. **Frontal body area (FBA)** – this is calculated as MBD * MBW (Sibbing and Nagelkerke, 2001).
25. **Hyoid / jaw-susp ratio (HyJsR) –** this is calculated as HyL / LJSL. A long hyoid bar allows the fish to increase head-volume, which in turn can indicate prey preference. The optimal ratio for speed is 0.71 (Sibbing and Nagelkerke, 2001).
    a. **Hyoid length (HyL) -** in mm. Measured from the joint of the hyoid and interhyoid to the most anterior point of the hyoid (Muller, 1989).
    b. **Lower jaw suspensorium length (LJSL) -** in mm. Measured from the joint of the hyoid and interhyoid to the most anterior part of the dentary (Muller, 1989).

For a more detailed description of the different morphological measurements, please refer to Sibbing and Nagelkerke (2001). Some measurements were left out in the FFM in this study for diverse reasons. Multiple reasons for exclusion were in accordance with the study of Van Onselen (2013) and therefore adopted from this study. They are indicated in the description of the morphological traits. The following list will present the left-out measurements with corresponding reasons.

26. **Pharyngeal tooth type 4 (TPT_4) -** present yes (1) or no (0). Type 3 is Incisiform (figure 9), which is suitable to shear the food (Sibbing, 1991; Sibbing and Nagelkerke, 2001). However, this tooth type was not present in the fish species and therefore left out of the FFM.
27. **Oral tooth type 4 (TOT4)** - present yes (1) or no (0). Type 3 is Incisiform (figure 9), which is suitable to shear the food (Sibbing, 1991 and Sibbing and Nagelkerke, 2001). However, this tooth type was not present in the fish species and therefore left out of the FFM.
28. **Total Weight (TW) -** in grams. Measured directly after defrosting with the fish being gently dabbed dry using a paper towel. This is an easily measured variable which could be used for making ratios with other variables. It was decided however to use Standard Length (SL) for this so TW was left out of the FFM (by Van Onselen, 2013).
29. **Length at maximum body width (LMBW)** - in mm. This variable provides a view on the shape of the fish, which then can give information in its swimming abilities (Sibbing and Nagelkerke, 2001). This is an easily measured variable which could be used for making ratios with other variables. It was decided however to use Standard Length (SL) for this so TW was left out of the FFM (by Van Onselen, 2013).
30. **Head width (HW) –** in mm. This variable provides a view on the shape of the head of the fish and its possible volume. Measured at head depth (HD) (Sibbing and Nagelkerke, 2001). This is an easily measured variable which could be used for making ratios with other variables. It was decided however to use Standard Length (SL) for this so TW was left out of the FFM (by Van Onselen, 2013) .
31. **Head depth (HD) –** in mm. This variable provides a view on the shape of the head of the fish and its possible volume (Sibbing and Nagelkerke, 2001). However, because already several variables provide information on this subject (such as MBD and RBD) it was decided to leave this parameter out of the FFM (by Van Onselen, 2013).
32. **Lower jaw width (LJW)** – in mm. Measured from left to right joint. This variable provides a view on the shape of the head of the fish (Sibbing and Nagelkerke, 2001). However, because already several variables provide information on this subject (such as HL) it was decided to leave this parameter out of the FFM (by Van Onselen, 2013).

33. **Lower jaw span (LJS)** – in mm. Measured from left to right joint, following the jaw. This variable can provide a view on the shape of the head of the fish (Sibbing and Nagelkerke, 2001). However, because already several variables provide information on this subject (such as HL) it was decided to leave this parameter out of the FFM (by Van Onselen, 2013).
34. **Number of teeth on lower jaw (#TLJ) -** Teeth can be distributed differently among the jaw (Barel *et al*., 1989). To get an overview of how the teeth are distributed the teeth are counted, measured and the total length of the jaw is measured in mm. Only the first row of teeth is counted (Sibbing and Nagelkerke, 2001). This could be of interest when looking at food preferences, because of limited knowledge on interpreting the relation between number of teeth and food preferences, a specialist dataset has not been made yet for this variable. For that reason it was left out of the FFM (by Van Onselen, 2013).
35. **Density of oral teeth on lower jaw (DOTL) -** The number of teeth per mm^2 as an average between left, right and centre of the lower jaw. The density of the teeth on the jaw can be of interest when looking at the ability of water to flow through or the amount of teeth in total (Sibbing and Nagelkerke, 2001). The density of the teeth on the jaw can be of interest when looking at the ability of water to flow through or the amount of teeth in total. However because of lack of knowledge in putting this into the specialist dataset, it was decided to leave it out of the FFM (by Van Onselen, 2013).
36. **Maximal tooth height (MTH) -** in mm. Measured from base to tip of the crown. Together with tooth width this could give information on the shape of the tooth. Together with tooth width this could give information on the shape of the tooth. However because teeth can be of different shapes entirely, just giving the absence or presence of a certain tooth type was thought to be a more reliable variable.
37. **Maximal tooth width (MTW) –** in mm. Measured at the widest part of the tooth. See MTH .
38. **Total number of gill rakers (TRNr) –** Counted on the second arch. The total number of gill rakers can be relevant when looking at the flow through of water, but only in combination with arch length and gill raker size (Sibbing and Nagelkerke, 2001). Because there are already variables looking at the same type of function (e.g. GiAR) it was decided to leave this variable out of the FFM (by Van Onselen, 2013).
39. **Gill-raker density (GrD)** - The actual number of gill-rakers per mm. Measured on the second arch. The number of gill rakers per mm. can again provide information on the capability to let water through or filter out particles. The number of gill rakers per mm. can again provide information on the capability to let water through or filter out particles. It was left out for the same reason as TRNr (by Van Onselen, 2013).
40. **Caudal fin area (CFAr) – in mm^2.** A tailfin area can increase thrust when striking while it also increases drag when swimming, this can indicate swimming and hunting habits (Sibbing and Nagelkerke, 2001; Webb, 1984). However, not all individuals examined had an intact caudal fin and it was decided to leave this variable out of the FFM (by Van Onselen, 2013).
41. **Total Length (TL) –** in mm. Measured from the most anterior point of the fish to the most posterior one. This is an easily measured variable which could be used for making ratios with other variables. It was decided however to use Standard Length (SL) for this so TW was left out of the FFM (by Van Onselen, 2013).
42. **Standard length, US way (SL_US)** – in mm. from most anterior point of the head to the articulation point of the tail. This is an easily measured variable which could be used for making ratios with other variables. It was decided however to use Standard Length (SL) for this so TW was left out of the FFM (by Van Onselen, 2013).
43. **Width of branchiostegal rays membrane (WBRM)** - in mm. Measured when fully extended. This variable provides information on the ability of the internal volume to increase which could provide information on maximum prey size or volume intake. However because this variable was not present in all fish species, it was decided to leave it out (by Van Onselen, 2013).
44. **Sex (S)** – male (1) or female (2). This variable is not very useful for making predictions about the food partitioning so it was left out of the FFM (by Van Onselen, 2013).
45. **Lower Pharyngeal jaw mass (PJM)** – in grams. The tougher the material to chew, the heavier the pharyngeal jaw needs to be (Sibbing and Nagelkerke, 2001). However, the species studied in this research had relatively small pharyngeal jaws which could not be measured precisely on the scale available. This resulted in unreliable measurements and it was decided to leave this variable out of the FFM (by Van Onselen, 2013).
46. **Lower pharyngeal length (LPL) –** in mm. Measured through the vertical centre axis of the jaw (Barel *et al*., 1976). In combination with the lower pharyngeal width, the LPL provides information on the shape of the pharyngeal jaw. However, some species used in this research did not have a pharyngeal jaw which could be measured in this way so it was decided to leave this variable out of the FFM (by Van Onselen, 2013).
47. **Lower pharyngeal width (LPW) –** in mm. Measured from left to right tip of pharyngeal bone in mm (Barel *et al*., 1976). However, some species used in this research did not have a pharyngeal jaw which could be measured in this way so it was decided to leave this variable out of the FFM (by Van Onselen, 2013).

3.6.2 Species selection

Fifteen fish species on the Saba bank were measured in this morphological part of the study. These fish species covered 13 fish species, 21 genera and 35 families of the 40 most abundant fish species (figure 10). These fifteen fish species were therefore a reasonable representation of reef fish assemblages on the Saba bank. With the exception of bar jack (*Caranx ruber*), rock beauty (*Holacanthus tricolor*), rosy razorfish (*Hemipteronotus martinicensis)* and sand tilefish (*Malacanthus plumieri*) at least 5 individuals of each species were analyzed (table 4). In total 70 individual fish were measured and all measurements can be found in Appendix VIII. The specimens were partly donated by local fishermen and partly caught by hand. Spear-fishing was used to catch fish species not landed by fishermen, taking into account not to damage tissue needed for morphological measurements. Fish were immediately frozen after obtaining and defrosted prior to dissection.

Table 4. Fish species used in this study. Standard length (SL) range and SL-average are indicated per species, as well as number of individuals measured per fish species.

Common name	**Scientific name**	**N** (measured)	**SL-range** (min-max, mm)	**SL-average** (mm)
Ocean surgeonfish	*Acanthurus bahianus*	5	126-202	166.4
Coney	*Cephalopholis fulva*	5	223-281	238.2
Bar jack	*Caranx ruber*	3	254-329	286
Queen triggerfish	*Balistes vetula*	5	263-387	354.4
Rosy razorfish	*Hemipteronotus martinicensis*	4	130-163	149.5
White grunt	*Haemulon plumierii*	6	170-233	195.6
Red hind	*Epinephelus guttatus*	5	287-351	325.4
Redband parrotfish	*Sparisoma aurofrenatum*	5	184-245	209.6
Banded butterflyfish	*Chaetodon striatus*	5	93-133	115
Sand tilefish	*Malacanthus plumieri*	4	338-368	346.8
Squirrelfish	*Holocentrus adscensionis*	5	200-216	208
Rock beauty	*Holacanthus tricolor*	3	198-215	206.7
Brown chromis	*Chromis multilineata*	5	97-114	108.4
Yelloweye snapper	*Sebastes ruberrimus*	5	194-225	210.4
Yellow goatfish	*Mulloidichthys vanicolensis*	5	151-296	187.4

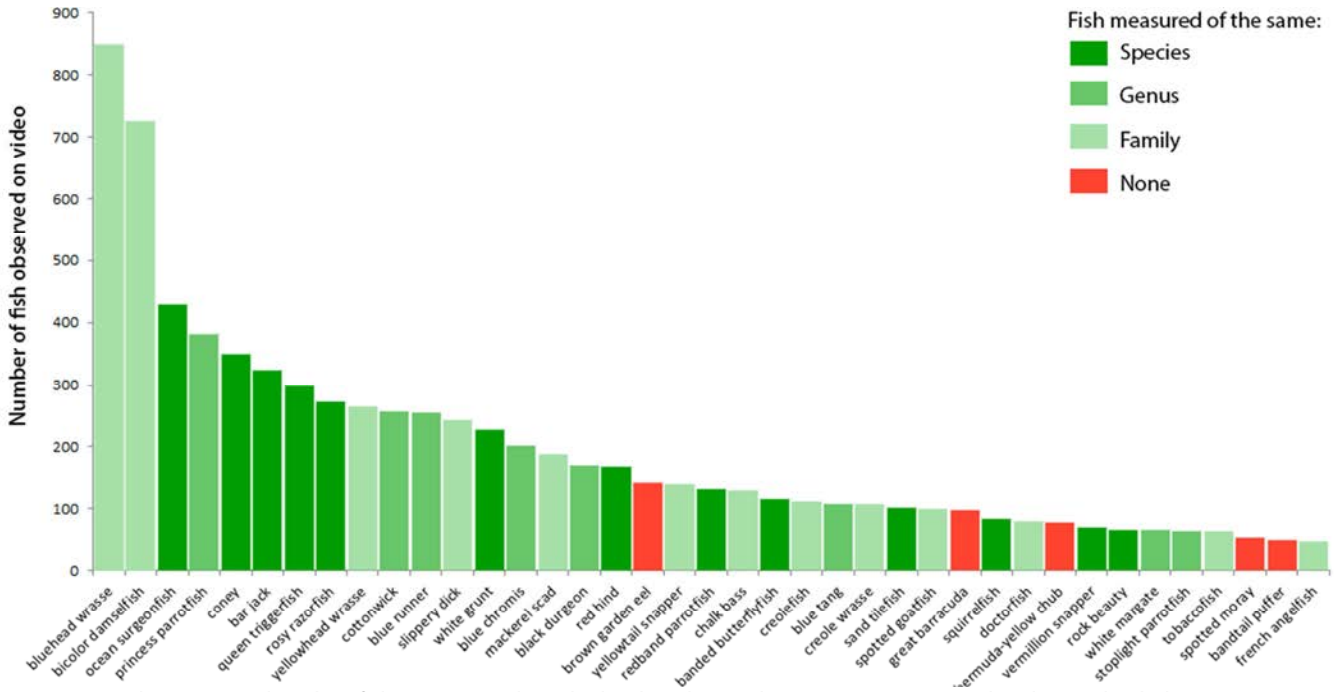

Figure 10. The 40 most abundant fish species on the Saba bank in this study. 15 species measured in this study (dark green) are covering 21 species on genus-level (lighter green) and 35 species on family-level (light green. Five species are not covered within family-level and therefore not used in further analysis.

For the measurements an electronic scale accurate up to 0-0.1 grams was used, as well as a dissection microscope with an ocular micro meter. A caliper (0.5 mm) and dissection set was used for measurements on the fish. A camera (Canon EOS 600D, 18 megapixels) was used to record all fish and dissected bones from different angles for meta-analysis and storage purposes. An example of the digital recordings of *Malacanthus plumieri* can be found in Appendix VI.

3.7 Data analysis

3.7.1 Fish community analysis

3.7.1.1 Data analysis

Fish length and abundance data sets were directly obtained from the video analysis software (Eventmeasure, Seagis). Species abundance in reef fish assemblages was calculated by adding up the maximum number of individuals per species (MaxN) for the different life stages (adult and juvenile). Species richness was measured with total number of species (Nsp) per sample location. Since it was not possible to directly measure weigth with BRUV surveys, biomass was calculated with the length-weight relationship: $W = a * L^b$ (Bohnsack *et al*., 1988). Weight parameters (a and b) were derived from fishbase (Froese and Pauly, 2006) and length parameters (L) were obtained from the length measurement data set. If weight parameters were not available, values from a close relative (same genus or family) were used, indicated by underlined measurements in Appendix V. For individuals with missing lengths the mean length of other individuals of the same species at the sample location was used to obtain biomass. For some species no data on close relatives or length data was available and they were left out of the biomass analysis. Non-demersal fish were also left out of the analysis (Langlois *et al*., 2012). All fish species were assigned to a trophic group and given a number representing trophic level, primarily based on food sources. This information was derived from fishbase (Froese and Pauly, 2006). A rough distinction in trophic group was made between herbivores, planktivores, invertebrate feeders, omnivores and piscivores. Trophic group classification per fish species can be found in Appendix VII. Furthermore, elasmobranch species were analyzed separately due to their large biomass and therefore their large influence on the analysis of reef fish assemblage structures. All statistics were performed using the statistical program R (version 3.1.0) and SPSS (IBM SPSS Statistics version 21). The R-scripts including the vegan-package (Oksanen *et al*., 2014) can be found in Appendix XI.

In order to conduct a comprehensive baseline survey on fish assemblages and investigate the influence of different (environmental) factors on the Saba bank, dependent variables Nsp, MaxN, biomass and trophic group were analysed for the explanatory factors. The explanatory factors habitat and depth were chosen based on the literature review, in which these factors were expected to be most explanatory for the structure of reef fish assemblages. These factors are highly variable among different geographical locations on the Saba bank (East, South, West, North and Center) and for this reason location was added as a factor in part of the analysis. For its summarizing character only data exploratory analyses are done with location as a explanatory factor. The influence of (small-scale) fisheries on reef fish assemblages on the Saba bank is largely unknown and therefore also included in this study as factor.

Mean number of fish (MaxN), mean number of species (Nsp), the log of mean biomass and differences in trophic groups were compared for the explanatory factors and (except the latter) were analyzed with one-way Analysis of Variance (ANOVA). Bonferroni correction was used as a post-hoc test to counteract the problem of multiple comparisons. Significant ($p<0.05$) differences after Bonferroni correction were indicated with letters. Letters shared in common between or among the groups indicated no significant difference. Error bars on the graphs indicated Standard Error (SE). MaxN was also separately analyzed for the factors using species accumulation curves (Oksanen *et al*., 2014). Species accumulation curves estimate the number of additional species that could be recorded with further effort (Chao and Shen, 2004; Colwell *et al*., 2004), indicating whether all reef fish species in the sampling area were detected. They gave an indication of the quality of the data set used in this study. Fish length was analyzed seperately with standardized length-frequency diagrams for each factor. These length-frequency diagrams were standardized by dividing

number of fish of a particular length by the sum of all fish numbers. In this way the length-frequency diagrams could be compared to each other and between the factors. To determine the influence of fisheries on mean fish length of key target species on the Saba bank, fish length data was also seperately analysed for a selection of important commercial species, indicated in the study by Van Gerwen (2013). Most landed fish species in 2013 based on abundances were *Haemulon plumieri* (white grunt: 27%), *Acanthurus bahianus* (ocean surgeonfish: 15%), *Epinephelus guttatus* (red hind: 11%), *Haemulon melanurum* (cottonwick: 8%) and *Balistes vetula* (queen triggerfish: 6%). In the analysis (ANOVA) of these fish species they were used as dependent variables, with habitat, depth, fisheries and their interaction as fixed factors. Bonferroni-correction was applied as previously described. Error bars on the graphs indicate Standard Error (SE).

3.7.1.2 Multivariate analysis

The dataset contained a lot of samples and species and therefore visualization of the variation between assemblages can be a very helpful tool (Legendre and Gallagher, 2001; Anderson and Millar, 2004). For this visualization a non-metric multidimensional scaling (NMDS) was used, which is an ordination method that fits data to a predetermined number of dimensions (Minchin, 1987) and is used in many fish assemblage studies (Toller *et al*., 2010; Zintzen *et al*., 2012; Kelaher *et al*., 2014). Fish abundance data was transformed by using a Bray-Curtis dissimilarity matrix (square root), based on the distance between samples in ordination space (Beals, 1984; Clark, 1993), which was then used to create a NMDS plot (Faith *et al*., 1987). The Bray-Curtis dissimilarity method emphasized the abundance differences within samples (Anderson and Willis, 2003) and it was used in many ecological studies as ordination method (Minchin, 1987; Legendre and Gallagher, 2001). Because it emphasizes the abundance differences, the outcome was not affected by the absence of species in the various samples. In other words, less abundant (rare) species way less heavy when comparing samples than abundant fish species (Field *et al*., 1982). The resulting nMDS plots visualized variation in species composition of reef fish assemblages for the different factors (habitat, depth, fisheries and location) with 95% confidence elipses. The package vegan (Oksanen *et al*., 2014) in the statistical program R (version 3.1.0) was used in this study to create two-dimensional NMDS plots.

A detrended correspondence analysis (DCA) was used in this study to visually obtain the way species abundance was influenced by the explanatory factors, because a NMDS was not sufficient for this purpose (Hill and Gauch, 1980). The DCA method is a modification of the correspondence analysis (CA) (Anderson and Willis, 2003), based on chi-square distances. The axis of the DCA plot is scaled in units of standard deviation and therefore relative easy to interpret (Hill and Gauch, 1980; Peet *et al*., 1988). The DCA plot only displayed species that had a correlation higher than 0.5 with the first axis. For this visualization of the relation between fish abundances and the factors habitat, depth and fisheries, the statistical program R (version 3.1.0) with the vegan package (Oksanen *et al*., 2014) was used.

3.7.1.3 PERMANOVA

The same software package was used to test for effects of the explanatory factors on reef fish communities. With a permutational analysis of variance (PERMANOVA) (Anderson, 2001) the influence of habitat, depth and fisheries and their interaction was tested for the dependent variables MaxN, Nsp and average biomass. Factors were tested with the model: Y = habitat + depth + fisheries + habitat*depth + habitat*fisheries + depth*fisheries + habitat*depth*fisheries + error. MaxN, Nsp and average biomass were tested separately as output variable Y. Before analysis first a Bray-Curtis dissimilarity matrix was created from the abundance data, after which by default 999 permutations of the data were computed to obtain P-values. Outcomes were presented in table form and significant differences were indicated in bold. Because depth was the most significant factor in explaining differences on reef fish assemblages, a seperate PERMANOVA was done to test the influence of habitat and fisheries on the fish assemblage variables within the different depth layers (15m, 25m and 40m). In this way the influence of the other highly significant factor habitat was dissociated from depth.

3.7.1.4 Elasmobranch analysis

One of the objectives of this study was to conduct a baseline shark survey, involving spatial distribution, species composition, relative abundance, length frequency on the shark population of the Saba bank. To

show elasmobranch distribution, two maps of the Saba bank were made based on elasmobranch abundances (Google Earth, 2014). Separate maps were made for shark and ray spatial distribution. Abundances were expressed as Catch Per Unit of Effort (CPUE), which is the number of sharks/rays per species per hour of BRUV recording time (Brooks *et al*. 2011; Bond *et al*. 2012). Both shark and ray species composition was shown in a species composition diagram in percentages of the total abundances. Mean fork length was analysed using one-way ANOVA and error bars indicate standard error (SE). Only for the shark species *Carcharhinus perezii* (Caribbean reef shark) and *Ginglymostoma cirratum* (nurse shark) a length frequency diagram was made, due to insufficient abundances of other elasmobranch species for this type of analysis. To study the influence of habitat, depth and fisheries on the elasmobranch population, CPUE (shark/rays per hour) was tested for these explanatory factors. This was done with one-way ANOVA with Bonferroni correction as post-hoc test and error bars indicate standard error (SE). Data was normally distributed, meeting the criterium for ANOVA analysis. Elasmobranch species were also tested for for overall effects of the explanatory factors. Their abundances were pooled and tested for variance with a PERMANOVA. Factors were tested with the model: Y = habitat + depth + fisheries + habitat*depth + habitat*fisheries + depth*fisheries + habitat*depth*fisheries + error. And MaxN was tested separately as output variable Y.

3.7.2 Ecomorphological approach

3.7.2.1 Principal Component Analysis (PCA) with raw data

To provide insight in trophic morphology of reef fish assemblages, the morphological traits related to the feeding process of fifteen fish species were analyzed. This was done with a Principal Component Analysis (PCA), which visually presents morphological variables of the species. PCA is a multivariate statistical method which uses linear transformations of the measured variables to create new orthogonal variables, the principal components. These principal components are uncorrelated and describe the variability present in the measured variables (Freund and Littell, 1991; Abdi and Williams, 2010). In this way most essential morphological information is extracted from the data set without correlation effects. PCA was performed with the vegan package (Oksanen *et al*., 2014) in R (version 3.1.0). All variables may indicate differences and similarities in fish species and therefore the first PCA involved all untransformed variables measured in this study, although not all variables were used in the Fish Food Model (FFM).

3.7.2.2 Data processingand the Fish Food Model (FFM)

Variability in the data was better described after data transformations and data reduction. Most individual fish, also of the same species, differed in size and therefore the size-dependent variables were standardized for standard length (SL). This was done by dividing the size-dependent variables by SL. Present/absent values, degrees and values already expressed as a ratio or calculation were not divided by SL. Also the data set was reduced to 26 variables based on a similar study of Van Onselen (2013). This reduction was done because most variables were measuring similar morphological characteristics and were therefore redundant. In the description of the variables the reason for deletion can be found (Van Onselen, 2013). Please refer to Sibbing and Nagelkere (2001) for a more detailed description of why certain variables were chosen for certain food types. Furthermore, $\log^{10}$ transformations for variables consisting of multiplied factors, were performed on the length-adjusted data set to even out extreme values. Table 5 shows a list of the variables used in the FFM and their corresponding transformations.

Table 5. All variables used in the FFM with their corresponding transformations.

Variable	Transformation	Variable	Transformation	Variable	Transformation
Ba	None	TOT1	None	RBD/SL	None
MBD/SL	Log10	TOT2	None	LJFEiC	None
CPD/SL	Log10	TOT3	None	VCOp	None
HL/SL	None	RL/SL	None	OpAr	None
ED/SL	None	GiRD/SL	None	GiAr	Log10
Pr/SL	None	PLOW/SL	None	RGA	Log10
OGAx	None	TPT_1	None	HyJsR	None
GL/SL	Log10	TPT_2	None	HyL/SL	None
LJL/SL	Log10	TPT_3	None		

The specialist dataset used in this study (table 3) consists of values derived for food specialists from Sibbing and Nagelkerke (2001) and was used as base of the FFM. Furthermore, van Onselen (2013) added some extra variables to the specialist data set, based in the study of Sibbing (1991) and therefore also were used in this study. These variables included type of oral (TOT1-TOT4) and pharyngeal teeth (TPT1-TPT4). In order for each measured variable to be compared with the value in the specialist data set, it was centered and standardized. Standardization was done by subtraction of the mean value of the variable and dividing it by the standard deviation. This resulted in values with a mean of one and standard deviation of zero. The same process was done for the specialist data set. For comparison between the two data sets, correlations were performed and the resulting values were scaled on a range from 0 to 1. To create a compact table on species level, measurements of individual fish from the same species were taken together. Measurements were already corrected for size differences and therefore mean values for each variable per species were calculated, with the exception of present/absent values, degrees and values already expressed as a ratio or calculation. The result of these processes was a compact table with food scores for food types and fish species, obtained with a correlation matrix. These scores per species were also put in a figure to graphically show optimal food type per species.

3.7.2.3 Translation to reef fish assemblages

For many of the 40 most abundant species occurring on the Saba bank a set of 'suitability-scores' per food type was obtained by using the food scores of the 15 fish species analysed in this study for their close relatives. Fish species without any close relatives were left out of further analysis (see red bars in figure 10), therefore 5 fish species were left out. For each site, the abundance data (N) of every fish species was multiplied by the food-suitability score per food type. Hereby obtaining a matrix of abundance-related food scores per site. By adding up the food scores per site and then dividing this number by the total number of fish on that site, a matrix of the average score per food type per site was obtained. An example of the matrix is shown in table 6.

Table 6. An example of the averagescores per food source matrix for the first 13 sites of this study. For each fish species in the abundance data set the suitability score of each food type was multiplied by its abundance (fish) on each site. Hereby obtaining a matrix of abundance-related food scores. By adding up the food scores per site and then dividing this number by the total number of fish on that site, a matrix of the average score per food type per site was obtained

Site	Phy_t	Phy_p	Alg_s	Alg_b	Detr	MiCr_t	MiCr_p	Crust	Lar_wrm	Mollusc	Fish_a	Fish_p
Center_1_1	0.238	-0.610	0.294	0.703	0.147	0.161	-0.267	0.326	0.576	0.177	-0.500	0.019
Center_1_2	0.313	-0.720	0.291	0.680	0.031	0.276	-0.388	0.253	0.725	-0.015	-0.462	0.105
Center_1_3	0.145	-0.682	0.056	0.705	-0.216	0.239	-0.481	0.657	0.399	0.338	-0.403	0.357
Center_1_5	0.252	-0.228	0.399	0.529	0.409	0.107	-0.408	0.364	0.233	0.288	-0.438	-0.134
Center_100	0.326	-0.826	0.253	0.616	-0.138	0.398	-0.512	0.389	0.676	-0.063	-0.461	0.333
Center_101	0.360	-1.100	0.443	0.816	0.261	0.298	-0.622	0.198	1.211	-0.147	-0.589	0.153
Center_102	-0.142	-0.807	-0.032	0.143	-0.090	-0.098	-0.700	-0.141	0.868	-0.397	0.116	0.539
Center_103	0.319	-0.680	0.176	0.484	-0.259	0.424	-0.417	0.414	0.449	-0.088	-0.383	0.359
Center_104	-0.048	-0.652	0.133	0.520	-0.132	-0.096	-0.500	0.325	0.576	0.035	-0.198	0.353
Center_105	0.280	-0.461	-0.001	0.349	-0.670	0.530	-0.365	0.643	-0.037	0.048	-0.291	0.574
Center_106	0.274	-0.416	-0.033	0.316	-0.736	0.547	-0.347	0.675	-0.126	0.062	-0.270	0.604
Center_107	0.223	-0.006	-0.318	0.016	-1.334	0.696	-0.181	0.962	-0.928	0.187	-0.078	0.874
Center_108	0.248	-0.205	-0.180	0.162	-1.044	0.624	-0.261	0.823	-0.539	0.126	-0.171	0.743

This translation of the 15 fish species scores to reef fish assemblage level on the Saba bank was completed by the conduction of a PCA with this data set. In the figure of this PCA, the influences of the different food sources on the fish assemblage structure were indicated with their vectors. In order to link ecomorphological differences in reef fish assemblages to the explanatory factors, PCA figures were made for all four explanatory factors used in this study. These differences in habitat, depth, fisheries and location were indicated with differently colored dots and the areas of similarity in factor characteristic were marked to highlight the differences.

3.7.2.4 Mantel test

To test the hypothesis that reef fish assemblages show less variability on a functional level than on species composition level, a comparison of data sets was necessary. A PCA of the fish abundance data per site with the same 35 fish species was executed and was visually compared with the PCA analysis of the ecomorphological data set. Only habitat differences were indicated in the figure because most differences in PCA were observed for this factor. Because no real conclusions can be drawn from this visual comparison, an Mantel test was used to test for differences. A Mantel test measures the correlation between two matrices typically containing measures of distance (Legendre and Fortin, 1989; Anderson and Millar, 2004; Oksanen, 2009). For this, both datasets were transformed by using a Bray-Curtis dissimilarity matrix and after comparison correlation between the data sets was obtained. This correlation is a measure of (dis)similarity between the functional and the abundance data. To check for differences within habitat, a Mantel test was also done for the different habitat types. Results of the Mantel test were shown in both table and figure.

4. Results

4.1 Fish community analysis

4.1.1 Data analysis

A total of 8579 individual fish belonging to 135 species were identified on the Saba bank in 165 BRUV deployments between October 2012 and February 2014. The eleven most abundant species represented eight families and accounted for nearly 50% of the total number of individual fish (figure 11). These eleven species were *Thalassoma bifasciatum* (*Labridae*: 9.8%), *Stegastus partitus* (*Pomacentridae*: 8.4%), *Acanthurus bahianus* (*Acanthuridae*: 5.0%), *Scarus taeniopterus* (*Scaridae*: 4.4%) , *Epinephelus fulva* (*Serranidae*: 4.0%), *Caranx ruber* (*Carangidae*: 3.8%), *Balistes vetula* (*Balistidae*: 3.5%), *Hemipteronotus martinicensis* (*Labridae*: 3.2%), *Halichoeres garnoti* (*Labridae*: 3.1%), *Haemulon melanurum* (*Haemulidae*: 3.0%) and *Caranx crysos* (*Carangidae*: 3.0%). Species distribution on family level was shown in figure 12. The eight most abundant fish families accounted for nearly 90% of total number of individual fish, with *Labridae* (22%) as most abundant fish family found on the Saba bank. Some fish families represented only a few species, but their numerical abundance dominated many sites. Especially small fish from the *Pomacentridae* family were very abundant in a wide range of locations.

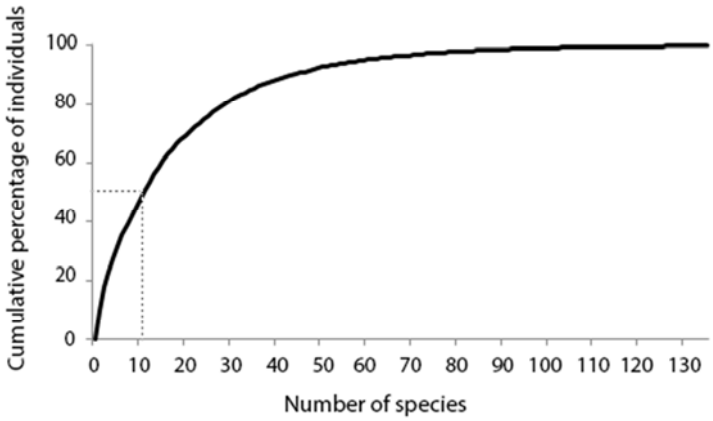

Figure 11. Fish abundance curve per species in percentage of total fish abundance. Number of individuals per species was added up according to its number of occurance on the Saba bank. The dotted line indicates the number of species necessary for reaching 50% of the total amount of individual fish observed in this study.

Mean number of fish was significantly different for low habitat complexity (0-1) and intermediate (2-3) and high complexity levels (4) (figure 13A). When fish abundance (MaxN) for different habitat complexity levels was compared, a clear positive relation was observed between habitat complexity and the mean number of fish. Generally, if habitat structure became more complex, reef fish assemblages increased in fish abundance. On the other hand, when habitat complexity was very low (0-1), fewer fish observations were made. Similar patterns were observed when habitat complexity level was analyzed for number of species (Nsp) and biomass (figures 13E and 13I). Variability in the data for habitat categories is highest in Nsp as dependent variable. Despite the differences in biomass were less clear, still significant differences were seen between low complexity (0) and high complexity (3-4). Depth also explained a some of the variability in MaxN and a negative correlation was found between depth and MaxN (figure 13B). Differences in depth were even larger in Nsp compared to MaxN (figure 13F), whereas biomass was less influenced by depth differences (figure 13J). Generally, all dependent variables were negatively related to an increase in depth. The effect of fisheries on the dependent variables was less clear. Mean MaxN, Nsp and biomass were lower in sites with low fisheries activity, compared with sites with high fishing pressure (figures 13C, 13G and 13K). Sites with intermediate fishing activity show highest levels in all dependent variables. Mean number of fish (MaxN) per site is highest at sites located in the South and Eastern part of the Saba bank, whereas rather similar levels of fish number were observed in the West, Center and Northern part (figure 13D). A similar pattern was observed for mean number of species (Nsp) (figure 13H). Mean biomass is also highest in the South and Eastern part of the Saba bank (figure 13L). However, mean biomass is also high for the Western part, where both Nsp and MaxN levels are relatively low. Biomass levels for the Center and Northern part of the Saba bank are lowest.

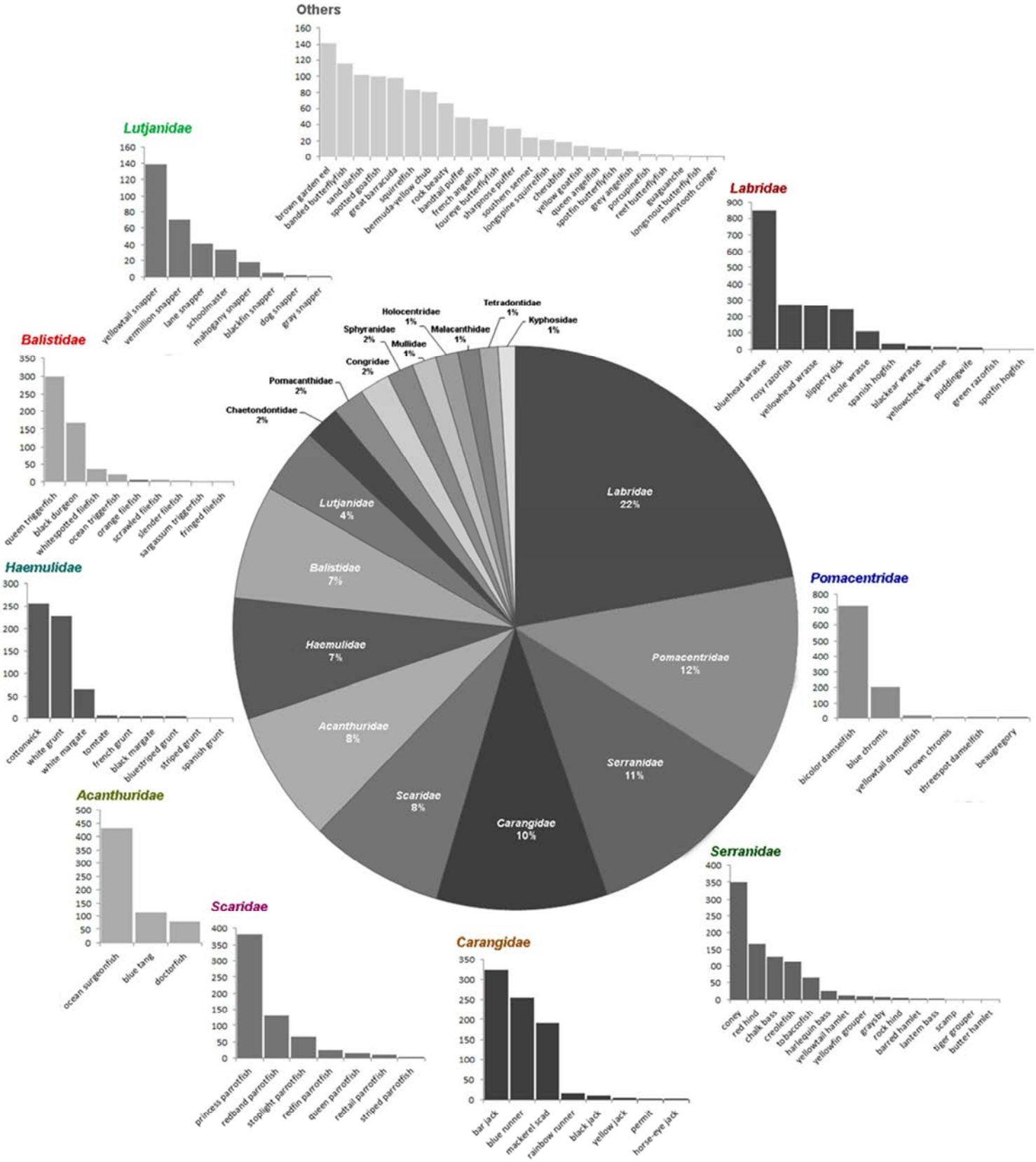

Figure 12. Species distribution per family and species identified on the Saba bank (Dutch Caribbean). The central pie-chart shows percentage of fish family occurrence, with *Labridae*, *Pomacentridae*, *Serranidae* and *Carangidae* as most abundant families, accounting for more than 50% of the individual fish on the Saba bank. Individual graphs show the species distribution within family level, with number observations on the y-axis.

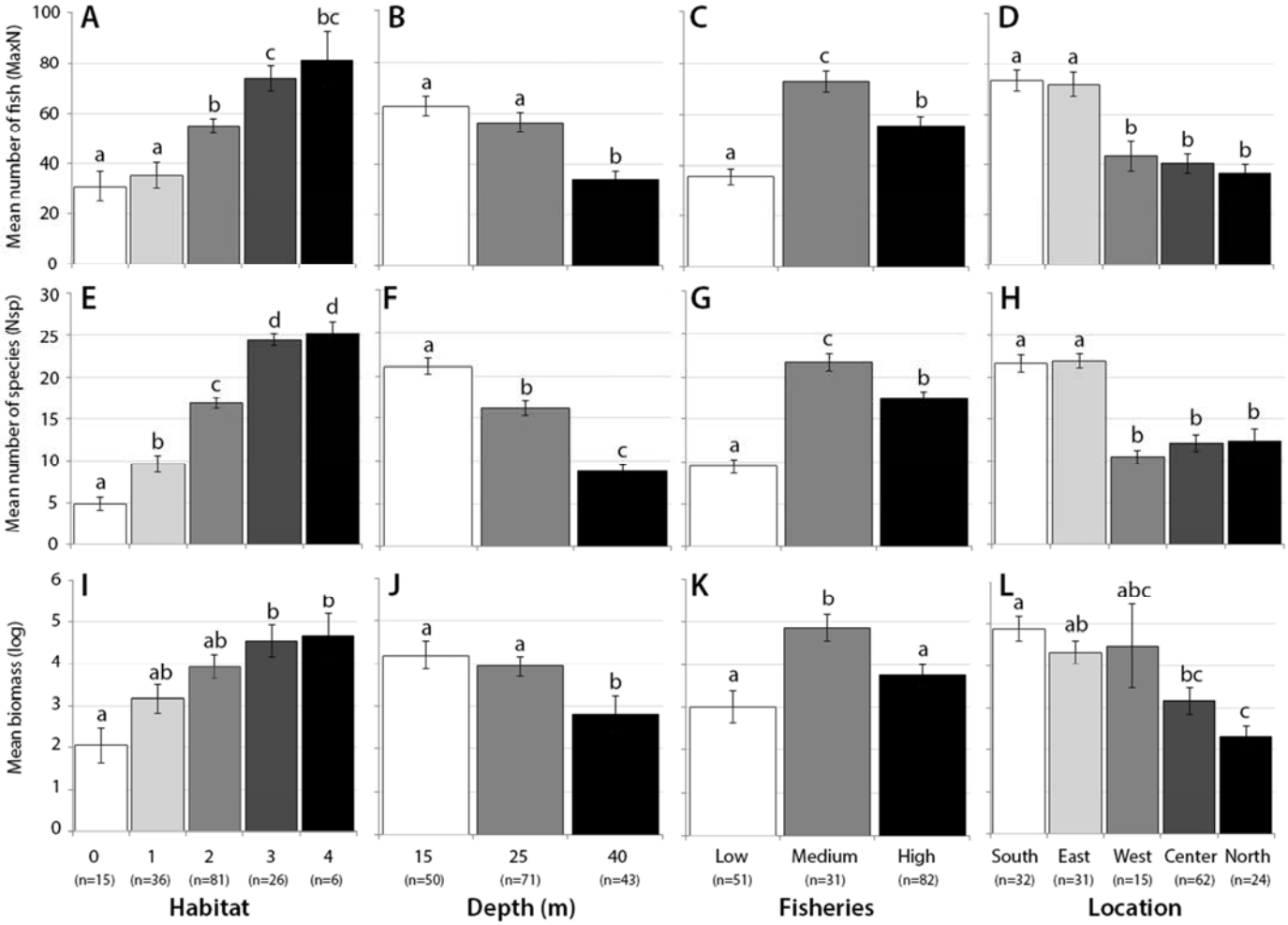

Figure 13 Mean (±1 SE) number of fish (MaxN), fish species (Nsp) and biomass for the explanatory factors habitat (0-4), depth (15, 25 and 40), fisheries (low, medium and high) and location (N/W/S/E/C). Means with different letters are significant according to one-way ANOVA testing with Bonferroni correction.

