Categories of habitat and depth are structuring reef fish assemblages over no-fishing and fishing zones in the Saba Marine Park (Caribbean Netherlands).

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Abstract

Reef fish assemblages are structured by many factors like depth, habitat and zonation' s in marine protected areas (MPAs). These fish assemblages can be determined by different sampling methods and design. For instance, stereo Baited Remote Underwater Video (stereo-BRUV) allows for monitoring fishes at various depths (>40m) beyond the reach of conventianol diver-based methodologies. This is relevant in a way that fish diversity, biomass and species richness changes with depth. Furthermore, the spatial distribution and composition in fish assemblages can have a strong correlation with fine-scale habitat differences. However, fine-scale measureremens of habitats are rarely available for marine research, particularly for deeper (>40m) marine environments. Stereo-BRUV studies lacking this information prior of sampling reef fish assemblages had to rely upon hierarchical classifications of habitat. One of the aims of this study was to examine which habitat classification was most sensitive to the detection of small-scale changes in fish assemblages by sampling different habitats and depths (e.g, 15, 50 and 100 meters) in the Saba Marine Park (SMP) area. We compared three categorization methods of habitat commonly used in literature 1) two scale on "habitat"; low (sand) and high (reef) relief (Colton et al. 2010); 2) three scale on "relief"; low, medium and high relief (Watson et al. 2005) and 3) fine-scale consisting of 6 types of "habitat complexity" (Polunin et al. 1993). The "habitat complexity" category method produced less variance among fish populations' mean within each habitat. This increased the probability of finding a significant difference between two fish populations' mean, as smaller variations lowered the possibility of overlapping standard deviations. For this reason we found a significant interaction effect of zonations (fishing vs. no-fishing zone) within the habitat complexity category on fish biomass, density and species richness, in all depths within the SMP boundary (15 and 50m). This effect was not found when using the habitat or relief category. However, the differences among the habitat category methods were less significant on the statistical power of detecting those changes in fish biomass, density and species richness. Overall, habitat characteristics, such as sand bottom or low complexity in substrate structure, were associated with lower values of fish biomass, density and species richness. These values increased gradually with habitats containing more complex, reef-based structures. From the shallow (15m) to deeper (50 and 100m) areas the habitat complexity in terms of reef structures significantly declined. Along this depth gradient, the structure of reef fish assemblages changed from higher densities of herbivorous species at 15 meter depth and higher carnivorous species richness and

densities found at 50 and 100 meters depth. Some species (within families of Lutjanidae and Serranidae), also important to fisheries, were distributed over the full depth range. Moreover, stereo-BRUV detected high densities of larger predatory species (*Carcharhinus perezii, Ginglymostoma cirratum)*, especially at depths of 50 meters. The changes found in fish assemblages were less determined by the effect of the no-fishing zone. On the contrary, the mean fish biomass and density were higher in the zone without protection from fisheries, indicating that fishing pressure was low in the SMP. In conclusion, depth and finer-scale habitat complexity were the main drivers that structure reef fish assemblages. These results indicate that the chosen categories of habitat and depth have a significant effect on studying reef fish assemblages across different zones in the SMP.

1. Introduction

Reef fish assemblages are strongly structured by key environmental factors, like habitat (Carpenter et al. 1981, Ferreira et al. 2001) and depth (Fujita et al. 1995, Brokovich et al. 2008). Anthropogenic impacts like fishery can also play a significant role in changing reef fish assemblages. To protect marine habitats from unsustainable exploitation many countries worldwide established Marine Protected Areas (MPAs) along territorial waters (Australia; Malcolm 2007, Caribbean; Polunin et al. 1993, Philippines; Russ et al 1996). Zonation systems were established in which fishing is reduced or prohibited in certain zones (Polunin et al. 1993). Many studies demonstrated a recovery of fish populations after the implementation of no-fishing zones or reserves (Russ and Alcala 1996, Chapman and Kramer 1999). No-fishing and fishing zones were found to be different in abundance, biomass and numbers of fish species (Roberts 1995, McClanahan et al. 2006, Noble et al. 2013). Targeted species of fisheries were often in greater abundance, length and biomass after the establishment of no-fishing zones (Harborne et al. 2008, Watson et al. 2009). However, most of these studies were focused on studying the difference between fishing and no-fishing zone without paying attention to environmental factors like habitat and depth which also may explain the difference observed between the zones (Willis and Babcock 2000, Cappo et al. 2004, Langlois et al. 2012).

The effect of no-fishing zones can be investigated by comparing reef fish assemblages inside open and closed zones for fishing (Watson et al. 2009, Langlois et al. 2012). Furthermore an understanding of fish distribution at a spatial scale is needed, where mainly habitat and depth are found to have strong potential in explaining the distribution and occurrence of fish species (Malcolm et al. 2007). These factors, such as depth (Malcolm et al. 2011, Zintzen et al. 2012), substratum type (Howard 1989, Harman et al. 2003), and vertical relief of habitat complexity (Watson et al. 2005) have been shown to represent patterns of fish diversity. Coral reefs form complex frameworks of living corals that can support a wide variety of habitats which leads to an increase in the diversity of fish (Carpenter et al. 1981, Ferreira et al. 2001). More studies showed that different habitat structures were the main drivers in changing fish assemblages (Carpenter et al. 1981, Ferreira et al. 2001), even at a fine scale of change in habitat characteristics (Moore et al. 2010).