The distribution of biomass over different trophic groups changed with habitat complexity level (figure 14A). The percentage of planktivorous fish species was highest for low complexity habitat (0), whereas this percentage steadily drops in more complex habitat types to nearly zero in habitat category 4. For herbivorous fish species it is the other way around: they were absent in the lowest habitat category, whereas they have the highest percentage of total biomass in complex habitat types (3-4). Differences in levels of piscivorous fish species were less profound, they were present in all habitat categories. However their relative percentage of total biomass was higher in low habitat complexity levels (43%) compared to the highest category (13%). Invertebrate feeders were constant troughout habitat differences, with relative percentages of biomass between 20-40%, except for the lowest category (5%). Omnivorous fish species were overall less present with percentages of total biomass around 2%. When the distribution of biomass over different depths was compared, clear differences in herbivorous fish biomass were observed (figure 14B). Their relative biomass is high at 15m (30%) and 25m (40%), whereas their presence at 40m depth dropped to 2% of the total biomass. Planktivorous fish species, on the other hand, were more present in deeper water (30%) compared to shallow water (12%). Omnivous species were less present at all depths compared to the other trophic groups. Piscivorous fish and invertebrate feeders showed relatively few changes in relative percentage of biomass over different depthss. Changes in biomass distributions in different levels of fisheries activity were not as clear as for habitat and depth changes. Changes observed by an increase of fisheries activity were corresponding with the changes observed by an increase in habitat complexity.

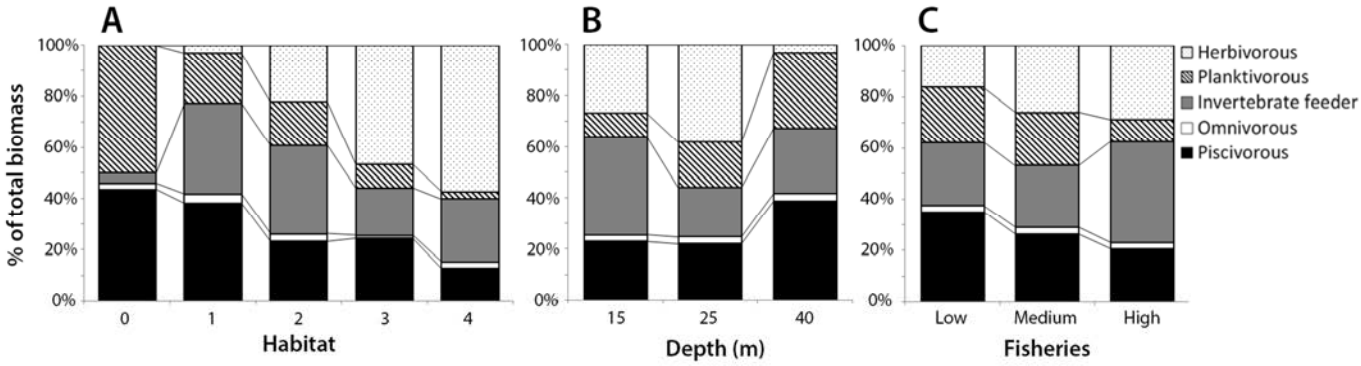

Figure 14 The relative percentage of total biomass for the trophic groups. Fish species are classified by food source: herbivorous, planktivorous, invertebrate feeder, omnivorous and piscivorous. Differences per explanatory factors habitat (A), depth (B) and fisheries (C) are indicated with lines.

Mean fish length differed within different habitat complexity levels. Complex habitat sites (2-4) were characterized with relatively small fish (22.4cm±0.3SE), whereas relatively large fish (24.6cm ±0.81SE) were more abundant in sites with low complexity levels (0-1). Length frequency diagrams are shown in figure 15 without categorization and between habitat, depth and fisheries categories. In the general shape of the diagram two peaks were observed, one between 5-8cm and one between 18-25cm. Inbetween these peaks, between 9-15cm an area of lower frequency was observed. After the second peak of around 20cm the frequence diagram gradually decreased until 45cm after which larger fish were not frequently observed. Differences in length frequency were apparent between habitat complexity categories (figure 15A). Whereas frequency diagrams of habitat type 2 and 3 were highly similar compared to the one without categorization, habitat type 0,1 and 4 were different. Two distinct peaks were observed in the diagram of habitat complexity level 0. In this category fish frequencies were highest for length between 3-10cm and 30-40cm, whereas relatively few fish had a length between 10-30cm. Also more larger fish (>50cm) were observed in this habitat category. The fish lengths in the most complex habitat types (3-4) were more concentrated around 20cm with a gradual decline in frequencies in both larger and smaller fish. These habitat categories also had more small peaks compared to other categories. Furthermore, relatively more larger fish (>70cm) were found in habitat category 4. For the different depth categories also 2 peaks were observed in the length frequency diagrams (figure 15B). In deeper water (40m) relatively more smaller fish (5-10cm) occurred compared to less deeper (15m and 25m) waters. More relatively larger fish (20-30cm) were observed in these shallower waters. Fisheries as explanatory factor was not observed to alter length frequency diagrams in a similar way as habitat, and in lesser extend, depth did. However, peaks were more distinct in areas with low fisheries activity, but those peaks do not differ much from the diagram without categorization.

To look more closely at the influence of fisheries on mean fish length of key target species on the Saba bank, fish length data was analysed for a selection of important commercial species, indicated in the study by Van Gerwen (2013). Most landed fish species in 2013 based on abundances were *Haemulon plumieri* (white grunt: 27%), *Acanthurus bahianus* (ocean surgeonfish: 15%), *Epinephelus guttatus* (red hind: 11%), *Haemulon melanurum* (cottonwick: 8%) and *Balistes vetula* (queen triggerfish: 6%). Mean fish length of the five mostly targeted fish species per fisheries category were shown in figure 16. Figure 16A showed the overall mean fish length of all species on the Saba bank per fisheries category. Mean fish length for the lowest and highest category was highly similar, whereas mean length for sites with medium fisheries activity was different from the others. Both *Haemulon plumieri* (16C) and *Acanthurus bahianus* (16D) showed similar differences between the different categories. *Haemulon melanurum* (16B) however, was significantly larger (cm) at sites with high fishing activity and lower at sites with medium fishing activity, compared to sites with low activity. *Balistes vetula* (16F) also tends to be larger at sites with high fisheries activity compares to sites with the lowest fishing pressure. No significant changes in mean length *Epinephelus guttatus* (16E) was observed between sites.

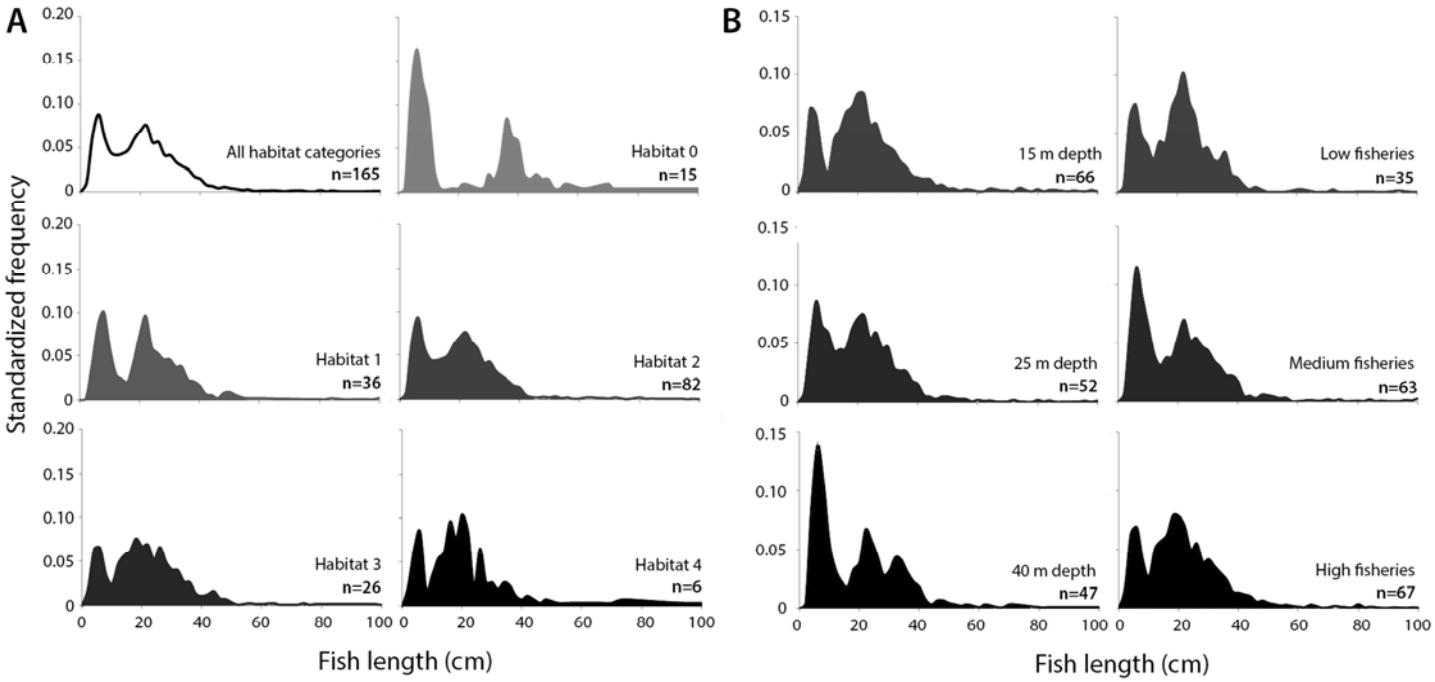

Figure 15 Lengt frequency diagram in a continuous line form. Lengths are categorized for habitat types (A), depth and fisheries activity (B). Frequencies are standardized by dividing number of fish of a particular length by the sum of all fish numbers.

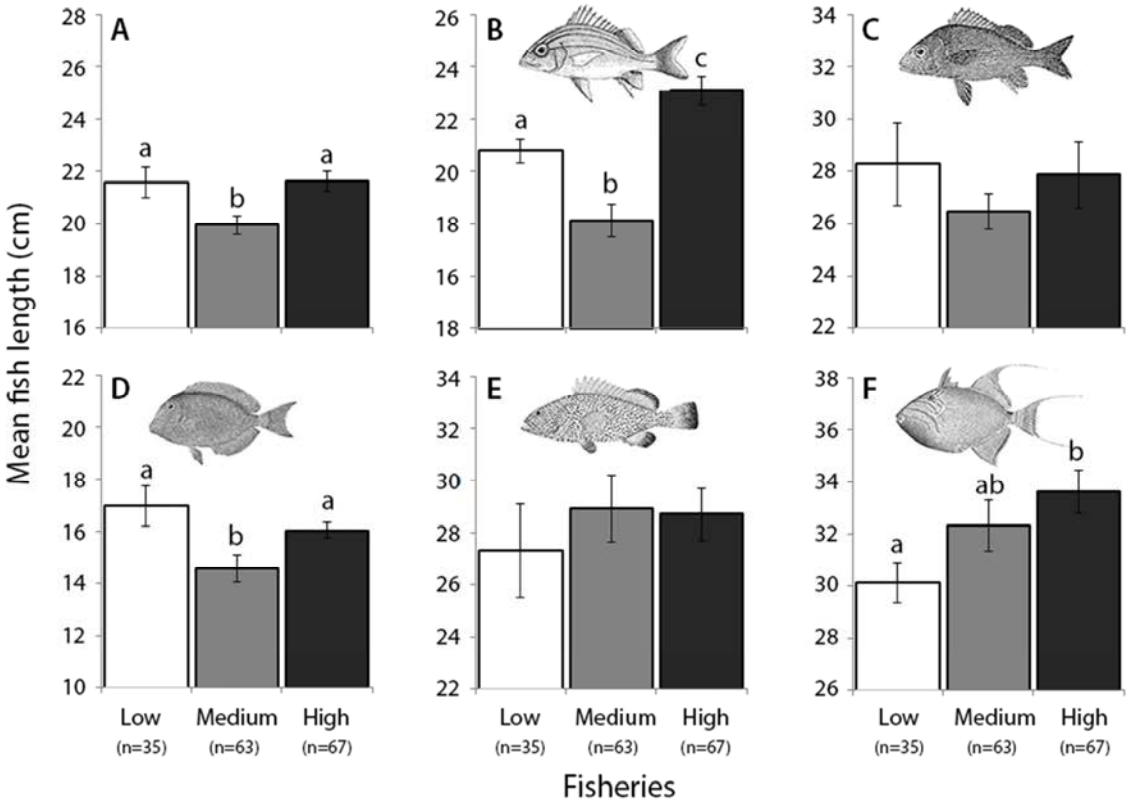

Figure 16 Mean fish length of key target species on the Saba bank per fisheries category.A: the overall mean fish length of all species on the Saba bank B: *Haemulon melanurum,* C:*Haemulon plumieri,* D: *Acanthurus bahianus,* E: *Epinephelus guttatus* and F: *Balistes vetula* Means with different letters are significant according to one-way ANOVA testing with Bonferroni correction.

The species accumulation curve in figure 17A shows that over 70% of all species already were observed within the first 20 samples and over 90% of all species was observed within 50 samples. The rate of species addition eventually slowed down until with a total number of samples (N=165) around 130 species were observed. It can be observed that the species accumulation curve is not reaching it asymptote yet, indicating that with increased effort most likely resulted in the observation of more new species. Differences in the rate at which new species were observed was different between habitat complexity categories (figure 17B). The curve of the most habitat categories (1-4) rises quickly with a rapid species accumulation in the first 20 samples, after which the curve gradually levels off. The curve of the lowest habitat category however, shows a steady increase in species accumulation with an increase in samples. The influence of depth on the species accumulation curves was less clear (figure 17C). The same shape was maintained within the depth categories with a lower rate of species accumulation deeper water (40m). For fisheries as explanatory factor highly similar curves are observed with similar standard deviations of around 10 species for all categories (figure 17D).

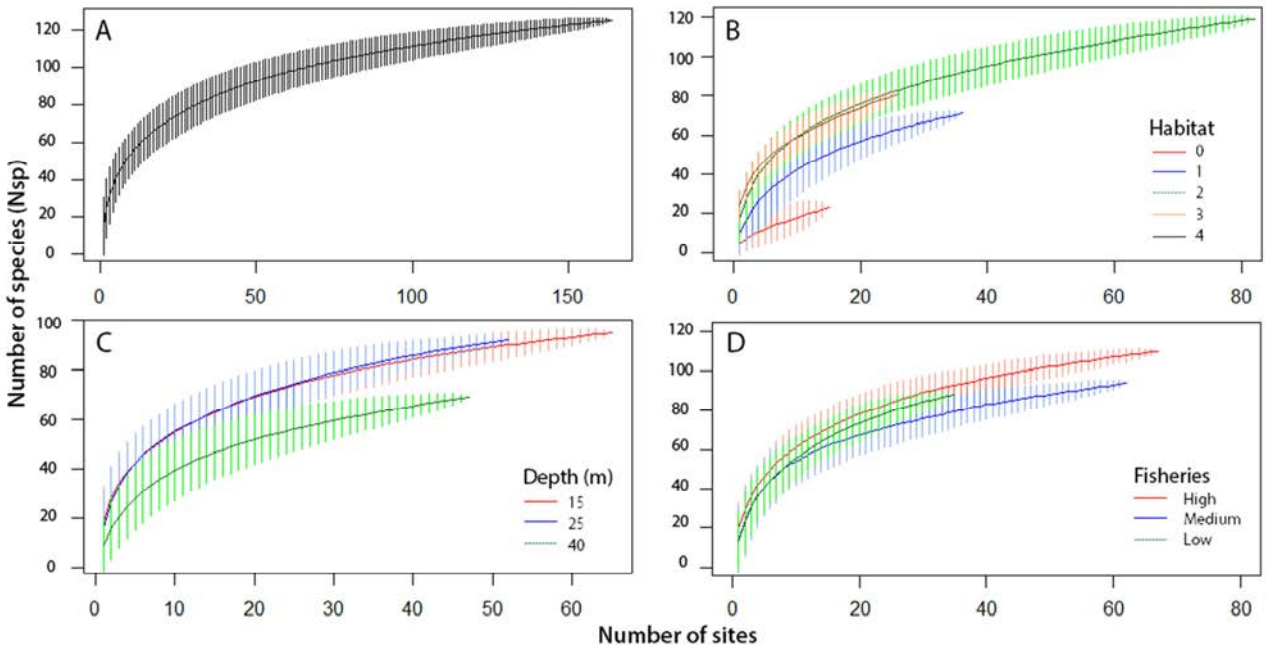

Figure 17 Species accumulation curves calculated for the total number of samples. A cumulative representation of the total number of species recorded with the BRUV method (A). Standard deviation of recording a new species per extra sample is indicated with vertical lines. Samples are grouped in different treatment characteristics: habitat complexity (B), depth (C) and fisheries activity (D).

4.1.2 Multivariate analysis

Variation between of fish assemblages for the explanatory factors is shown by the nMDS ordination plots in figure 18. According to Clarke (1993), for interpreting differences between fish assemblages a stress value of less than 0.2 was required. The stress value of these nMDS plots was 0.15, indicating that between-sample similarity was adequately represented. There was a clear influence of habitat on fish assemblage composition (figure 18A). Reef fish assemblages associated with high habitat complexity (3-4) were separated from the assemblages on sites with low habitat complexity (0-1). Furthermore, the dense clustering of sites with high habitat complexity indicates high similarity in reef fish assemblages. This clustering was also seen in shallow water (15m) and less in deeper water (25 and 40m), indicating that similarity of assemblages decreases with depth (figure 18B). The effect of fisheries was less conspicuous with highly overlapping clusters at different fisheries activity levels (figure 18C), whereas location as explanatory factor showed partly overlapping clusters in the two-dimensional space (figure 18D).

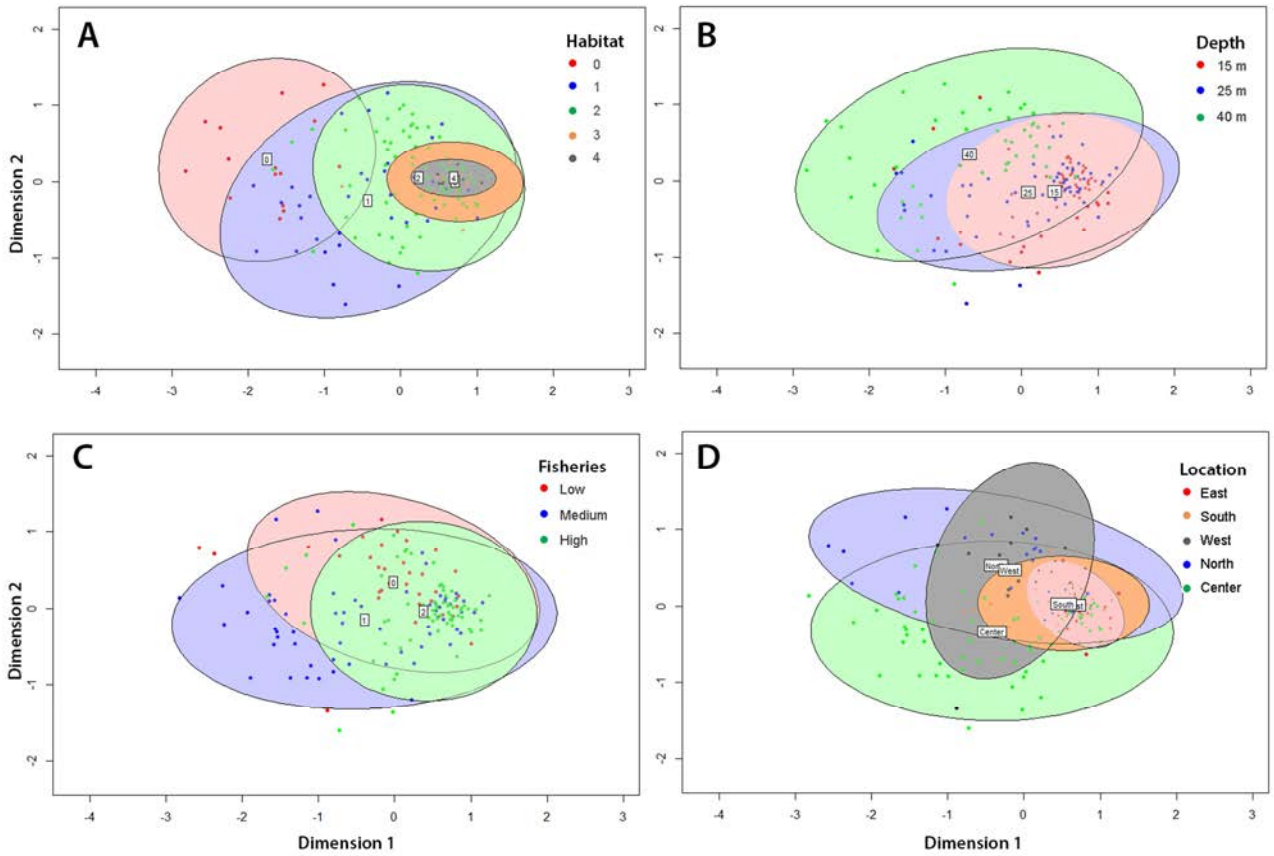

Figure 18. nMDS ordination plots for each of the four treatments examined. N= 165 sites, 135 species. Stress value was 0.15, indicating that between-sample similarity was adequately represented in these nMDS plots. Plots represent different explanatory factors: habitat (A), depth (B), fisheries activity (C) and location (D).

Because the NMDS method was mainly focused on species composition patterns, a Detrended Correspondence Analysis (DCA) was used in this study to visually obtain the way species abundance was influenced by the explanatory factors. The differences in species abundance of reef fish assemblages was best explained by different habitat complexity levels, followed by depth, whereas the presence of certain fish species in assemblages was least explained by fisheries activity (figure 19). The abundances of fish species near the center of the distribution, such as queen triggerfish (*Balistes vetula*), squirrelfish (*Holocentrus adcensionis*) and sand tilefish (*Malacanthus plumieri*) were least explained by the treatments. On the other hand, brown garden eel (*Heteroconger longissimus*), blue runner (*Caranx crysos*) and rosy razorfish (*Hemipteronotus martinicensis*) were found at the outer edges of the distribution and were associated with low complexity levels in their habitat. High numbers of the white grunt (*Haemulon plumieri*), rock beauty (*Holacanthus tricolor*) and blue tang (*Acanthurus coeruleus*) were found at sites with a more complex habitat structure, indicated by their presence more on the left side on the distribution. Regarding depths, presence of cottonwick (*Haemulon melanurum*) was more restricted to shallow water, whereas abundances of chalk basses (*Serranus tortugarum*), harlequin basses (*Serranus tigrinus*) and tobaccofish (*Serranus tabacarius*) were higher in deeper water. Both scientific and common name of the abbreviations of fish species used in the DCA analysis in figure 19 are shown in table 7.

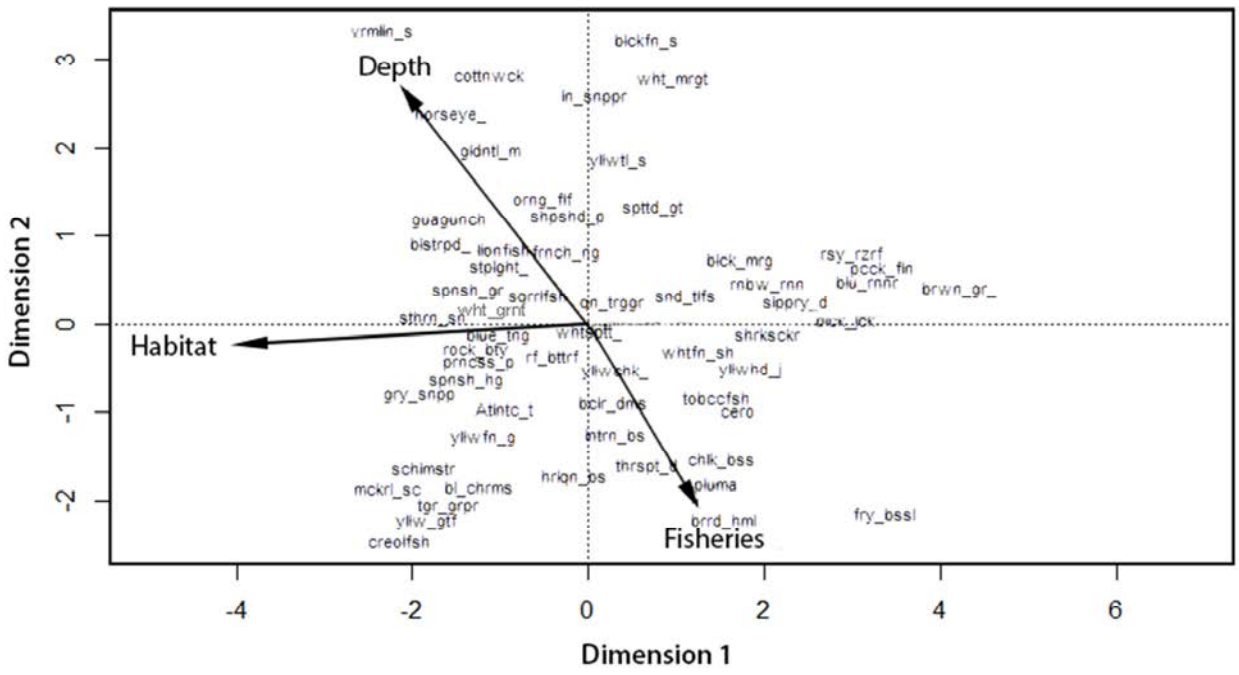

Figure 19. Detrended Correspondence Analysis (DCA) of the interaction of species abundance with explaining variables. Variables were most explained by the variation in reef fish occurrence are habitat type, followed by depth (length of the arrows). This plot only displayed species that had a correlation higher than 0.5 with the first axis.

4.1.3. PERMANOVA

With a permutational analysis of variance (PERMANOVA) the influence of habitat, depth and fisheries and their interaction was tested for the dependent variables MaxN, Nsp and average biomass (table 8). Highly significant differences in biomass (P=0.001), species richness (P=0.001) and fish abundance (P=0.001) with depth as explanatory factor were observed. Also habitat as explanatory factor was significant for all dependent variables (Biomass: P=0.001; Nsp: P=0.001; MaxN: P=0.001). Fisheries was also tested and significant differences were observed for biomass (P=0.003) and MaxN (P=0.018), Nsp was not significant for fisheries activity. Biomass (P=0.026) and MaxN (P=0.003) were also significantly different when tested for the interaction of fisheries with depth. If the interaction of depth and habitat was tested with PERMANOVA, in all dependent variables significant differences were observed (Biomass: P=0.001; Nsp: =0.002; MaxN: P=0.001). The interaction of depth with habitat and fisheries was only significant for Nsp P=0.037).

Because depth was the most significant factor in explaining differences on reef fish assemblages, a seperate PERMANOVA (table 9) was executed to test for both habitat and fisheries influences on the dependent variables within the different depth layers (15m, 25m and 40m). In this way the influence of the other highly significant factor habitat was dissociated from depth. Within-depth differences were observed with habitat as explanatory variables. The effect of habitat on Nsp, MaxN and biomass was significant at all depthss, except on fish abundance and biomass in shallow water (15m) and the biomass effect in deeper water (25m). No effect of fisheries activity per se was observed, only its interaction with habitat had an effect on biomass in both shallow (P=0.050) and deep water (P=0.010).

1	**Atlntc_t**	**bndd_btt**	**bndtl_pf**	**bar_jack**	**brrd_hml**	**beagrgry**	**bermyell**	**bclr_dms**	**blck_drg**	**blck_jck**
2	Atlantic trumpetfish	banded butterflyfish	bandtail puffer	bar jack	barred hamlet	beaugregory	bermuda-yellow chub	bicolor damselfish	black durgeon	black jack
3	*Aulostomus maculatus*	*Cheatodon striatus*	*Sphoeroides spengleri*	*Caranx ruber*	*Hypoplectrus puella*	*Stegastes leucostictus*	*Kyphosus sectatrix*	*Stegastes partitus*	*Melichthys niger*	*Caranx lugubris*
1	**blck_mrg**	**blckr_wr**	**blckfn_s**	**bl_chrms**	**blu_rnnr**	**blue_tng**	**bluehead**	**blspttd_**	**blstrpd_**	**brwn_chr**
2	black margate	blackear wrasse	blackfin snapper	blue chromis	blue runner	blue tang	bluehead	bluespotted cornetfish	bluestriped grunt	brown chromis
3	*Anisotremus surinensis*	*Halichoeres poeyi*	*Lutjanus buccanella*	*Chromis cyanea*	*Caranx crysos*	*Acanthurus coeruleus*	*Thalassoma bifasciatum*	*Fistularia tabacaria*	*Haemulon sciurus*	*Chromis multilineata*
1	**brwn_gr_**	**bttr_hml**	**cero**	**chlk_bss**	**chnnl_fl**	**cherbfsh**	**coney**	**cottnwck**	**crl_wrss**	**creolfsh**
2	brown garden eel	butter hamlet	cero	chalk bass	channel flounder	cherubfish	coney	cottonwick	creole wrasse	creolefish
3	*Heteroconger halis*	*Hypoplectrus unicolor*	*Scomberomorus regalis*	*Serranus tortugarum*	*Syacium micrurum*	*Centropyge argi*	*Cepholopholis fulva*	*Haemulon melanurum*	*Clepticus parrae*	*Paranthias furcifer*
1	**doctrfsh**	**dg_snppr**	**fry_bssl**	**fry_bttr**	**frnch_ng**	**frnch_gr**	**frngd_fl**	**glssy_sn**	**gldntl_m**	**gry_snpp**
2	doctorfish	dog snapper	fairy basslet	foureye butterflyfish	french angelfish	french grunt	fringed filefish	glasseye snapper	goldentail moray	gray snapper
3	*Acanthurus chirurgus*	*Lutjanus jocu*	*Gramma loreto*	*Cheatodon capistratus*	*Pomacanthus paru*	*Haemulon flavolineatum*	*Manocanthus ciliatus*	*Priacanthus cruentatus*	*Gymnothorax miliaris*	*Lutjanus griseus*
1	**graysby**	**grt_brrc**	**gren_mry**	**grn_rzrf**	**gry_nglf**	**guagunch**	**hrlqn_bs**	**highhat**	**horseye_**	**jlthd_pr**
2	graysby	great barracuda	green moray	green razorfish	grey angelfish	guaguanche	harlequin bass	highhat	horse-eye jack	jolthead porgy
3	*Cephalopholis cruentata*	*Sphyrae barracuda*	*Gymnothorax funebris*	*Hemipteronotus splendens*	*Pomacanthus arcuatus*	*Sphyrae guachancho*	*Serranus tigrinus*	*Equetus acumitus*	*Caranx latus*	*Calamus bajodo*
1	**kltl_ndl**	**lncr_drg**	**ln_snppr**	**lntrn_bs**	**lionfish**	**lngsnt_b**	**lngspn_s**	**mckrl_sc**	**mhgny_sn**	**mnytth_c**
2	keeltail needlefish	lancer dragonet	lane snapper	lantern bass	lionfish	longsnout butterflyfish	longspine squirrelfish	mackerel scad	mahogany snapper	manytooth conger
3	*Playbelone argalus*	*Paradiplogrammus bairdi*	*Lutjanus sygris*	*Serranus baldwini*	*Pterois volitans*	*Cheatodon aculeatus*	*Holocentrus rufus*	*Decapterus macarellus*	*Lutjanus mahogoni*	*Conger triporiceps*
1	**ocn_srgn**	**ocn_trgg**	**orng_flf**	**pcck_fln**	**permit**	**pluma**	**prcpnfsh**	**prncss_p**	**puddngwf**	**qn_nglfs**
2	ocean surgeonfish	ocean triggerfish	orange filefish	peacock flounder	permit	pluma	porcupinefish	princess parrotfish	puddingwife	queen angelfish
3	*Acanthurus bahianus*	*Canthidermis sufflamen*	*Aluterus schoepfi*	*Bothus lutus*	*Trachinotus falcatus*	*Calamus pentula*	*Diodon hystrix*	*Scarus taeniopterus*	*Halichoeres radiatus*	*Holacanthus ciliaris*
1	**qn_prrtf**	**qn_trggr**	**rnbw_rnn**	**red_hind**	**rdbnd_pr**	**rdfn_prr**	**rdtl_prr**	**rf_bttrf**	**rock_bty**	**rock_hnd**
2	queen parrotfish	queen triggerfish	rainbow runner	red hind	redband parrotfish	redfin parrotfish	redtail parrotfish	reef butterflyfish	rock beauty	rock hind
3	*Scarus vetula*	*Balistes vetula*	*Elagatis bipinnulata*	*Epinephelus guttatus*	*Sparisoma aurofretum*	*Sparisoma rubripinne*	*Sparisoma chrysopterum*	*Cheatodon sedentarius*	*Holacanthus tricolor*	*Epinephelus adscensionsis*
1	**rsy_rzrf**	**snd_tlfs**	**srgssm_t**	**scry_prg**	**scamp**	**schlmstr**	**scrwld_f**	**swd_blnn**	**shrksckr**	**shrpns_p**
2	rosy razorfish	sand tilefish	sargassum triggerfish	saucereye porgy	scamp	schoolmaster	scrawled filefish	seaweed blenny	sharksucker	sharpnose puffer
3	*Hemipteronotus martinicensis*	*Malacanthus plumieri*	*Xanthichthys ringens*	*Calamus calamus*	*Myceroperca phex*	*Lutjanus apodus*	*Aluterus scriptus*	*Parablennius marmoreus*	*Echeneis ucrates*	*Canthigaster rostrata*
1	**shpshd_p**	**slndr_fl**	**slppry_d**	**smth_trn**	**sthrn_sn**	**spnsh_gr**	**spnsh_hg**	**sptfn_bt**	**sptfn_hg**	**spttd_g_**
2	sheepshead porgy	slender filefish	slippery dick	smooth trunkfish	southern sennet	spanish grunt	spanish hogfish	spotfin butterflyfish	spotfin hogfish	spotted eagle ray
3	*Calamus penna*	*Manocanthus tuckeri*	*Halichoeres bivittatus*	*Lactophrys triqueter*	*Sphyrae picudilla*	*Haemulon macrostomum*	*Bodianus rufus*	*Cheatodon ocellatus*	*Bodianus pulchellus*	*Aetobatus riri*
1	**spttd_gt**	**spttd_mr**	**sqrrlfsh**	**stplght_**	**strpd_gr**	**strpd_pr**	**thrspt_d**	**tgr_grpr**	**tobccfsh**	**tomtate**
2	spotted goatfish	spotted moray	squirrelfish	stoplight parrotfish	striped grunt	striped parrotfish	threespot damselfish	tiger grouper	tobaccofish	tomtate
3	*Pseudopeneus maculatus*	*Gymnothorax moringa*	*Holocentrus adscensionis*	*Sparisoma viride*	*Haemulon striatum*	*Scarus iserti*	*Stegastes planifrons*	*Myceroperca tigris*	*Serranus tabacarius*	*Haemulon aurolineatum*
1	**trunkfsh**	**vrmlln_s**	**wht_grnt**	**wht_mrgt**	**whtfn_sh**	**whtsptt_**	**yllw_gtf**	**yllw_jck**	**yllwchk_**	**yllwfn_g**
2	trunkfish	vermillion snapper	white grunt	white margate	whitefin sharksucker	whitespotted filefish	yellow goatfish	yellow jack	yellowcheek wrasse	yellowfin grouper
3	*Lactophrys trigonus*	*Rhomboplites aurorubens*	*Haemulon plumieri*	*Haemulon album*	*Echeneis neucratiodes*	*Cantherhines macrocerus*	*Mulloidichthys martinicus*	*Caranx bartholomaei*	*Halichoeres cyanocephalus*	*Myceroperca venenosa*
1	**yllwhd_j**	**yllwhd_w**	**yllwtl_d**	**yllwtl_h**	**yllwy_s**	**yllwtl_s**				
2	yellowhead jawfish	yellowhead wrasse	yellowtail damselfish	yellowtail hamlet	yelloweye snapper	yellowtail snapper				
3	*Opistogthus aurifrons*	*Halichoeres garnoti*	*Microspathodon chrysurus*	*Hypoplectrus chlorurus*	*Sebastes ruberrimus*	*Ocyurus chrysurus*				

Table 7 Explanation of abreviations (1) used in figure 19, giving common name (2) and genus species name

Table 8 Permutational Analysis of Variance (PERMANOVA). Factors were tested with the model: Y= habitat + depth + fisheries + habitat*depth + habitat*fisheries + depth*fisheries + habitat*depth*fisheries + error. MaxN, Nsp and average biomass were tested separately as output variable Y. Differences were significant when p<0.05 and were selected bold.

PERMANOVA (n=163)	**Biomass**				**Nsp**				**MaxN**			
Explanatory factors	Df	MS	Pseudo-F	P (perm)	Df	MS	Pseudo-F	P (perm)	Df	MS	Pseudo-F	P (Perm)
Depth	1	2.3401	6.9804	**0.001**	1	2.11067	59.611	**0.001**	1	4.3674	16.9781	**0.001**
Habitat	1	1.3603	4.0578	**0.001**	1	1.82372	51.507	**0.001**	1	2.2967	8.9284	**0.001**
Fisheries	1	0.8081	2.4105	**0.003**	1	0.06891	1.946	0.121	1	0.5607	2.1797	**0.018**
Depth x Habitat	1	0.9318	2.7794	**0.001**	1	0.52603	14.856	**0.002**	1	1.2779	4.968	**0.001**
Depth x Fisheries	1	0.632	1.8853	**0.026**	1	0.00528	0.149	0.840	1	0.6396	2.4865	**0.003**
Habitat x Fisheries	1	0.3058	0.9123	0.556	1	0.00784	0.221	0.760	1	0.4172	1.622	0.066
Depth x Habitat x Fisheries	1	0.3185	0.9499	0.502	1	0.1264	3.57	**0.037**	1	0.348	1.3528	0.132

Table 9 Permutational Analysis of Variance (PERMANOVA). The model tested the explanatory treatments habitat, location, fisheries zone and their interactions on MaxN, Nsp and biomass for three different depth layers (15, 25 and 40m). Differences were significant when p<0.05 and were selected bold.

PERMANOVA	**15m** (n=50)				**25m** (n=70)				**40m** (n=43)			
	df	MS	Pseudo-F	P(perm)	df	MS	Pseudo-F	P(perm)	df	MS	Pseudo-F	P(perm)
Habitat												
MaxN	1	0.23105	0.93375	0.540	1	0.48493	1.7350	**0.040**	1	2.03777	8.0167	**0.001**
Nsp	1	0.41990	13.4602	**0.002**	1	0.32903	9.4768	**0.004**	1	1.19886	24.4204	**0.001**
Biomass	1	0.4575	1.40628	0.097	1	0.48557	1.5457	0.093	1	0.76360	2.3691	**0.005**
Fisheries												
MaxN	1	0.41820	1.69012	0.055	1	0.35709	1.2776	0.191	1	0.22502	0.8852	0.512
Nsp	1	0.06063	1.9435	0.168	1	0.01105	0.3182	0.697	1	0.00742	0.1512	0.800
Biomass	1	0.34955	1.07429	0.383	1	0.43727	1.3919	0.133	1	0.38760	1.2025	0.271
Habitat x Fisheries												
MaxN	1	0.35664	1.44131	0.107	1	0.45254	1.6191	0.069	1	0.25529	1.0043	0.405
Nsp	1	0.00941	0.3017	0.662	1	0.12228	3.5220	0.051	1	0.02496	0.5085	0.511
Biomass	1	0.52370	1.60952	**0.050**	1	0.31609	1.0062	0.417	1	0.68140	2.1141	**0.010**

4.1.4 Elasmobranch analysis

Shark presence on the Saba bank was mainly observed along the shallow edges in the Eastern en Southern part (figure 20). *Carcharhinus perezii* (Caribbean reef shark) (N=29) was most numerous along these edges, followed by *Ginglymostoma cirratum* (nurse shark) (N=21) Together, these shark species were representing over 90% of total shark observations at these locations. Not only shark abundances, but also number of sharks per hour was higher near the edges compared to other locations. Sharks observations were also done at shallow sites in the center of the Saba bank, but species number and composition was different in these locations. Compared to the shallow edges both *C. perezii* (N=3) and *G. cirratum* (N=10) were less abundant. The deeper sites near the Northern part of the bank were characterized by general absence of sharks, whereas some sharks were present in deeper waters in the West.

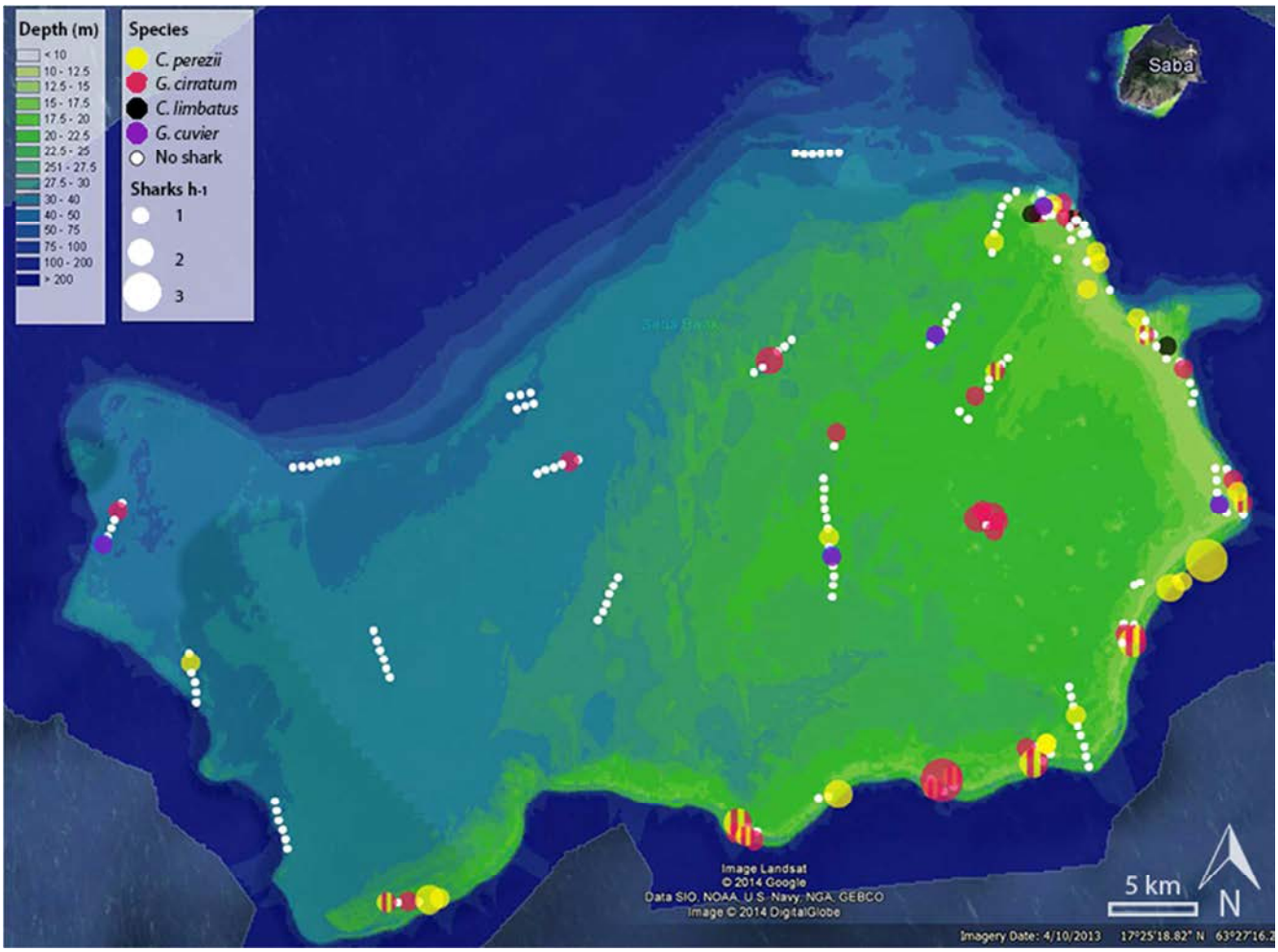

Figure 20 Spatial distribution of sharks on the Saba bank**.** On the depth map of the Saba bank were shark species indicated with differently colored dots. Pink dots for *Ginglymostoma cirratum*(nurse shark), yellow for *Carcharhinus perezi*i (Caribbean reef shark), blue for *Galeocerdo cuvier* (tiger shark) and black for *Carcharhinus limbatus* (blacktip reef shark). The amount of sharks per site is indicated with differently sized dots. Sites with no shark presence are shown as white dots.

A total of 85 shark observations were made in this study. *Ginglymostoma cirratum* (nurse shark) was the most abundant shark species in this study (N=41). Over 48% of shark observations were of this species (figure 21A). *Carcharhinus perezii* (Caribbean reef shark) was recorded 36 times (42%) and *Galeocerdo cuvier* (tiger shark) was observed five times (6%). Only three observations (4%) of *Carcharhinus limbatus* (blacktip shark) were made in this study. The number of sharks per hour (CPUE) was for both most abundant shark species between 0.22-0.25 (figure 21B), whereas *G cuvier* and *C. limbatus* were less abundant with a CPUE of less than 0.04. *G. cuvier* was the largest shark species observed with a mean fork length of 235.4cm(±35.5SE) (figure 21C). The smallest shark species in this study is *C. perezii* with a mean for length of 94.7cm (±8.2SE). The length frequency diagram of the two most abundant species shows one high peak for *C. perezii*

between 65-75cm and another smaller peak around 100cm (figure 21D). Larger individuals of this species were less frequent. More variability in length was observed in *G. cirratum* with multiple peaks. The largest peak is between 175-185cm, whereas smaller peaks were present around 150, 105 and 70cm.

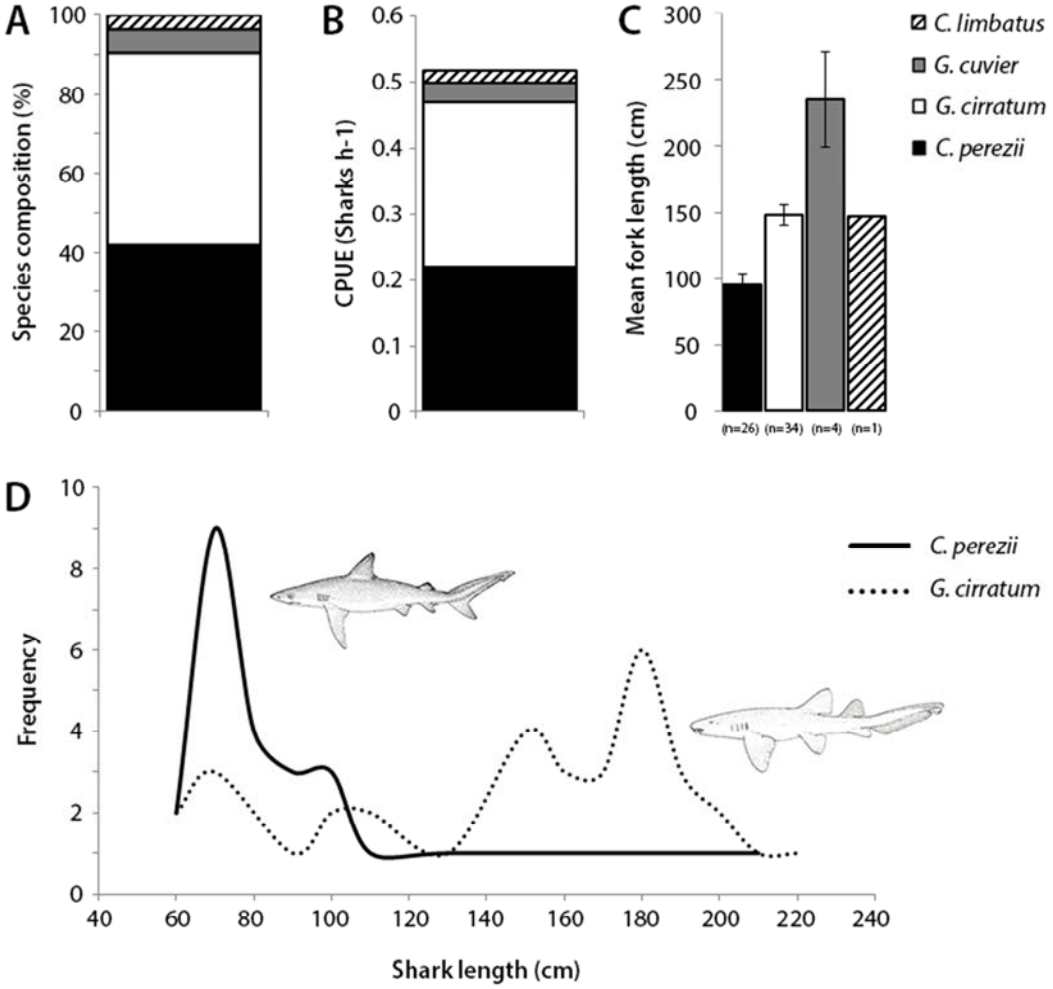

Figure 21 Shark abundances on the Saba bank. Species compostion (%) (A), number of sharks per hour (CPUE) (B), mean fork length (C) and a length frequency diagram (D) were shown. Only data of *C. perezii* and *G. cirratum* were shown in the length frequency diagram due to the insufficient abundances of *G. cuvier* and *C. limbatus*. Lengths were shown in cm and error bars in mean fork length analysis indicated standard error (SE).

The presence of rays was less restricted to shallow parts of the Saba bank compared to shark presence (figure 22). Ray species were present over the whole bank, from shallow reef edges to deeper water. They were less numerous (N=33) than sharks and the species composition was restricted to four species. Twenty recordings (61%) of *Dasyatis americana* (southern stingray) were done. Eight (24%) times a *Dasyatis centroura* (roughtail stingray) was observed, four (12%) *Aetobatus narinari* (spotted eagle ray) were seen and one (3%) *Manta birostris* (manta ray) was observed (figure 23A). The number of rays per hour was highest for *D. americana* with 0.12, followed by *D. centroura* with a CPUE of 0.05 (figure 23B). With a mean width of 49.0cm (±6.2SE) *D. america* was by far the smallest ray species observed on the Saba bank (figure 23C). Its close-relative *D. centroura* had a mean disc width of 137.0cm (±14.8SE) and *A. narinari* was the largest ray species that was measured with a mean width of 159.1 (±8.7SE). Unfortunately, disc width of *M. birostris* was not measured.

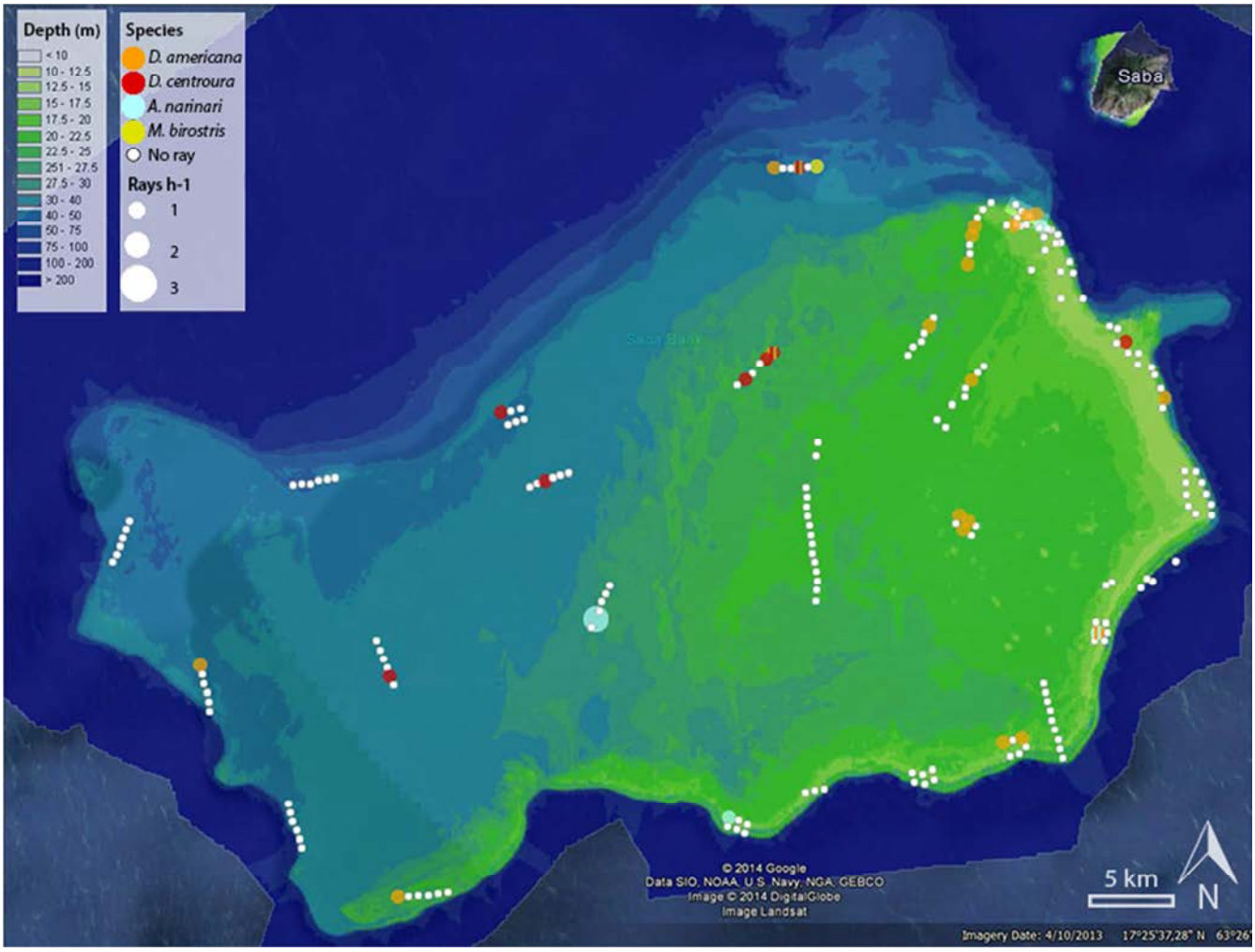

Figure 22 Spatial distribution of rays on the Saba bank**.** On the depth map of the Saba bank were ray species indicated with differently colored dots. Orange dots for *Dasyatis americana* (southern stingray), red for *Dasyatis centroura* (roughtail stingray), lightblue for *Aetobatus narinari* (spotted eagle ray) and a yellow dot for *Manta birostris* (manta ray). The amount of rays per site is indicated with differently sized dots. Sites with no ray presence are shown as white dots.

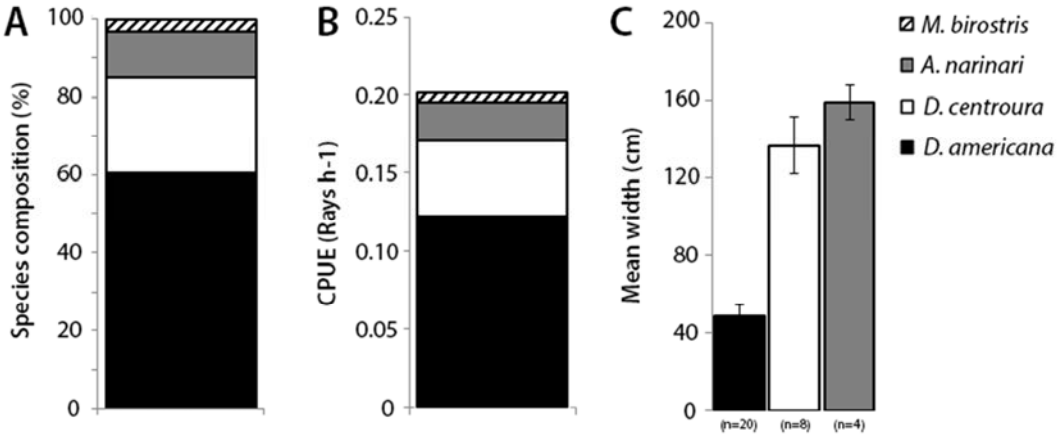

Figure 23 Ray abundances on the Saba bank. Species compostion (%) (A), number of rays per hour (CPUE) (B), and mean disc length (C) were shown. Lengths were shown in cm and error bars in mean fork length analysis indicated standard error (SE).

All shark species were pooled and tested for variance with a PERMANOVA (table 10). Shark abundance (CPUE) was analyzed for the explanatory factors habitat, depth and fisheries. No significant differences in shark abundance was observed for the explanatory factors. However, when the correlation effect of depth x habitat (P=0.030) and depth x fisheries (P=0.039) was analyzed, significant differences in shark numbers were observed. Ray species were also pooled and tested with PERMANOVA (table 10). Ray abundance was significantly different for habitat complexity (P=0.031) and for the correlation effect of depth x habitat (P=0.034).

Table 10 Permutational Analysis of Variance (PERMANOVA) for shark and ray abundances on the Saba bank . Factors were tested with the model: Y= habitat + depth + fisheries + habitat*depth + habitat*fisheries + depth*fisheries + habitat*depth*fisheries + error. MaxN, was tested separately as output variable Y. Differences were significant when p<0.05 and were selected bold.

PERMANOVA Shark abundance (N=58)	**MaxN**			
	Df	MS	Pseudo-F	P (Perm)
Depth	1	0.25111	1.0859	0.327
Habitat	1	0.41538	1.7962	0.166
Fisheries	1	0.59088	2.5551	0.084
Depth x Habitat	1	0.87487	3.7832	**0.030**
Depth x Fisheries	1	0.74848	3.2367	**0.039**
Habitat x Fisheries	1	0.19594	0.8473	0.429
Depth x Habitat x Fisheries	1	0.25575	1.1059	0.312
PERMANOVA Ray abundance (N=28)	**MaxN**			
	Df	MS	Pseudo-F	P (Perm)
Depth	1	0.52931	2.666	0.088
Habitat	1	0.77433	3.9001	**0.031**
Fisheries	1	0.05931	0.2987	0.762
Depth x Habitat	1	0.78604	3.9591	**0.034**
Depth x Fisheries	1	0.03211	0.1617	0.834
Habitat x Fisheries	1	0.23318	1.1745	0.317
Depth x Habitat x Fisheries	1	0.10508	0.5293	0.590

Elasmobranch species were individually tested (ANOVA) for differences in abundances (CPUE) for habitat, depth and fisheries as explanatory factors (figure 24). With 0.6-1.0 sharks per hour the abundance of *C. perezii* was significantly higher for locations with high habitat complexity compared to the sites with lower complexities (0-2) (CPUE<0.2). No individuals of this species were observed at sites with the lowest habitat complexity level (0) (figure 24A). The same distribution pattern per habitat was observed in *G. cirratum*, whereas G. cuvier and C. limbatus were less abundant overall (CPUE<0.05). Ray species were more evently distributed over habitat categories, with relatively high abundance levels (CPUE~0.5) of *D. americana* in habitat type 4 and both *D. Americana* (CPUE between 0.3-0.35) and *D. centroura* (CPUE between 0.05-0.25) abundances in lower habitat complexities (0-2) (figure 24B). Both *C. perezii* and *G. cirratum* were most abundant in relatively shallow waters (15m and 25m) compared to their abundance in deeper water (40m) (figure 24C). *C. limbatus* was only observed in waters of 15m depth and *C. cuvier* was absent in the 25m depth layer. Ray species were abundant in all depth layers with the exception of A. narinari, which was absent in deeper waters (40m) (figure 24D). When the abundance of elasmobranch species was tested with fisheries as explanatory factor, the different effect per species was observed. Both *C. perezii* and *G. cirratum* were most abundant at sites with medium and high fishing activity, whereas *C. limbatus* and *G. cuvier* were most abundant at sites with high fisheries (figure 24E). For *D. americana* an increase in abundances was observed for more fisheries activity and for *A. narinari* it is the other wat around (figure 24F)

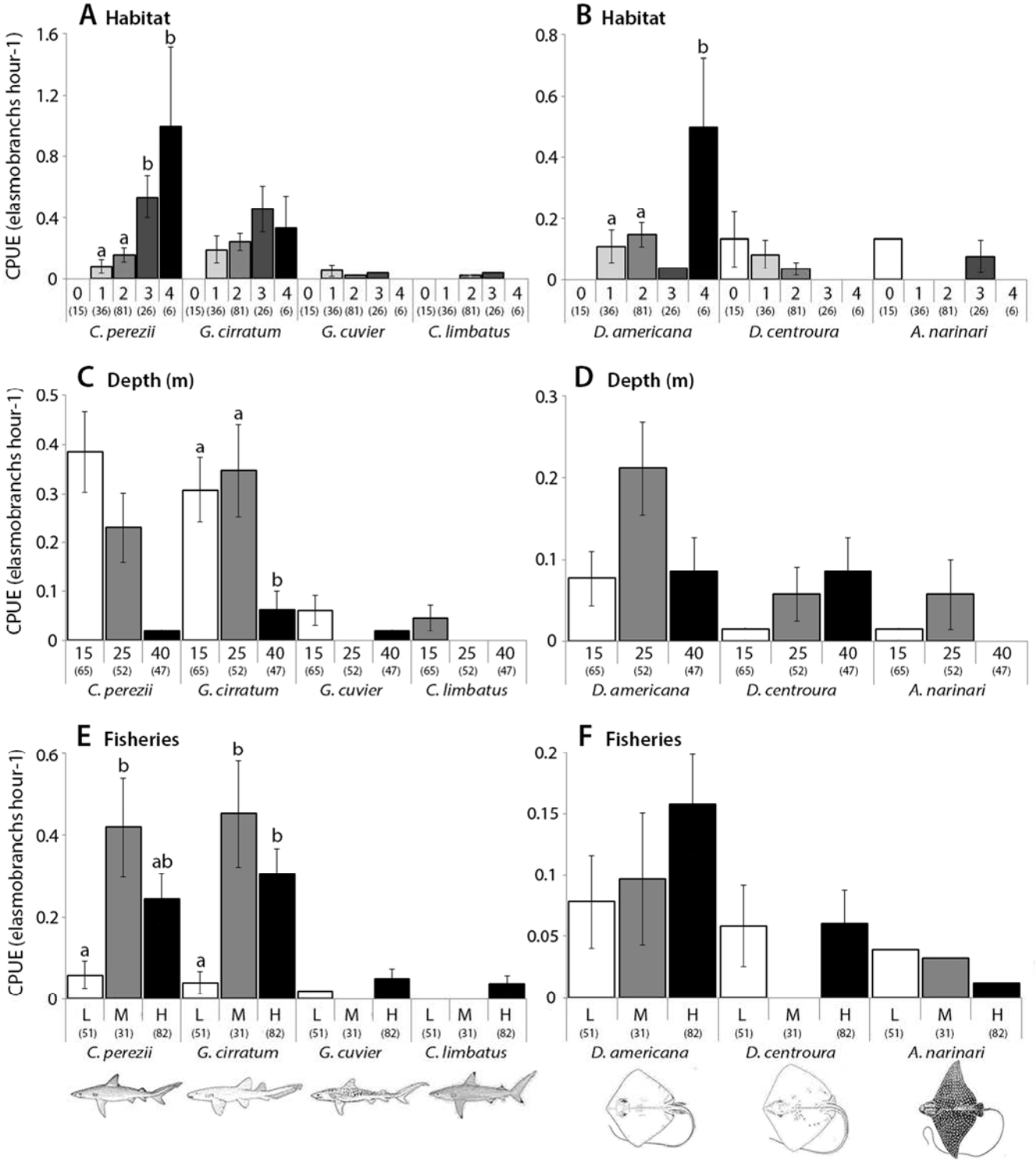

Figure 24 Elasmobranch abundances (CPUE) on the Saba bank for habitat, depth and fisheries as explanatory factors. Abundance of elasmobranch species was analyzed as catch per unit of effort (CPUE), which is the amount of sharks/rays observed per hour of video footage. Effects on shark species were seen in figure A, C and E. Effects on rays were given in figure B,D and F.. Means with different letters are significant according to one-way ANOVA testing with Bonferroni correction

4.2 Ecomorphological approach

PCA analysis was done to indicate differences and similarities in morphological characteristics of reef fish species on the Saba bank. The PCA analysis was done for the untransformed measurements of fifteen fish species and raw data can be found in Appendix X. The PCA gave a good visual representation of the variation between different species, explained by the first (PC1: 58.4%) and second (PC2: 17.7%) principal component. However, size differences of the measured fish were responsible for most of the variability in the dataset and the first axis, associated with size, was neglected. The second and third axis, explaining respectively 17.7% and 6.2% of the variability, were associated with the actual morphological traits and therefore used in this analysis. PCA analysis was also executed with normalized and size-adjusted data, resulting in similar explanatory values of PC2 and PC3. Size-adjustment of the data set resulted in a considerable improvement of the distinctive power of the graph and was therefore used for indicating differences and similarities in morphological characteristics of reef fish species.

The graph of the size-adjusted PCA is shown in figure 25. A clear distinction was observed between almost all fish species, indicated with differently colored circles. Only yellow eye snapper (*Sebastes ruberrimus*) shows overlapping morphological characteristics with white grunt (*Haemulon plumieri*), and sand tilefish (*Malacanthus plumieri*) with rosy razorfish (*Hemipteronotus martinicensis*).

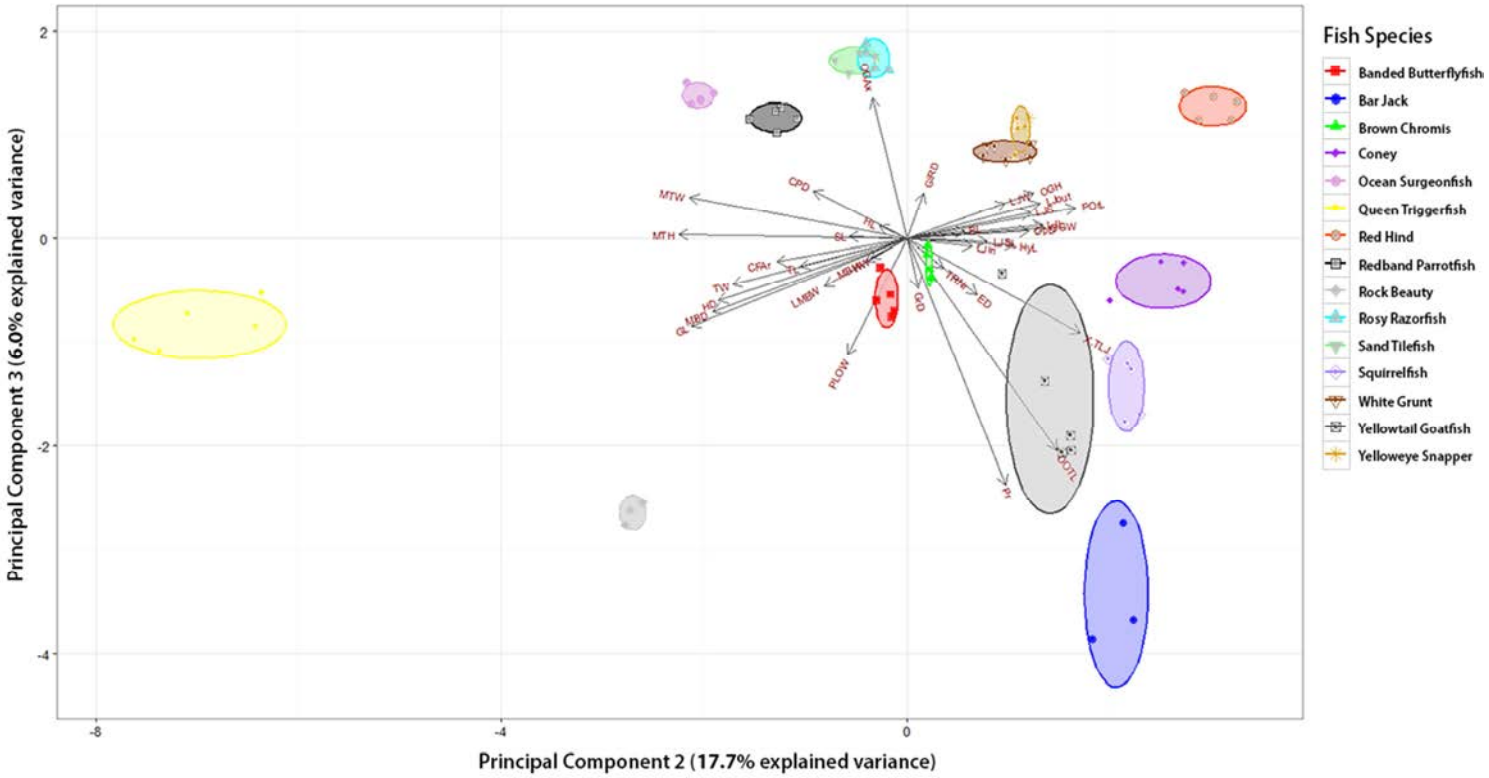

Figure 25 Principal Component Analysis (PCA) with size-adjusted data. Axis 2and 3 explain variability of respectively 17.7% and 6.0%. Fifteen different species are indicated with differently colored circles, whereas the explanatory variables are indicated by arrows. Their length indicates influence on species distribution. More explanation on the abbreviations for morphological traits can be found in appendix VIII.

Two sets of variables explain most of the difference between the fish species. At one side the traits were observed involving a predatory life style, including OGW (oral gape width), OGH (oral gape height), HyL (hyoid length), LJL (lower jaw length) and DOTL (density of teeth on lower jaw). Whereas on the opposite side of the graph more characteristics involving a herbivorous life style explained the variance in fish species: GL (gut length), MTH (maximum tooth height), MTW (maximum tooth width), MBD (maximum body depth) and HD (head depth). OGAx (oral gape axis) and Pr (protrusion) explain most of the variance on the third PC axis. This relation may be explained by the fact that fish species that use protrusion in their food-intake process are mostly predators that hunt by sight and suck their prey in with high velocity. Those type of predators tend to have a terminal oral gape instead of a subterminal one.

In many species variation within the species was observed, especially the larger species such as queen triggerfish (*Balistes vetula*), bar jack (*Caranx ruber*), rock beauty (*Holacanthus tricolor*) and coney (*Cephalopholis fulva*) (figure 25). The smaller species, such as ocean surgeonfish (*Acanthurus bahianus*) and brown chromis (*Chromis multilineata*), seemed to be quite concentrated on the graph, indicating small variation within the species. An exception is the yellowtail goatfish, in which an high degree of variation within the species was observed.

	wht_grnt	rock_bty	coney	rdbnd_pr	ocn_srgn	yllwy_s	bndd_btt	sqrrlfsh	qn_trggr	yllw_gtf	brwn_chr	snd_tlfs	red_hind	bar_jack	rsy_rzrf
Phy_t	0.17	0.61	0.02	0.81	0.49	0.31	0.81	0.83	0.25	0.92	0.64	0.17	0.19	0.68	0.63
Phy_p	0.31	0.83	0.38	1.00	0.20	0.30	0.59	0.75	0.00	0.71	0.80	0.22	0.58	0.58	0.00
Alg_s	0.22	1.00	0.10	0.81	0.92	0.00	0.63	0.46	0.40	0.76	0.53	0.52	0.00	0.44	0.67
Alg_b	0.33	0.57	0.00	0.64	0.73	0.30	0.18	0.15	1.00	0.38	0.58	0.90	0.21	0.59	0.83
Detr	0.00	0.94	0.21	0.31	1.00	0.31	0.98	0.30	0.74	0.95	0.00	0.51	0.35	0.00	0.59
MiCr_t	0.22	0.26	0.09	0.80	0.25	0.73	0.45	1.00	0.13	0.76	0.36	0.26	0.47	0.88	0.60
MiCr_p	0.40	0.26	0.15	0.56	0.41	0.71	0.98	0.84	0.13	1.00	1.00	0.00	0.32	0.50	0.21
Crust	0.92	0.87	0.11	0.60	0.48	0.10	0.36	0.00	0.71	0.35	0.58	0.99	0.19	1.00	0.56
Lar_wrm	0.28	0.00	0.53	0.00	0.72	0.63	0.71	0.05	0.86	0.78	0.00	0.83	0.57	0.18	1.00
Mollusc	0.57	0.87	0.12	0.51	0.63	0.25	1.00	0.05	0.92	0.00	0.60	0.75	0.18	0.66	0.41
Fish_p	1.00	0.05	0.87	0.13	0.09	0.67	0.00	0.25	0.30	0.37	0.21	1.00	0.83	0.96	0.54
Fish_a	0.90	0.17	1.00	0.17	0.00	1.00	0.16	0.25	0.17	0.76	0.49	0.49	1.00	0.55	0.22

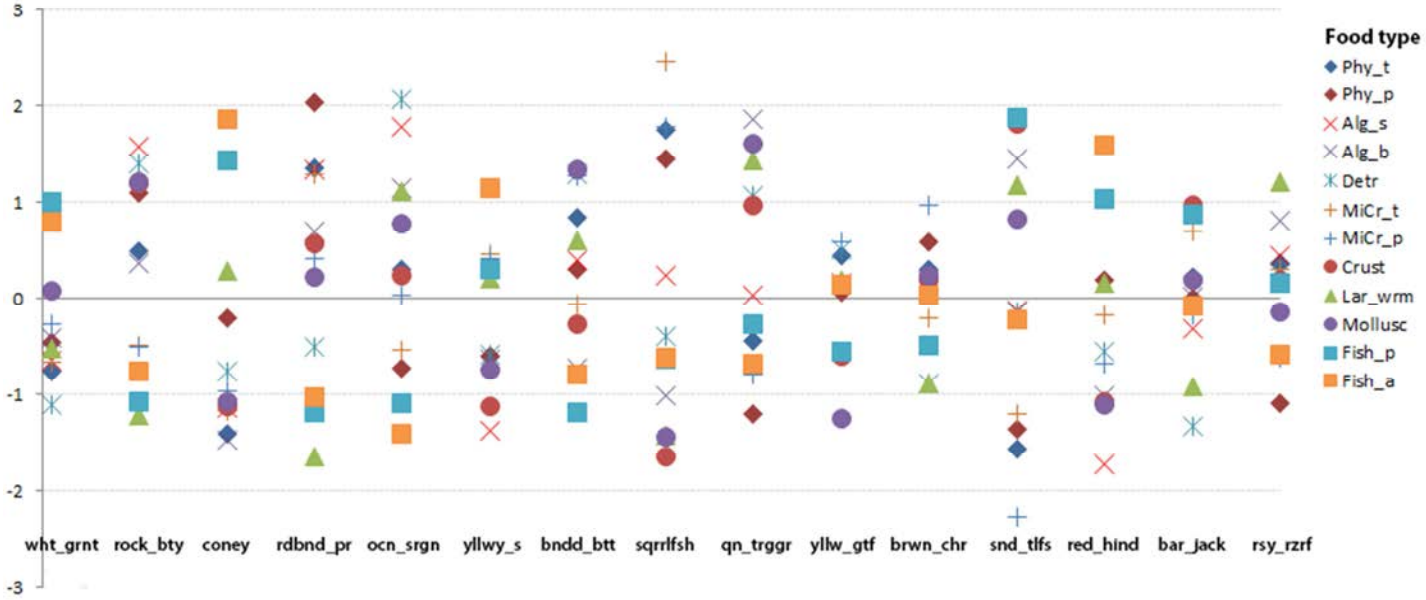

Figure 26 Fish Food Model (FFM) analysis. (A) The data matrix for the Fish Food Model (FFM) obtained by matrix multiplication. Colors in the data tables indicate species' 'afinity' with the food type (green is high, red is low). Fish abbreviations can be found in table 7. Food type abbreviations: phytoplankton-townet (Phy_t), phytoplankton-pump (Phy_p), algae-scraping (Alg_s), algae-biting (Alg_b), detritus (Detr), Micro-crustaceans-townet (MiCr_t), micro-crustaceans-pump (MiCr_p), crustaceans (Crust), larvae-worms (Lar_wrm), mollusc (Mollusc), fish-pursuit (Fish_p), fish-ambush (Fish_a).

The data matrix for the Fish Food Model (FFM) was obtained by the method of matrix multiplication and the output was presented in figure 26. According to the FFM-analysis trophic diversity in the samples is high, with fish species representing all food types analyzed. Best suited food types were fish (5/6), algae (2/5) and micro-crustaceans (3/4) followed by phytoplankton (1/1), mollusca (1/0), crustaceans (1/0), larvae/worms (1/0) and detritus (1/0). White grunt (*Haemulon plumieri*) is a real food-specialist in both analysis (figure 26), morphologically best fitted for fish (both pursuit as ambush) as a food source, followed by crustaceans, whereas it is less suited for feeding on algae and detritus. The same applies to yelloweye snapper (*Sebastes ruberrimus*), which is mainly suited for eating fish and as a consequence poorly adapted for eating plant material. Fish species that are specialized in eating plant material are rock beauty (*Holacanthus tricolor*), redband parrotfish (*Sparisoma aurofrenatum*), ocean surgeonfish (*Acanthurus bahianus*) and rosy razorfish (*Hemipteronotus martinicensis*). Fish species that are structural generalists are able to feed on a wide range of food sources, based on their morphological traits. Few species are called structural generalists: banded

butterflyfish (*Cheatodon striatus*) and yellow goatfish (*Mullidae mulloidichthys*) score relatively high for nearly all food types. A food specialist possesses a set of morphological traits suited for optimal feeding on a particular food source. Bar jack (*Caranx ruber*) is mainly suited for eating crustaceans and fish, whereas coney (*Cephalopholis fulva*) and red hind (*Cephalopholis guttatus*) are morphologically fitted for exclusively eating fish and therefore considered food specialists. Micro-crustaceans as a food type is best fitted for brown chromis (*Chromis multilineata*) and squirrelfish (*Holocentrus adscensionis*). Brown chromis is considered to be more suited in applying the pump-mechanism, whereas squirrelfish has higher scores for applying the townet-mechanism. Queen triggerfish (*Balistes vetula*) is best suited for mollusks and algae (biting), whereas sand tilefish (*Malacanthus plumieri*) is a fish species specialized in high protein food types, such as mollusks, crustaceans, fish, larvae and worms.

The outcomes of the FFM analysis were translated to reef fish assemblages level and a matrix of the average score per food type per site was obtained. The influences of the different food types on the fish assemblage structure was obtained with a PCA (figure 27). In order to link ecomorphological differences in reef fish assemblages to the explanatory factors, PCA figures were made for the explanatory factors habitat, depth, fisheries and location. Differences were indicated with differently colored dots and the areas of similarity in factor characteristic were marked to highlight the differences.

Table 11 Results of the PCA on food type influence of reef fish assemblages on the Saba bank. The first five axes (principal component) are shown in this table, with a total of 94% of the variance explained by these axes. Food types in bold are explaining most variance on the first two axis and therefore are in fish assemblages.