To determine the effect of no-fishing zones on fish assemblages, all other potential explanatory variables, such as differences in habitat and depth between the no-fishing and fishing zones need to be taken into account. This means that spatial

variability of habitats needs to be similar between samples of fish assemblages of no-fishing and fishing zones. Stereo-BRUV (Baited Remote Underwater Video) studies that had access to accurate habitat maps showed that fine scale habitat differences are strongly correlated with the fish assemblages spatial distribution and composition (Moore et al. 2010, Moore et al. 2011). Many other stereo-BRUV studies (Colton et al. 2010, Polunin et al. 1993, Watson et al. 2005) had limited information on the specific habitat characteristics of the research area, particularly for investigating deeper marine environments. These studies had to rely upon hierarchical classifications of the sampled habitat and chose for simpler habitat categories; on habitat, e.g. sand or reef (Colton and Swearer 2010), relief, e.g. low, medium or high relief (Watson et al. 2005), or a finer-scale category; on habitat complexities with 6 levels categorization based on the complexities of habitat structures (Polunin and Roberts 1993). Finer scales in categories may decrease variation per level of categorization (Malcolm et al. 2011). When the sampling area consists of high spatial variability of habitats, a more diverse and higher variation on fish assemblages can be detected. This may suggest the use of more levels of categorization to detect small-scale changes in fish assemblages within habitats. This will eventually increase similarities of environmental conditions between replicate samples. More similarity between samples will improve statistical power of detecting changes in fish populations (Harvey et al. 2007b). So far, there is a need of knowledge in how different habitat classifications influence results of stereo-BRUV studies that associate fish assemblages to habitat differences (Harman et al. 2003, Colella et al. 2010, Watson et al. 2010, Malcolm et al. 2011). In this study, it was hypothesized that using different categories, chosen from low to higher degree of habitat scaling previously used by other studies (Polunin and Roberts 1993, Watson et al. 2005, Colton and Swearer 2010), wil affect how much of the variability of reef fish assemblages was attributed to factor habitat.

Moreover, the fish density, diversity and composition can change along a depth gradient (Malcolm et al. 2011, Zintzen et al. 2012). Physical and biotic factors change along a depth gradient resulting in less complexity of coral reef structures (Brokovich et al. 2008). Light levels are decreasing which leads to decreased algae growth rates (Russ 2003) and modified coral assemblages and habitat structures. Through less food availability and decreasing light levels in deeper areas, it is harder for herbivorous fish species to forage in those depth ranges (Rickel and Genin 2005). On the other hand, some fish migrate vertically during the day and use deeper areas as a refuge (Brokovich et al. 2008). Depth is therefore a useful factor in determining differences of observed fish assemblage structures, and hence representation of

biodiversity. However, until now, reef fish assemblages were only examined in shallow reefs (<15m) within the Saba Marine Park (SMP) (Polunin and Roberts 1993, Roberts 1995, Noble et al. 2013). In many other cases, similar studies were not able to measure reef fish assemblages at depths greater than 40 meters due to limitations introduced by using diver-based methodologies. In present study, the use of stereo Baited Remote Underwater Video (stereo-BRUV) may provide new information on the spatial distribution and composition of reef fish assemblages from shallow (15m) to deeper depths (50 and 100m) that have not been investigated so far in the SMP area.

The widespread application of BRUV surveys is now leading to an expanded literature which investigates the relative effect of the biases and implications on BRUV-derived data compared to other sampling techniques (Cappo et al. 2004, Watson et al. 2005, Shortis et al. 2007, Colton and Swearer 2010, Langlois et al. 2010, Brooks et al. 2011, Harvey et al. 2012). One of the advantages of stereo-BRUV over diver-based methodologies is to obtain more and higher numbers of carnivorous species (Watson et al. 2005, Harvey et al. 2007b). Various studies have suggested that larger predatory fish may be repelled in the presence of divers (Chapman and Atkinson 1986, Willis and Babcock 2000). Previous studies monitored fish in the Saba Marine Park using diver point-count census and recorded a 68% loss of carnivorous fish in shallow areas (5 m depth) across all zones since the Marine Park was established in 1987 (Noble et al. 2013). These species are more vulnerable to fisheries and therefore important to conservation programs. In general, most of the fishing occurred offshore on the Saba Bank and only some recreational fishing took place at Saba' s reefs, mainly consisted of hand-lining and a few fishing traps placed close inshore at the south side of the Island (Polunin and Roberts 1993). It is possible that previous recordings of declining numbers in carnivorous species were coming from the biases introduced by the sampling method being used, rather than through the impact of fishing. Thus, using stereo-BRUV may provide a better understanding of the spatial distribution of larger predatory fish.

The general aim of the present study was to establish a stereo-BRUV sampling design of categories on different depths and habitats useful to effectively monitor reef fish assemblages in the Saba Marine Park. In more detail, we investigated the underlying aspects introduced by monitoring and assessing reef fish assemblages through the following objectives: (1) different habitat categories were examined on the statistical power of detecting changes in reef fish assemblage metrics and towards sampling efficiency in reaching that power, (2) changes in the structure of habitat and

associated fish assemblages were investigated over different depths, and (3) we examined the present biomass and length of herbivore and carnivore species across fishing and no-fishing zones at different depths.

2. Literature review

The aim of this literature review is to provide an overview of the advantages and disadvantages of each sampling method that has been used for collecting data on fish assemblages. As we used stereo Baited Remote Underwater Video (stereo-BRUV) method, comparisons are made between this method and other methods being reviewed.

2.1 Introduction

A variety of sampling methods have been used to study the effect of Marine Protected Areas (MPAs) on the conservation of reef fish assemblages. An important consideration in designing any robust ecological study is the choice of sampling method (Willis et al. 2000, Watson et al. 2010). Different sampling methods may result in different estimates of the fish population' s mean and variance. Bias in methods can be caused by factors that are intrinsic to the species being observed (MacNeil et al. 2008), as well as by the survey methodology itself (Cappo et al. 2004, Harvey et al. 2004, Colton and Swearer 2010, Watson et al. 2010, Harvey et al. 2012). Here, we reviewed the pros and cons of most sampling techniques commonly used to assess fish assemblages, with special reference to stereo-BRUV method.