	PC1	**PC2**
Eigenvalue	0.2573	0.2305
Proportion explained	0.3406	0.3051
Cumulative proportion	0.3406	0.6458
Phy_t	-0.0135	0.3399
Phy_p	**-0.715**	**0.7819**
Alg_s	0.40459	0.4128
Alg_b	0.39506	0.0817
Detr	0.62291	-0.31
MiCr_t	-0.3221	0.0162
MiCr_p	**-0.5464**	0.4216
Crust	-0.2734	0.074
Lar_wrm	0.47604	**-1.037**
Mollusc	-0.0904	0.1811
Fish_a	**-1.0359**	**-0.535**
Fish_p	**-0.8673**	**-0.887**

Table 11 shows that 65% of total variance was explained by the first two axis (PC1=34%, PC2=31%), hereby giving a good visual representation of the data. Most variance on the first axis (PC1) was explained by four food types (scores in bold): fish-ambush, fish-pursuit, phytoplankton-pump and micro-crustaceans-pump. On the second axis (PC2) similar food types were explaining most of the variance in the data, only larvae/worms took the place of phytoplankton-pump.

Figure 27 gives a graphical representation (PCA analysis) of the influence of different sets of morphological characteristics (FFM-values) on reef fish communities. As shown in table 11, fish, phytoplankton (pump) and micro-crustaceans (pump) as food source were responsible for explaining most of the variance, whereas crustaceans and mollusks had little explanatory power. The differences in fish assemblage structure within habitat complexity levels (0-4) were mostly explained by a set of morphological characteristics involved in eating fish (Fish_a, Fish_p) and algae (Alg_s) (figure 27A). For feeding on fish, variables were mainly related to the jaw apparatus. Hyoid length (HyL), hyoid/Jaw suspension ratio (HyJsR), lower jaw length (LjL) and post lingual organ width (PLOW) were mostly related to a piscivorous lifestyle (table 11). For algae as food source other variables such as lower jaw force efficiency in closing (LJFEiC), pharyngeal teeth (TPT1/2) and gut length (GL), are important (table 11). Differences of fish assemblages within the depth layers were less apparent, but still changes in assemblages were observed between the deepest category (40m) and other depths (15 and 25m) (figure 27B). These differences can be related to fish traits mostly involved in eating fish (Fish_a, Fish_p), worms and larvae (Lar_wrm), algae (Alg_s) and phytoplankton (Phy_t). Among those variables are barbels (Ba), oral gape axis (OGAx), both belonging to larvae and worms as food source, and relative body depth (RBD), gill raker length (RL) and relative gape area (RGA) (table 11). Those latter three characteristics are optimized for feeding on phytoplankton with a townet mechanism. Reef fish assemblages categorized for fisheries activity show a huge amount of overlap and therefore no real differences can be found in food sources creating variability (figure 27C). The same applies more or less for assemblages categorized for location, all five distributions are centralized and therefore no real ecomorphological differences were observed (figure 27D).

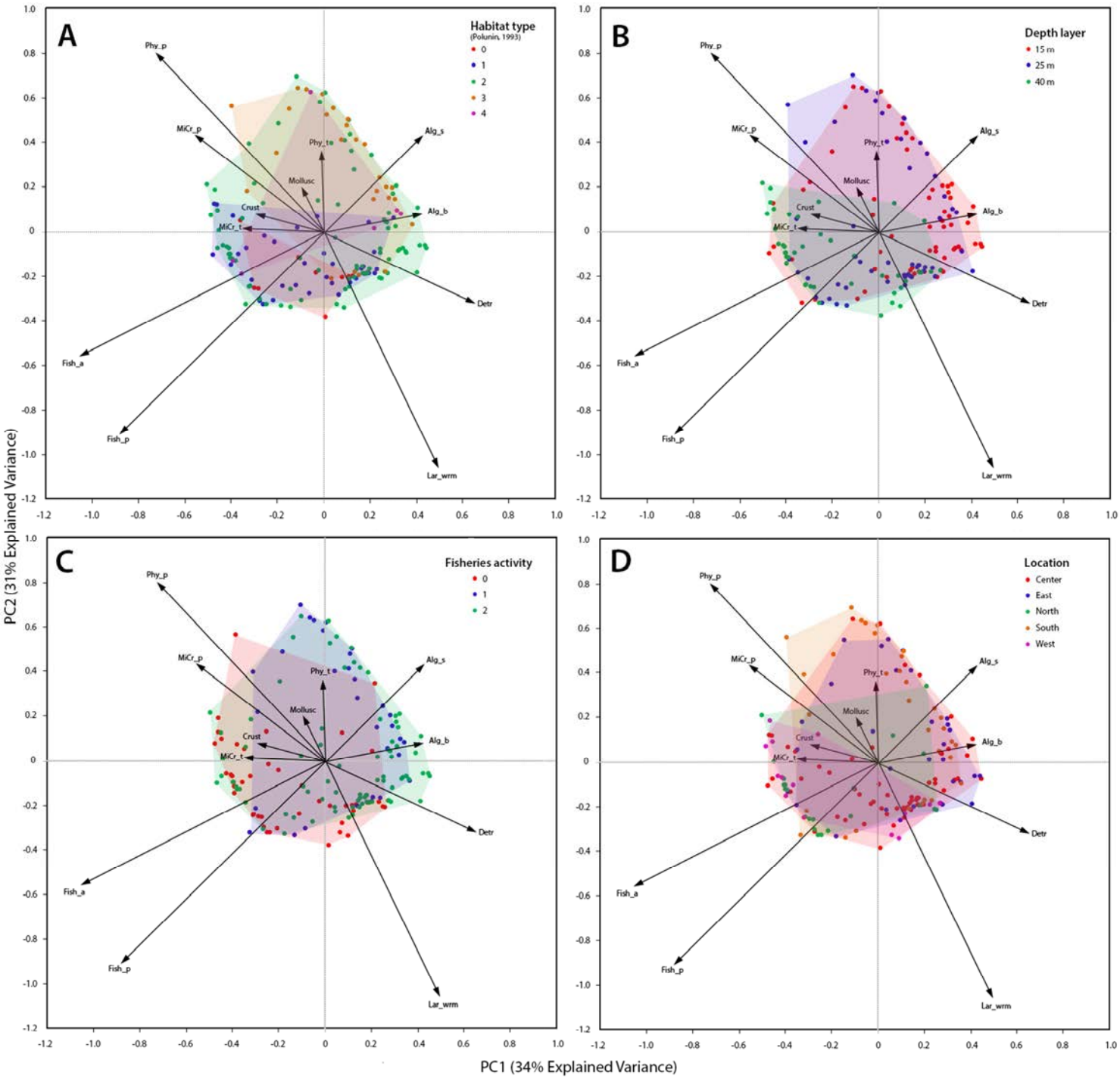

Figure 27 PCA for ecomorphological characteristics in reef fish assemblages. Four graphs give a graphical representation of the influence of different sets of morphological characteristics (FFM-values) on reef fish communities. Reef fish assemblages are categorized by type of habitat complexity (A), depth (B), fisheries activity (C) and location on the Saba bank (D). Nearly 65% of total variance is explained by the first two axis (PC1=34%, PC2=31%)

To test the hypothesis that reef fish assemblages show less variability on a functional level than on species composition level, a comparison of data sets was made. A PCA of the fish abundance data per site with 35 fish species was executed and was visually compared with the PCA analysis of the ecomorphological data set. Both a PCA of species diversity and trophic diversity for habitat differences are found in figure 28. Habitat was chosen as explanatory variable because most variability in figure 27 was observed for this factor.

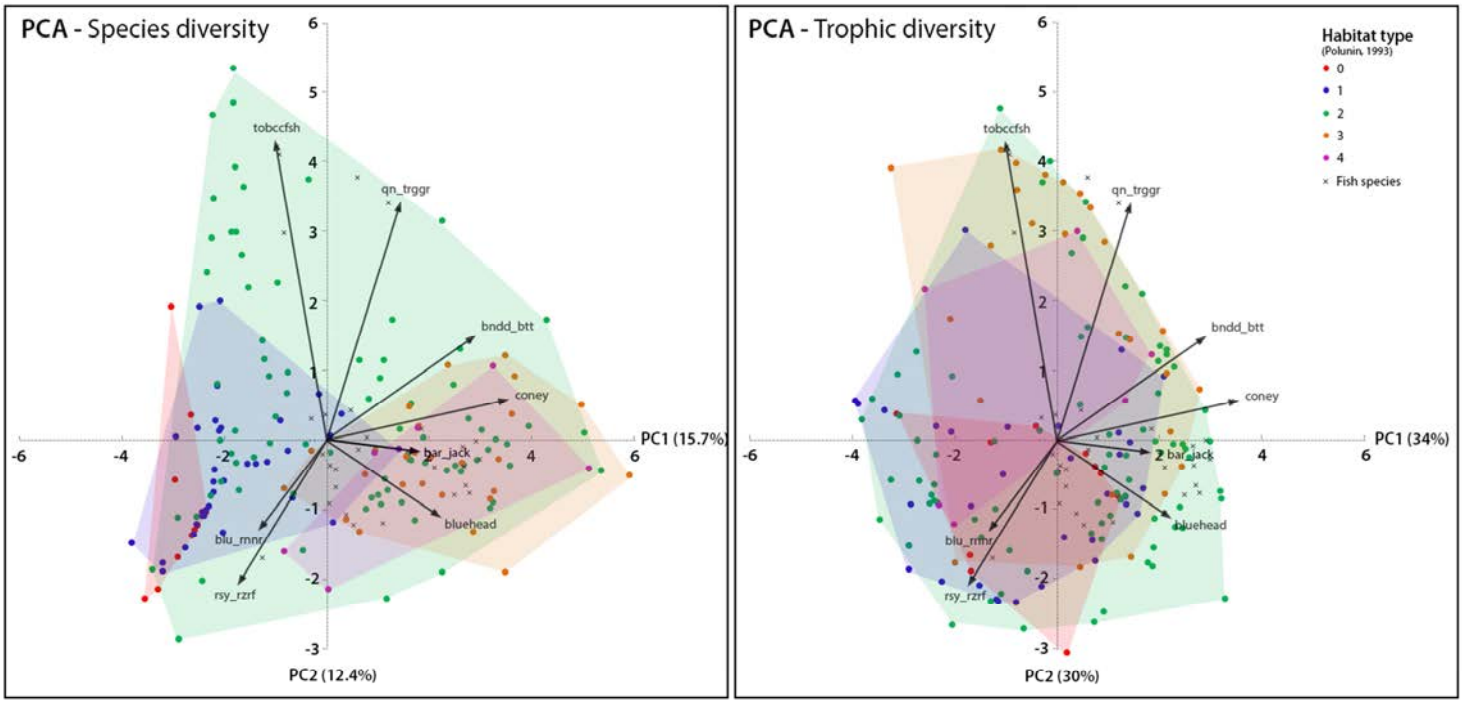

Figure 28 PCA for species and trophic diversity data. Two graphs give a graphical representation of the differences in fish assemblages for trophic diversity and species diversity. Nearly 30% of total variance is explained by the first two axis (PC1=15.7%, PC2=12.4%) of species diversity data, whereas 64% of total variance is explained by the first two axis (PC1=34%, PC2=30%) of the trophic diversity data.

More overlap and more centralization in trophic diversity data was observed compared to species diversity data (figure 28). In both analyses fish assemlages in habitat category 2 (green) showed most variability. Fish assemblages found in habitat category 0 (red) are most distinct in both analyses, with no overlap of assemblages with habitat type 3 and 4 in the species abundance analysis. Fish assemblages in habitat category 3 and 4 showed high overlap in species diversity analysis and were found more to the right of the distribution. In trophic diversity data this was less clear and the clusters are more centralized. Differences in explanatory character of the PCA analyses wereobserved. Nearly 28% of total variance was explained by the first two axis (PC1=15.7%, PC2=12.4%) of the species diversity data set, whereas 64% of total variance was explained by the first two axis (PC1=34%, PC2=30%) of the trophic diversity data.

A Mantel test was used to measure correlations between the two matrices. Correlations are a measure of (dis)similarity of the data sets. Correlation were measures for both the complete data sets and for the data stratified for habitat categories. Table 12 shows the overall correlation and between data of different habitat categories.

Table 12 Correlations between two data sets (species diversity and trophic diversity) and their significant, obtained with a Mantel test. Correlation were measures for both the complete data sets and for the data stratified for habitat categories.

MANTEL TEST	**Habitat category**					
	All (N=164)	0 (N=15)	1 (N=36	2 (N=81)	3 (N=26)	4 (N=6)
Correlation (r)	0.4827	0.1694	0.4339	0.3271	0.4917	-0.2563
Significance (p)	**0.001**	0.136	**0.001**	**0.001**	**0.001**	0.819

Overall there was a significant correlation found between species diversity and trophic diversity. For habitat categories 1-3 also a signifant correlation was observed, whereas habitat types 0 and 4 showed no significant correlations. Figure 29 shows the correlation data sets in a scatter plot. Correlation was present, but the values on the x and y-axis were not similar, indicating differences in diversity between the data sets.

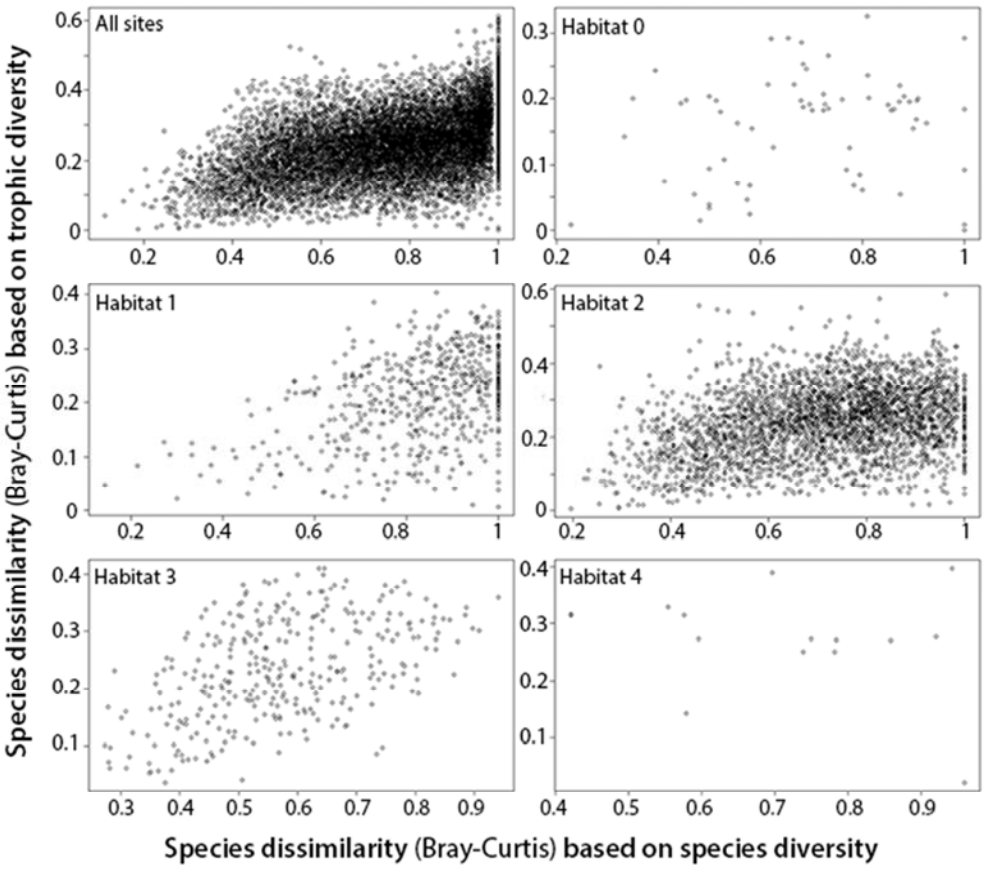

Figure 29 Scatter plots of the correlation datasets (species diversity and trophic diversity). Data was transformed by using a Bray-Curtis dissimilarity matrix (square root), based on the distance between samples in ordination space. Correlation were measures for both the complete data sets and for the data stratified for habitat categories.

5. Discussion

5.1 General diversity

Toller *et al*. (2010) found in their study in the Southeastern part of the Saba bank a total of 97 fish species. Their study area (40km^2, <30m) was only a fraction of the area of this study in both spatial (2,200km^2) and depth coverage (<58m). Furthermore, they focused on one reef system of the Saba bank, whereas present study covered the whole bank with associated types of habitat, in which more different fish species were observed. A total of 135 fish species were identified, belonging to 39 families. Higher species richness was found by Williams *et al*. (2010) in a more comprehensive research focused on species richness on the Saba bank, involving ichthyiocide sampling and visual surveys at 25 different locations. They reported 270 different fish species, of which 132 were observed during visual census. Total species richness on the Saba bank was even estimated higher, varying between 320 and 411 species (Williams *et al*., 2010). Because BRUV surveys were not designed for species richness assessments (Watson *et al*., 2005; Langlois et al., 2010), lower levels of species richness were expected to be found in this study compared to Williams *et al*. (2010). For the purpose of conducting a baseline survey on reef fish assemblages covering the whole Saba bank, it is not necessary to give a comprehensive overview of species richness.

5.2 Factors influencing fish abundances

5.2.1 Depth

Changes in fish assemblage structures were most clear when shallow (15m) and deeper (25m) sites were compared with the deepest (40m) locations. Both species richness and mean biomass was highest for shallow sites (N=102, biomass=21.8kg), followed by deeper locations (N=95, biomass=16.1kg) and deepest sites (N=74, biomass=14.0kg). The differences in mean biomass of reef fish assemblages were largest between sites located in the 15m and 25m depth layer, which was mainly caused by the fact that maximum number of individual fish (MaxN) was highest at shallow sites (MaxN=4236), compared to other locations (25m: MaxN=2731, 40m: MaxN=1703). Although MaxN was lowest in 40m-sites, the species observed in deeper water fish were relatively larger, hereby contributing to the relatively high mean biomass for these sites. The same strong correlation of depth with fish community structure was found by other research groups focussed on more temperate regions (Hyndes et al., 1999; Williams *et al*., 2001). Hyndes *et al*. (1999) found in their study off the Southwest coast of the Australian continent significant decrease in mean MaxN and Nsp levels of fish faunas from near-shore depths (~2m) to further offshore (5-15m and 20-35m) sites. Some fish species were far more abundant in depths of 5-15m, whereas other species mainly occurred in deeper waters.

Change of depth may have major impact on the kind of habitat fish encounter, mainly due to changes in light penetration, pressure and temperature. The percentage of bare rock as habitat substratum increases with depth (Ferreira *et al*., 2001), whereas corals, algae and other photosynthetic organisms were more abundant in shallow waters. Herbivorous fish species were most abundant in shallow water, whereas their presence in deep water (40m) was almost zero. This was mainly because of the availability of their food source in shallow water. This assumption was supported by research in both the Great Barrier Reef (Russ, 1984) and the Hawaiian island Hanaley (Friendlander and Parrish, 1998). Both studies found more herbivorous fish species together with higher levels of algal cover in shallow water, compared to deeper waters. Whereas the depth range of suitable habitat types for herbivores seemed to be rather small, invertebrate feeders occupied a much broader depth range and rather similar percentages in herbivore abundance (in biomass) was found for all depths. Mean length distribution for depth showed both slightly higher frequencies of larger fish and a relatively large peak for small fish in deep water (40m), compared to more shallow water. Fish of intermediate lengths (15-20cm) were relatively absent at this depth. The large peak at smaller fish lengths may be explained by the low levels of relief in deeper waters compared to shallower depths. When fish grow larger, less sheltering opportunities are present and they are more visible to predators.

Because the influences of depth on reef fish assemblages as co-varied with levels habitat complexity (Bouchon-Navaro *et al*., 2005), distance to shore (Malcolm *et al*., 2010) and food availability (Ferreira *et al*., 2001) it was difficult to relate this factor to patterns in reef fish assemblages. However, the distribution of certain fish species was higher in particular depth layers, despite similarities in habitat complexity. With their relatively high trophic level (TL>3.1), small seabasses (*Serranidae*) such as *Serranus tortugarum* (invertebrate feeder), *Serranus baldwini* (piscivore) and *Serranus tabacarius* (invertebrate feeder) and the snapper *Rhomboplites aurorubens* (piscivore) were more observed in deeper waters (>25m). Hereby responsible for the relatively high percentages of piscivores and omnivores in deeper water. On the other hand, most parrotfish species (herbivores) almost exclusively occur in shallow waters (<25m), hereby contributing to relatively low mean trophic level of fish assemblages in shallow water. These diverse spatial distributions over different depth layers, together with their trophic level differences, provide an explanation for the patterns observed in reef fish assemblages between depths.

5.2.2 Habitat

Habitat complexity is assumed to be strongly correlated with depth (Anderson *et al*., 2004; Ferreira *et al*., 2001; Harman *et al*., 2003; Toller *et al*., 2010), especially when habitat complexity is based on algal structures, which are dependent on light penetration. Only few studies observed variability in reef fish assemblage structures between and within different habitat complexity levels along a depth gradient (Moore *et al*., 2010; Malcolm *et al*., 2011; Zintzen *et al*., 2012). Prior to sampling, specific information on environmental conditions on the Saba bank was limited. A GIS-map (2007) and depth map of the Saba bank was available to make sure evenness in sampling habitat complexity types was maintained throughout this study. Relatively more samples (N=85) were taken in the shallow areas (<20m) along the edges of the bank (East and South), where range of habitat types was expected to be widest. However, fine-scale variability on habitat complexity at any sampling location was unknown prior to sampling. Hence, sampling over different habitat types (0-4) was not uniformly distributed with respectively 15, 35, 80, 25, 6 samples taken per habitat category. This implies that habitat category 2 (Polunin and Roberts, 1993), which was characterized by 'low but widespread relief', was by far the most abundant habitat type along the shallow edges of the Saba bank. This fine-scale categorization for analysis of habitat influences was chosen because it decreased variation between treatments and thereby increased the probability of finding differences ($p<0.05$) in fish assemblage structures related by habitat complexity.

Within all depth layers, a strong positive correlation was observed between habitat complexities, species richness (Nsp), fish abundances (MaxN) and mean biomass of fish assemblages. This general increase in number of fish, biomass and number of species with an increase in habitat complexiy was also observed in the study of Toller *at al*. (2010) on the Saba bank. High levels of reef fish diversity and abundance were found in complex habitats when compared with the lagoon, where habitat is less complex. Herbivorous fish species in complex shallow reef systems, such as ocean surgeonfish (*Acanthurus bahianus*), princess parrotfish (*Scarus taeniopterus*) and rock beauty (*Holacanthus tricolor*) contributed most to this correlation. Complex reef systems provide important resources and shelter opportunities for many fish species. Its vertical relief and rugosity of substratum supports high numbers of fish (Jones, 1988; Hixon and Beets, 1993; Auster *et al*., 1995; La Mesa *et al*., 2011), which explained the high similarity of fish abundance structures found in shallow water. A strong linear relationship was found by Friedlander and Parrish (1998) between mean volume of holes and mean reef fish length, indicating the importance of shelter possibilities for small fish species. No strong relation between mean biomass of fish assemblages and habitat complexity was found in shallow and deeper waters. This may be explained with the relatively higher abundance of mobile piscivores, such as larger jacks and snappers, that do not have close affinity with a particular kind of substratum (Friendlander and Parrish, 1998). Because they were found at a large range of habitat types they compensate biomass level for the absence of small herbivorous fish (*Labridae* and *Pomacentridae*) at sites with lower habitat complexity. This was supported by observations on mean trophic level and trophic groups. Trophic level was significantly ($p<0.05$) higher (TL>3.55) for sites with low habitat complexity (0-1) compared to other habitat types (2-4) (TL<3.18). Low spatial relief and lack of shelter possibilities at sites classified with habitat type 0 and 1 probably resulted in poor habitat and probably cause the absence of many small non-piscivorous fish species.

Fish length distributions were different for the different habitat categories. Large fish species (>30cm) were more frequently observed at lowest habitat complexity levels, compared to smaller fish. This may be due to the general absence of fish of intermediate (15-30cm) lengths at these sites, hereby increasing the relative percentage of larger species. A more concentrated length distribution was observed in more complex habitat (2-4) with high numbers of smaller fish (3-25cm).

5.2.3 Fisheries activity

Many foreign vessels used to fish on the Saba bank (Guidicelli and Villegas, 1981; Dilrosun, 2000; Lundvall, 2008; Hoetjes and Carpenter, 2010), but since the implementation of a Dutch fishery law in 1993, the Saba bank was exclusively available for Saban fishermen as part of the Exclusively Economic Zone (EEZ) of Saba. Only the lobster fishery with fish (mixed fish) as bycatch was considered as possible influence on reef fish assemblages in this study, because this takes place on the Saba bank. Approximately 7.8 – 9.8 tonnes mixed fish caught on the Saba Bank was landed annually (Van Gerwen, 2013). This was considered to be a relatively low amount of fish. For a comparison, in 2006 the Dominican Republic landed over 1,000 times more tonnes of fish in an area only 100 times larger the the EEZ of Saba (Herrara *et al*., 2011). On Saba, most landed fish species in 2013 based on abundances were *Haemulon plumieri* (white grunt: 27%), *Acanthurus bahianus* (ocean surgeonfish: 15%), *Epinephelus guttatus* (red hind: 11%), *Haemulon melanurum* (cottonwick: 8%) and *Balistes vetula* (queen triggerfish: 6%) (Van Gerwen, 2013). In 2006, Dominican by catch of lobster fishery consisted mainly of *Haemulon plumieri*, *Haemulon melanurum* and *Pseudopeneus maculatus* (spotted goatfish), showing similarities with the by catch of Saban lobster fishery (Herrara *et al*., 2011). Significant differences in mean fish length of the fish species on the by catch of Saba fishery was not observed between locations with different fishing pressure. *B. vetula* showed differences in mean fish length that were significant between areas of high and low fisheries activity. Their mean length was 30.1cm (±7.8SE) for low and 33.6cm (±8.1SE) for high fisheries activity areas. This is the opposite of what one would expect regarding the effect of fisheries on mean fish length. High intensities of trap fishing may cause serious overfishing, alter ecosystem structure and reduce biodiversity (Hawkins *et al.,* 2007). One reason for the effects found could be that the fishing on the Saba bank takes place on such low intensities, that its effect was not observed in the fish species studied in this study. On the other hand, a general absence of piscivores such as large snappers and groupers in this study is an indication of the indelible effects of past fisheries on the Saba bank (Dilrosun, 2000). Despite the absence of large grouper and snappers, still apex predators such as sharks were abundant if compared to other regions in the Caribbean (Newman *et al*., 2006; Brooks *et al*., 2011; Bond *et al.,* 2012).

5.3 Elasmobranchs

Despite the decline of shark populations worldwide due to chronic overfishing and slow reproductive life-history characteristics (Myers *et al.,* 2007), high shark numbers were found on the Saba bank. Compared to other shark research by Brooks *et al*. (2011) in the Bahamas and Bond *et al*. (2012) in Belize, shark numbers on the bank seem to be higher than in those areas. Brooks *et al.* (2011) found on a bank at the Bahamas shark CPUE (sharks per hour) levels ranging from 0.2 along the edges (intermediate habitat complexity) to 0.35 in the mid-banks zone (high habitat complexity) and 0.1 on the bank itself (low habitat complexity). On the Saba bank corresponding CPUE levels of 1.0 ,0.5 and 0.1 were found. Especially on the shallow edges of the bank, where the ocean floor continues in a steep drop-off, high numbers of elasmobranchs were found. Shark abundance (CPUE) was positively correlated with habitat complexity, whereas depth exerted a negative influence on shark abundances. Rays were present in all habitat types and less influences by depth. High shark abundances on the Saba bank could be explained by the lack of destructive industrial fishery methods, such as long-lining, gillnetting and directed fisheries for shark fins. High shark numbers on the Saba bank are a good sign for the health of the Saba Bank ecosystem, since sharks are apex predators, making them a prime indicator for ecosystem health.

5.4 Ecomorphological approach

5.4.1 Fish Food Model (FFM)

Strong differences in morphology and little overlap could be observed for all different fish species in the morphological analysis. Two sets of traits explain most of the variance between the fish species. One was involved in predatory life style, whereas the other set explained most of the variance in fish species associated with an herbivorous lifestyle. A predatory lifestyle was mainly associated with morphological traits concerning the jaw-apparatus, such as gape size, hyoid and lower jaw length. Maximum prey size can be determined by gape traits, whereas lower jaw and hyoid length are important in calculating force transmission and thereby strength of the feeding apparatus (Wainwright and Richard, 1995). The jaw apparatus is one of the most diverse morphological systems among fish (Goatley and Bellwood, 2009) and gape size is one of the most frequently used measures in morphological research on fish (Kotrschal, 1988; Wainwright and Richard, 1995; Persson *et al*., 1996; Truemper and Lauer, 2005). Teeth type, gut length and body depth-related morphological traits explained most of the variance associated with an herbivorous lifestyle. Teeth in herbivorous fish are very important in scraping off algae from hard substrate and grinding the badly digestible plant material, whereas high body depth ensures high levels of maneuverability in the search for plant material (Liem, 1973; Hulsey *et al*., 2006). Gut length is associated with food type, with corallivores possessing narrow and long guts, whereas herbivores have relatively long and wide intestines. Carnivores possess wide and relatively short guts (Elliott and Bellwood, 2003).

Most variation in the data was explained by the queen triggerfish (*Balistes vetula*), which is an invertebrate feeder and herbivore, the herbivorous rock beauty (*Holacanthus tricolor*) and the piscivorous bar jack (*Caranx ruber*). These species have clear distinctive features that separate them from 'standard' reef fish species such as brown chromis (*Chromis multilineata*) and banded butterflyfish (*Cheatodon striatus*), which were assessed as omnivores by their morphological characteristics. FFM-analysis partially confirmed the observed division of fish species into two main groups (herbivorous and piscivorous), and even added a third one (micro-crustaceans). A total of 37% (5.5/15) of the fish species were classified as piscivores, due to their highest association of their morphological features with fish as a food source. Futhermore, 30% (5/15) of the species were classified as herbivores and 23% (3.5/15) were classified as microcrustacean-feeders. This rough division in trophic groups is consistent with other research on fish assemblages on the Saba bank (Toller *et al*., 2010). Furthermore, this study found also a rather similar species distribution based on trophic groups from fishbase with 32% of the fish species being piscivorous, 30% is invertebrate feeder and 20% is herbivorous.

Eye diameter is commonly used as indicator for predatory fish under low light conditions in deeper waters (Job and Bellwood, 2000; Goatley and Bellwood, 2009). This study found no relation between water depth and eye diameter, probably due to relative shallow sampling depth. Goatley and Bellwood (2009) also found that certain trophic groups were highly correlated with eye diameter and oral gape axis. Highly selective feeders, such as *Pomacentridae* and *Chaetodontidae* species, were associated with relatively large eye diameter and small oral gape axis, whereas grazing herbivores had both small eye diameter and oral gape axis (Goatley and Belwood, 2009). This study affirmatively found that large eye diameter in combination with small oral gapes axis was associated with micro-crustaceans feeders (pump) and banded butterflyfish (*Chaetodontidae*) and brown chromis (*Pomacentridae*) were found to be highly suited for feeding on micro-crustaceans (figure 26). Patterns of eye diameter and oral gape axis in grazing herbivores were less apparent.

5.4.2 Assemblage structures

The variance in the trophic analysis of the data when categorized by habitat complexity was best explained by the abundance of algal-feeders (scraping) and piscivores. Piscivorous fish species were relatively most abundant in non-complex habitat, whereas fish species specialized in algal-scraping were most numerous in complex habitat structures. Similar relations were found in total biomass analysis for trophic groups obtained from fishbase (figure 14A). High percentage of algal cover due to high availability of substrate and

high light penetration levels in complex reef systems compared to less complex habitat types probably explains this relation. The morphological characteristics involved in explaining habitat differences in fish assemblage structures are mainly jaw-related for piscivores: hyoid length (HyL), hyoid/Jaw suspension ratio (HyJsR), lower jaw length (LjL) and post lingual organ width (PLOW). These are involved in respectively grabbing and tasting potential food sources. For algae as food source more digestion-involved characteristics such as lower jaw force efficiency in closing (LJFEiC), pharyngeal teeth (TPT1/2) and gut length (GL), are important. (Sibbing and Nagelkerke, 2001)

Trophic differences of fish assemblages within the depth were less apparent compared with habitat structure. However, changes in assemblages were observed between the deepest category (40m) on one side and 15 and 25m on the other. These differences were best explained by to fish traits involved in eating fish (Fish_a, Fish_p), worms and larvae (Lar_wrm) on one side (40m) and algae (Alg_s) and phytoplankton (Phy_t) on the other (15 and 25m). Analysis of biomass for trophic groups obtained similar results, with almost no herbivorous fish species present in deep water high numbers in shallow waters (figure 14). Among the traits responsible for the variation in trophic analysis were barbels (Ba), oral gape axis (OGAx), both belonging to larvae and worms as food source, and relative body depth (RBD), gill raker length (RL) and relative gape area (RGA) Those latter three characteristics were optimized for feeding on phytoplankton with a townet mechanism. No clear ecomorphological differences for fisheries and location were found, indicating minor influences on trophic character of assemblages of these explanatory factors. The similarity of reef fish assemblages for these fisheries may be explained by low levels of current fishing pressure on the Saba bank, whereas the similarity for location may be ascribed to high variability of habitat types within samples of different locations.

When species diversity and trophic diversity were directly compared for different habitat complexity levels, the distribution for the habitat types of trophic diversity data was more centralized, whereas species diversity data showed habitat type clusters with less overlap. This may indicate more robustness of reef fish assemblages on a functional level compared to species composition level. An example of robustness in niche differentiation for habitat was given by two abundant fish species of the *Caranx*-family on the Saba bank (figure 28). Niche differentiation is found in bar jack (*Caranx ruber*) and blue runner (*Caranx crysos*), which were highly similar in feeding characteristics since they are from the same genus. However, bar jack was relatively more abundant in shallow complex reef systems, whereas blue runner was mainly found in sand-dominated areas in deeper waters. This hypothesis was partially supported by species dissimilarity levels (Bray-Curtis) based on trophic and species diversity data (figure 29). The dissimilarity levels based on trophic diversity ranged from 0-0.6, indicating relatively high similarity in the data compared to dissimilarity levels of the species diversity data, which ranged from 0.1-1.0. On the other hand, significant correlation levels (Mantel test) were found between the two data sets for all habitat complexity levels except 0 and 4. Lower correlation levels between the data sets for habitat types 0 and 4 was most likely explained by low sample numbers in these areas (0: N=15, 4: N=6) (table12).

5.5 Methodology

BRUV surveys are a useful and important method in comparing and assessing reef fish assemblages on the Saba bank, due to its rough character. Both short (1 to 10km) and long scale (1 to 60km) bioregional differences in assemblage structure was detected. Variation in species richness was observed on similar scale by studies on shallow rocky reefs using UVC (Underwater Visual Census) techniques (Curley *et al.* , 2002; Anderson and Millar, 2004). BRUV surveys use bait to attract fish, hereby creating elevated activity levels in front of the cameras. This commotion may attract opportunistically feeding fish species of other trophic groups and may enable BRUV studies to sample a greater section of a fish assemblage than more traditional methods and it is able to detect (large) mobile animals that avoid divers during SCUBA surveys (Cappo *et al*., 2004, Watson *et al*., 2005, Stobart *et al*., 2007). A rover diving (RD) survey by Toller *et al.* (2010) on the Saba bank, in which a diver swam in a random direction for 10 minutes and noted every fish species observed, observed a total of 97 different fish species on 40 different sites. A RD survey is often used to increase species richness of a SCUBA survey (Toller *et al*., 2010) and should therefore be able to observe more different species than UVC. Current BRUV study observed 38 additional species in more than 100

additional samples. With 40 samples the total number of species observed by this study was between 75 and 95 species (figure 17). This indicated that a SCUBA survey with additional RD survey was able to observe higher species richness than BRUV surveys. However, current study sampled many sites that were low in species richness (habitat category 0 and 1), whereas Toller *et al*. (2010) sampled exclusively areas in or nearby the reef in the Southeastern part of the Saba bank. This particular area (South and East) was characterized by highest levels of MaxN, Nsp and biomass in current study (figure 13). Therefore caution is advised when comparing both studies.

In BRUV surveys, the extent of the bait plume is unknown and subject to environmental conditions such as current velocity, habitat complexity and the sense of smell in fish species (Willis and Babcock, 2000). In water with low visibility and turbid waters fish species using smell over sight may be more present in the data (Bassett and Montgomery, 2011). It is also possible that with the use of bait fish assemblage will be biased towards predatory and scavenger species and that the abundances of herbivorous and omnivorous species will be underestimated (Harvey *et al*., 2007). This effect was observed in fish traps when bait is used to attract piscivorous species (Newman, 1990). However, this seems not the case, as indicated by independent studies of Watson *et al.* (2005) and Harvey *et al.* (2007). In these studies baited and unbaited stereo video surveys were compared. Both studies showed an increase in piscivorous, omnivorous and herbivorous fish species when bait was used. This could be explained by a so-called 'sheep effect': the activity and excitement in the area of the bait, caused mainly by the attracted piscivorous species, attracts in their turn herbivorous and omnivorous fish species. Not only higher species richness will be established in this way, it also attracts more individuals per species (Harvey *et al*., 2007). With a higher number of individuals from a wider range of species, the statistical power of the tests will be improved when using BRUV for analyzing fish assemblages (Cappo *et al.* 2006). Species accumulation curves of the dataset were not approaching their asymptotic length yet, indicating that with an increase in sampling effort more species will be detected. This assumption is supported by the fact that total species richness is on the Saba bank is estimated much higher (320-411 species) than observed in this study (135 species) (Williams *et al*., 2010). Watson *et al*. (2005) stated in their study that especially in complex habitat types, diver surveys are still warranted to create a more complete idea of the structure of reef fish assemblages.

Sampling is this study was only done in short periods (October-February), hereby not including seasonal differences in reef fish assemblages. Seasonal aggregation patterns of certain fish species (*Balistes vetula*: spawning, *Epinephelus guttatus*: spawning) in particular areas on the Saba bank were observed in the past (Dilrosun, 2000), and therefore additional research is necessary to account for this variability. This study was done during the spawning period of *Epinephelus guttatus*, therefore relatively more individuals of this species may be observed than in non-spawning periods. Furthermore, fisheries information related to specific quadrants on the bank was provided by fishermen and since there was reasonable competition between them, may not always be relied upon. Some fisheries effect may therefore be falsely interpreted or simply not be noticed. However, this was the only way of obtaining any information on fisheries activity and therefore used in this study. Just as the obtaining of fisheries data, the process of habitat categorization and video analysis was done manually, this creates room for observer error.

Nearly all trophic guilds occurring in fish assemblages on the Saba bank were included in the FFM analysis. The emphasis is on smaller and intermediately-sized (<40cm) fish species, which were easily obtained. Larger, more mobile, piscivorous fish such as sharks and great barracuda (*Sphyraena barracuda*) were not available and therefore left out of the analysis. However, these larger fish species were very abundant at certain locations. Despite 35 of 40 most abundant fish species were 'covered' in the FFM-analysis, it provided a slightly shifted image of Saba banks' fish assemblages towards smaller species. Furthermore, the model includes a large number of variables. Some of them may be highly correlated due to measurement of the same characteristic or body area. This may increase the weight on certain morphological characteristics, causing unbalance in the distribution and a decrease of sensitivity in the model. However, some fish characteristics are more important in the feeding process than others and should be more emphasized on in the analysis. To decrease the number of descriptive variables, a selection based on importance (explanatory power) could be made and included in further studies (Norton, 1995).

6. Conclusions

(1) Habitat complexity and depth have highest explanatory value for differences in reef fish assemblages structure. Habitat complexity was found to be positively correlated with species richness, fish abundance and mean biomass, whereas depth was found to be negatively correlated with these variables. High quantities of vertical relief and rugosity of substratum in shallow areas were found to support high numbers of fish species, whereas sand flats in deeper water were characterized by general absence of species.

(2) A minor part of the variability in the structure of reef fish assemblages was explained by differences in fisheries activity, indicating that no clear fisheries effect was observed in fish assemblages in this study. Furthermore, no significant differences in average size of target species were observed between areas with different fishing pressure. However, the general absence of piscivores such as large snappers and groupers was an indication of the indelible effects of past fisheries on the Saba bank.