2.2 Fishery independent data

The majority of fishery independent data collected to investigate reef fish assemblages were conducted by diver-based Underwater Visual Census (UVC) surveys (Russ and Alcala 1996, English et al. 1997). Such an observational, non-destructive sampling technique is preferred in an ecologically sensitive or protected area. The uses of destructive sampling techniques, such as fish trapping and trawling, are for the most part prohibited in MPAs. However, due to biases and limitations by UVC

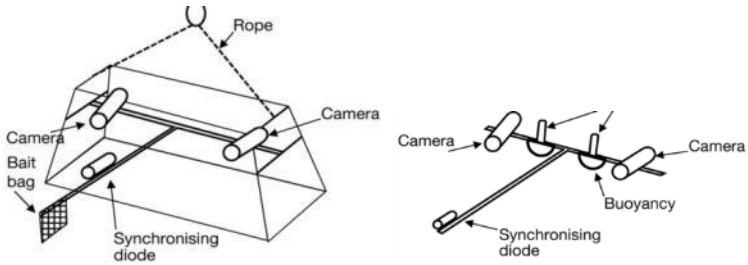


Figure 1. Schematic representation of a stereo Baited Remote Underwater Video system (stereo-BRUV) and stereo Underwater Video Census system (stereo-UVC).

alternative techniques were developed, including remote video census (Fig.1). Remote underwater video systems can be deployed with bait or without. Here, we reviewed the biases of measuring fish using diver-based methodologies compared to stand-alone remote video stations, as well as the effect of using bait to remote video stations.

2.2.1 BRUV

First, stand-alone remote video stations, are non-extractive and do not cause major disturbance to the substrate and its epifauna (Cappo et al. 2006). Secondly, stand-alone remote video systems can be deployed at depths beyond the reach of SCUBA divers (>40m) with video stations being sampled consecutively without the need of interval or limiting sampling time (Watson et al. 2007). Remote video census is therefore highly efficient in monitoring large areas. This will increase the amount of replicates in monitoring different habitat types and associated fish assemblages, which in turn improves statistical power and precision of the results. In comparison, remote video stations were found to be more cost-efficient in terms of total time spent in the field compared to diver-based methods (Harvey et al. 2002, Langlois et al. 2010). In addition, the observed data including length measurements can be obtained both via visual estimation from divers and via stereo remote video stations (Harvey and Shortis 1998). Stand-alone BRUV provide accurate and precise length measurement data of reef fishes. Length measurements obtained from divers during UVC suffer from inter-observer variability or the relative experience of the diver (Langlois et al. 2010). In general, remote video stations obtained estimates of fish biomass, density and diversity with less variance, resulting in greater power to detect spatial and temporal changes in the fish assemblage metrics (Harvey et al. 2001, Langlois et al. 2010).

With stand-alone BRUV fish density is being defined as the maximum number of individuals of a species observed at a single frame within the recorded time period (hereafter referred as MaxN). MaxN is a measure of relative density that avoids recounting of individuals that repeatedly visit the bait (Willis and Babcock 2000). However, there is an upper limit to the number of fish that can be viewed in a frame, in particular to those species that formed dense schools (Willis et al. 2000). The most severe drawback of BRUV is that the sampled area is not known. When studies tried to estimate the attraction area of the bait plume, they had to deal with many assumptions making it difficult to draw rightful conclusions (See RUV). For these two reasons, only a relative estimate of density can be acquired, not an absolute estimate.

2.2.2 UVC

UVC surveys are conducted by divers and various studies have suggested that some species of fish may either be attracted to or repelled by divers (Chapman and Atkinson 1986, Willis and Babcock 2000). This behavioral response means that fish abundance estimates will reflect or will be influenced by the behavior of the fish (Willis et al. 2000). Large carnivorous species, such as species of shark, are most sensitive to disturbance from divers and the abundance of such species is often underestimated by UVC surveys (Harvey, 2004). Stand-alone BRUV have been shown to provide better estimates of large predatory fish (Watson et al. 2005, Langlois et al. 2006, Malcolm et al. 2007).

On the other hand, UVC often recorded more of the smaller sized cryptic species than BRUV (Willis 2001, Watson et al. 2005), suggesting that at least some of the differences between methods were based on the ability of divers to record cryptic and territorial species (Fig.2). However, from the perspective of not using underwater video techniques, several studies found that divers are better than cameras at observing cryptic species because divers are able to search complex habitats in ways that cameras cannot (Stobart et al. 2007).

Furthermore, there is spatial and temporal variability between sampling designs of the two techniques. The field-of-view from the remote video cameras, depending on water visibility, was on average 8 meters and sampling took approximately 1 hour. UVC transects can cover an area of 100 to 500 m^2 of habitat, taking on average not more than 10 minutes per survey. Thus divers conducting a UVC are likely to pass through many individuals' territories, while a BRUV unit will usually land in a single individuals' territory or the junction area between a few individuals' territories (Colton and Swearer 2010). This difference between the two methods suggests that UVC surveyed higher habitat diversity and therefore a higher species diversity than BRUV (Colton and Swearer 2010).

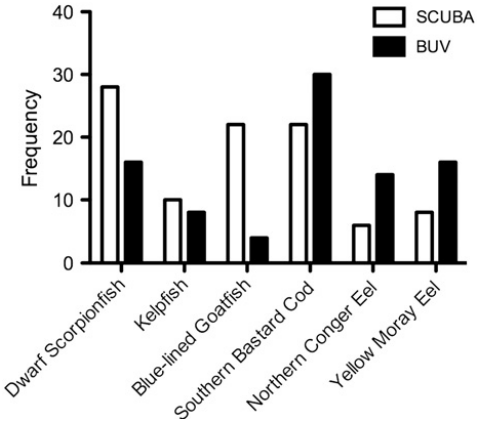


Figure 2. The frequency of occurrence of various fish between BRUV (black bars) and UVC (white bars). Mobile predators (southern bastard cod, yellow moray eel, northern conger eel) show increased occurrence at baited underwater video drops. The opposite

In conclusion, most of the studies that compared UVC to stand-alone BRUV have found BRUV to be superior to UVC in terms of measuring fish diversity (Willis et al. 2000, Watson et al. 2005, Harvey et al. 2007a), only a few studies recorded more individuals, of all species (Fig.2: cryptic and most territorial species), and higher biodiversity using UVC (Stobart et al. 2007, Colton and Swearer 2010). At any time BRUV recorded proportionally more mobile predators (Fig.2).

2.2.3 RUV

RUV (Remote Underwater Video) is different from BRUV as it does not use additional bait. Watson et al. (2005) compared fish assemblage data measured from UVC, baited (BRUV) and unbaited (RUV) remote video stations. Results showed that the use of bait (BRUV) recorded the highest species diversity and most individuals over different habitat types (Fig.3). Harvey et al. (2007b) found an increase in similarity of samples of fish assemblages within a habitat which generated greater statistical power to detect

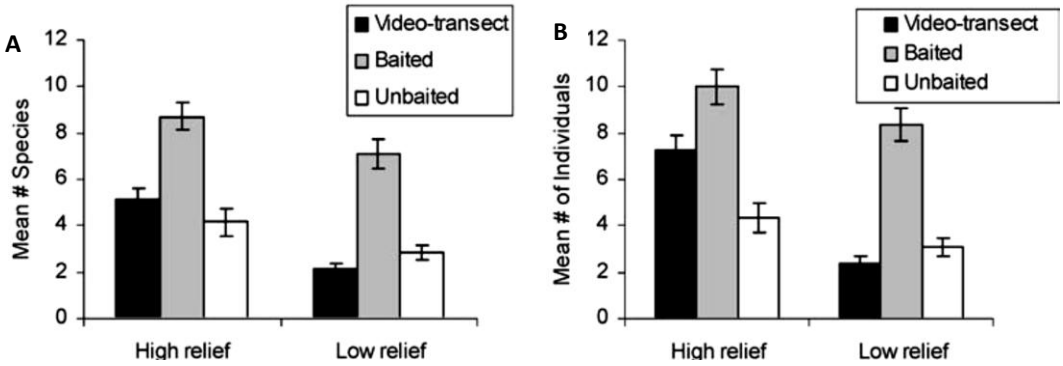


Figure 3. Mean number of species (A) and individuals (B) grouped within habitat type, recorded by Video-transect, Baited and Unbaited Underwater Video census. Source: (Watson et al. 2005)

changes in the observed fish assemblages (Harvey et al. 2007a). Additionally, bait attracts species closer to the cameras providing more accurate measurements of fish lengths (Fig. 4) using stereo-video systems (Harvey et al. 2001, Harvey et al. 2004). Furthermore, BRUV is known to sample relatively higher biomass of larger predatory fish with no differences in sampling biomass of herbivores (Watson et al. 2005, Harvey et al. 2007a).

Figure 4. Bait attracted more individuals and species (picture; *Lutjanus bucanella* at 50 meters depth) into the field-of-view of the cameras.

Carnivorous fishes feed on the bait which also stimulated herbivorous species to approach (Watson et al. 2005). Herbivorous species, although not directly attracted to the bait, are interested in the activity caused by fish feeding on the bait (Cappo et al. 2003). From present study, more behavioral traits from species of different trophic groups were found to be attracted to the bait (Fig.3). Such as sharks and rays come not only just to feed, but were often found to investigate the bait. Others, like some herbivorous species of the family Scaridae and Chaetodontidae were interested in the general activity around the bait. Some large predatory species of the family Carangidae and Sphyraenidae (Fig. 5) were probably attracted by the presence of small prey species. Thus, the use of bait to Remote Underwater Video systems stimulates fish, due to different behavioral traits, towards the cameras for counting and measurement (Bassett and Montgomery 2011).

The complexity of BRUV over RUV is to determine the sampling area of the bait plume (Harvey et al. 2007a). The sampling area is hard to investigate due to variable current velocity which affects the bait plume area (Taylor et al. 2013). One of the studies using BRUVS targeting deepwater scavengers (Priede and Merrett 1996) has modelled the area of attraction from the bait plume. They used MaxN and arrival time to determine the absolute fish density with the parameters of current velocities, fish swimming speeds and models of bait plume behaviour. However, it was too difficult to determine each one of those parameters with absolute certainty which made it still unclear to define the exact sampling area (Priede and Merrett 1996).

Figure 5. Fish were attracted to the bait through different behavioral cues. A great barracuda (*Sphyraena barracuda*) investigated the bait and the much smaller species, brown chromis (*Chromis multilineata*), were interested in the general activity around it.

2.3 Fishery dependent data

Research based on fishery dependent data has to deal with many biases that rely on the use of fishing gear selective for catching fish with certain sizes and species composition (Willis et al. 2000). Many of these potential biases can be eliminated

through the sampling approach offered by stereo- BRUV. Here, we reviewed studies that used fishing gear to obtain fish assemblage data and compared that with data derived by stereo-BRUV studies.