(3) Relatively high shark abundances were observed on the Saba bank compared with other Caribbean regions. Shark abundance (CPUE) was positively correlated with habitat complexity, whereas depth exerted a negative influence on shark abundances. High shark numbers are a good sign for the health of the Saba Bank ecosystem, since sharks are apex predators, making them a prime indicator for ecosystem health.

(4) On a functional level reef fish assemblages showed less variability than on species composition level, this may be an indication for high levels of robustness in niche differentiation in reef fish communities on the Saba bank.

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Appendix I: Habitat images

OpCode	Depth (m)	Image	Relief (Watson, 2004)	Habitat type (Polunin and Roberts, 1993)	Habitat (%)		Range of view (m)	Visibility	Position of Cams
			Low/Medium/High	0-5	Sand	Other			
SB_North_36	26,0		Medium	2	30	70	>8	Very good	Straight
SB_North_35	34,0		Medium	2	25	75	>8	Very good	Straight
SB_North_34	32,0		Low	1	85	15	>8	Good	Straight
SB_North_33	18,0		Medium	2	50	50	>8	Very good	Straight
SB_North_32	29,0		Medium	2	40	60	>8	Good	Straight
SB_North_31	25,0		Low	1	70	30	>8	Medium	Straight
SB_North_30	25,0		Medium	2	60	40	>8	Medium	Straight

OpCode	Depth (m)	Image	Relief (Watson, 2004)	Habitat type (Polunin and Roberts, 1993)	Habitat (%)		Range of view (m)	Visibility	Position of Cams
			Low/Medium/High	0-5	Sand	Other			
SB_North_29	23,0		Medium	2	50	50	>8	Good	Straight
SB_East_138	17,0		Medium	3	30	70	>8	Good	Straight
SB_East_139	17,0		Medium	3	25	75	2=20% >8=80%	Very good	Straight
SB_South_13	20,0		Medium	2	70	30	>8	Medium	Straight
SB_South_14	25,0		Low	1	75	25	>8	Medium	Straight
SB_South_15	25,0		High	4	20	80	4=50% >8=50%	Good	Downwards
SB_South_17	17,0		Medium	2	50	50	>8	Good	Straight
SB_South_18	17,0		Medium	2	50	50	>8	Good	Straight

OpCode	Depth (m)	Image	Relief (Watson, 2004)	Habitat type (Polunin and Roberts, 1993)	Habitat (%)		Range of view (m)	Visibility	Position of Cams
			Low/Medium/High	0-5	Sand	Other			
SB_South_63	15,0		Medium	3	40	60	>8	Very good	Straight
SB_South_62	24,0		Medium	3	40	60	>8	Very good	Straight
SB_South_61	18,0		Medium	3	40	60	>8	Medium	Upwards
SB_South_66	20,0		Medium	3	40	60	>8	Good	Straight
SB_South_65	20,0		Medium	2	70	30	>8	Very good	Straight
SB_South_64	18,0		Medium	3	40	60	>8	Good	Straight
SB_East_67	18,0		Medium	2	60	40	>8	Good	Straight
SB_East_68	15,0		Medium	2	50	50	>8	Good	Upwards

OpCode	Depth (m)	Image	Relief (Watson, 2004)	Habitat type (Polunin and Roberts, 1993)	Habitat (%)		Range of view (m)	Visibility	Position of Cams
			Low/Medium/High	0-5	Sand	Other			
SB_East_69	14,0		Medium	3	40	60	>8	Good	Downwards
SB_East_71	17,0		Medium	3	30	70	>8	Good	Upwards
SB_East_72	17,0		Medium	3	20	80	>8	Good	Straight
SB_East_132	19,0		Medium	3	30	70	4=40% >8=60%	Good	Downwards
SB_East_133	25,0		High	4	20	80	2=30% >8=70%	Medium	Straight
SB_South_7	28,0		Medium	2	70	30	>8	Medium	Straight
SB_South_8	25,0		Medium	2	60	40	>8	Medium	Upwards
SB_South_9	22,0		High	4	20	80	2=20% >8=80%	Medium	Straight

OpCode	Depth (m)	Image	Relief (Watson, 2004)	Habitat type (Polunin and Roberts, 1993)	Habitat (%)		Range of view (m)	Visibility	Position of Cams
			Low/Medium/High	0-5	Sand	Other			
SB_South_10	22,0		High	4	10	90	6=50% >8=50%	Medium	Straight
SB_South_11	23,0		Medium	2	60	40	>8	Medium	Straight
SB_Center_73	23,0		Low	1	80	20	>8	Very good	Straight
SB_Center_74	23,0		Low	1	80	20	>8	Very good	Straight
SB_Center_75	22,0		Medium	2	60	40	>8	Very good	Straight
SB_Center_76	23,0		Medium	2	60	40	>8	Very good	Straight
SB_Center_77	23,0		Medium	2	60	40	>8	Very good	Straight
SB_Center_78	23,0		Low	1	75	25	>8	Very good	Straight

OpCode	Depth (m)	Image	Relief (Watson, 2004)	Habitat type (Polunin and Roberts, 1993)	Habitat (%)		Range of view (m)	Visibility	Position of Cams
			Low/Medium/High	0-5	Sand	Other			
SB_South_114	22,0		Medium	2	60	40	>8	Low	Upwards
SB_South_116	19,0		Medium	2	70	30	>8	Medium	Straight
SB_East_200	25,0		Medium	2	70	30	>8	Very good	Downwards
SB_East_201	24,0		Medium	2	75	25	>8	Very good	Straight
SB_East_202	22,0		Low	1	85	15	>8	Good	Straight
SB_East_204	24,0		Low	1	80	20	>8	Very good	Straight
SB_East_205	26,0		Medium	2	60	20	>8	Good	Upwards
SB_East_206	24,0		Medium	2	70	30	>8	Very good	Straight

OpCode	Depth (m)	Image	Relief (Watson, 2004)	Habitat type (Polunin and Roberts, 1993)	Habitat (%)		Range of view (m)	Visibility	Position of Cams
			Low/Medium/High	0-5	Sand	Other			
SB_East_207	23,0		Medium	3	35	65	>8	Very good	Straight
SB_East_208	24,0		Medium	2	40	60	>8	Very good	Straight
SB_East_209	19,0		Medium	2	50	50	2=40% >8=60%	Very good	Straight
SB_East_210	17,0		Medium	2	40	60	>8	Good	Straight
SB_East_211	17,0		Medium	2	40	60	>8	Good	Straight
SB_East_212	34,0		Medium	2	50	50	>8	Good	Straight
SB_East_213	19,0		Medium	2	40	60	>8	Good	Straight
SB_East_214	20,0		Medium	2	40	60	>8	Good	Straight

OpCode	Depth (m)	Image	Relief (Watson, 2004)	Habitat type (Polunin and Roberts, 1993)	Habitat (%)		Range of view (m)	Visibility	Position of Cams
			Low/Medium/High	0-5	Sand	Other			
SB_Center_79	29,0		Low	1	85	15	>8	Medium	Straight
SB_Center_80	27,0		Medium	2	75	25	>8	Medium	Straight
SB_Center_81	27,0		Medium	2	75	25	>8	Medium	Straight
SB_Center_82	28,0		Low	1	80	20	>8	Medium	Straight
SB_Center_83	28,0		Low	1	95	5	>8	Medium	Straight
SB_Center_92	30,0		Low	0	99	1	>8	Medium	Straight
SB_Center_94	28,0		Low	0	99	1	>8	Medium	Straight
SB_Center_95	29,0		Low	0	98	2	>8	Medium	Straight

OpCode	Depth (m)	Image	Relief (Watson, 2004)	Habitat type (Polunin and Roberts, 1993)	Habitat (%)		Range of view (m)	Visibility	Position of Cams
			Low/Medium/High	0-5	Sand	Other			
SB_Center_96	28,0		Low	0	98	2	>8	Good	Straight
SB_Center_102	40,0		Low	0	95	5	>8	Good	Straight
SB_Center_101	38,0		Low	0	100	0	>8	Medium	Straight
SB_Center_100	39,0		Low	0	99	1	>8	Good	Straight
SB_Center_99	36,0		Low	0	100	0	>8	Good	Straight
SB_Center_98	37,0		Low	1	90	10	>8	Medium	Straight
SB_Center_97	37,0		Low	1	90	10	>8	Good	Straight
SB_North_46	46,0		Low	0	99	1	>8	Good	Straight

OpCode	Depth (m)	Image	Relief (Watson, 2004)	Habitat type (Polunin and Roberts, 1993)	Habitat (%)		Range of view (m)	Visibility	Position of Cams
			Low/Medium/High	0-5	Sand	Other			
SB_North_47	44,0		Low	1	95	5	>8	Medium	Straight
SB_North_48	42,0		Low	0	100	0	>8	Medium	Straight
SB_North_43	45,0		Low	1	90	10	>8	Medium	Straight
SB_North_44	43,0		Low	0	99	1	>8	Medium	Straight
SB_North_45	43,0		Low	0	99	1	>8	Good	Straight
SB_East_215	31,0		Medium	2	70	30	>8	Good	Straight
SB_East_216	28,0		Medium	2	70	30	>8	Good	Straight
SB_East_217	26,0		Medium	2	50	50	>8	Very good	Upwards

OpCode	Depth (m)	Image	Relief (Watson, 2004)	Habitat type (Polunin and Roberts, 1993)	Habitat (%)		Range of view (m)	Visibility	Position of Cams
			Low/Medium/High	0-5	Sand	Other			
SB_East_218	17,0		Medium	2	50	50	>8	Very good	Upwards
SB_East_220	19,0		Medium	2	50	50	>8	Very good	Straight
SB_South_1	26,0		Medium	3	40	60	2=15% >8=85%	Good	Straight
SB_South_2	25,0		Medium	2	50	50	>8	Good	Straight
SB_South_3	26,0		Medium	3	50	50	>8	Good	Downwards
SB_South_4	27,0		Medium	2	70	30	>8	Very good	Straight
SB_South_5	29,0		Medium	2	70	30	>8	Good	Straight
SB_South_6	27,0		Medium	2	60	40	>8	Very good	Straight

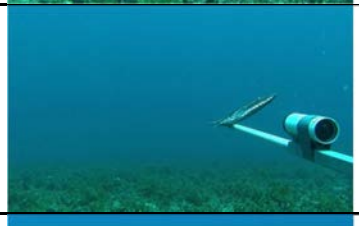
OpCode	Depth (m)	Image	Relief (Watson, 2004)	Habitat type (Polunin and Roberts, 1993)	Habitat (%)		Range of view (m)	Visibility	Position of Cams
			Low/Medium/High	0-5	Sand	Other			
SB_West_19	41,0		Low	0	99	1	>8	Very good	Straight
SB_West_20	43,0		Low	1	80	20	>8	Very good	Upwards
SB_West_21	43,0		Low	1	90	10	>8	Good	Straight
SB_West_22	45,0		Low	1	90	10	>8	Good	Straight
SB_West_23	44,0		Low	1	95	5	>8	Good	Straight
SB_West_24	45,0		Low	1	95	5	>8	Good	Straight
SB_West_25	52,0		Medium	2	40	60	>8	Good	Straight
SB_West_26	44,0		Medium	2	40	60	>8	Medium	Upwards

OpCode	Depth (m)	Image	Relief (Watson, 2004)	Habitat type (Polunin and Roberts, 1993)	Habitat (%)		Range of view (m)	Visibility	Position of Cams
			Low/Medium/High	0-5	Sand	Other			
SB_West_27	45,0		Medium	2	40	60	>8	Good	Downwards
SB_West_28	43,0		Medium	2	40	60	>8	Good	Straight
SB_West_29	44,0		Medium	2	40	60	>8	Good	Straight
SB_West_30	43,0		Medium	2	40	60	>8	Good	Straight
SB_North_55	50,0		Medium	2	40	60	>8	Good	Straight
SB_North_57	46,0		Medium	2	40	60	>8	Good	Straight
SB_North_58	48,0		Medium	2	40	60	>8	Good	Straight
SB_North_59	50,0		Medium	2	40	60	>8	Medium	Straight

OpCode	Depth (m)	Image	Relief (Watson, 2004)	Habitat type (Polunin and Roberts, 1993)	Habitat (%)		Range of view (m)	Visibility	Position of Cams
			Low/Medium/High	0-5	Sand	Other			
SB_North_60	50,0		Medium	2	40	60	>8	Good	Straight
SB_Center_103	38,0		Low	1	85	15	>8	Good	Straight
SB_Center_104	40,0		Low	1	90	10	>8	Good	Straight
SB_Center_105	39,0		Low	1	95	5	>8	Good	Straight
SB_Center_106	40,0		Low	1	95	5	>8	Good	Straight
SB_Center_107	40,0		Low	1	95	5	>8	Good	Straight
SB_Center_108	40,0		Low	1	95	5	>8	Very good	Straight
SB_West_31	50,0		Medium	2	40	60	>8	Very good	Straight

OpCode	Depth (m)	Image	Relief (Watson, 2004)	Habitat type (Polunin and Roberts, 1993)	Habitat (%)		Range of view (m)	Visibility	Position of Cams
			Low/Medium/High	0-5	Sand	Other			
SB_West_33	51,0		Medium	2	40	60	>8	Good	Straight
SB_West_34	52,0		Medium	2	40	60	>8	Good	Straight
SB_West_35	54,0		Medium	2	35	65	>8	Medium	Upwards
SB_North_37	56,0		Low	1	60	40	>8	Good	Straight
SB_North_38	58,0		Low	0	98	2	>8	Good	Straight
SB_North_39	56,0		Low	0	99	1	>8	Good	Straight
SB_North_40	49,0		Medium	2	40	60	>8	Good	Straight
SB_North_41	51,0		Medium	2	35	65	>8	Good	Straight

OpCode	Depth (m)	Image	Relief (Watson, 2004)	Habitat type (Polunin and Roberts, 1993)	Habitat (%)		Range of view (m)	Visibility	Position of Cams
			Low/Medium/High	0-5	Sand	Other			
SB_North_42	49,0		Medium	2	45	55	>8	Good	Straight
C1_1	20		Low	1	60	40	>8	Medium	Downwards
C1_2	21.3		Low	1	80	20	>8	Good	Straight
C1_3	21		Low	1	40	60	>8	Medium	Straight
C1_4	19.2		Low	1	80	20	>8	Medium	Straight
C1_5	21		Low	1	50	50	>8	Good	Straight
C1_6	21		Medium	2	10	90	>8	Good	Straight
C2_1	19		Medium	2	10	90	>8	Good	Straight

OpCode	Depth (m)	Image	Relief (Watson, 2004)	Habitat type (Polunin and Roberts, 1993)	Habitat (%)		Range of view (m)	Visibility	Position of Cams
			Low/Medium/High	0-5	Sand	Other			
C2_2	20		Medium	2	20	80	>8	Good	Downwards
C2_3	19		Medium	2	15	85	>8	Good	Straight
C2_4	19		Medium	2	15	85	>8	Good	Straight
C2_5	19		Medium	2	15	85	>8	Good	Straight
C2_6	19		Medium	2	20	80	>8	Good	Straight
C2_7	19.5		Medium	2	15	85	>8	Good	Straight
C4_1	20.1		Medium	2	25	75	>8	Good	Straight
C4_2	20.7		Medium	2	10	90	>8	Good	Upwards

OpCode	Depth (m)	Image	Relief (Watson, 2004)	Habitat type (Polunin and Roberts, 1993)	Habitat (%)		Range of view (m)	Visibility	Position of Cams
			Low/Medium/High	0-5	Sand	Other			
C4_4	20.7		Medium	2	30	70	>8	Good	Straight
C4_6	20.4		Medium	2	30	70	>8	Good	Straight
C4_7	20.1		Low	1	80	20	>8	Good	Straight
C4_8	20		Low	1	75	25	>8	Good	Straight
C4_10	20		Medium	2	75	25	>8		Straight
C4_11	20		Low	1	90	10	>8	Good	Straight
C4_12	20		Low	1	90	10	>8	Medium	Straight
C4_14	21		Medium	2	25	75	>8	Good	Straight

OpCode	Depth (m)	Image	Relief (Watson, 2004)	Habitat type (Polunin and Roberts, 1993)	Habitat (%)		Range of view (m)	Visibility	Position of Cams
			Low/Medium/High	0-5	Sand	Other			
E1_1	16		Medium	2	30	70	>8	Very good	Straight
E1_2	14		Medium	3	20	60	>8	Very good	Straight
E1_4	17		Medium	3	20	80	>8	Good	Straight
E1_5	13		Medium	2	20	80	>8	Good	Straight
E1_8	21		Medium	3	30	70	3=30% >8=70%	Good	Straight
E1_9	20		Medium	3	20	80	>8	Good	Upwards
E1_11	20		Medium	2	20	80	>8	Good	Straight
E1_12	12.5		Low	1	80	20	>8	Good	Straight

OpCode	Depth (m)	Image	Relief (Watson, 2004)	Habitat type (Polunin and Roberts, 1993)	Habitat (%)		Range of view (m)	Visibility	Position of Cams
			Low/Medium/High	0-5	Sand	Other			
E2_2	13		Medium	2	10	90	>8	Good	Straight
E2_3	13		Medium	2	10	90	>8	Good	Straight
E2_5	13		Medium	2	30	70	>8	Good	Downwards
E2_6	13		Medium	2	20	80	>8	Good	Straight
E2_7	13		Medium	2	20	80	>8	Good	Straight
E2_8	15		Low	1	95	5	>8	Good	Straight
E2_9	12		Medium	2	10	90	>8	Good	Straight
E2_10	19		Low	1	95	5	>8	Good	Straight

OpCode	Depth (m)	Image	Relief (Watson, 2004)	Habitat type (Polunin and Roberts, 1993)	Habitat (%)		Range of view (m)	Visibility	Position of Cams
			Low/Medium/High	0-5	Sand	Other			
E3_4	18		Medium	3	50	50	>8	Good	Straight
E3_5	13		Medium	2	50	50	>8	Good	Straight
E3_6	13		Medium	3	60	40	6=80% >8=20%	Very good	Downwards
E3_7	13		Medium	3	50	50	>8	Good	Upwards
E3_8	19.1		Medium	3	50	50	>8	Good	Upwards
E3_10	20.7		Medium	3	60	40	>8	Good	Straight
E4_1	17.7		Medium	3	50	50	>8	Good	Straight
E4_2	18		Medium	3	40	60	>8	Good	Straight

OpCode	Depth (m)	Image	Relief (Watson, 2004)	Habitat type (Polunin and Roberts, 1993)	Habitat (%)		Range of view (m)	Visibility	Position of Cams
			Low/Medium/High	0-5	Sand	Other			
E4_3	18.3		High	4	20	80	4=30% >8=70%	Good	Straight
E4_4	25		High	4	30	70	1=20% >8=80%	Good	Downwards
E4_6	22		Medium	3	25	75	>8	Good	Upwards
E4_6_2	15		High	4	10	90	4=50% >8=50%	Good	Straight
E4_7	19		Medium	3	20	80	>8	Good	Upwards

Appendix II: Habitat characteristics

OpCode	Depth	Site	Fisheries zone	Habitat type	Relief (Polunin, 1993)	Relief (Watson, 2005)
Center_1_1	15	Center	2	Sand	1	Low
Center_1_2	25	Center	2	Sand	1	Low
Center_1_3	25	Center	2	Sand	1	Low
Center_1_5	15	Center	2	Sand	1	Low
Center_100	40	Center	1	Sand	0	Low
Center_101	40	Center	1	Sand	0	Low
Center_102	40	Center	1	Sand	0	Low
Center_103	40	Center	1	Sand	1	Low
Center_104	40	Center	1	Sand	1	Low
Center_105	40	Center	1	Sand	1	Low
Center_106	40	Center	1	Sand	1	Low
Center_107	40	Center	1	Sand	1	Low
Center_108	40	Center	1	Sand	1	Low
Center_2_3	15	Center	2	Sand	2	Medium
Center_2_4	15	Center	2	Sand	2	Medium
Center_2_5	15	Center	2	Sand	2	Medium
Center_2_6	15	Center	2	Sand	2	Medium
Center_2_7	15	Center	2	Sand	2	Medium
Center_4_1	15	Center	1	Sand	2	Medium
Center_4_10	15	Center	1	Sand	2	Medium
Center_4_11	15	Center	1	Sand	1	Low
Center_4_12	15	Center	1	Sand	1	Low
Center_4_14	25	Center	1	Sand	2	Medium
Center_4_2	15	Center	1	Sand	2	Medium
Center_4_4	15	Center	1	Sand	2	Medium
Center_4_6	15	Center	1	Sand	2	Medium
Center_4_7	15	Center	1	Sand	1	Low
Center_4_8	15	Center	1	Sand	1	Low
Center_73	25	Center	1	Sand	1	Low
Center_74	25	Center	1	Sand	1	Low
Center_75	25	Center	1	Sand	2	Medium
Center_76	25	Center	1	Sand	2	Medium
Center_77	25	Center	1	Sand	2	Medium
Center_78	25	Center	1	Sand	1	Low
Center_79	25	Center	2	Sand	1	Low
Center_80	25	Center	2	Sand	2	Medium
Center_81	25	Center	2	Sand	2	Medium
Center_82	25	Center	2	Sand	1	Low
Center_83	25	Center	2	Sand	1	Low
Center_92	25	Center	1	Sand	0	Low
Center_94	25	Center	1	Sand	0	Low
Center_95	25	Center	1	Sand	0	Low
Center_96	25	Center	1	Sand	0	Low
Center_97	40	Center	1	Sand	1	Low
Center_98	40	Center	1	Sand	1	Low
Center_99	40	Center	1	Sand	0	Low
East_1_1	15	Center	2	Reef	2	Medium
East_1_11	15	Center	2	Reef	2	Medium
East_1_12	15	Center	2	Reef	1	Low
East_1_2	15	Center	2	Reef	3	Medium
East_1_4	15	Center	2	Reef	3	Medium
East_1_5	15	Center	2	Reef	2	Medium
East_1_8	25	Center	2	Reef	3	Medium
East_1_9	15	Center	2	Reef	3	Medium
East_114	25	South	1	Reef	2	Medium
East_116	15	South	1	Reef	2	Medium
East_132	15	East	2	Reef	3	Medium
East_133	25	East	2	Reef	4	High
East_138	15	East	2	Reef	3	Medium
East_139	15	East	2	Reef	3	Medium
East_2_10	15	Center	2	Sand	1	Low
East_2_2	15	Center	2	Sand	2	Medium
East_2_3	15	Center	2	Reef	2	Medium
East_2_4	15	Center	2	Reef	2	Medium
East_2_5	15	Center	2	Reef	2	Medium
East_2_6	15	Center	2	Sand	2	Medium

OpCode	Depth	Site	Fisheries zone	Habitat type	Relief (Polunin, 1993)	Relief (Watson, 2005)
East_2_7	15	Center	2	Sand	2	Medium
East_2_8	15	Center	2	Sand	1	Low
East_2_9	15	Center	2	Sand	2	Medium
East_200	25	South	1	Sand	2	Medium
East_201	25	South	1	Sand	2	Medium
East_202	25	South	1	Sand	1	Low
East_204	25	South	1	Sand	1	Low
East_205	25	South	1	Sand	2	Medium
East_206	25	South	1	Reef	2	Medium
East_207	25	South	1	Reef	3	Medium
East_208	25	South	1	Reef	2	Medium
East_209	15	East	2	Reef	2	Medium
East_210	15	East	2	Reef	2	Medium
East_211	15	East	2	Reef	2	Medium
East_212	40	East	2	Reef	2	Medium
East_213	15	East	2	Reef	2	Medium
East_214	15	East	2	Reef	2	Medium
East_215	40	East	2	Reef	2	Medium
East_216	25	East	2	Reef	2	Medium
East_217	25	East	2	Reef	2	Medium
East_218	15	East	2	Reef	2	Medium
East_220	15	East	2	Reef	2	Medium
East_3_10	15	East	2	Reef	3	Medium
East_3_4	15	East	2	Reef	3	Medium
East_3_5	15	East	2	Reef	2	Medium
East_3_6	15	East	2	Reef	3	Medium
East_3_7	15	East	2	Reef	3	Medium
East_3_8	15	East	2	Reef	3	Medium
East_4_1	15	East	2	Reef	3	Medium
East_4_3	15	East	2	Reef	4	High
East_4_4	25	East	2	Reef	4	High
East_4_6	25	East	2	Reef	3	Medium
East_4_7	15	East	2	Reef	3	Medium
East_67	15	East	2	Reef	2	Medium
East_68	15	East	2	Reef	2	Medium
East_69	15	East	2	Reef	3	Medium
East_71	15	East	2	Reef	3	Medium
East_72	15	East	2	Reef	3	Medium
North_29	25	North	0	Sand	2	Medium
North_30	25	North	0	Sand	2	Medium
North_31	25	North	0	Sand	1	Low
North_32	25	North	0	Reef	2	Medium
North_33	15	North	0	Reef	2	Medium
North_34	40	North	0	Sand	1	Low
North_35	40	North	0	Reef	2	Medium
North_36	25	North	0	Reef	2	Medium
North_37	40	North	0	Sand	1	Low
North_38	40	North	0	Sand	0	Low
North_39	40	North	0	Sand	0	Low
North_40	40	North	0	Reef	2	Medium
North_41	40	North	0	Reef	2	Medium
North_42	40	North	0	Reef	2	Medium
North_44	40	North	1	Sand	0	Low
North_45	40	North	1	Sand	0	Low
North_46	40	North	1	Sand	0	Low
North_47	40	North	1	Sand	1	Low
North_48	40	North	1	Sand	0	Low
North_55	40	North	2	Reef	2	Medium
North_57	40	North	2	Reef	2	Medium
North_58	40	North	2	Reef	2	Medium
North_59	40	North	2	Reef	2	Medium
North_60	40	North	2	Reef	2	Medium
South_1	25	South	0	Reef	3	Medium
South_2	25	South	0	Reef	4	High
South_3	25	South	0	Reef	2	Medium
South_4	15	South	0	Reef	2	Medium
South_5	25	South	0	Reef	1	Low
South_6	25	South	0	Reef	4	High

OpCode	Depth	Site	Fisheries zone	Habitat type	Relief (Polunin, 1993)	Relief (Watson, 2005)
South_7	15	South	1	Reef	2	Medium
South_8	15	South	1	Reef	2	Medium
South_9	25	South	1	Reef	2	Medium
South_10	25	South	1	Reef	3	Medium
South_11	25	South	1	Sand	2	Medium
South_13	25	South	1	Reef	2	Medium
South_14	25	South	1	Reef	2	Medium
South_15	15	South	1	Reef	3	Medium
South_17	25	South	1	Reef	3	Medium
South_18	15	South	1	Reef	3	Medium
South_61	15	South	1	Reef	3	Medium
South_62	15	South	1	Reef	2	Medium
South_63	15	South	1	Reef	3	Medium
South_64	25	South	1	Reef	2	Medium
South_65	25	South	1	Reef	2	Medium
South_66	25	South	1	Reef	4	High
West_19	40	West	0	Sand	0	Low
West_20	40	West	0	Sand	1	Low
West_21	40	West	0	Sand	1	Low
West_22	40	West	0	Sand	1	Low
West_23	40	West	0	Sand	1	Low
West_25	40	West	0	Reef	2	Medium
West_26	40	West	0	Reef	2	Medium
West_27	40	West	0	Reef	2	Medium
West_28	40	West	0	Reef	2	Medium
West_29	40	West	0	Reef	2	Medium
West_30	40	West	0	Reef	2	Medium
West_31	40	West	0	Reef	2	Medium
West_33	40	West	0	Reef	2	Medium
West_34	40	West	0	Reef	2	Medium
West_35	40	West	0	Reef	2	Medium

Appendix III: Sample location information

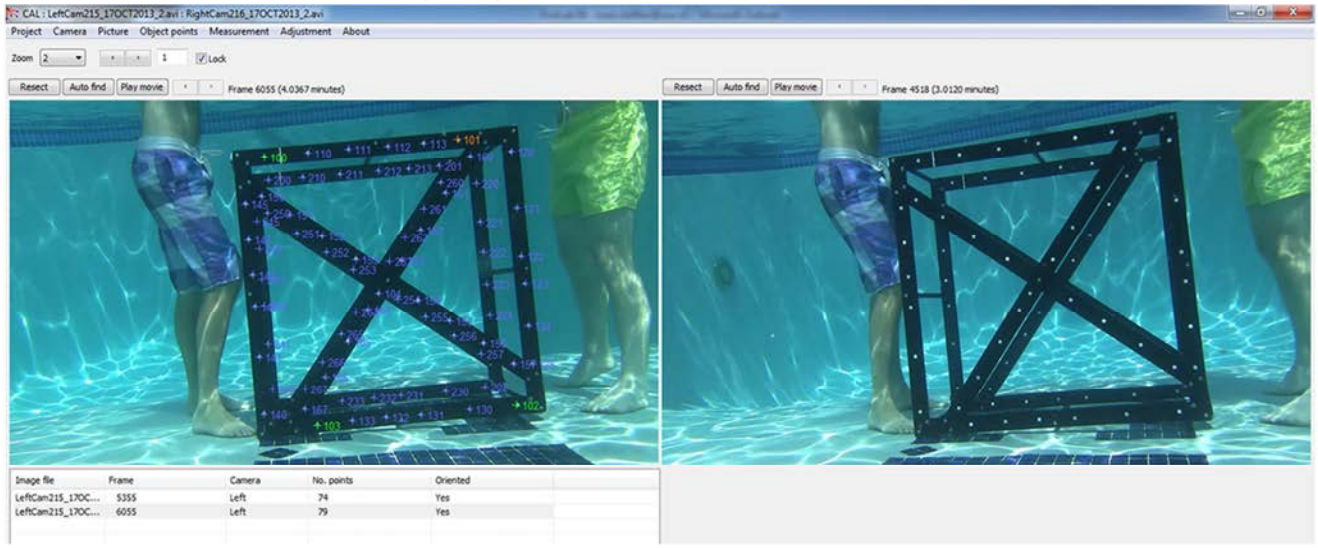
Data OpCode	Date Deployed	Depth (m)	Time in	Time out	Latitude	Longitude
	mm/dd/yy		hh:mm	hh:mm	Edd mm.mmm	Sdd mm.mmm
SB_North_36	10-19-13	26.0	11:56	12:56	63 18.237	17 33.984
SB_North_35	10-19-13	34.0	12:06	13:06	63 18.340	17 34.273
SB_North_34	10-19-13	32.0	12:20	13:20	63 18.787	17 34.241
SB_North_01	10-19-13	22.0	13:04	14:04	63 18.727	17 34.033
SB_North_02	10-19-13	33.0	13:30	14:30	63 18.734	17 34.040
SB_North_33	10-19-13	18.0	13:43	14:43	63 19.279	17 33.980
SB_North_32	10-20-13	29.0	11:30	12:30	63 19.514	17 33.714
SB_North_31	10-20-13	25.0	11:37	12:37	63 19.598	17 33.432
SB_North_30	10-20-13	25.0	11:45	12:45	63 19.697	17 33.139
SB_North_03	10-20-13	23.0	12:40	13:40	63 19.786	17 32.846
SB_North_04	10-20-13	24.0	12:50	13:50	63 19.780	17 32.567
SB_North_29	10-20-13	23.0	13:00	14:00	63 19.859	17 32.248
SB_East_138	10-22-13	17.0	14:23	15:23	63 17.132	17 33.266
SB_East_139	10-22-13	17.0	14:30	15:30	63 17.390	17 33.402
SB_East_140	10-22-13	17.0	14:40	15:40	63 17.115	17 33.031
SB_South_13	10-31-13	20.0	11:45	12:45	63,354,112	17,264,162
SB_South_14	10-31-13	25.0	11:58	12:58	63,359,271	17,262,054
SB_South_15	10-31-13	25.0	12:10	13:10	63,365,136	17,263,152
SB_South_16	10-31-13	24.0	13:00	14:00	63,354,942	17,269,389
SB_South_17	10-31-13	17.0	13:13	14:13	63,360,387	17,266,928
SB_South_18	10-31-13	17.0	13:24	14:24	63,366,226	17,268,002
SB_East_63	10-31-13	15.0	15:18	16:18	63,302,771	17,280,395
SB_East_62	10-31-13	24.0	15:24	16:24	63,306,643	17,276,849
SB_East_61	10-31-13	18.0	15:30	16:30	63,311,617	17,275,514
SB_East_66	11-1-13	20.0	10:56	11:56	63,304,878	17,285,102
SB_East_65	11-1-13	20.0	11:01	12:01	63,310,081	17,283,956
SB_East_64	11-1-13	18.0	11:08	12:08	63,315,489	17,283,040
SB_East_67	11-1-13	18.0	13:15	14:15	63,258,215	17,336,498
SB_East_68	11-1-13	15.0	13:21	14:21	63,256,530	17,340,750
SB_East_69	11-1-13	14.0	13:26	14:26	63,257,310	17,345,640
SB_East_70	11-1-13	18.0	14:41	15:41	63,263,768	17,336,577
SB_East_71	11-1-13	17.0	14:54	15:54	63,261,961	17,340,805
SB_East_72	11-1-13	17.0	15:05	16:05	63,262,803	17,346,222
SB_East_132	11-6-13	19.0	13:37	14:37	-6,322,386.00	1,745,939.00
SB_East_133	11-6-13	25.0	13:47	14:47	-6,322,254.00	1,746,437.00
SB_East_134	11-6-13	25.0	14:04	15:04	-6,322,467.00	1,746,955.00
SB_South_7	11-7-13	28.0	11:40	12:40	-6,346,919.00	1,724,071.00
SB_South_8	11-7-13	25.0	11:49	12:49	-6,346,414.00	1,723,912.00
SB_South_9	11-7-13	22.0	12:00	13:00	-6,345,978.00	1,723,704.00
SB_South_10	11-7-13	22.0	12:45	13:45	-6,346,836.00	1,724,555.00
SB_South_11	11-7-13	23.0	12:57	13:57	-6,346,301.00	1,724,398.00
SB_South_12	11-7-13	21.0	13:09	14:09	-6,345,824.00	1,724,166.00
SB_Center_73	11-6-13	23.0	10:33	11:33	-6,333,777.00	1,740,406.00
SB_Center_74	11-6-13	23.0	10:45	11:45	-6,333,274.00	1,740,086.00
SB_Center_75	11-6-13	22.0	10:50	11:50	-6,332,880.00	1,739,803.00
SB_Center_76	11-6-13	23.0	11:34	12:34	-6,333,988.00	1,739,954.00
SB_Center_77	11-6-13	23.0	11:48	12:48	-6,333,562.00	1,739,626.00
SB_Center_78	11-6-13	23.0	12:00	13:00	-6,333,135.00	1,739,313.00
SB_South_114	11-7-13	22.0	14:46	15:46	-6,342,573.00	1,725,841.00
SB_South_115	11-7-13	18.0	14:53	15:53	-6,342,045.00	1,725,941.00
SB_South_116	11-7-13	19.0	15:07	16:07	-6,341,524.00	1,726,006.00
SB_East_200	12-13-13	25.0	11:35	12:35	-6,328,240.00	1,727,411.00
SB_East_201	12-13-13	24.0	11:43	12:43	-6,328,389.00	1,727,910.00
SB_East_202	12-13-13	22.0	11:50	12:50	-6,328,472.00	1,728,391.00
SB_East_203	12-13-13	20.0	13:17	14:17	-6,328,667.00	1,728,941.00
SB_East_204	12-13-13	24.0	13:26	14:26	-6,328,814.00	1,729,449.00

Data OpCode	Date Deployed	Depth (m)	Time in	Time out	Latitude	Longitude
	mm/dd/yy		hh:mm	hh:mm	Edd mm.mmm	Sdd mm.mmm
SB_East_205	12-13-13	26.0	13:32	14:32	-6,328,896.00	1,729,976.00
SB_East_206	12-13-13	24.0	14:52	15:52	-6,329,044.00	1,730,456.00
SB_East_207	12-13-13	23.0	14:59	15:59	-6,329,143.00	1,730,930.00
SB_East_208	12-13-13	24.0	15:07	16:07	-6,329,240.00	1,731,420.00
SB_East_209	12-18-13	19.0	12:00	13:00	-6,330,509.00	1,755,744.00
SB_East_210	12-18-13	17.0	12:13	13:13	-6,330,148.00	1,755,688.00
SB_East_211	12-18-13	17.0	12:31	13:31	-6,329,073.00	1,755,578.00
SB_East_212	12-18-13	34.0	14:10	15:10	-6,329,223.00	1,756,366.00
SB_East_213	12-18-13	19.0	14:20	15:20	-6,329,761.00	1,756,274.00
SB_East_214	12-18-13	20.0	14:29	15:29	-6,330,313.00	1,756,162.00
SB_Center_79	12-29-13	29.0	10:33	11:33	-6,343,989.00	1,749,206.00
SB_Center_80	12-29-13	27.0	10:40	11:40	-6,344,370.00	1,748,872.00
SB_Center_81	12-29-13	27.0	10:48	11:48	-6,344,751.00	1,748,615.00
SB_Center_82	12-29-13	28.0	11:59	12:59	-6,345,169.00	1,748,094.00
SB_Center_83	12-29-13	28.0	12:05	13:05	-6,345,559.00	1,747,778.00
SB_Center_84	12-29-13	28.0	12:13	13:13	-6,346,029.00	1,747,482.00
SB_Center_91	12-29-13	31.0	14:36	15:36	-6,353,273.00	1,736,945.00
SB_Center_92	12-29-13	30.0	14:44	15:44	-6,353,502.00	1,736,503.00
SB_Center_93	12-29-13	29.0	14:52	15:52	-6,353,737.00	1,736,085.00
SB_Center_94	12-29-13	28.0	15:59	16:59	-6,353,862.00	1,735,589.00
SB_Center_95	12-29-13	29.0	16:05	17:05	-6,354,058.00	1,735,187.00
SB_Center_96	12-29-13	28.0	16:10	17:10	-6,354,321.00	1,734,766.00
SB_Center_102	1-3-14	40.0	10:12	11:12	-6,357,638.00	1,742,254.00
SB_Center_101	1-3-14	38.0	10:23	11:23	-6,357,221.00	1,742,435.00
SB_Center_100	1-3-14	39.0	10:31	11:31	-6,356,763.00	1,742,548.00
SB_Center_99	1-3-14	36.0	11:30	12:30	-6,356,337.00	1,742,719.00
SB_Center_98	1-3-14	37.0	11:38	12:38	-6,355,935.00	1,742,843.00
SB_Center_97	1-3-14	37.0	11:45	12:45	-6,355,466.00	1,742,950.00
SB_North_46	1-3-14	46.0	13:05	14:05	-6,358,791.00	1,745,574.00
SB_North_47	1-3-14	44.0	13:13	14:13	-6,358,357.00	1,745,733.00
SB_North_48	1-3-14	42.0	13:18	14:18	-6,357,903.00	1,745,856.00
SB_North_43	1-3-14	45.0	14:27	15:27	-6,358,087.00	1,746,420.00
SB_North_44	1-3-14	43.0	14:33	15:33	-6,358,630.00	1,746,303.00
SB_North_45	1-3-14	43.0	14:38	15:38	-6,359,181.00	1,746,244.00
SB_East_215	1-14-04	31.0	10:00	11:00	-6,330,379.00	1,756,873.00
SB_East_216	1-14-14	28.0	10:12	11:12	-6,330,049.00	1,756,508.00
SB_East_217	1-14-24	26.0	10:19	11:19	-6,329,650.00	1,756,274.00
SB_East_218	1-14-14	17.0	11:17	12:17	-6,329,810.00	1,755,763.00
SB_East_219	1-14-04	17.0	11:23	12:23	-6,330,354.00	1,755,774.00
SB_East_220	1-14-14	19.0	11:28	12:28	-6,330,907.00	1,755,753.00
SB_South_1	1-17-14	26.0	9:25	10:25	-6,362,515.00	1,720,765.00
SB_South_2	1-17-14	25.0	9:33	10:33	-6,363,055.00	1,720,699.00
SB_South_3	1-17-14	26.0	9:39	10:39	-6,363,599.00	1,720,611.00
SB_South_4	1-17-14	27.0	10:39	11:39	-6,364,166.00	1,720,612.00
SB_South_5	1-17-14	29.0	10:44	11:44	-6,364,713.00	1,720,574.00
SB_South_6	1-17-14	27.0	10:50	11:50	-6,365,294.00	1,720,565.00
SB_West_19	1-17-14	41.0	12:09	13:09	-6,370,610.00	1,723,250.00
SB_West_20	1-17-14	43.0	12:14	13:14	-6,370,719.00	1,723,720.00
SB_West_21	1-17-14	43.0	12:19	13:19	-6,370,869.00	1,724,191.00
SB_West_22	1-17-14	45.0	13:22	14:22	-6,371,104.00	1,724,652.00
SB_West_23	1-17-14	44.0	13:28	14:28	-6,371,222.00	1,725,137.00
SB_West_24	1-17-14	45.0	13:33	14:33	-6,371,316.00	1,725,615.00
SB_West_25	1-17-14	52.0	15:06	16:06	-6,375,635.00	1,730,563.00
SB_West_26	1-17-14	44.0	15:11	16:11	-6,375,667.00	1,731,064.00
SB_West_27	1-17-14	45.0	15:16	16:16	-6,375,746.00	1,731,561.00
SB_West_28	1-17-14	43.0	16:23	17:23	-6,375,936.00	1,732,043.00
SB_West_29	1-17-14	44.0	16:28	17:28	-6,376,009.00	1,732,537.00
SB_West_30	1-17-14	43.0	16:33	17:33	-6,376,105.00	1,733,030.00