2.3.1 Fish traps

Studies investigating fish assemblages from the catch of fish traps have shown that some herbivorous species were caught more using unbaited traps than baited traps on coral reefs (Munro 1974). The opposite was found for remote video techniques, whereas BRUVS sampled no difference or even more herbivorous species than unbaited RUVS (Watson et al. 2005). It could be that predators and scavengers attracted to the baited fish traps might feed on or scare away the non-predatory or herbivorous species inside the traps, which reduces density and diversity of individuals, species and trophic groups being recorded from fish traps. A study which placed cameras inside the fish traps showed that some species have escape rates of up to 25% (Newman and Australia 2012). Some species were not or less caught by fish traps, but has been recorded outside the traps by the cameras and also on the stereo-BRUVs. The species not caught by traps were many non-commercial species. On the other hand, BRUV recorded much more species and individuals than fishing traps (Fig. 6).

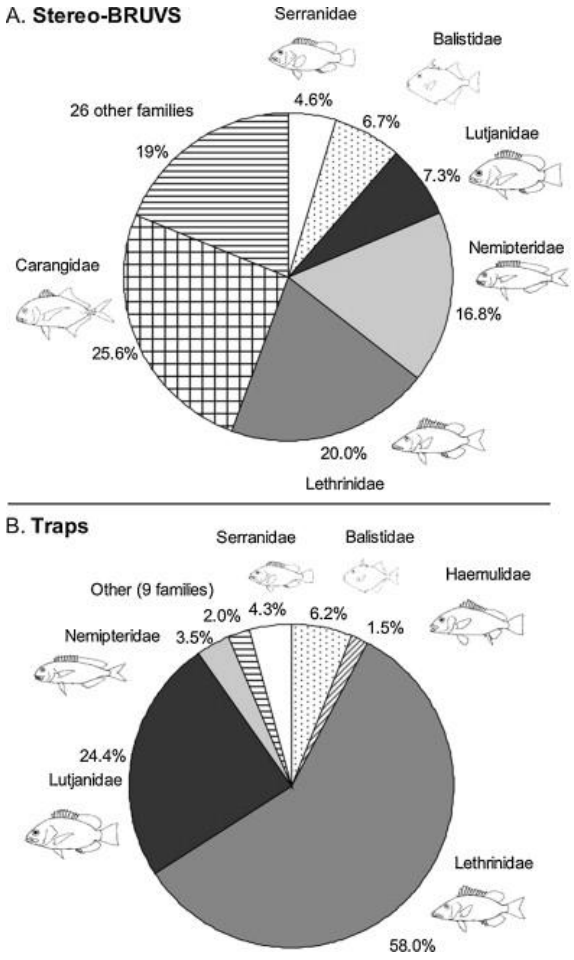


Figure 6. The composition (family) of fish assemblages recorded by (A) stereo-BRUVS and (B) fish traps. Source; (Harvey et al. 2012).

BRUVs measured very similar length frequency data on targeted fish species compared to that from fish traps (Harvey et al. 2012). Trap catches was therefore a good representation of determining the length frequency structures of targeted fish stocks, which is important for stock assessment models that depend on fish length and size data. As there is almost no difference in data obtained on length frequencies of targeted species between the two methods, it indicates that fish collected from fish traps are well respresenting the natural occurring length frequencies. Unless, stereo-BRUV and fishing traps were both methods that recorded only a particular range of the lengths from the targeted fish (Newman and Australia 2012). Nonetheless, stereo-BRUVs obtained more various length frequency data from more species than fish traps (Fig. 7). It is for these reasons that stereo-BRUVs is a more powerful method than fish traps to obtain data on fish assemblages for investigating multi-species fisheries (Fig. 6) (Harvey et al. 2012).

Figure 7. Baited Remote Underwater Video (left; Scaridae and Pomacentridae species) recorded more herbivorous species than fishing traps (right; Lutjanidae species).

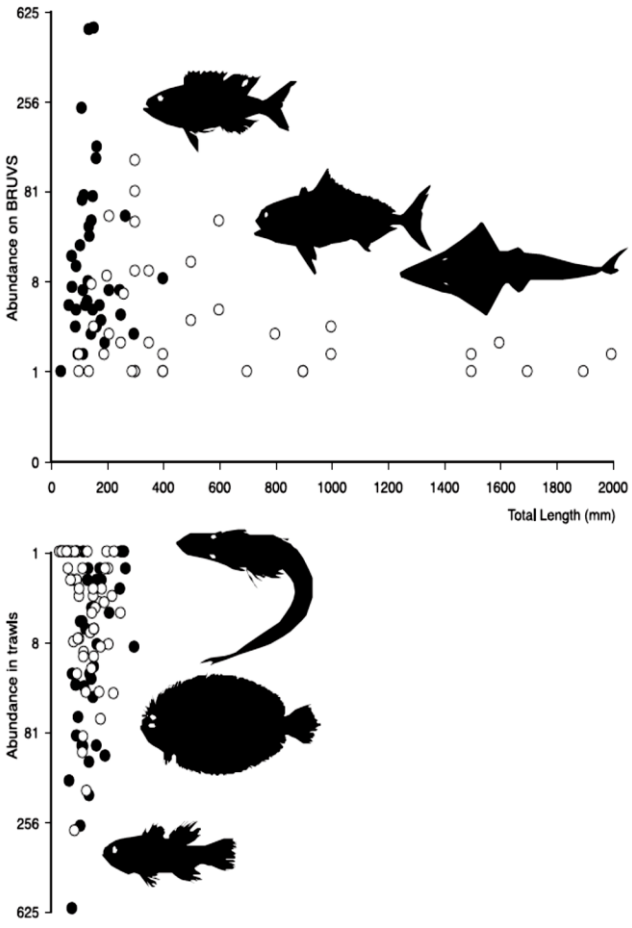


Figure 8. Scatterplots on the average total length of each species recorded by BRUV and trawl surveys. BRUV recorded more species from larger size ranges, where trawling collected more smaller sedentary and cryptic species. Source; (Cappo et al. 2004).