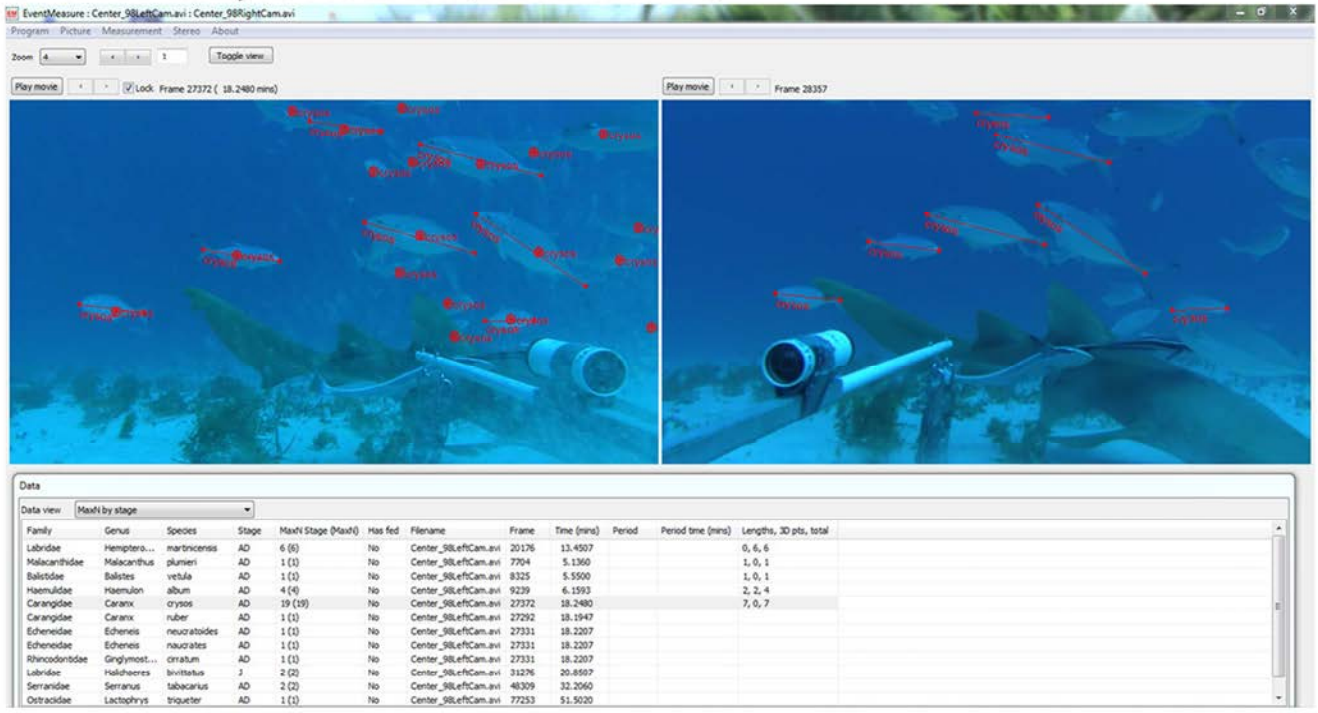
Data OpCode	Date Deployed	Depth (m)	Time in	Time out	Latitude	Longitude
	mm/dd/yy		hh:mm	hh:mm	Edd mm.mmm	Sdd mm.mmm
SB_North_55	1-20-14	50.0	13:21	14:21	-6,343,783.00	1,758,995.00
SB_North_56	1-20-14	48.0	13:31	14:31	-6,343,311.00	1,758,954.00
SB_North_57	1-20-14	46.0	13:37	14:37	-6,342,859.00	1,758,949.00
SB_North_58	1-20-14	48.0	14:46	15:46	-6,342,391.00	1,758,993.00
SB_North_59	1-20-14	50.0	14:51	15:51	-6,341,904.00	1,759,008.00
SB_North_60	1-20-14	50.0	14:55	15:55	-6,341,418.00	1,759,038.00
SB_Center_103	1-21-14	38.0	8:46	9:46	-6,365,360.00	1,731,837.00
SB_Center_104	1-21-14	40.0	8:53	9:53	-6,365,572.00	1,732,299.00
SB_Center_105	1-21-14	39.0	8:59	9:59	-6,365,709.00	1,732,766.00
SB_Center_106	1-21-14	40.0	9:59	10:59	-6,365,909.00	1,733,238.00
SB_Center_107	1-21-14	40.0	10:05	11:05	-6,366,084.00	1,733,700.00
SB_Center_108	1-21-14	40.0	10:10	11:10	-6,366,285.00	1,734,219.00
SB_West_31	1-21-14	50.0	12:00	13:00	-6,380,929.00	1,738,569.00
SB_West_32	1-21-14	51.0	12:06	13:06	-6,380,682.00	1,738,961.00
SB_West_33	1-21-14	51.0	12:11	13:11	-6,380,496.00	1,739,384.00
SB_West_34	1-21-14	52.0	13:13	14:13	-6,380,342.00	1,739,811.00
SB_West_35	1-21-14	54.0	13:19	14:19	-6,380,159.00	1,740,263.00
SB_West_36	1-21-14	55.0	13:25	14:25	-6,379,960.00	1,740,707.00
SB_North_37	1-21-14	56.0	15:38	16:38	-6,370,806.00	1,742,531.00
SB_North_38	1-21-14	58.0	15:44	16:44	-6,370,323.00	1,742,582.00
SB_North_39	1-21-14	56.0	15:50	16:50	-6,369,845.00	1,742,573.00
SB_North_40	1-21-14	49.0	16:50	17:50	-6,369,389.00	1,742,756.00
SB_North_41	1-21-14	51.0	16:54	17:54	-6,368,895.00	1,742,810.00
SB_North_42	1-21-14	49.0	17:00	18:00	-6,368,464.00	1,742,875.00

Appendix IV: Data analysis screenshots

A Calibration software (CAL)



B Video analysis software (EventMeasure)



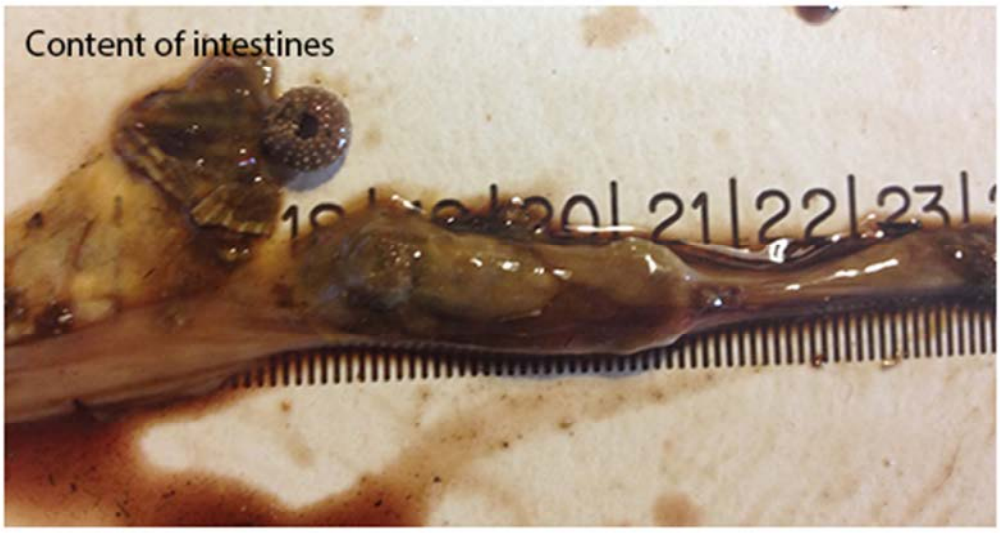
Appendix V: Fish species table

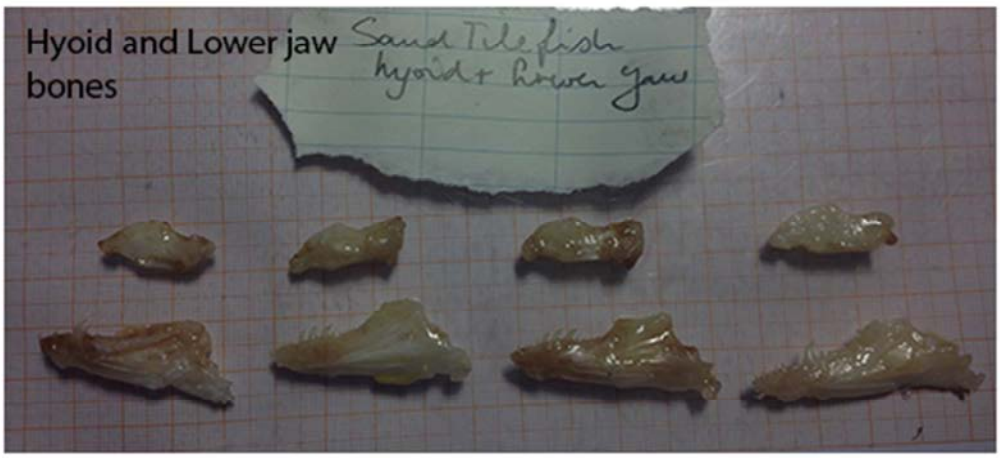
Scientific name	Common name	Trophic level	Mean Depth (m)	Abundant Stage (Ad/Juv)	MaxN in 1 frame	Total number analyzed	Maximum length (mm)	Maximum weight (g)	Sample length (mm) Mean +/- SD	Mean sample length as % of maximum
Aulostomus maculatus	Atlantic trumpetfish	4.3	19	A	2	45	580	446	236 ± 0	41
Cheatodon striatus	banded butterflyfish	3.2	24	A	4	116	235	424	107 ± 6	46
Sphoeroides spengleri	bandtail puffer	3.2	26	A	5	49	134	49	80 ± 4	60
Caranx ruber	bar jack	4.4	23	A	32	323	623	3748	235 ± 16	38
Hypoplectrus puella	barred hamlet	3.7	22	A	1	3	114	NA	38 ± 0	33
Stegastes leucostictus	beaugregory	3.1	52	A	5	5	52	3	48 ± 5	93
Kyphosus sectatrix-incisor	bermuda-yellow chub	2	20	A	53	77	492	NA	393 ± 55	80
Stegastes partitus	bicolor damselfish	2	25	A	39	725	521	3718	27 ± 4	5
Melichthys niger	black durgeon	2.4	20	A	11	168	372	1125	220 ± 22	59
Caranx lugubris	black jack	4.5	29	A	3	11	636	3371	360 ± 3	57
Anisotremus surimensis	black margate	3.3	41	A	1	1	458	2269	458 ± 0	100
Halichoeres poeyi	blackear wrasse	3.4	20	A	4	23	139	37	62 ± 3	44
Lutjanus buccanella	blackfin snapper	3.9	48	J	3	4	285	355	196 ± 23	69
Carcharhinus limbatus	blacktip shark	4.2	16	A	1	3	1473	25333	491 ± 0	33
Chromis cyanea	blue chromis	3.1	26	A	33	202	209	119	42 ± 9	20
Caranx crysos	blue runner	4.4	34	A	49	254	615	2703	330 ± 14	54
Acanthurus coeruleus	blue tang	2	19	A	5	108	314	846	143 ± 7	46
Thalassoma bifasciatum	bluehead wrasse	3.3	20	J	37	849	367	475	45 ± 6	12
Fistularia tabacaria	bluespotted cornetfish	3.5	30	A	1	4	1343	NA	798 ± 0	59
Haemulon sciurus	bluestriped grunt	3.4	14	A	3	4	264	323	250 ± 12	95
Chromis multilineata	brown chromis	3	18	A	4	9	63	4	28 ± 2	44
Heteroconger halis	brown garden eel	3.1	48	A	48	141	133	3	10 ± 4	8
Hypoplectrus unicolor	butter hamlet	4	46	A	1	1	38	1	38 ± 0	100
Scomberomorus regalis	cero	4.5	40	A	1	7	1113	16186	584 ± 0	52
Serranus tortugarum	chalk bass	3.1	47	A	20	129	138	36	52 ± 11	38
Syacium micrurum	channel flounder	3.3	13	A	1	1	NA	NA	NA	NA
Centropyge argi	cherubfish	2	49	A	5	19	74	10	45 ± 3	61
Cephalopholis fulva	coney	4.1	24	A	10	349	339	681	176 ± 23	52
Haemulon melanurum	cottonwick	2.2	22	A	52	256	372	992	206 ± 13	55
Clepticus parrae	creole wrasse	3.3	20	A	48	107	198	97	57 ± 14	29
Paranthias furcifer	creolefish	3.1	22	A	80	112	257	264	96 ± 7	37
Acanthurus chirurgus	doctorfish	2	17	A	15	80	242	224	142 ± 10	59
Lutjanus jocu	dog snapper	4.3	28	A	1	2	277	375	139 ± 0	50
Gramma loreto	fairy basslet	3.3	40	A	1	3	52	2	25 ± 0	48
Cheatodon capistratus	foureye butterflyfish	3	21	A	4	37	128	84	78 ± 6	61
Pomacanthus paru	french angelfish	2.8	27	A	3	47	477	3132	241 ± 15	51
Haemulon flavolineatum	french grunt	3.3	20	A	2	5	205	136	68 ± 0	33
Manocanthus ciliatus	fringed filefish	2.7	23	A	1	1	43	1	43 ± 0	100
Priacanthus cruentatus	glasseye snapper	3.8	14	A	1	1	NA	NA	NA	NA
Gymnothorax miliaris	goldentail moray	3.9	25	A	1	1	NA	NA	NA	NA
Lutjanus griseus	gray snapper	4.3	20	A	1	1	255	224	255 ± 0	100
Cephalopholis cruentata	graysby	4.2	22	A	3	3	NA	NA	NA	NA
Sphyrae barracuda	great barracuda	4.5	27	A	7	98	1174	12196	736 ± 6	63
Gymnothorax funebris	green moray	4	21	A	1	4	NA	NA	NA	NA
Hemipteronotus splendens	green razorfish	3.1	21	A	1	1	NA	NA	NA	NA
Pomacanthus arcuatus	grey angelfish	2.9	31	A	2	7	394	1767	310 ± 26	79
Sphyrae guachancho	guaguanche	3.9	13	A	1	1	NA	NA	NA	NA
Serranus tigrinus	harlequin bass	3.7	33	A	2	11	127	33	66 ± 0	52
Equetus acumitus	highhat	3.6	49	A	8	8	87	9	75 ± 11	86
Caranx latus	horse-eye jack	4.4	19	A	2	2	511	2692	479 ± 46	94
Calamus bajodo	jolthead porgy	3.2	38	A	2	3	463	2052	381 ± 12	82
Playbelone argalus	keeltail needlefish	4.5	13	A	1	1	NA	NA	NA	NA
Paradiplogrammus bairdi	lancer dragonet	3.3	46	A	1	1	NA	NA	NA	NA
Lutjanus sygris	lane snapper	3.8	29	A	28	40	293	331	227 ± 17	78
Serranus baldwini	lantern bass	4.1	21	A	1	1	58	3	58 ± 0	100
Pterois volitans	lionfish	4.5	28	A	1	1	164	62	164 ± 0	100
Cheatodon aculeatus	longsnout butterflyfish	3.2	46	A	1	1	53	4	53 ± 0	100
Holocentrus rufus	longspine squirrelfish	3.5	16	A	3	20	261	156	104 ± 3	40
Decapterus macarellus	mackerel scad	3.4	26	A	70	188	289	321	211 ± 28	73
Lutjanus mahogoni	mahogany snapper	4.5	36	A	17	18	271	339	224 ± 19	83
Manta birostris	manta	3.5	50	A	1	1	NA	NA	NA	NA
Conger triporiceps	manytooth conger	4	14	A	1	1	NA	NA	NA	NA
Ginglymostoma cirratum	nurse shark	3.8	22	A	3	40	2179	81016	1259 ± 63	58
Acanthurus bahianus	ocean surgeonfish	2	22	A	27	430	327	635	129 ± 22	39
Canthidermis sufflamen	ocean triggerfish	3.2	31	A	15	20	314	768	132 ± 12	42

Scientific name	Common name	Trophic level	Mean Depth (m)	Abundant Stage (Ad/Juv)	MaxN in 1 frame	Total number analyzed	Maximum length (mm)	Maximum weight (g)	Sample length (mm) Mean +/- SD	Mean sample length as % of maximum
Aluterus schoepfi	orange filefish	2	18	A	1	5	409	1194	161 ± 0	39
Bothus lutus	peacock flounder	4.5	30	A	2	12	208	156	53 ± 0	25
Trachinotus falcatus	permit	3.2	23	A	2	3	520	3539	485 ± 10	93
Calamus pentula	pluma	3.5	49	A	2	2	301	451	236 ± 91	79
Diodon hystrix	porcupinefish	3.4	24	A	1	4	660	11644	345 ± 0	52
Scarus taeniopterus	princess parrotfish	2	19	J	17	380	354	596	194 ± 12	55
Halichoeres radiatus	puddingwife	3.3	21	A	2	12	298	395	159 ± 5	53
Holacanthus ciliaris	queen angelfish	3	19	A	2	12	359	1077	254 ± 3	71
Scarus vetula	queen parrotfish	2	22	J	6	15	385	658	292 ± 23	76
Balistes vetula	queen triggerfish	3.4	26	A	15	298	594	5085	276 ± 22	46
Elagatis bipinnulata	rainbow runner	3.6	22	A	15	17	713	3183	529 ± 8	74
Epinephelus guttatus	red hind	3.9	22	A	10	167	486	1970	220 ± 32	45
Sparisoma aurofretum	redband parrotfish	2	21	J	8	131	396	1228	159 ± 6	40
Sparisoma rubripinne	redfin parrotfish	2	22	J	12	25	365	947	230 ± 19	63
Sparisoma chrysopterum	redtail parrotfish	2	20	A	2	11	402	1216	255 ± 3	63
Cheatodon sedentarius	reef butterflyfish	2.8	52	A	2	2	101	31	97 ± 5	96
Carcharhinus perezii	reef shark	4.5	20	A	3	36	2085	73078	647 ± 20	31
Holacanthus tricolor	rock beauty	3	20	A	3	67	311	802	114 ± 7	37
Epinephelus adscensionsis	rock hind	3.5	18	A	2	6	186	155	77 ± 1	41
Hemipteronotus martinicensis	rosy razorfish	3.5	32	A	46	272	196	110	63 ± 7	32
Dasyatis centroura	roughtail stingray	3.8	33	A	1	8	1893	185214	1027 ± 0	54
Malacanthus plumieri	sand tilefish	3.6	28	A	4	101	558	1805	224 ± 6	40
Xanthichthys ringens	sargassum triggerfish	3.1	43	A	1	1	179	124	179 ± 0	100
Calamus calamus	saucereye porgy	3.3	26	A	6	37	369	919	229 ± 7	62
Myceroperca phex	scamp	4.5	25	A	1	1	358	852	358 ± 0	100
Lutjanus apodus	schoolmaster	4.2	21	A	26	34	531	2425	248 ± 6	47
Aluterus scriptus	scrawled filefish	2.8	21	A	2	3	367	877	335 ± 16	91
Parablennius marmoreus	seaweed blenny	2.5	49	A	1	1	44	1	44 ± 0	100
Echeneis ucrates	sharksucker	3.4	25	A	2	7	545	820	469 ± 12	86
Canthigaster rostrata	sharpnose puffer	3	24	A	2	35	96	18	41 ± 2	43
Calamus pen	sheepshead porgy	3.4	25	A	2	4	335	823	256 ± 5	77
Manocanthus tuckeri	slender filefish	2.7	23	A	2	4	43	3	20 ± 2	46
Halichoeres bivittatus	slippery dick	3.3	29	J	43	243	348	559	79 ± 10	23
Lactophrys triqueter	smooth trunkfish	3.1	22	A	1	37	216	259	113 ± 0	52
Sphyrae picudilla	southern sennet	4.5	18	A	18	24	430	392	195 ± 14	45
Dasyatis america	southern stingray	3.5	28	A	1	20	1186	49801	396 ± 0	33
Haemulon macrostomum	spanish grunt	3.3	17	A	1	1	439	1975	439 ± 0	100
Bodianus rufus	spanish hogfish	3.4	18	A	3	34	350	744	179 ± 3	51
Cheatodon ocellatus	spotfin butterflyfish	3.2	22	A	2	10	301	819	118 ± 20	39
Bodianus pulchellus	spotfin hogfish	3.6	25	A	1	1	288	351	288 ± 0	100
Aetobatus riri	spotted eagle ray	3.2	23	A	2	4	1781	NA	1624 ± 64	91
Pseudopeneus maculatus	spotted goatfish	3.5	22	A	9	100	337	231	158 ± 4	47
Gymnothorax moringa	spotted moray	4.5	22	A	3	53	474	167	16 ± 0	3
Holocentrus adscensionis	squirrelfish	3.5	24	A	5	84	309	309	138 ± 4	45
Sparisoma viride	stoplight parrotfish	2	20	A	3	65	467	2184	222 ± 5	48
Haemulon striatum	striped grunt	3.4	20	A	2	2	122	40	122 ± 0	100
Scarus iserti	striped parrotfish	2	15	A	2	3	356	824	285 ± 0	80
Megalops atlanticus	tarpon	4.5	13	A	1	1	NA	NA	NA	NA
Stegastes planifrons	threespot damselfish	2.6	45	A	3	8	73	10	47 ± 2	64
Myceroperca tigris	tiger grouper	4.5	19	A	1	2	524	2746	486 ± 0	93
Galeocerdo cuvier	tiger shark	4.5	18	A	1	4	3094	272821	2354 ± 0	76
Serranus tabacarius	tobaccofish	4.2	37	A	5	64	268	273	80 ± 11	30
Haemulon aurolineatum	tomtate	3.2	19	A	2	7	231	170	152 ± 4	66
Lactophrys trigonus	trunkfish	3.1	33	A	2	13	411	1233	175 ± 3	43
Rhomboplites aurorubens	vermillion snapper	4.3	43	A	70	70	375	772	285 ± 42	76
Acanthocybium solandri	wahoo	4.4	14	A	1	1	844	3620	844 ± 0	100
Haemulon plumieri	white grunt	3.6	20	A	87	228	439	1385	226 ± 6	51
Haemulon album	white margate	3.2	24	A	29	66	557	3207	274 ± 8	49
Echeneis neucratiodes	whitefin sharksucker	3.3	23	A	2	16	562	907	309 ± 6	55
Cantherhines macrocerus	whitespotted filefish	3	25	A	2	36	501	2145	280 ± 7	56
Mulloidichthys martinicus	yellow goatfish	3.2	23	A	9	14	256	301	198 ± 11	77
Caranx bartholomaei	yellow jack	4.5	19	A	5	5	659	5494	579 ± 75	88
Halichoeres cyanocephalus	yellowcheek wrasse	3.6	23	A	2	15	413	1065	174 ± 1	42
Myceroperca venenosa	yellowfin grouper	4.5	20	A	2	11	601	4295	298 ± 9	50
Opistogthus aurifrons	yellowhead jawfish	3.1	40	A	3	10	145	16	42 ± 5	29
Halichoeres garnoti	yellowhead wrasse	3.5	28	J	26	265	292	412	80 ± 5	27

Scientific name	Common name	Trophic level	Mean Depth (m)	Abundant Stage (Ad/Juv)	MaxN in 1 frame	Total number analyzed	Maximum length (mm)	Maximum weight (g)	Sample length (mm) Mean +/- SD	Mean sample length as % of maximum
Microspathodon chrysurus	yellowtail damselfish	2.1	20	A	6	15	386	1686	56 ± 0	14
Hypoplectrus chlorurus	yellowtail hamlet	3.8	18	A	5	12	87	14	30 ± 1	34
Ocyurus chrysurus	yellowtail snapper	4	23	A	25	138	591	2157	233 ± 7	39

Appendix VI: Digital recording dissection example





Appendix VII: Life history characteristics

Family	Genus	Species	Code	K	L_m	L_{50}	Biomass (a)	Biomass (b)	Trophic level	Trophic group
Acanthuridae	*Acanthurus*	*bahianus*	ocean surgeonfish	0.40	355	155	0.0257	2.9000	2.0	herbivorous
Acanthuridae	*Acanthurus*	*chirurgus*	doctorfish	0.25	390	170	0.0204	2.9200	2.0	herbivorous
Acanthuridae	*Acanthurus*	*coeruleus*	blue tang	0.11	369	130	0.0324	2.9500	2.0	herbivorous
Aulostomidae	*Aulostomus*	*maculatus*	Atlantic trumpetfish	NA	1000	NA	0.0040	2.8650	4.3	piscivorous
Balistidae	*Aluterus*	*schoepfi*	orange filefish	0.30	610	NA	0.0263	2.89	2.0	herbivorous
Balistidae	*Aluterus*	*scriptus*	scrawled filefish	0.30	1100	NA	0.0263	2.89	2.8	herbivorous
Balistidae	*Balistes*	*vetula*	queen triggerfish	0.60	600	235	0.02239	3.0200	3.4	invertebrates
Balistidae	*Cantherhines*	*macrocerus*	whitespotted filefish	0.30	460	NA	0.0263	2.89	3.0	invertebrates
Balistidae	*Canthidermis*	*sufflamen*	ocean triggerfish	0.60	650	NA	0.0275	2.9700	3.2	invertebrates
Balistidae	*Manocanthus*	*ciliatus*	fringed filefish	0.30	200	NA	0.01995	2.8800	2.7	herbivorous
Balistidae	*Manocanthus*	*tuckeri*	slender filefish	0.30	100	NA	0.0302	3.0700	2.7	herbivorous
Balistidae	*Melichthys*	*niger*	black durgeon	0.60	500	NA	0.02188	3.0000	2.4	herbivorous
Balistidae	*Xanthichthys*	*ringens*	sargassum triggerfish	0.60	250	NA	0.02188	3.0000	3.1	invertebrates
Belonidae	*Playbelone*	*argalus*	keeltail needlefish	NA	500	NA	NA	NA	4.5	piscivorous
Blenniidae	*Parablennius*	*marmoreus*	seaweed blenny	NA	85	NA	0.01096	3.0300	2.5	herbivorous
Bothidae	*Bothus*	*lutus*	peacock flounder	0.16	460	NA	0.01349	3.0800	4.5	piscivorous
Callionymidae	*Paradiplogrammus*	*bairdi*	lancer dragonet	NA	114	NA	NA	NA	3.3	invertebrates
Carangidae	*Caranx*	*bartholomaei*	yellow jack	0.14	1000	450	0.0257	2.9300	4.5	piscivorous
Carangidae	*Caranx*	*crysos*	blue runner	0.32	700	274	0.01549	2.9300	4.4	planktivorous
Carangidae	*Caranx*	*latus*	horse-eye jack	0.14	1010	370	0.0245	2.9500	4.4	piscivorous
Carangidae	*Caranx*	*lugubris*	black jack	0.12	1000	380	0.01549	2.9600	4.5	piscivorous
Carangidae	*Caranx*	*ruber*	bar jack	0.14	590	310	0.0191	2.9500	4.4	planktivorous
Carangidae	*Decapterus*	*macarellus*	mackerel scad	0.80	460	NA	0.0138	2.9900	3.4	planktivorous
Carangidae	*Elagatis*	*bipinnulata*	rainbow runner	0.60	1800	NA	0.01288	2.9100	3.6	piscivorous
Carangidae	*Trachinotus*	*falcatus*	permit	0.18	1220	547	0.0331	2.9300	3.2	invertebrates
Carcharhinidae	*Carcharhinus*	*limbatus*	blacktip shark	0.27	2750	1200	0.00617	3.0500	4.2	piscivorous
Carcharhinidae	*Carcharhinus*	*longimanus*	oceanic whitetip	0.10	3960	1800	0.00724	3.0300	4.2	piscivorous
Carcharhinidae	*Carcharhinus*	*perezii*	reef shark	0.27	3000	1520	0.00617	3.0500	4.5	piscivorous
Carcharhinidae	*Galeocerdo*	*cuvier*	tiger shark	0.20	7500	2500	0.00437	3.1300	4.5	piscivorous
Chaetondontidae	*Cheatodon*	*capistratus*	foureye butterflyfish	1.10	140	92	0.02818	3.1400	3.0	omnivorous
Chaetondontidae	*Cheatodon*	*ocellatus*	spotfin butterflyfish	1.10	200	139	0.0263	3.0400	3.2	omnivorous
Chaetondontidae	*Cheatodon*	*striatus*	banded butterflyfish	1.10	160	120	0.0263	3.0700	3.2	omnivorous
Cheatondontidae	*Cheatodon*	*aculeatus*	longsnout butterflyfish	1.10	100	NA	0.02344	3.0400	3.2	omnivorous
Cheatondontidae	*Cheatodon*	*sedentarius*	reef butterflyfish	1.10	150	80	0.0263	3.0600	2.8	omnivorous
Congridae	*Conger*	*triporiceps*	manytooth conger	NA	1000	NA	0.00068	3.1600	4.0	piscivorous
Congridae	*Heteroconger*	*halis*	brown garden	NA	510	NA	0.00102	3.0600	3.1	planktivorous
Dasyatidae	*Dasyatis*	*america*	southern stingray	NA	2000	660	0.0739	2.8100	3.5	omnivorous
Dasyatidae	*Dasyatis*	*centroura*	roughtail stingray	NA	2200	660	0.0739	2.8100	3.8	omnivorous
Echeneidae	*Echeneis*	*neucratiodes*	whitefin sharksucker	NA	750	NA	0.00302	3.1300	3.3	omnivorous
Echeneidae	*Echeneis*	*ucrates*	sharksucker	NA	1100	NA	0.00302	3.1300	3.4	omnivorous
Fistulariidae	*Fistularia*	*tabacaria*	bluespotted cornetfish	NA	2000	NA	NA	NA	3.5	piscivorous
Grammatidae	*Gramma*	*loreto*	fairy basslet	NA	80	30	0.01122	3.0400	3.3	invertebrates
Haemulidae	*Anisotremus*	*surimensis*	black margate	0.19	760	305	0.0195	3.0500	3.3	omnivorous
Haemulidae	*Haemulon*	*album*	white margate	0.19	790	305	0.0178	3.0100	3.2	invertebrates
Haemulidae	*Haemulon*	*aurolineatum*	tomtate	0.18	250	140	0.0138	3.0000	3.2	omnivorous
Haemulidae	*Haemulon*	*flavolineatum*	french grunt	0.24	300	160	0.01479	3.0200	3.3	invertebrates
Haemulidae	*Haemulon*	*macrostomum*	spanish grunt	0.24	430	NA	0.0209	3.0300	3.3	invertebrates
Haemulidae	*Haemulon*	*melanurum*	cottonwick	0.30	330	190	0.0200	2.9900	2.2	omnivorous
Haemulidae	*Haemulon*	*plumieri*	white grunt	0.16	530	190	0.01698	2.9900	3.6	invertebrates
Haemulidae	*Haemulon*	*sciurus*	bluestriped grunt	0.22	460	185	0.01585	3.0300	3.4	invertebrates
Haemulidae	*Haemulon*	*striatum*	striped grunt	0.22	280	NA	0.0175	3.0990	3.4	planktivorous
Holocentridae	*Holocentrus*	*adscensionis*	squirrelfish	0.90	610	145	0.01122	2.9800	3.5	omnivorous
Holocentridae	*Holocentrus*	*rufus*	longspine squirrelfish	0.90	350	135	0.01072	2.9400	3.5	invertebrates
Kyphosidae	*Kyphosus*	*sectatrix-incisor*	bermuda-yellow chub	NA	760	NA	NA	NA	2.0	herbivorous
Labridae	*Bodianus*	*pulchellus*	spotfin hogfish	NA	285	NA	0.01288	3.0400	3.6	invertebrates
Labridae	*Bodianus*	*rufus*	spanish hogfish	NA	400	NA	0.0144	3.0530	3.4	invertebrates
Labridae	*Clepticus*	*parrae*	creole wrasse	NA	300	NA	0.01023	3.0700	3.3	planktivorous
Labridae	*Halichoeres*	*bivittatus*	slippery dick	0.60	350	NA	0.0100	3.0800	3.3	piscivorous
Labridae	*Halichoeres*	*cyanocephalus*	yellowcheek wrasse	1	300	NA	0.01	3.1100	3.6	invertebrates
Labridae	*Halichoeres*	*garnoti*	yellowhead wrasse	0.70	193	NA	0.01	3.1500	3.5	invertebrates
Labridae	*Halichoeres*	*poeyi*	blackear wrasse	1	200	NA	0.01023	3.1100	3.4	invertebrates
Labridae	*Halichoeres*	*radiatus*	puddingwife	0.60	510	NA	0.0131	3.0380	3.3	invertebrates
Labridae	*Hemipteronotus*	*martinicensis*	rosy razorfish	1.00	150	NA	0.01288	3.0400	3.5	invertebrates
Labridae	*Hemipteronotus*	*splendens*	green razorfish	1.00	175	NA	0.01288	3.0400	3.1	invertebrates
Labridae	*Thalassoma*	*bifasciatum*	bluehead	0.70	250	NA	0.00891	3.0200	3.3	planktivorous
Lutjanidae	*Lutjanus*	*apodus*	schoolmaster	0.18	672	250	0.01622	3.0000	4.2	piscivorous
Lutjanidae	*Lutjanus*	*buccanella*	blackfin snapper	0.10	750	310	0.01479	3.0100	3.9	piscivorous

Family	Genus	Species	Code	K	L_m	L_{50}	Biomass (a)	Biomass (b)	Trophic level	Trophic group
Lutjanidae	*Lutjanus*	*griseus*	gray snapper	0.10	890	320	0.01349	3.0000	4.3	piscivorous
Lutjanidae	*Lutjanus*	*jocu*	dog snapper	0.10	1280	229	0.0182	2.9900	4.3	piscivorous
Lutjanidae	*Lutjanus*	*mahogoni*	mahogany snapper	0.10	480	130	0.0195	2.9600	4.5	piscivorous
Lutjanidae	*Lutjanus*	*sygris*	lane snapper	0.13	600	253	0.01413	2.9800	3.8	piscivorous
Lutjanidae	*Ocyurus*	*chrysurus*	yellowtail snapper	0.10	863	237	0.01445	2.9200	4.0	piscivorous
Lutjanidae	*Rhomboplites*	*aurorubens*	vermillion snapper	0.20	600	200	0.01698	2.9600	4.3	piscivorous
Malacanthidae	*Malacanthus*	*plumieri*	sand tilefish	NA	700	NA	0.01175	2.9700	3.6	invertebrates
Megalopidae	*Megalops*	*atlanticus*	tarpon	0.07	2500	1600	0.00891	3.0200	4.5	piscivorous
Mobulidae	*Manta*	*birostris*	manta	NA	9100	3800	NA	NA	3.5	planktivorous
Mullidae	*Mulloidichthys*	*martinicus*	yellow goatfish	0.40	394	170	0.011	3.1500	3.2	invertebrates
Mullidae	*Pseudopeneus*	*maculatus*	spotted goatfish	0.30	300	180	0.00543	3.0300	3.5	invertebrates
Muraenidae	*Gymnothorax*	*funebris*	green moray	NA	2500	NA	0.00145	3.1400	4.0	piscivorous
Muraenidae	*Gymnothorax*	*miliaris*	goldentail moray	NA	700	NA	0.00174	3.1100	3.9	piscivorous
Muraenidae	*Gymnothorax*	*moringa*	spotted moray	NA	2000	NA	0.00081	3.1700	4.5	piscivorous
Myliobatidae	*Aetobatus*	*riri*	spotted eagle	NA	3300	998	NA	NA	3.2	invertebrates
Opistogthidae	*Opistogthus*	*aurifrons*	yellowhead jawfish	NA	100	NA	0.00389	3.1200	3.1	planktivorous
Ostraciidae	*Lactophrys*	*trigonus*	trunkfish	NA	550	NA	0.0178	3.0000	3.1	invertebrates
Ostraciidae	*Lactophrys*	*triqueter*	smooth trunkfish	NA	470	NA	0.05012	2.7800	3.1	invertebrates
Paralichtyidae	*Syacium*	*micrurum*	channel flounder	0.16	400	NA	0.00851	3.0800	3.3	invertebrates
Pomacanthidae	*Centropyge*	*argi*	cherubfish	NA	80	NA	0.02884	2.9200	2.0	herbivorous
Pomacanthidae	*Holacanthus*	*ciliaris*	queen angelfish	0.20	450	220	0.0309	2.9200	3.0	invertebrates
Pomacanthidae	*Holacanthus*	*tricolor*	rock beauty	0.20	350	158	0.03388	2.9300	3.0	invertebrates
Pomacanthidae	*Pomacanthus*	*arcuatus*	grey angelfish	0.20	600	226	0.03467	2.9500	2.9	herbivorous
Pomacanthidae	*Pomacanthus*	*paru*	french angelfish	0.20	411	220	0.03236	2.9700	2.8	herbivorous
Pomacentridae	*Chromis*	*cyanea*	blue chromis	0.33	150	NA	0.01479	2.9600	3.1	planktivorous
Pomacentridae	*Chromis*	*multilineata*	brown chromis	0.33	200	NA	0.01479	2.9600	3.0	planktivorous
Pomacentridae	*Microspathodon*	*chrysurus*	yellowtail damselfish	0.33	210	NA	0.0282	3.0100	2.1	omnivorous
Pomacentridae	*Stegastes*	*leucostictus*	beaugregory	0.33	100	NA	0.02239	2.96	3.1	invertebrates
Pomacentridae	*Stegastes*	*partitus*	bicolor damselfish	0.33	100	NA	0.0224	3.0400	2.0	herbivorous
Pomacentridae	*Stegastes*	*planifrons*	threespot damselfish	0.33	130	NA	0.0269	2.9700	2.6	omnivorous
Priacanthidae	*Priacanthus*	*cruentatus*	glasseye snapper	NA	507	NA	0.0204	2.9200	3.8	piscivorous
Rhincodontidae	*Ginglymostoma*	*cirratum*	nurse shark	0.14	4300	2300	0.00457	3.1000	3.8	piscivorous
Scaridae	*Scarus*	*iserti*	striped parrotfish	0.20	350	160	0.0158	3.0400	2.0	herbivorous
Scaridae	*Scarus*	*taeniopterus*	princess parrotfish	0.20	350	NA	0.0135	3.0000	2.0	herbivorous
Scaridae	*Scarus*	*vetula*	queen parrotfish	0.60	610	NA	0.01	3.0400	2.0	invertebrates
Scaridae	*Sparisoma*	*aurofretum*	redband parrotfish	0.20	280	150	0.0123	3.1300	2.0	herbivorous
Scaridae	*Sparisoma*	*chrysopterum*	redtail parrotfish	0.80	460	NA	0.0129	3.1000	2.0	herbivorous
Scaridae	*Sparisoma*	*rubripinne*	redfin parrotfish	0.50	478	160	0.01413	3.0900	2.0	herbivorous
Scaridae	*Sparisoma*	*viride*	stoplight parrotfish	0.60	640	163	0.017	3.0600	2.0	herbivorous
Sciaenidae	*Equetus*	*acumitus*	highhat	NA	230	NA	0.01023	3.1300	3.6	invertebrates
Scombridae	*Acanthocybium*	*solandri*	wahoo	0.34	2500	993	0.00309	3.1500	4.4	piscivorous
Scombridae	*Scomberomorus*	*regalis*	cero	0.20	1830	405	0.0112	3.0100	4.5	piscivorous
Scorpaenidae	*Pterois*	*volitans*	lionfish	NA	380	160	0.01202	3.0600	4.5	piscivorous
Serranidae	*Cephalopholis*	*cruentata*	graysby	0.34	426	160	0.01288	3.0700	4.2	piscivorous
Serranidae	*Cephalopholis*	*fulva*	coney	0.15	410	160	0.01413	3.0600	4.1	piscivorous
Serranidae	*Epinephelus*	*adscensionsis*	rock hind	0.11	610	250	0.0174	3.1100	3.5	piscivorous
Serranidae	*Epinephelus*	*guttatus*	red hind	0.12	760	250	0.01413	3.0500	3.9	invertebrates
Serranidae	*Hypoplectrus*	*chlorurus*	yellowtail hamlet	NA	127	NA	0.01995	3.0100	3.8	invertebrates
Serranidae	*Hypoplectrus*	*puella*	barred hamlet	NA	152	NA	NA	NA	3.7	invertebrates
Serranidae	*Hypoplectrus*	*unicolor*	butter hamlet	NA	127	NA	0.0178	3.0300	4.0	invertebrates
Serranidae	*Myceroperca*	*phex*	scamp	0.09	1070	460	0.01445	3.0700	4.5	piscivorous
Serranidae	*Myceroperca*	*tigris*	tiger grouper	0.11	1010	460	0.01445	3.0700	4.5	piscivorous
Serranidae	*Myceroperca*	*venenosa*	yellowfin grouper	0.09	1000	510	0.01549	3.0600	4.5	piscivorous
Serranidae	*Paranthias*	*furcifer*	creolefish	0.22	300	NA	0.0135	3.0430	3.1	planktivorous
Serranidae	*Serranus*	*baldwini*	lantern bass	0.22	120	NA	0.0129	3.0360	4.1	piscivorous
Serranidae	*Serranus*	*tabacarius*	tobaccofish	0.22	220	NA	0.01202	3.0500	4.2	invertebrates
Serranidae	*Serranus*	*tigrinus*	harlequin bass	0.22	290	NA	0.0138	3.0600	3.7	invertebrates
Serranidae	*Serranus*	*tortugarum*	chalk bass	0.22	80	NA	0.01202	3.0500	3.1	planktivorous
Sparidae	*Calamus*	*bajodo*	jolthead porgy	0.20	760	300	0.0316	2.8900	3.2	invertebrates
Sparidae	*Calamus*	*calamus*	saucereye porgy	0.20	560	NA	0.02188	2.9500	3.3	invertebrates
Sparidae	*Calamus*	*pen*	sheepshead porgy	0.20	460	NA	0.0347	2.8700	3.4	invertebrates
Sparidae	*Calamus*	*pentula*	pluma	0.20	370	NA	0.01905	2.9600	3.5	invertebrates
Sphyraenidae	*Sphyrae*	*barracuda*	great barracuda	0.09	2000	660	0.00912	2.9600	4.5	piscivorous
Sphyraenidae	*Sphyrae*	*guachancho*	guaguanche	NA	2000	350	NA	NA	3.9	piscivorous
Sphyraenidae	*Sphyrae*	*picudilla*	southern sennet	NA	610	NA	0.00692	2.9100	4.5	piscivorous
Tetradontidae	*Canthigaster*	*rostrata*	sharpnose puffer	0.51	120	NA	0.02239	2.9600	3.0	omnivorous
Tetradontidae	*Diodon*	*hystrix*	porcupinefish	0.12	910	NA	0.07586	2.8500	3.4	invertebrates
Tetradontidae	*Sphoeroides*	*spengleri*	bandtail puffer	0.51	300	NA	0.02344	2.9500	3.2	invertebrates