2.3.2 Trawling

Trawl surveys can only be done in sand and muddy rubble habitat, where the possibility is to damage the benthos (Jones 1992). Additionally, trawl surveys are time consuming to conduct and are therefore expensive (Newman, 2012). Video sampling is non-extractive and, unlike research trawling, does not affect the seabed, so it allows for the collection of data on fish species

in protected areas. Unlike fishing techniques, video also gives a detailed image of the habitat types in the sampling area (Cappo et al. 2003). Furthermore, the catch of the fish trawls were highly variable between replicate samples. The high variability in trawl catches in which only sandy habitat can be sampled resulted in trawls not being considered to be a robust method for developing a long-term monitoring program (Newman and Australia 2012).

On the other hand, trawls can be used in any level of water clarity and provide direct estimates of fish density. A study, conducted in the Great Barrier Reef, compared the two techniques and found trawl surveys recording 30% more species than the stereo-BRUVs (Cappo et al. 2004). Further, the two techniques recorded significantly different components of the fish fauna on the similar habitat type (Fig.8). Trawls caught mainly small, sedentary or cryptic species, (Cappo et al. 2004). The BRUVS recorded larger, mobile species from a much wider size range of families, including pelagic species. The authors concluded that the complementary use of trawls and BRUVS would enable a more comprehensive assessment of fish diversity in the area.

2.3.3 Long-line fishing

Ellis and Demartini (1995) compared data on fish abundance derived from the BRUV method and longline Catch per Unit Effort (CPUE) data. Long-line fishing collected fish of larger mean size may due to hook selectivity for larger fish (Willis et al. 2000). Another disadvantage of longlining is hook competition of fish begin to saturate available hooks. Also, hook loss can happen where fish bite through the leader above the hook (Ellis and Demartini 1995). Therefore, BRUV recorded a higher diversity of reef associated species that were not caught by long-line fishing.

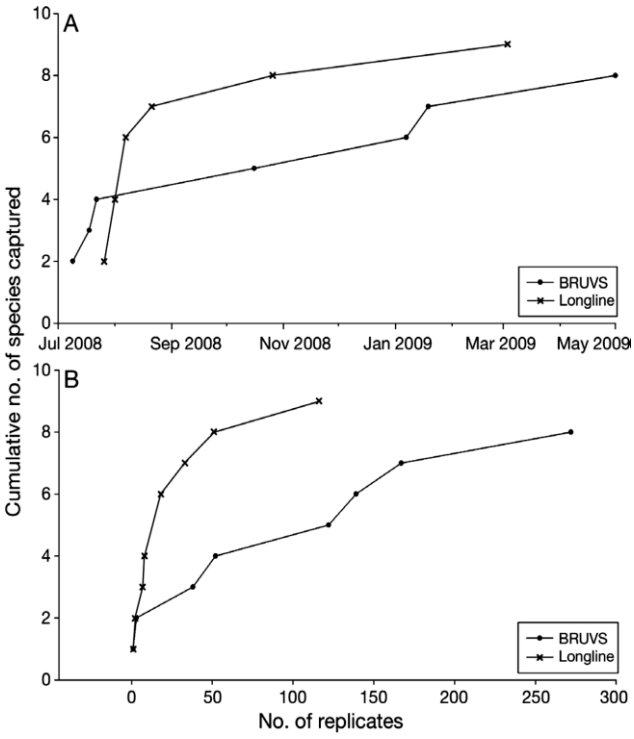


Figure 9. A cumulative number of species recorded through a different number of samples used between BRUVS and Longline surveys. Longline reached the total number of species faster and with fewer samples than BRUVS. Source; (Brooks et al. 2011)

Scientific longline surveys were often used to collect data on shark populations. However, this kind of surveys will introduce damage to the animals being investigated by hooking and retrieval of the longline (Brooks et al. 2011). BRUVS offer a non-invasive alternative to longline surveys for monitoring the relative abundance of sharks. In further comparison, BRUV has been demonstrated to be less size selective, where hook can be effective to retrieve data of only a certain size range (Cappo et al. 2006). Brooks et al. (2011) found similar values of species richness for shark families. Only, longline surveys reached these values faster and with fewer replicates than BRUVS (Fig.9). On the hand, some species recorded with BRUVS can be difficult to identify. Like some species of sharks of the family Carcharhinidae are difficult to identify due to similar body types, body patterns. From the retrieval of longlines with fish on board it will give access to get a closer look at the species and the fish can be tagged afterwards for more detailed information (Heithaus et al. 2007).

In terms of cost efficiency, longline surveys are on the long run more expensive than BRUVS, and are therefore less cost effective (Brooks et al. 2011). The major costs for BRUVS are initial equipment costs, whereas personnel, bait and boat costs are far lower than for longline surveys.

2.3.4 Ichthyocide

In the detection spectrum, cryptic species are at the opposite end to conspicuous species. These fishes are rarely detected in visual surveys, which are well known to underestimate their density (Willis 2001). In fact, the only way to accurately survey cryptic species may be with the application of an ichthyocide. The use of toxicants or rotenone enables detection of species that inhabit reef burrows and therefore are not usually seen. As mentioned before, the chance of detecting cryptic species is low but rather detectable on UVC. However, the chance is even smaller when the underwater video is stationary, such as in the case of BRUV (Stobart et al. 2007). Assemblages of small, cryptic fishes that are strongly associated with the benthos have been either largely ignored, or sampled using UVC with little consideration of methodological bias (Willis 2001). Accurate estimates of overall reef-fish diversity, abundance, biomass and productivity may require extractive sampling with the use of ichthyocide, so that cryptic fishes are not underestimated.

Table 1. The pros (+) and cons (-) of each sampling method that was independent or dependent of fishery data.

Method	Non-Destructive	Not Depth-limited	Not Size-selective	Not Species-selective: Shy and Cryptic species		Absolute (+) or Relative (-) fish density
BRUV	+	+	+	+	-	-
RUV	+	+	+	+	-	-
UVC	+	-	+/-	-	+	+
Fish traps	-	+	-	+	-	+
Trawling	-	+	+	+	+	+
Long-line fishing	-	+	-	+	-	+
Ichthyocide	-	-	+	+	+	+

2.4 Conclusion

The disadvantages (Table 1; size- and species-selectivity) of some extractive techniques, such as fish trapping, can result in low power to detect large changes in sample means, requiring levels of replication that would be unacceptable in areas such as marine parks (Cappo et al. 2003). Of all destructive techniques (Table 1), ichthyocide is potentially the least selective, although large mobile species frequently move away, leaving only smaller species within the rotenone plume (Smith 1973). Many studies demonstrated that stereo-BRUVs had greater statistical power than most other sampling methods to detect changes in abundance. The most difficult part in comparing studies is to standardize the sampling designs of each method on the difference between sample unit areas. Comparing methods should occur in predetermined (fixed) locations to minimize variability associated with fine scale spatial variation in the fish assemblages from sampling different habitats. Nonetheless, in an area unknown of the habitat being sampled would BRUV offer a better estimate on most of the species that can be recorded from the fish assemblage. We conclude that baited video techniques afford the only sampling option for some situations, but more often can complement other traditional methods to enhance the scope and capabilities of monitoring and stock assessment programs.

3. Methods

3.1 Study area

The survey was conducted between July and December 2012 in and around the Saba Marine Park (SMP) area (13 km^2) (17° 39'N, 63° 14'W) (Fig.10). This Marine Protected Area (MPA) was established in 1987 and has, from that moment, been subdivided in four zones: recreational diving zone, anchorage zone, all-purpose recreational zone and multiple use zones. The recreational diving zone is the only area where fishing is not allowed (hereafter referred as no-fishing zone). This zone covered an area of 4.29 km^2 (approximately 33% of the SMP) and here mainly reefs with a carbonate framework was developed (Polunin et al. 1993). These reefs generally slope either gently from the shallows (5-10 m) into deep (±50 m) water, or onto a shallow platform (±10m) before dropping into deep water (Noble et al. 2013). Fishing is allowed in the remaining three zones (hereafter referred as fishing zone). This area was mainly covered by corals, gorgonians and other reef-related organisms that formed a veneer over the volcanic-rock substratum (Polunin et al. 1993).