Appendix VIII: Morphological traits

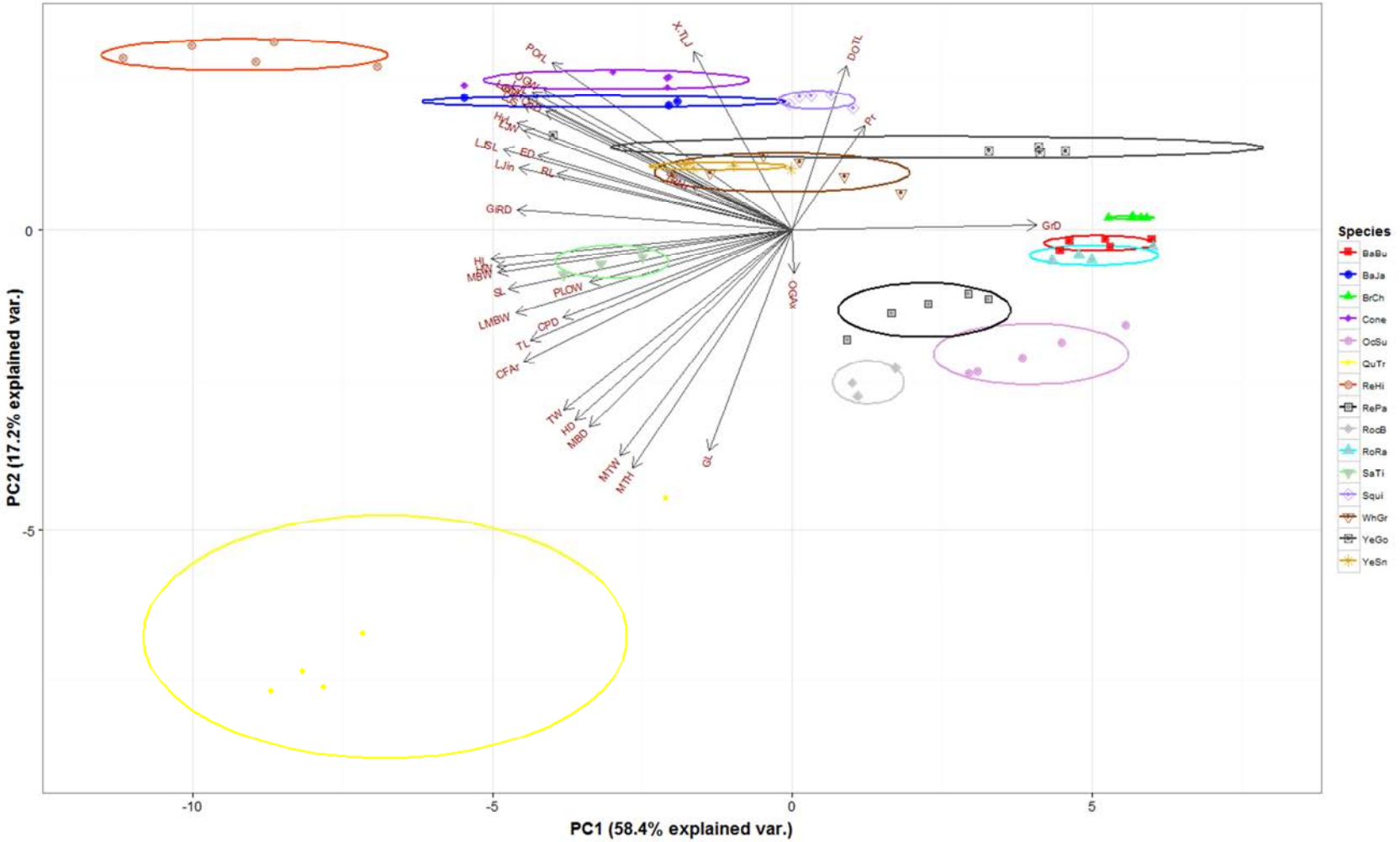
Morphological parameter	Abbreviation	Unit	Fish 1	Fish 2	Fish 3	Fish 4	Fish 5	Fish 6	Fish 7	Fish 8	Fish 9	Fish 10	Fish 11	Fish 12	Fish 13	Fish 14	Fish 15	Fish 16	Fish 17	Fish 18	Fish 19	Fish 20	Fish 21	Fish 22	Fish 23	Fish 24
			Haemulon plumieri						*Holacanthus tricolor*			*Cephalopholis fulva*					*Sparisoma aurofrenatum*					*Acanthurus bahianus*				
Barbels	Ba	Y/N	N	N	N	N	N	N	N	N	N	N	N	N	N	N	N	N	N	N	N	N	N	N	N	N
Total Weigth	TW	g	91	126	127	154	222	256	208	257	269	158	161	162	191	375	108	120	155	179	250	47	86	108	156	161
Total Length	TL	mm	190	205	212	228	247	257	198	243	235	223	225	227	235	281	186	200	206	227	254	132	168	193	205	232
Standard Length	SL	mm	170	185	197	204	222	238	198	207	215	223	225	227	235	281	184	197	208	219	245	126	152	172	180	202
Standard Length (US)	SL_US	mm	148	163	172	184	195	208	156	174	179	179	181	180	196	245	152	155	177	185	205	105	130	147	154	171
Length at Maximum Body Width	LMBW	mm	54	57	57	57	57	57.5	77	76.9	76.5	71	68	70	65	77	43.8	43.2	51.8	53.4	55.1	42.8	55.3	63	68.5	64.9
Maximum Body Depth	MBD	mm	54	54	57.5	59.5	71	76	87	94.4	96.6	57.8	59.5	57.7	64.4	84.5	56	57.4	63.8	65.8	79.3	53.4	62.5	67.9	76.4	74.7
Caudal Peduncle Depth	CPD	mm	14.5	16.5	16	17.5	19	21	23	25	25.5	22	22.1	22.1	22.6	29.6	17.2	16.9	19.6	19.9	21.6	11.3	12.5	14.1	15.8	16.1
Head Length	HL	mm	48	53.5	56	59	63.5	71	40	44.2	47.6	65.3	64.2	64	65.4	83.3	40.5	41	48.6	51.1	56	22.7	33.5	39.4	39.7	44.5
Eye Diameter	ED	mm	12.5	14	14.5	15	15.5	16	10.5	9.9	10.8	14.1	14.3	13.7	14.4	15.3	10.2	10.2	11.5	11.4	11.9	8.8	10.8	12.3	12.7	12.5
Protrusion	Pr	mm	0.8	1.5	1.3	1	1	1.4	9.5	11.8	11	5.2	7.5	5	6.1	8.1	1.5	1.7	1.3	1.3	1.2	1	1.3	1.1	0.8	0.8
Oral Gape Axis	OGAx	degrees	64	67	59	56	59	52	23	18	13	42	38	39	42	38	49	53	53	54	55	87	88	89	89	89
Lower Jaw Length	LJL	mm	25	33	32	39	39	42.5	15.5	16.1	17.7	44	42.5	43.1	45.2	50.5	9.6	9.1	10.6	11.1	12.3	7.1	9	10.2	10	10.4
Oral Tooth Type 1	TOT1	Y/N	0	0	0	0	0	0	1	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Oral Tooth Type 2	TOT2	Y/N	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1	1	1	1	1	1	1	1
Oral Tooth Type 3	TOT3	Y/N	1	1	1	1	1	1	0	0	0	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0
Oral Tooth Type 4	TOT4	Y/N	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Oral Tooth Type 5	TOT5	Y/N	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Bony Gill Raker Length	RL	mm	0.5	0.5	0.5	0.7	0.8	0.9	0.5	0.8	0.9	0.6	0.7	0.6	0.9	1.3	0.9	1.3	1.3	1.4	1.4	0.1	0.2	0.4	0.3	0.3
Gill Inter Raker Distance	GIRD	mm	0.8	0.9	0.9	0.9	0.9	0.9	1.2	0.9	1	1	1.2	1.2	1.2	1.4	0.5	0.4	0.6	0.6	0.7	0.6	0.6	0.4	0.5	0.5
Postlingual Organ Width	PLOW	mm	12.5	14	15.5	15	18	19	12	14.8	15	8.4	9.5	10.2	11	14.2	7.8	8.2	8.1	9.9	11.8	2.3	3	3.1	5.4	6.6
Pharyngeal Tooth Type 1	TPT_1	Y/N	0	0	0	0	0	0	1	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Pharyngeal Tooth Type 2	TPT_2	Y/N	1	1	1	1	1	1	0	0	0	0	0	0	0	0	1	1	1	1	1	0	0	0	0	0
Pharyngeal Tooth Type 3	TPT_3	Y/N	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Pharyngeal Tooth Type 4	TPT_4	Y/N	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Maximum Body Width	MBW	mm	23.5	27.5	28	29.5	32	35	31	35	34.6	36.5	35.9	36	40	48	26.4	29.3	30.9	34.4	35.4	17.2	23.4	23.9	26.5	26.9
Lower Jaw In-lever	LJin	mm	8	8	11.5	12	13	13.5	3.9	4.2	3.9	19.8	21.2	21.2	21.3	26.9	3.9	3.9	4	4.9	5.6	2.7	3	3.8	4.3	4.2
Lower Jaw Out-lever	LJout	mm	24	25.5	29.5	34.5	35	37	8.8	10.1	9.5	40.1	40.6	40.7	43.9	51.5	13.2	14	14.1	14.4	16.9	5.3	7	9	10.5	9.8
Postorbital Length	POrL	mm	17	19.5	20	21	23	24.5	12.5	15.7	14.8	32	32	31	33.8	40.3	15.2	18.8	18.8	19.5	20	4	4.7	5.3	7	7.3
Operculum Depth	OpD	mm	27	30	31	35.5	41	44	27.5	26.8	25.8	28	29	28.5	30.9	35.8	25.5	28.8	32.3	32.7	33.3	16.1	21.5	22	24.9	27.2
Oral Gape Height	OGH	mm	30.5	32	37	37	42	44	9	12.8	11.4	38.5	39.2	39	40.5	41	14.1	15.3	17.2	18	18.9	7.5	8.7	11.5	11.9	12.1
Oral Gape Width	OGW	mm	11.5	11.5	15	12.5	14	16.5	8.5	13.3	13.5	39.5	40	37.1	43.8	48.8	11.6	12.2	12.5	15.8	16	6.9	7.5	8.9	9.9	10.3
Gut Length	GL	mm	165	190	200	220	230	260	860	1200	980	170	165	175	160	250	290	280	275	320	410	405	450	500	545	550
Hyiod Length	HyL	mm	21	20.5	24.5	25	25	25.5	11	12.7	13.8	34.2	32	31.9	35.7	39.2	14.4	13.9	14.2	16	15.5	5	7.2	8.5	11.1	10.5
Lower Jaw Suspensorium Length	LJSL	mm	42	45	50	50	52	53	33	30.9	31.2	54.5	53.5	53	59.1	73	29.2	29	29.5	29.6	30.5	10.4	12	14.1	18.5	18.8
Head Width	HW	mm	25	27	28	29.5	32	35	29	31.5	32	36.5	35.9	36	40	48	26.4	29.3	30.9	34.4	35.4	16	21.4	22.2	25.1	24.9
Head Depth	HD	mm	54	54	57.5	59.5	71	76	90	81.2	83.3	57.8	59.5	57.7	64.4	84.5	56	57.4	63.8	65.8	79.3	46.8	54.6	60.5	65	67.5
Sex	S	M/F																								
Lower Jaw Width	LJW	mm	13	17	22.5	24	25.5	26.5	11	13.2	12.9	33.4	33	31	35.1	36.8	15	16	16.2	17.2	18.1	8.2	9	9.8	10.9	10.8
Lower Jaw Span	LJS	mm	50	66	72	76	78	82	29	28.8	28.4	85	82	86	85.5	104	19	23	22.7	28	30.8	11.2	13.8	15.2	19.1	18.8
Number of Teeth on Lower Jaw	#TLJ	#	40	52	60	72	76	60	46	44	48	396	336	396	460	468	fused	fused	fused	fused	fused	18	18	18	18	18
Density of Teeth on Lower Jaw	DOTL	#	3	3	2.5	2.5	2.5	2	3	2.9	2.7	3	2.7	3	3.3	3	fused	fused	fused	fused	fused	1.8	1.7	1.7	1.8	1.7
Maximal Tooth Height	MTH	mm	1	1	1	1	1.5	1.5	3.5	4.2	3.8	3.9	3.5	3.8	4.4	3.5	3.5	3.4	3.5	4.2	4.2	1.2	1.7	1.9	2.1	1.9
Maximal Tooth Width	MTW	mm	0.5	0.5	0.7	0.7	0.9	0.9	0.4	0.4	0.4	1	0.7	1.2	1.7	1.7	fused	fused	fused	fused	fused	0.8	0.9	1.2	1.4	1.3
Total Number of Gill Rakers	TRNr	#	28	32	36	36	36	36	17	18	18	21	22	20	22	24	20	18	17	19	20	13	15	16	15	15
Gill Raker Density	GrD	#	1	1	1	1	1	1	0.8	1	1	1	1	1	1	1	2	2	1.8	1.7	1.6	1	1.2	1.3	1.1	1.2
Lower Pharyngeal Jaw Mass	PJM	g	-	-	-	-	-	-									0.4	0.7	0.7	0.9	1.1					
Lower Pharyngeal Length	LPL	mm	-	-	-	-	-	-									6.2	7	7.1	9.9	11.4					
Lower Pharyngeal Width	LPW	mm	-	-	-	-	-	-									6	6.5	6.5	8.8	10.7					
Caudal Fin Area	CFAr	mm2	1000	1200	1100	1500	2000	1800	2000	2500	2600	1600	1650	1600	2000	3000	750	850	900	1200	1400	900	1100	1350	1450	1500
Comment GUT CONTENT															Bicolor Damselfish				Algae							

Morphological parameter	Abbreviation	Unit	Fish 25	Fish 26	Fish 27	Fish 28	Fish 29	Fish 30	Fish 31	Fish 32	Fish 33	Fish 34	Fish 35	Fish 36	Fish 37	Fish 38	Fish 39	Fish 40	Fish 41	Fish 42	Fish 43	Fish 44	Fish 45	Fish 46	Fish 47	Fish 48	Fish 49
			Sebastes ruberrimus					*Choetodon striotus*					*Holocentrus adscensionis*					*Balistes vetulo*					*Mulloidichthys vanicolensis*				
Barbels	Ba	Y/N	N	N	N	N	N	N	N	N	N	N	N	N	N	N	N	N	N	N	N	N	Y 22,1	Y 28,1	Y 26,8	Y 31,7	Y 59,8
Total Weigth	TW	g	118	134	159	170	175	24	40	41	61	70	126	135	139	157	170	455	1265	1350	1370	1550	53	64	59	86	468
Total Length	TL	mm	210	214	228	235	242	93	111	112	126	133	235	245	251	254	263	340	450	493	570	535	172	179	175	201	339
Standard Length	SL	mm	194	201	214	218	225	93	111	112	126	133	205	200	206	213	216	263	362	377	387	383	151	158	156	176	296
Standard Length (US)	SL_US	mm	157	163	172	177	181	76	91	95	103	113	181	185	184	192	195	222	315	323	338	334	133	142	140	162	280
Length at Maximum Body Width	LMBW	mm	56.1	62.9	67.2	74.4	70.7	36.2	43.1	40.2	47.4	48.6	51.8	54.5	52.6	55.1	59	74.7	102.3	110.2	107.1	106.8	39.3	39.8	40	42.5	78.4
Maximum Body Depth	MBD	mm	54.9	60.5	67.3	62	60.3	58.2	68.4	69.4	70.6	76	54.1	54.4	56.8	57.7	58.5	123.1	170.1	174.5	177.5	175.9	31.8	36	37.6	40.1	75.7
Caudal Peduncle Depth	CPD	mm	18.8	19.7	21.5	21.1	21	9.5	11.5	11.5	12.7	13.4	12.8	13	13.2	13.7	13.8	20.9	26.1	28.4	27.4	30.2	12.1	13.4	13.5	14.4	28.6
Head Length	HL	mm	57.2	61.8	65	68.6	66.4	23.5	28.5	27.4	31.4	32.2	48.5	49.4	48.7	52.3	53.6	77.3	105.5	108.1	111.4	112.4	38.1	38.3	39.6	43.6	77
Eye Diameter	ED	mm	17.6	17.1	18.2	19.4	19.6	8.4	9.7	9.6	11.1	10.9	19.4	20.7	19.6	19.7	19.6	16.3	20	17.3	19.1	19.2	12.2	12.3	13	13.3	22.2
Protrusion	Pr	mm	3.3	4	5.6	4.3	4.5	5.4	4.9	6	6.3	7.6	8	8.9	8	7.8	7.6	0	0	0	0	0	5.1	6.3	6.3	5.2	8.5
Oral Gape Axis	OGAx	degrees	34	35	31	30	33	19	22	18	18	17	35	38	39	41	40	40	42	45	51	47	51	49	52	47	55
Lower Jaw Length	LJL	mm	27.7	27.1	27.2	32	31.2	14.1	15.2	15.5	17.9	18.6	25.8	26.7	24.9	27.3	31	20.3	24.6	28.5	29.9	29.1	13.4	15.2	15	16.2	31.5
Oral Tooth Type 1	TOT1	Y/N	0	0	0	0	0	0	0	0	0	0	1	1	1	1	1	0	0	0	0	0	1	1	1	1	1
Oral Tooth Type 2	TOT2	Y/N	0	0	0	0	0	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Oral Tooth Type 3	TOT3	Y/N	1	1	1	1	1	1	1	1	1	1	0	0	0	0	0	1	1	1	1	1	0	0	0	0	0
Oral Tooth Type 4	TOT4	Y/N	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Oral Tooth Type 5	TOT5	Y/N	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Bony Gill Raker Length	RL	mm	1.8	2.9	3.2	3.3	3.1	0.3	0.4	0.3	0.3	0.3	2.2	1.9	3.5	2.4	2.7	1.4	2.8	2.1	2.6	2.8	0.5	0.5	0.5	0.6	1.8
Gill Inter Raker Distance	GiRD	mm	1	1.6	1.5	1.4	1.6	0.4	0.4	0.4	0.3	0.4	0.7	0.8	1	1	0.9	1.2	1.6	1.5	1.6	1.7	0.3	0.3	0.4	0.4	0.8
Postlingual Organ Width	PLOW	mm	9	8	7.8	8.2	8.1	2.1	2.5	2.6	3	3.2	9.6	9.4	8.4	10.5	10.2	19.4	24.1	25	25.8	27.4	12.1	11.6	11.5	11	32
Pharyngeal Tooth Type 1	TPT_1	Y/N	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1	1	1
Pharyngeal Tooth Type 2	TPT_2	Y/N	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Pharyngeal Tooth Type 3	TPT_3	Y/N	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0	1	1	1	1	1	0	0	0	0	0
Pharyngeal Tooth Type 4	TPT_4	Y/N	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Maximum Body Width	MBW	mm	25.7	29.2	34.1	30.9	29.6	12.9	13.8	15.9	18.8	19.6	26.6	29	28.3	28.5	29.7	39.3	55.7	63	60	60.8	21.3	23.2	22.3	26.9	45
Lower Jaw In-lever	LJin	mm	18.2	22	22.4	19.2	21.2	7.3	7.7	8.8	11.3	9.9	15.9	15.7	15.1	16.7	16.6	13.9	23.7	24.6	25.2	26.3	6.6	6.5	6.5	7.3	14.6
Lower Jaw Out-lever	LJout	mm	27.9	33.1	31.5	33.3	32.3	13.9	15.7	15	18.2	17.2	25.8	26.8	27.1	28.2	28.3	19.8	27.6	29.1	30	30.1	11.6	13.5	13.5	14.6	32.7
Postorbital Length	POrL	mm	22.5	22.9	24.6	23.5	25.5	7.3	8.1	7.9	9.4	10.3	20.2	21.7	20.6	22.8	21.7	7.6	13.3	13.6	14.5	17.2	12.7	13	11.8	14.6	26
Operculum Depth	OpD	mm	34.2	32.9	35.9	34.1	34.5	19.7	22.7	20.9	25.2	24.9	38	40.1	37.6	39.2	37.4	24.6	31.9	32.4	32.9	32.7	24.2	27.4	24.2	28.6	57.7
Oral Gape Height	OGH	mm	28.4	29.3	32	33.7	33.3	6.2	6.8	7.1	8	8.2	23.7	25	28.1	30.1	28.7	24.6	28.2	29	28.7	27.2	17.1	17.2	17.7	19.4	38.9
Oral Gape Width	OGW	mm	33.3	33.8	39	39.1	40.1	6	6.1	7	8.3	8.3	26.8	30.3	32.2	34.6	34	19.3	28.3	24.7	24.5	29.1	17.3	17.2	17.3	18.6	39
Gut Length	GL	mm	170	190	190	200	215	370	360	380	450	510	300	260	280	270	300	550	710	900	850	910	160	180	170	190	250
Hyiod Length	HyL	mm	24.6	29.5	32.5	33.6	30.1	6.4	7.2	8.3	8	7.5	22.1	23.1	22.4	21.7	23.3	21.3	29.4	31.8	30.7	32.1	16.5	22.2	20	23.3	45
Lower Jaw Suspensorium Length	LJSL	mm	35.7	42.3	39.5	43.4	43	18.9	21.5	21.8	22.7	23.7	38.5	38.4	42.6	41.8	43.9	42	53.5	53.8	61.5	60.2	25.9	25.6	24.4	30.5	50.8
Head Width	HW	mm	25.7	29.2	34.1	30.9	29.6	12.4	14	15.6	16.6	18.5	26.6	29	28.3	28.5	29.7	39.3	55.7	63	60	60.8	21.3	23.2	22.3	26.9	45
Head Depth	HD	mm	54.9	60.5	67.3	62	60.3	42.6	56.1	56.5	57.4	60	46.1	46.5	46.8	47.3	48	123.1	170.1	174.5	177.5	175.9	31.8	36	37.6	40.1	75.7
Sex	S	M/F																									
Lower Jaw Width	LJW	mm	20	21.3	22.7	23	22.3	4.3	5.8	6.6	7	6.8	16.9	17.4	16.8	16	16.2	15.2	22	20.4	23.1	24.2	7.8	8.2	6.9	8.8	33.1
Lower Jaw Span	LJS	mm	68.8	71	65	72.5	69.8	27.7	29	30.8	36.2	38.6	49.8	56	57.5	58.2	58	42.8	61.8	63.4	65	69.5	22.3	24.6	23.6	26.2	74
Number of Teeth on Lower Jaw	#TLJ	#	25	27	24	25	28	36	40	50	48	48	>100	>100	>100	>100	>100	8	8	8	8	8	>100	>100	>100	>100	>100
Density of Teeth on Lower Jaw	DOTL	#	0.9	0.8	0.7	0.7	0.6	2	2.2	2.8	2.7	2.5	5	5	5	5	5	0.3	0.2	0.2	0.2	0.2	6	6	6	6	4
Maximal Tooth Height	MTH	mm	1.6	1.5	1.8	1.7	1.4	0.2	0.1	0.2	0.3	0.1	0.05	0.05	0.05	0.05	0.05	10.3	14.3	12.9	14.3	15.2	0.05	0.05	0.05	0.05	0.1
Maximal Tooth Width	MTW	mm	0.6	0.7	0.7	0.8	0.7	0.1	0.1	0.1	0.1	0.1	0.05	0.05	0.05	0.05	0.05	3.2	4.7	5.9	5	5.7	0.05	0.05	0.05	0.05	0.1
Total Number of Gill Rakers	TRNr	#	17	14	17	15	15	11	12	14	12	11	15	17	17	16	16	20	20	20	21	20	15	17	18	18	20
Gill Raker Density	GrD	#	0.5	0.5	0.5	0.4	0.4	2	2	2.1	2.2	2.2	1.5	1.5	1.1	1	1.1	0.8	0.6	0.7	0.7	0.5	2.7	2.6	2.3	2.1	1.3
Lower Pharyngeal Jaw Mass	PJM	g																0.15	0.3	0.2	0.3	0.35					
Lower Pharyngeal Length	LPL	mm																6.2	7.7	7.8	7.1	7.2					
Lower Pharyngeal Width	LPW	mm																5.6	6.2	6.9	6.8	6.8					
Caudal Fin Area	CFAr	mm2	1700	1700	1950	2050	2300	350	400	550	700	700	1500	1550	1600	1600	1800	3400	5850	6350	5900	6000	500	700	650	900	2350
Comment GUT CONTENT													TOOTHPLATE		Mollusc						Crushed shell						Detritus

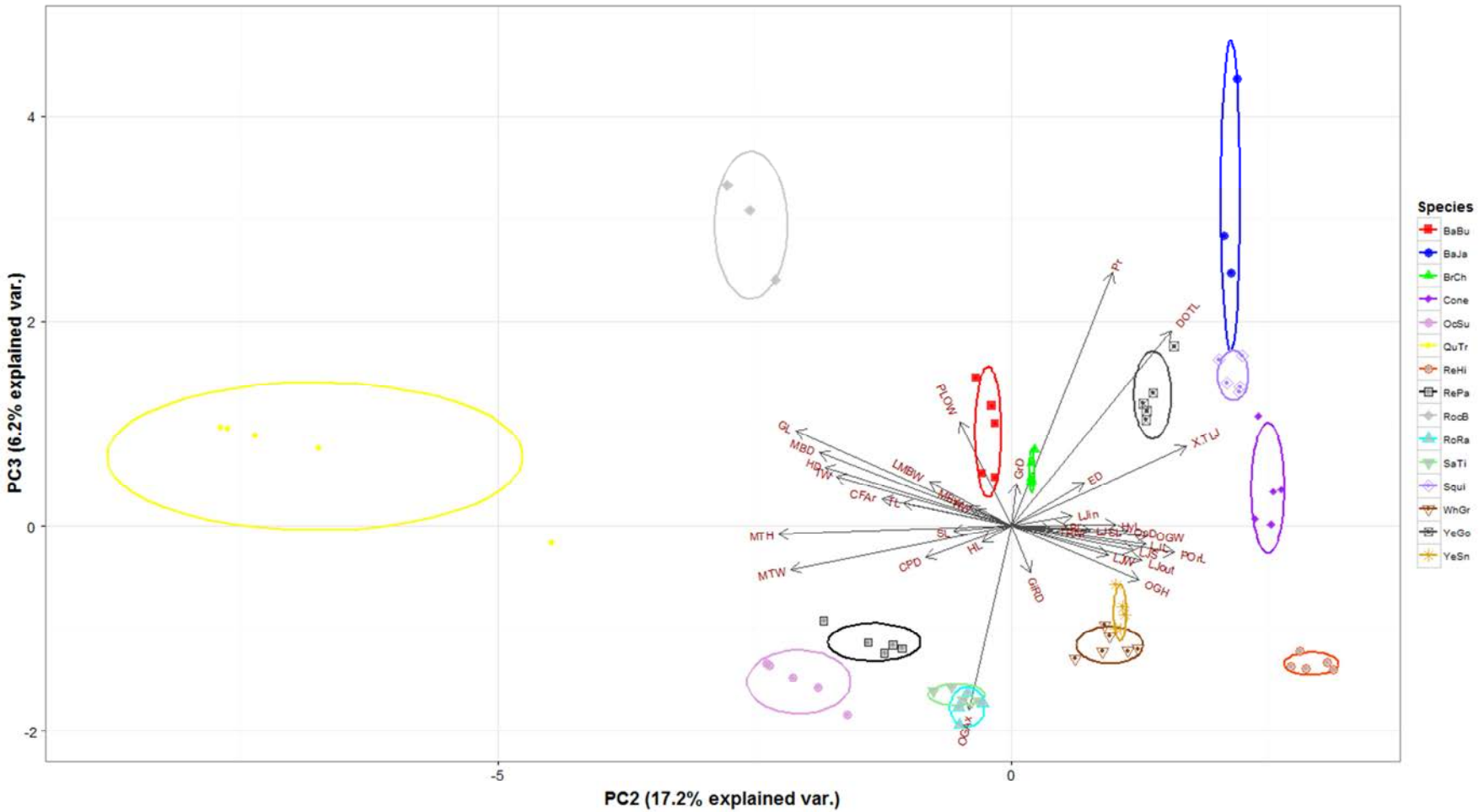
Morphological parameter	Abbreviation	Unit	Fish 50	Fish 51	Fish 52	Fish 53	Fish 54	Fish 55	Fish 56	Fish 57	Fish 58	Fish 59	Fish 60	Fish 61	Fish 62	Fish 63	Fish 64	Fish 65	Fish 66	Fish 67	Fish 68	Fish 69	Fish 70
			Chromis multilineata					*Malacanthus plumieri*				*Epinephelus guttatus*					*Caranx ruber*			*Hemipteronotus martinicensis*			
Barbels	Ba	Y/N	N	N	N	N	N	N	N	N	N	N	N	N	N	N	N	N	N	N	N	N	N
Total Weigth	TW	g	34	35	40	31	33	278	297	330	371	298	445	428	510	642	269	305	598	21.8	35.2	36.6	45
Total Length	TL	mm	136	135	140	122	127	389	388	398	420	287	322	327	340	351	328	300	378	130	149	156	163
Standard Length	SL	mm	111	112	114	97	108	338	336	345	368	287	322	327	340	351	275	254	329	130	149	156	163
Standard Length (US)	SL_US	mm	99	98	102	93	96	312	311	321	343	240	266	269	283	295	262	241	306	106	125	132	144
Length at Maximum Body Width	LMBW	mm	33.5	32.9	34.6	28.6	29.1	64.1	67.1	74.8	73.5	82	78.2	94.4	93	95.6	70.4	75.1	92.9	26.4	33.3	35.7	39.9
Maximum Body Depth	MBD	mm	38	38.9	43	39.6	37.4	46.3	50	60	53.5	81.2	84.2	88	84.6	105.4	73.9	78.9	97.4	29.2	37.4	36.5	37.7
Caudal Peduncle Depth	CPD	mm	12.9	12.7	13.6	12.5	12.8	22	20.7	21.2	23.5	19.4	23.8	22.9	26.7	27	9	9.1	11.4	12	13.7	14.6	16.1
Head Length	HL	mm	25.2	23.8	26.2	24.4	24.8	74.7	73.3	81.3	84	91.9	104.3	111.1	114.4	108	58.8	63.8	84.2	26.4	29.7	30.4	32.2
Eye Diameter	ED	mm	8.8	8.6	9.1	8.3	8.5	13.4	13.7	13.9	14.3	21	23.8	24.8	22.7	24.1	19.5	18.7	20.1	5.7	5.8	5.9	5.9
Protrusion	Pr	mm	4.6	5.8	5.2	4.4	4.7	0	0	0	0	0	0	0	0	0	9.5	9.7	13.2	3	2.1	2.9	2.4
Oral Gape Axis	OGAx	degrees	17	15	15	17	17	39	35	40	39	50	48	46	50	54	28	27	24	67	73	67	68
Lower Jaw Length	LJL	mm	9.6	9.7	11	8.7	9.2	34.5	33.2	34.6	38.8	49.7	60	63.4	61.4	67.5	34.3	36.1	41.8	11.2	13.5	13.9	13.5
Oral Tooth Type 1	TOT1	Y/N	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Oral Tooth Type 2	TOT2	Y/N	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Oral Tooth Type 3	TOT3	Y/N	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
Oral Tooth Type 4	TOT4	Y/N	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Oral Tooth Type 5	TOT5	Y/N	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Bony Gill Raker Length	RL	mm	0.4	0.5	0.5	0.4	0.4	1.2	1	1	1.2	4.4	4.3	3.4	5.1	4.8	2.1	2	2.7	0.6	0.5	0.7	0.9
Gill Inter Raker Distance	GIRD	mm	0.3	0.2	0.3	0.2	0.2	2	2.1	2	1.8	2.1	2	2.1	2.1	3	1.2	1.2	1.3	0.3	0.4	0.4	0.6
Postlingual Organ Width	PLOW	mm	8.2	9	9.3	8.3	8.6	19.4	16	18	16.9	15.4	15.5	13.5	13.8	14.1	22.4	26	40.4	6.2	8.3	10	9.8
Pharyngeal Tooth Type 1	TPT_1	Y/N	1	1	1	1	1	0	0	0	0	0	0	0	0	0	1	1	1	0	0	0	0
Pharyngeal Tooth Type 2	TPT_2	Y/N	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Pharyngeal Tooth Type 3	TPT_3	Y/N	0	0	0	0	0	1	1	1	1	1	1	1	1	1	0	0	0	0	0	0	0
Pharyngeal Tooth Type 4	TPT_4	Y/N	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Maximum Body Width	MBW	mm	18	18.8	18.3	18.1	18.4	36.2	37.2	38.9	41.4	49.2	57.1	61	65.6	60.8	33.8	37.6	48.4	10.6	14.8	13.1	16.1
Lower Jaw In-lever	LJin	mm	6.5	7.2	8.8	7.5	7.4	19.6	18.3	18.9	19.5	23.9	27.8	28.6	29.5	33.5	20	20.1	23.2	5.4	6.9	8.3	9.5
Lower Jaw Out-lever	LJout	mm	10.7	10.8	11.1	10.6	10.5	33.7	31.4	37.7	40.8	53.1	60.3	62.6	63.2	68.3	31.5	31.4	41.8	10.4	11	12.8	14.8
Postorbital Length	POrL	mm	11.6	11.8	12.3	11.9	10.9	29.3	29	27.8	31.4	40.2	46.5	44.6	49	59.4	25.1	26.4	36.6	10.5	11.8	10.8	11.4
Operculum Depth	OpD	mm	17.6	17.4	20.5	16.1	17	29.7	34	37.7	38.2	57.5	58	60.2	68.1	69.3	39.8	37.3	53.7	19.8	23.4	24.2	22.1
Oral Gape Height	OGH	mm	10.9	11.4	12.4	11.2	11.5	37.6	38.3	38.7	37.7	54.2	62.8	58.4	62.7	61.8	32.2	33.1	38.2	9.6	13.2	13.3	13.5
Oral Gape Width	OGW	mm	11.5	11.4	12.5	11	11.3	23.3	25.6	26.8	28.2	71.7	80.5	74	81.8	84	36	36.9	44.7	10.6	13.6	13.9	13.8
Gut Length	GL	mm	140	146	161	150	150	300	280	300	410	260	310	380	420	400	220	240	280	120	140	130	140
Hyiod Length	HyL	mm	8.9	9.1	9.1	8.1	8.2	21	21.8	22.6	22	45.9	49.4	49.4	51.5	59.8	29.7	28.2	36.8	8.3	10.5	10.6	12
Lower Jaw Suspensorium Length	LJSL	mm	16.9	17.1	17.2	14.7	15.3	53	51.7	58.5	60.8	76.7	83.5	90.1	88.7	90	56.3	55.5	66.4	16.4	21	22.2	22.2
Head Width	HW	mm	18	18.8	18.3	18.1	18.4	36.2	37.2	38.9	41.4	49.2	57.1	61	65.6	60.8	33.8	37.6	48.4	10.6	14.8	13.1	16.1
Head Depth	HD	mm	38	38.9	43	39.6	37.4	46.3	50	60	53.5	81.2	84.2	88	84.6	105.4	73.9	78.9	97.4	29.2	37.4	36.5	37.7
Sex	S	M/F																					
Lower Jaw Width	LJW	mm	7	7.1	7.9	7.5	7.4	20.5	17.6	18.1	22.2	33.5	37.8	35.7	42.6	37	19.2	19.4	26.3	5.8	7.4	7.8	7.4
Lower Jaw Span	LJS	mm	22.4	23.5	24	23.6	23	78.9	75	79.9	84.7	114.7	130	129.5	128.6	141.2	75.5	74.2	96.7	23.9	27.1	27.5	26.5
Number of Teeth on Lower Jaw	#TLJ	#	36	36	36	36	36	34	30	38	33	160	162	150	172	166	>100	>100	>100	18	20	24	22
Density of Teeth on Lower Jaw	DOTL	#	2.5	2.5	2.4	2.5	2.5	0.3	0.2	0.4	0.3	2	1.8	1.7	1.9	2.2	5	5.5	6	0.9	0.8	0.9	0.8
Maximal Tooth Height	MTH	mm	0.3	0.3	0.3	0.25	0.3	3.5	2.7	3.4	4.6	2.1	2.3	2.4	2	3	0.2	0.2	0.25	1.9	2.2	2.4	2.3
Maximal Tooth Width	MTW	mm	0.4	0.4	0.4	0.35	0.4	1.5	1.9	2	2.3	1.2	0.9	0.8	0.9	1.9	0.2	0.2	0.2	0.7	0.8	0.8	0.7
Total Number of Gill Rakers	TRNr	#	16	15	15	16	16	16	14	16	16	18	19	19	18	19	25	26	28	17	16	16	18
Gill Raker Density	GrD	#	2.8	3	2.7	3.1	3	0.5	0.5	0.5	0.6	0.4	0.4	0.3	0.3	0.3	0.8	0.8	1	2.6	2.3	2.2	2
Lower Pharyngeal Jaw Mass	PJM	g																					
Lower Pharyngeal Length	LPL	mm																					
Lower Pharyngeal Width	LPW	mm																					
Caudal Fin Area	CFAr	mm2	500	550	600	500	550	2700	3150	2800	3300	3250	3350	3300	3900	4100	2250	1950	3400	550	900	1000	1050
Comment GUT CONTENT								Sea urchins + mollusks + crabs									small fish						

Appendix X: Principal Component Analysis (PCA)

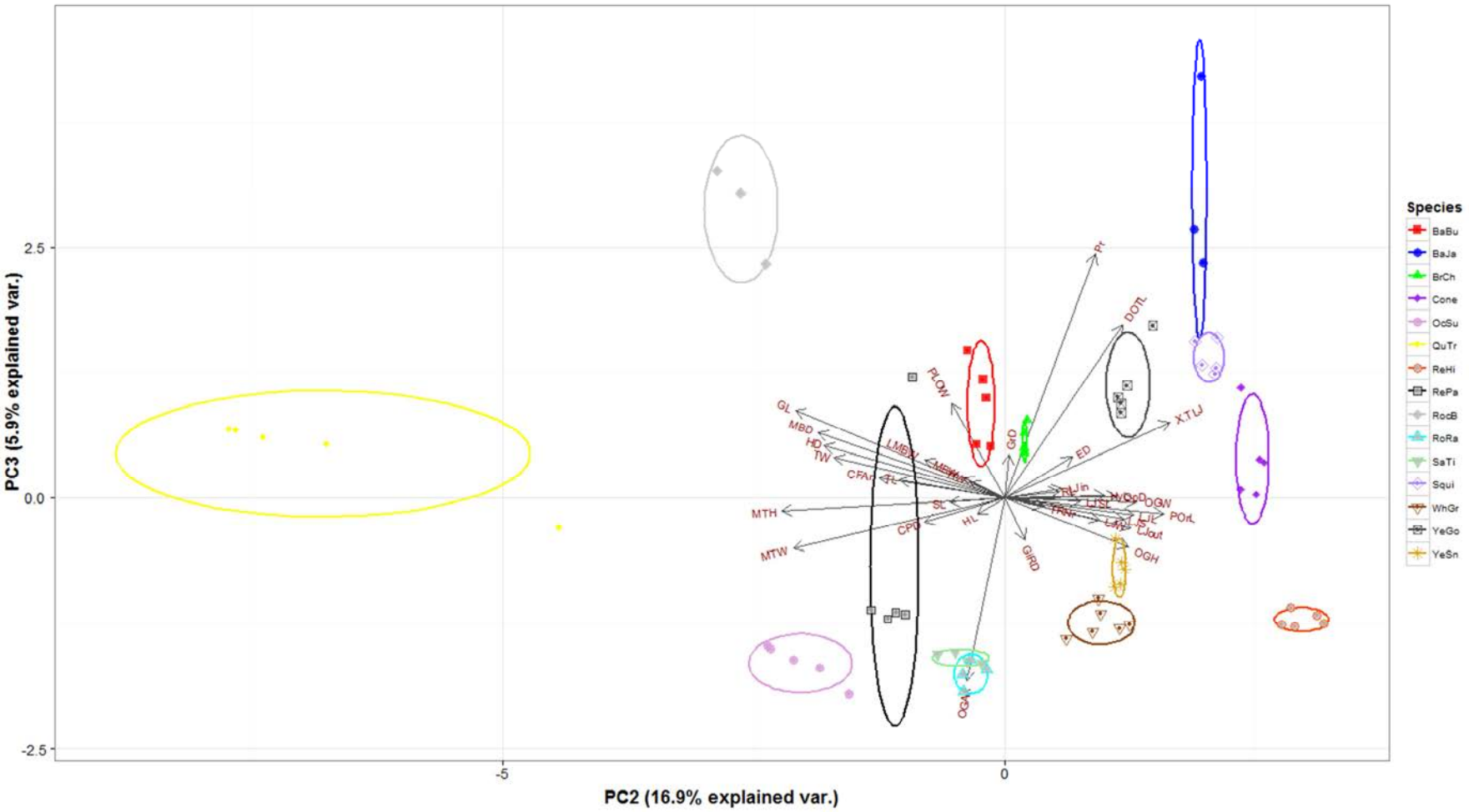
Raw PC1-PC2



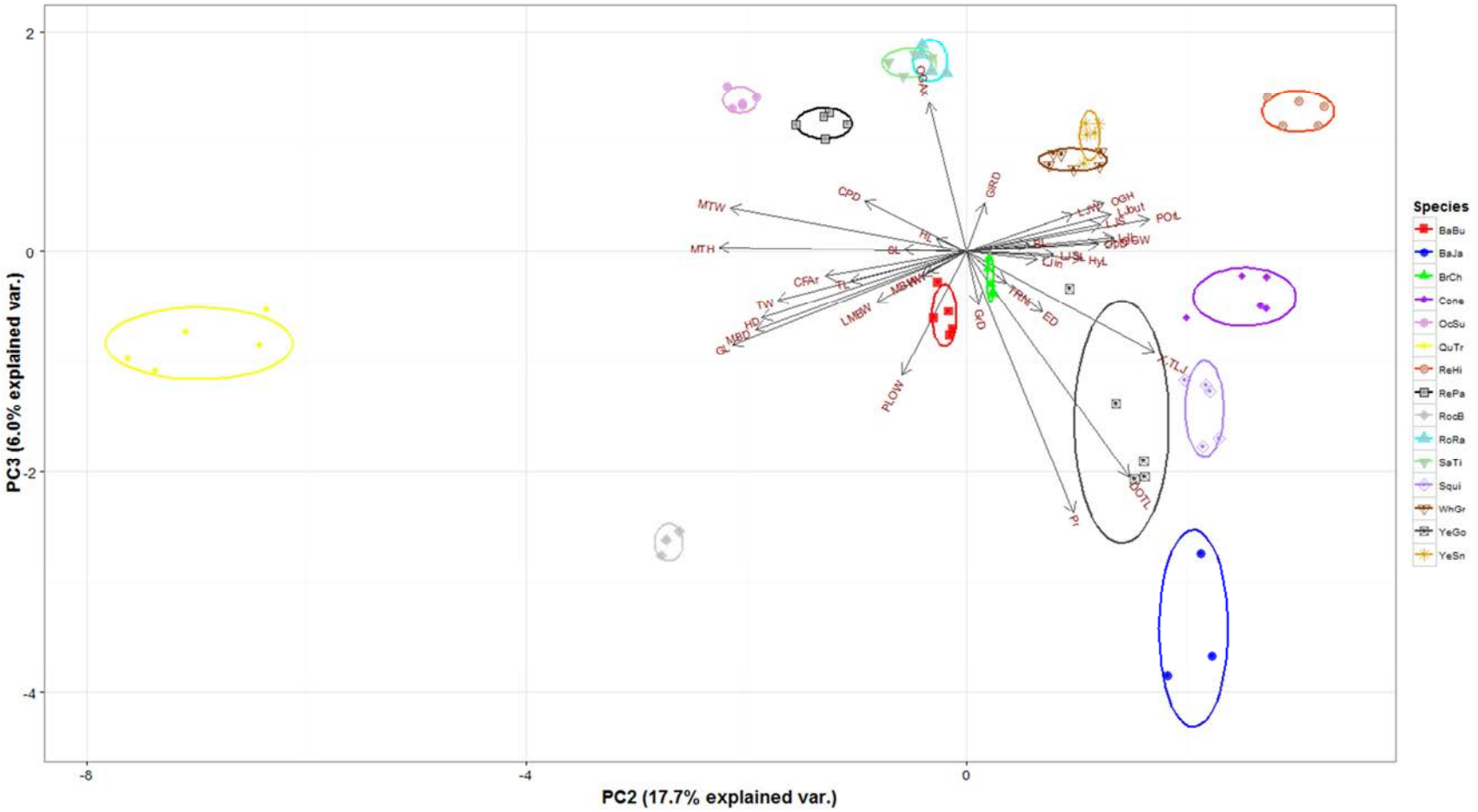
Raw PC2-PC3


PC3 (6.2% explained var.)
PC2 (17.2% explained var.)
4
2
0
-2
-5
0
Species
BaBu
BaJa
BrCh
Cone
OcSu
QuTr
ReHi
RePa
RocB
RoRa
SaTi
Squi
WhGr
YeGo
YeSn
PLOW
GrD
Pt
DDTL
XTLJ
ED
GL
MBD
HD
TW
CFAr
LMBW
MTH
MTW
CPD
SL
HL
LJin
LJW
LJout
POrL
OGW
OGH
GRD
OGHx

Normalized PC2-PC3



Size adjusted PC2-PC3



Appendix XI: R-script

```
# Set working directory
remove(list=ls(all=TRUE))  #remove all objects
setwd("C:/Users/Twan/Documents/MSc Thesis AFI/ANALYSE/R analyse/Twan/R Datasets")

# Load permute package
# install.packages('permute', C:/Users/Twan/Documents/MSc Thesis AFI/ANALYSE/R analyse/Twan/Packages', dep=TRUE)
require('permute', lib.loc='C:/Users/Twan/Documents/MSc Thesis AFI/ANALYSE/R analyse/Twan/Packages')
require('xlsReadWrite', lib.loc='C:/Users/Twan/Documents/MSc Thesis AFI/ANALYSE/R analyse/Twan/Packages')

# Load vegan package
# install.packages('vegan', C:/Users/Twan/Documents/MSc Thesis AFI/ANALYSE/R analyse/Twan/Packages', dep=TRUE)
require('vegan', lib.loc='C:/Users/Twan/Documents/MSc Thesis AFI/ANALYSE/R analyse/Twan/Packages')
require('rJava', lib.loc='C:/Users/Twan/Documents/MSc Thesis AFI/ANALYSE/R analyse/Twan/Packages')


citation()

#-----------------------------------------------------R scripts-----------------------------------------------------------

# Permutational Anova tests
 # For Biomass, commsh stands for fish communities in shallow depth range, opcode for factors
 # Upload data sheets

commsh<-as.data.frame(read.csv(file="Biomass_Comm_Shallow_Twan.csv", header=TRUE, row.names=1, sep=";"))
opcodesh<-as.data.frame(read.csv(file="Factors_Shallow_Twan.csv", header=TRUE, row.names=1, sep=";"))
abunsh<-as.data.frame(read.csv(file="Relabun_Shallow_Twan.csv", header=TRUE, row.names=1, sep=";"))
nspsh<-as.data.frame(read.csv(file="Nsp_Shallow_Twan.csv", header=TRUE, row.names=1, sep=";"))
nsp<-as.data.frame(read.csv(file="Nsp_Twan.csv", header=TRUE, row.names=1, sep=";"))

opcodetotal<-as.data.frame(read.csv(file="Factors_Twan.csv", header=TRUE, row.names=1, sep=";"))
opcodetotalsharks<-as.data.frame(read.csv(file="Factors_Twan_sharks.csv", header=TRUE, row.names=1, sep=";"))
opcodetotalrays<-as.data.frame(read.csv(file="Factors_Twan_rays.csv", header=TRUE, row.names=1, sep=";"))

relabuntotal<-as.data.frame(read.csv(file="Relabun_Comm_Twan.csv", header=TRUE, row.names=1, sep=";"))
relabuntotalsharks<-as.data.frame(read.csv(file="Relabun_Comm_sharks.csv", header=TRUE, row.names=1, sep=";"))
relabuntotalrays<-as.data.frame(read.csv(file="Relabun_Comm_rays.csv", header=TRUE, row.names=1, sep=";"))
commtotal<-as.data.frame(read.csv(file="Biomass_Comm_Twan.csv", header=TRUE, row.names=1, sep=";"))

adonis(commtotal ~ Relief_POL1993, opcodetotal)
adonis(nsp ~ Depth_layer * Relief_POL1993 * Zone, opcodetotal)
adonis(relabuntotalsharks ~ Depth_layer * Relief_POL1993 * Zone, opcodetotalsharks)
adonis(relabuntotalrays ~ Depth_layer * Relief_POL1993 * Zone, opcodetotalrays)


# Test communities on Location, habitat category of Polunin and Zone
adonis(commsh ~ Site * Relief_POL1993 * Zone, opcodesh)
adonis(abunsh ~ Site * Relief_POL1993 * Zone, opcodesh)
adonis(nspsh ~ Site * Relief_POL1993 * Zone, opcodesh)
# also for Relief_WAT2005
adonis(commsh ~ Site * Relief_WAT2005 * Zone, opcodesh)
adonis(abunsh ~ Site * Relief_WAT2005 * Zone, opcodesh)
adonis(nspsh ~ Site * Relief_WAT2005 * Zone, opcodesh)

# Select for deep fish communities and drops
commdeep<-as.data.frame(read.csv(file="Biomass_Comm_Deep_Twan.csv", header=TRUE, row.names=1, sep=";"))
opcodedeep<-as.data.frame(read.csv(file="Factors_Deep_Twan.csv", header=TRUE, row.names=1, sep=";"))
abundeep<-as.data.frame(read.csv(file="Relabun_Deep_Twan.csv", header=TRUE, row.names=1, sep=";"))
nspdeep<-as.data.frame(read.csv(file="Nsp_Deep_Twan.csv", header=TRUE, row.names=1, sep=";"))

#Polunin
adonis(commdeep ~ Site * Relief_POL1993 * Zone, opcodedeep)
adonis(abundeep ~ Site * Relief_POL1993 * Zone, opcodedeep)
adonis(nspdeep ~ Site * Relief_POL1993 * Zone, opcodedeep)
#And Watson
adonis(commdeep ~ Site * Relief_WAT2005 * Zone, opcodedeep)
adonis(abundeep ~ Site * Relief_WAT2005 * Zone, opcodedeep)
adonis(nspdeep ~ Site * Relief_WAT2005 * Zone, opcodedeep)

# And deeper areas
commdeeper<-as.data.frame(read.csv(file="Biomass_Comm_Deeper_Twan.csv", header=TRUE, row.names=1, sep=";"))
opcodedeeper<-as.data.frame(read.csv(file="Factors_Deeper_Twan.csv", header=TRUE, row.names=1, sep=";"))
abundeeper<-as.data.frame(read.csv(file="Relabun_Deeper_Twan.csv", header=TRUE, row.names=1, sep=";"))
nspdeeper<-as.data.frame(read.csv(file="Nsp_Deeper_Twan.csv", header=TRUE, row.names=1, sep=";"))
```

```
#Polunin
adonis(commdeeper ~ Site * Relief_POL1993 * Zone, opcodedeeper)
adonis(abundeeper ~ Site * Relief_POL1993 * Zone, opcodedeeper)
adonis(nspdeeper ~ Site * Relief_POL1993 * Zone, opcodedeeper)
#And Watson
adonis(commdeeper ~ Site * Relief_WAT2005 * Zone, opcodedeeper)
adonis(abundeeper ~ Site * Relief_WAT2005 * Zone, opcodedeeper)
adonis(nspdeeper ~ Site * Relief_WAT2005 * Zone, opcodedeeper)

# See http://phylodiversity.net/skembel/r-workshop/biodivR/SK_Biodiversity_R.html for explanation #
# comm is the community data, species in columns, in the rows opcodes and biomass or abundance of each species
# opcode is opcodes with the factors

#-----------------------------------------------------------------------------------------------------------------------

# remove other data

rm(list = ls())

# Upload data sheets
comm<-as.data.frame(read.csv(file="Relabun_comm_Twan.csv", header=TRUE, row.names=1, sep=";"))
opcode<-as.data.frame(read.csv(file="Relabun_comm_Twan.csv", header=TRUE, row.names=1, sep=";"))
attach(comm)
names(comm)
str(comm)


# Load ape package
# install.packages('ape', C:/Users/Twan/Documents/MSc Thesis AFI/ANALYSE/R analyse/Twan/Packages', dep=TRUE)
require('ape', lib.loc='C:/Users/Twan/Documents/MSc Thesis AFI/ANALYSE/R analyse/Twan/Packages')
# Load picante package
# install.packages('picante', C:/Users/Twan/Documents/MSc Thesis AFI/ANALYSE/R analyse/Twan/Packages', dep=TRUE)
require('picante', lib.loc='C:/Users/Twan/Documents/MSc Thesis AFI/ANALYSE/R analyse/Twan/Packages')
# Load spa package
# install.packages('spa', C:/Users/Twan/Documents/MSc Thesis AFI/ANALYSE/R analyse/Twan/Packages', dep=TRUE)
require('spa', lib.loc='C:/Users/Twan/Documents/MSc Thesis AFI/ANALYSE/R analyse/Twan/Packages')

library(picante)
class(comm)
dim(comm)
rownames(comm)

head(colnames(comm))
comm[1:5, 1:5]

data<-as.data.frame(read.csv(file="Factors_Twan.csv", header=TRUE, row.names=1, sep=";"))
head(data)
savefont <- par(font=3)
par(savefont)
str(data)

#Species accumulation curves
par(mfrow=c(1,1))
par(mar=c(4,4,1,1))
par(oma=c(1,1,1,1))
plot(specaccum(comm), xlab = "# of samples", ylab = "# of species",las=2,cex.axis=1,cex.lab=1.2, ci.col="black", ci.type="polygon")
sp.comm <- specaccum(comm, xlab = "# of samples", ylab = "# of species",las=2,cex.axis=1,cex.lab=1.2)
plot(sp.comm)

# spec acc for each depth in one graph
#factors
shallow<-as.data.frame(read.csv(file="Factors_Shallow_Twan.csv", header=TRUE, row.names=1, sep=";"))
deep<-as.data.frame(read.csv(file="Factors_Deep_Twan.csv", header=TRUE, row.names=1, sep=";"))
deeper<-as.data.frame(read.csv(file="Factors_Deeper_Twan.csv", header=TRUE, row.names=1, sep=";"))
#species
comm_sh<-as.data.frame(read.csv(file="Relabun_Shallow_Twan.csv", header=TRUE, row.names=1, sep=";"))
comm_deep<-as.data.frame(read.csv(file="Relabun_Deep_Twan.csv", header=TRUE, row.names=1, sep=";"))
comm_deeper<-as.data.frame(read.csv(file="Relabun_Deeper_Twan.csv", header=TRUE, row.names=1, sep=";"))

plot(specaccum(comm_sh, method="exact"), col="red", xlab="# of samples", ylab="# of species", ci.col="tomato")
plot(specaccum(comm_deep),col="blue", add=T, ci.col="royalblue1")
plot(specaccum(comm_deeper), col="darkgreen",add=T, ci.col="green")

# spec acc for each level of habitat in one graph #
comm_0<-as.data.frame(read.csv(file="Relabun_0_Twan.csv", header=TRUE, row.names=1, sep=";"))
comm_1<-as.data.frame(read.csv(file="Relabun_1_Twan.csv", header=TRUE, row.names=1, sep=";"))
comm_2<-as.data.frame(read.csv(file="Relabun_2_Twan.csv", header=TRUE, row.names=1, sep=";"))
comm_3<-as.data.frame(read.csv(file="Relabun_3_Twan.csv", header=TRUE, row.names=1, sep=";"))
```

```
comm_4<-as.data.frame(read.csv(file="Relabun_4_Twan.csv", header=TRUE, row.names=1, sep=";"))
plot(specaccum(comm_0, method="exact"),col="red", ci.col="tomato", xlab="# of samples", ylab="# of species",xlim=c(0,80), ylim=c(0,120))
plot(specaccum(comm_1),col="blue", add=T, ci.col="royalblue1")
plot(specaccum(comm_2), col="darkgreen",add=T, ci.col="green")
plot(specaccum(comm_3),col="chocolate4", add=T, ci.col="chocolate1")
plot(specaccum(comm_4), col="black",add=T, ci.col="gray40")


#spec acc for fisheries
abun_fisheries0<-comm_0<-as.data.frame(read.csv(file="Relabun_Fish0.csv", header=TRUE, row.names=1, sep=";"))
abun_fisheries1<-comm_0<-as.data.frame(read.csv(file="Relabun_Fish1.csv", header=TRUE, row.names=1, sep=";"))
abun_fisheries2<-comm_0<-as.data.frame(read.csv(file="Relabun_Fish2.csv", header=TRUE, row.names=1, sep=";"))
plot(specaccum(abun_fisheries2, method="random"),col="red", ci.col="tomato", xlab="# of samples", ylab="# of species",xlim=c(0,80), ylim=c(0,120))
plot(specaccum(abun_fisheries1, method="random"),col="blue", add=T, ci.col="royalblue1")
plot(specaccum(abun_fisheries0, method="random"), col="darkgreen",add=T, ci.col="green")


# check for mismatches/missing species

all.equal(rownames(comm), rownames(data))

# compare species richness between categories of habitats
str(data)
par(mfrow=c(1,3))
par(mar=c(4,4,0,1))
par(oma=c(1,0,0,0))

data$Habitat_type = factor(data$Habitat_type,c("Sand","Reef"))
data$Relief_WAT2005 = factor(data$Relief_WAT2005,c("Low","Medium","High"))
data$Relief_POL1993 = factor(data$Relief_POL1993,c("0","1","2","3","4"))

boxplot_data1<-specnumber(comm) ~ data$Habitat_type

boxplot(specnumber(comm) ~ data$Habitat_type, ylab = "# of species",las=1, names=c("Sand","Reef"), col=c("grey90","grey30"))
boxplot(specnumber(comm) ~ data$Relief_WAT2005, xlab = "Watson (2005)", las=1, names=c("Low","Medium","High"), col=c("grey90","grey60","grey30"))
boxplot(specnumber(comm) ~ data$Relief_POL1993,xlab = "Polunin (1993)", las=1, names=c("0","1","2","3","4"), col=c("grey90","grey75","grey60","grey45","grey30"))

# compare species richness between depth, fisheries activity and location
str(data)
par(mfrow=c(1,3))
par(mar=c(4,4,0,1))
par(oma=c(1,0,0,0))


data$Depth_layer = factor(data$Depth_layer, c("40","25","15"))
data$Zone = factor(data$Zone,c("0","1","2"))
data$Site = factor(data$Site,c("0", "1", "2", "3", "4"))

boxplot_data1<-specnumber(comm) ~ data$Habitat_type


boxplot(specnumber(comm) ~ data$Depth_layer, las=1, names=c("15m","25m","40m"), col=c("grey90","grey60","grey30"))
boxplot(specnumber(comm) ~ data$Zone, las=1, names=c("0","1","2"), col=c("grey90","grey75","grey60","grey45","grey30"))
boxplot(specnumber(comm) ~ data$Site, ylab = "# of species",las=1, names=c("Center", "West", "North","South", "East"),
col=c("grey90","grey75","grey60","grey45","grey30"))


t.test(specnumber(comm) ~ data$Habitat_type)

#---------------------------------Bray-Curtis dissimilarity-----------------------------------------------------------------------------------------------------------



# How does the composition of fish communities vary across different samples? How are habitat type and environmental variables related to fish community composition?
# We will calculate Bray-Curtis dissimilarity among all the samples, an abundance-weighted measure of how similar two communities are in terms of their species composition
# calculate Bray-Curtis distance among samples

str(data)
par(mfrow=c(1,1))
par(mar=c(1,4,1,1))
par(oma=c(0,0,0,0))
#-----------------------------MANTELTEST-------------------------------------------------------
community<-as.data.frame(read.csv(file="Relabun_morph_fish_habitat.csv", header=TRUE, row.names=1, sep=";"))
community0<-as.data.frame(read.csv(file="COMHab0.csv", header=TRUE, row.names=1, sep=";"))
community1<-as.data.frame(read.csv(file="COMHab1.csv", header=TRUE, row.names=1, sep=";"))
community2<-as.data.frame(read.csv(file="COMHab2.csv", header=TRUE, row.names=1, sep=";"))
```

```
community3<-as.data.frame(read.csv(file="COMHab3.csv", header=TRUE, row.names=1, sep=";"))
community4<-as.data.frame(read.csv(file="COMHab4.csv", header=TRUE, row.names=1, sep=";"))

envfactors<-as.data.frame(read.csv(file="diet_per_drop_norm_habitat.csv", header=TRUE, row.names=1, sep=";"))
envfactors0<-as.data.frame(read.csv(file="TROHab0.csv", header=TRUE, row.names=1, sep=";"))
envfactors1<-as.data.frame(read.csv(file="TROHab1.csv", header=TRUE, row.names=1, sep=";"))
envfactors2<-as.data.frame(read.csv(file="TROHab2.csv", header=TRUE, row.names=1, sep=";"))
envfactors3<-as.data.frame(read.csv(file="TROHab3.csv", header=TRUE, row.names=1, sep=";"))
envfactors4<-as.data.frame(read.csv(file="TROHab4.csv", header=TRUE, row.names=1, sep=";"))

community.bray <- vegdist(community, method = "bray",data=community)
community0.bray <- vegdist(community0, method = "bray",data=community)
community1.bray <- vegdist(community1, method = "bray",data=community)
community2.bray <- vegdist(community2, method = "bray",data=community)
community3.bray <- vegdist(community3, method = "bray",data=community)
community4.bray <- vegdist(community4, method = "bray",data=community)

envfactors.bray<- vegdist(envfactors, method = "bray",data=envfactors)
envfactors0.bray<- vegdist(envfactors0, method = "bray",data=envfactors)
envfactors1.bray<- vegdist(envfactors1, method = "bray",data=envfactors)
envfactors2.bray<- vegdist(envfactors2, method = "bray",data=envfactors)
envfactors3.bray<- vegdist(envfactors3, method = "bray",data=envfactors)
envfactors4.bray<- vegdist(envfactors4, method = "bray",data=envfactors)

mantel(community.bray, envfactors.bray)
mantel(community0.bray, envfactors0.bray)
mantel(community1.bray, envfactors1.bray)
mantel(community2.bray, envfactors2.bray)
mantel(community3.bray, envfactors3.bray)
mantel(community4.bray, envfactors4.bray)

mantel(community.bray, envfactors.bray, method="spear")
plot(community.bray, envfactors.bray)
plot(community0.bray, envfactors0.bray)
plot(community1.bray, envfactors1.bray)
plot(community2.bray, envfactors2.bray)
plot(community3.bray, envfactors3.bray)
plot(community4.bray, envfactors4.bray)

community.bray

pc <- prcomp(community, scale = TRUE)
pc<- scores(pc, display = "sites", choices = 1:10)
edis <- vegdist(pc, method = "euclid")
vare.dis <- vegdist(wisconsin(sqrt(community)))
mantel(vare.dis, edis)
plot(vare.dis, edis)



#-------------------------------------------------------------------------------------
# cluster communities using average-linkage algorithm
comm.bc.clust <- hclust(comm.bc.dist, method = "average")
# plot cluster diagram
plot(comm.bc.clust, ylab = "Bray-Curtis dissimilarity")

str(data)
par(mfrow=c(1,1))
par(mar=c(3,3,1,1))
par(oma=c(0,0,0,0))

# non-metric multidimensional scaling to visualize the multivariate structure of these communities
# The metaMDS function automatically transforms data and checks solution robustness
comm.bc.mds <- metaMDS(comm, dist = "bray")
comm.bc.mds
# Assess goodness of ordination fit (stress plot)
stressplot(comm.bc.mds)
summary(comm.bc.mds)

# Names are opcodes
ordiplot(comm.bc.mds, display = "species", type = "text", data=data)
# automated plotting of results - tries to eliminate overlapping labels
ordipointlabel(comm.bc.mds)

# For Coral, Sand category
# ordination plots are highly customizable set up the plotting area but don't plot anything yet
mds.fig <- ordiplot(comm.bc.mds, type = "none")
mds.fig
```

```
vare.mds <- metaMDS(comm, trace = FALSE)
-------------------------------------------------------------------------
community<-as.data.frame(read.csv(file="Relabun_morph_fish_habitat.csv", header=TRUE, row.names=1, sep=";"))
prcomp(community)
summary(prcomp(community))
prcomp(community, scale = TRUE, center=TRUE)
prcomp(~
banded_butterflyfish+bar_jack+bicolor_damselfish+black_durgeon+blue_chromis+blue_runner+blue_tang+bluehead+chalk_bass+coney+cottonwick+creole_wrass
e+creolefish+doctorfish+french_angelfish+

harlequin_bass+mackerel_scad+ocean_surgeonfish+princess_parrotfish+queen_triggerfish+red_hind+redband_parrotfish+rock_beauty+rosy_razorfish+sand_tilefis
h+slippery_dick+spotted_goatfish+squirrelfish+stoplight_parrotfish+tobaccofish+white_grunt+white_margate+yellowhead_wrasse+yellowtail_snapper
     , data = community, scale = TRUE, center=TRUE)
plot(prcomp(community))
scores(prcomp(community, scale = TRUE, center=TRUE))
biplot(prcomp(community, scale = TRUE, center=TRUE))
prcomp(community, scale = TRUE, center=TRUE)

envfactors<-as.data.frame(read.csv(file="diet_per_drop_norm.csv", header=TRUE, row.names=1, sep=";"))

prcomp(envfactors, scale = TRUE, center=TRUE)
prcomp(~ Phy_t+Phy_p+Alg_b+Detr+MiCr_t+MiCr_p+Crust+Lar_wrm+Mollusc+Fish_p+Fish_a, data = envfactors, scale = TRUE, center=TRUE)
plot(prcomp(envfactors))
summary(prcomp(envfactors))
scores(prcomp(envfactors, scale = TRUE, center=TRUE))
biplot(prcomp(envfactors, scale = TRUE, center=TRUE))
prcomp(envfactors, scale = TRUE, center=TRUE)

#-------------------------------------------------------------------------
pc <- prcomp(community, scale = TRUE)
pc<- scores(pc, display = "sites", choices = 1:10)
edis <- vegdist(pc, method = "euclid")
vare.dis <- vegdist(wisconsin(sqrt(community)))
mantel(vare.dis, edis)
plot(vare.dis, edis)

pc <- prcomp(envfactors, scale = TRUE)
pc<- scores(pc, display = "sites", choices = 1:10)
edis <- vegdist(pc, method = "euclid")
vare.dis <- vegdist(wisconsin(sqrt(envfactors)))
mantel(vare.dis, edis)
plot(vare.dis, edis)
## the variances of the variables in the
## USArrests data vary by orders of magnitude, so scaling is appropriate
lalala<-USArrests
prcomp(USArrests)  # inappropriate
prcomp(USArrests, scale = TRUE)
prcomp(~ Murder + Assault + Rape, data = USArrests, scale = TRUE)
plot(prcomp(USArrests))
summary(prcomp(USArrests, scale = TRUE))
biplot(prcomp(USArrests, scale = TRUE))


# plot just the samples, colour by habitat, pch=19 means plot a circle
points(mds.fig, "sites", pch = 20, col = "red", select = data$Habitat_type ==  "Sand")
points(mds.fig, "sites", pch = 20, col = "blue", select = data$Habitat_type ==  "Reef")
# add confidence ellipses around habitat types
ordiellipse(comm.bc.mds, draw = "polygon", alpha=40, data$Habitat_type, col="grey", cex=0.7, conf = 0.95, label = TRUE)
legend(2,2, pch = c(20, 20), col = c("red", "blue"),legend = c("Sand", "Reef"), title = "Habitat types", cex=0.9)
# overlay the cluster results we calculated earlier

vare.mds

# For Polunin category
str(opcode)
# ordination plots are highly customizable set up the plotting area but don't plot anything yet
par(mfrow=c(1,1))
#c(bottom, left, top, right)
par(mar=c(4,4,1,1))
par(oma=c(0,0,0,0))
mds.fig <- ordiplot(comm.bc.mds, type = "none", xlab="Dimension  1", ylab="Dimension 2")
# plot just the samples, colour by habitat, pch=19 means plot a circle
points(mds.fig, "sites", pch = 20, col = "red", bg="red", select = data$Relief_POL1993 ==  "0")
points(mds.fig, "sites", pch = 20, col = "blue", bg="blue", select = data$Relief_POL1993 ==  "1")
points(mds.fig, "sites", pch = 20, col = "green", bg="green", select = data$Relief_POL1993 ==  "2")
points(mds.fig, "sites", pch = 20, col = "chocolate1",bg = "chocolate1",select = data$Relief_POL1993 == "3")
points(mds.fig, "sites", pch = 20, col = "black",bg="black", select = data$Relief_POL1993 ==  "4")
legend(2,2, pch = c(20, 20, 20, 20, 20), col = c("red", "blue", "green", "chocolate1", "black"), cex=0.9, legend = c("0", "1", "2", "3", "4"), title = "Habitat types")
```

```
ordiellipse(draw = "polygon", alpha=40, comm.bc.mds, data$Relief_POL1993, conf = 0.95, label = TRUE, col="grey", cex=0.7)
savefont <- par(font=1)
par(savefont)

# For depths
str(opcode)
mds.fig <- ordiplot(comm.bc.mds, type = "none", xlab="Dimension  1", ylab="Dimension 2")
# plot just the samples, colour by habitat, pch=19 means plot a circle
points(mds.fig, "sites", pch = 20, col = "red", bg="red", select = data$Depth_layer == "15")
points(mds.fig, "sites", pch = 20, col = "blue", bg="blue", select = data$Depth_layer ==  "25")
points(mds.fig, "sites", pch = 20, col = "green", bg="green", select = data$Depth_layer ==  "40")
legend(2,2, pch = c(20, 20, 20), col = c("red", "blue", "green"), cex=0.9, pt.bg = c("red", NA, "green"), legend = c("15 m", "25 m", "40 m"), title = "Depth Layer")

savefont <- par(font=1)
par(savefont)

# add confidence ellipses around habitat types
ordiellipse(draw = "polygon", alpha=40, comm.bc.mds, data$Depth_layer, conf = 0.95, label = TRUE, col = "grey", cex=0.7)
# overlay the cluster results we calculated earlier
ordicluster(comm.bc.mds, comm.bc.clust, col = "gray70")

# For Watson category
str(opcode)
mds.fig <- ordiplot(comm.bc.mds, type = "none")
# plot just the samples, colour by habitat, pch=19 means plot a circle

points(mds.fig, "sites", pch = 20, col = "red", select = data$Relief_WAT2005 == "Low")
points(mds.fig, "sites", pch = 20, col = "blue", select = data$Relief_WAT2005 ==  "Medium")
points(mds.fig, "sites", pch = 20, col = "green", select = data$Relief_WAT2005 ==  "High")
legend(2,2, pch = c(20, 20, 20), col = c("red", "blue", "green"), cex=0.9,  pt.bg = c("red", "blue", "green"), legend = c("Low", "Medium", "High"), title = "Habitat Types")
# add confidence ellipses around habitat types
ordiellipse(draw = "polygon", alpha=40, comm.bc.mds, data$Relief_WAT2005, conf = 0.95, label = TRUE, col = "grey", cex=0.7)
# overlay the cluster results we calculated earlier
ordicluster(comm.bc.mds, comm.bc.clust, col = "gray")

# How are environmental variables correlated with the ordination axes?
ordiplot(comm.bc.mds, xlab="Dimension 1",ylab="Dimension 2")
# calculate and plot environmental variable correlations with the axes use
# the subset of metadata that are environmental data
str(opcode)
plot(envfit(comm.bc.mds, opcode[, 1:50]))

data<-as.data.frame(read.csv(file="Factors_Twan.csv", header=TRUE, row.names=1, sep=";"))

#data$Zone <- factor(data$Zone, levels = c("0", "1", "2"), labels = c("Low","Medium", "High"))
# For Zone
str(opcode)
#data$Zone <- factor(data$Zone, levels = c("0", "1", "2"))
mds.fig <- ordiplot(comm.bc.mds, type = "none",xlab="Dimension 1",ylab="Dimension 2")
points(mds.fig, "sites", pch = 20, col = "red", bg="red", select = data$Zone == "0")
points(mds.fig, "sites", pch = 20, col = "blue", bg="blue", select = data$Zone ==  "1")
points(mds.fig, "sites", pch = 20, col = "green", bg="green", select = data$Zone ==  "2")
legend(2,2, pch = c(20, 20, 20), col = c("red", "blue", "green"), pt.bg = c("red", "blue", "green"), cex=0.9, legend = c("0", "1", "2"), title = "Fisheries Activity")

# add confidence ellipses around zones
ordiellipse(draw = "polygon", alpha=40, comm.bc.mds, data$Zone, conf = 0.95, label = TRUE, col = "grey", cex=0.7)
# overlay the cluster results we calculated earlier

# For site
mds.fig <- ordiplot(comm.bc.mds, type = "none")
points(mds.fig, "sites", pch = 20, col = "red", select = data$Site == "East")
points(mds.fig, "sites", pch = 20, col = "blue", select = data$Site ==  "North")
points(mds.fig, "sites", pch = 20, col = "black", select = data$Site ==  "West")
points(mds.fig, "sites", pch = 20, col = "chocolate1", select = data$Site ==  "South")
points(mds.fig, "sites", pch = 20, col = "green", select = data$Site ==  "Center")
legend(2,2.2, pch = c(20,20,20,20,20), col = c("red", "blue", "black", "chocolate1", "green"), cex=0.9, legend = c("East", "North", "West", "South", "Center"), title =
"Location")
# add confidence ellipses around cluster of  sites
ordiellipse(draw = "polygon", alpha=40, comm.bc.mds, data$Site, conf = 0.95, label = TRUE, col = "grey", cex=0.7)

# ------------------DCA: Ordination plot for species-----------------------------------

envfactors<-as.data.frame(read.csv(file="diet_per_drop_norm.csv", header=TRUE, row.names=1, sep=";"))
community<-as.data.frame(read.csv(file="Relabun_morph_fish.csv", header=TRUE, row.names=1, sep=";"))

library(vegan)
modsp <- decorana(envfactors)
?decorana
```

```
summary(modsp)
plot(modsp, dis="sp")
modsp

testing<-rda(envfactors)
summary(testing)
plot(testing)

library(vegan)
modsp <- decorana(opcode)
?decorana
summary(modsp)
plot(modsp, dis="sp")
modsp
row.names(opcode)[1:5]
# abbreaviation of names
shnam <- make.cepnames(row.names(opcode))
list(shnam[1:140])
names(opcode)
pl <- plot(modsp, dis="sites")
#identify(pl, "sites", labels=shnam) #Something goes wrong here!
#stems <- colSums(opcode)
plot(modsp, dis="sites", type="n")
sel <- orditorp(modsp, dis="sites", lab=shnam, pcol = "gray", pch="+")
plot(modsp, dis="sites", type="n")
ordilabel(modsp, dis="sites", lab=shnam)


# Now add variables to the species graph
library(picante)
habitat<-factor(data$Relief_POL1993)
str(opcode)
summary(modsp)
#c(bottom, left, top, right)
par(mfrow=c(1,1))
par(mar=c(4,4,4,4))
par(oma=c(0,0,0,0))
plot(modsp, dis="sites", type="n",xlab="Dimension 1",ylab="Dimension 2")
sel <- orditorp(modsp, dis="sites", lab=shnam, pcol = "gray", pch="+")
stat_hab<-envfit(comm.bc.mds, habitat)
stat_zone<-envfit(comm.bc.mds, data$Zone)
stat_depth<-envfit(comm.bc.mds, data$Depth_layer)
stat_hab
stat_zone
stat_depth
plot(envfit(comm.bc.mds, habitat),col= "red",p.max=0.05, cex=0.1)
plot(envfit(comm.bc.mds, data$Zone),col= "darkgreen",p.max=0.05, cex=0.1)
plot(envfit(comm.bc.mds, data$Depth_layer),col= "chocolate1",p.max=0.05, cex=0.1)
legend(4.5,3.5, lty=1:1, pch = c(20,20,20,20,20), col = c("red", "blue", "darkgreen", "chocolate1"), cex=0.9, legend = c("Relief - Polunin", "Relief - Watson", "Fisheries
Zone", "Depth Layer"), title = "Treatment")

#----------------------CCA-------------------------------------------------------------------------
envfactors<-as.data.frame(read.csv(file="diet_per_drop_norm.csv", header=TRUE, row.names=1, sep=";"))
community<-as.data.frame(read.csv(file="Relabun_morph_fish.csv", header=TRUE, row.names=1, sep=";"))

orig_twan <-cca(community~Phy_t+Phy_p+Alg_b+Detr+MiCr_t+MiCr_p+Crust+Lar_wrm+Mollusc+Fish_p+Fish_a, envfactors)
orig_twan
plot(orig_twan,choices=c(1,2))

summary(orig_twan)
anova.cca(orig_twan)
anova.cca(orig_twan, by="term")
anova(orig_twan, by="margin")
anova(orig_twan, by="axis")
```