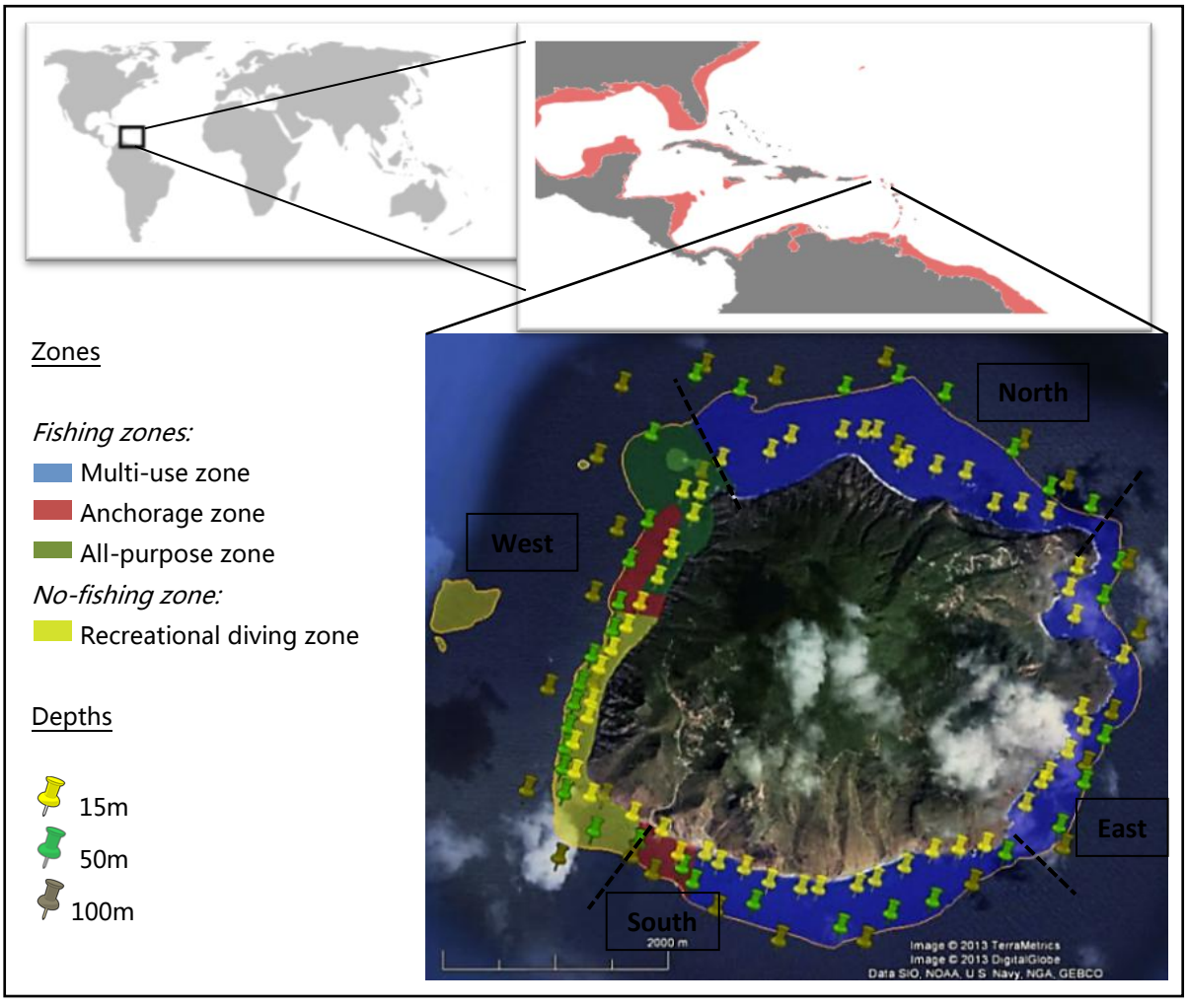


Fig. 10. Study area and study sites sampled inside (15 and 50 m depth) and outside (100 m) the Saba Marine Park.

3.2 Sampling technique

Three stereo-BRUV systems were used to assess reef fish assemblages inside (15 and 50m) and outside (100m) the SMP. Specific information on the design and calibration of the stereo-BRUVs can be found elsewhere (Harvey and Shortis 1995, Harvey and Shortis 1998, Harvey et al. 2002). Prior to field use, all stereo BRUVS were calibrated. Stereo-video imagery was calibrated using SeaGIS CAL V2.01 software (www.seagis.com.au). Calibration of the BRUV systems will provide accurate length measurements to be made during video analysis (Harvey et al. 2003, Shortis et al. 2007). Each BRUV system consists of two video cameras (Canon Legria HFG10) which were mounted within high-density PVC housings. The cameras were attached to an aluminium frame, orientated along a horizontal plane relative to the sea-floor. A rope was attached to the BRUV system with at the end a buoy to retrieve the systems back on board. A bait bag that contained ~800 grams of pilchards (Sardinops sp.) was mounted on a pole of 1.5 meters in front of the cameras. The BRUV was left to record on the sea bottom for at least 60 minutes before retrieval (Brooks et al. 2011). Consecutive BRUVs were separated by 250–400 m to reduce the probability of fish moving from one to another BRUV during overlapping recording time (Harvey et al. 2007b). The time, depth, position and duration were recorded for each set of BRUVS.

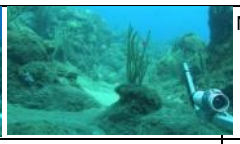
3.3 Sampling design

The BRUVs were randomly deployed over all habitat types along the three different depth layers (15, 50 and 100m). Study sites were characterized by type of habitat (see habitat characteristics), depth range and specific zone. Samples in the range of 15 meters depth (hereafter referred as "shallow") were thought to have more variation in habitat structures. Therefore relative more samples were obtained for shallow sites with an average of 12 samples on each side of the island (Fig 10; North, East, South and West). The total amount of samples at 50 meters depth (hereafter referred as "deep" area) was 31 and 23 were obtained at a depth of 100 meters ("deeper"). Extra samples were taken for the relative smaller no-fishing zone to meet the requirements in the amount of replicates (N>5) needed for statistical analysis. After sampling the video footage was checked on board for parameters, such as position of the cameras, range of view and visibility (see Appendix 3). Deployments that did not conform to the rules adjusted for each parameter than this study site was resampled. The rules were; position of the cameras need to be horizontal, the range of view should not be less than 8 meters depending on the visibility and through hard substrates blocking the range of view of the cameras.

3.4 Quantification of habitat characteristics

The habitat of each BRUV drop was classified according to three different scaling methods; two point scale (Colton et al., 2010) of sand and reef ; 3 point scale of low, medium and high relief (Watson et al. 2005) and 6 point scale (Polunin and Roberts 1993) of habitat complexity levels (Table 2).

Table 2. Quantification of habitat characteristics, where habitat images are categorized into three different classification systems ordered from low to higher degree of scaling. A higher scale than point 4 on habitat complexity, from the habitat classification of Polunin et al. (1993), was not recorded in present study.

Habitat images						NA
2 point scale (Colton et al. 2010)	Sand	Sand	Reef	Reef	Reef	Reef
3 point scale (Watson et al. 2005)	Low relief	Low relief	Medium relief	Medium relief	High relief	High relief
6 point scale (Polunin et al. 1993)	0=bare substratum	1=low and sparse relief	2=low but widespread relief	3=moderate complexity	4=high complexity with cave systems	5=extreme complexity

3.5 Image analysis

Tape recordings were analysed with the software program EventMeasure (http://www.seagis.com.au/event.html). The time of BRUVs settled on the seabed were recorded and for each study site a habitat image were made. For each species we measured the time of first sighting, time of first feeding at the bait, the maximum number seen together in any one time on the whole tape (MaxN) and time at which MaxN occurred. MaxN is a conservative measure of relative density that avoids the recounting of individuals that repeatedly visit the bait (Willis and Babcock 2000) and its use has been reviewed in detail by Cappo et al. (2003, 2004). Exception was made for sharks and where possible recorded for the maximum number of individuals seen over the whole tape (MaxN-A). Only here we were confident to distinguish individuals through significantly different body sizes (Bond et al. 2012). Fish MaxN and length measurements were made up to a range of ~8 m from the cameras (Cappo et al. 2004, Harvey et al. 2007). Fish were measured to the nearest mm fork length (FL, snout to fork). Rays were measured on disk width. To avoid making repeated measurements of the same individuals, measures of length were made at time of MaxN (Cappo et al. 2004).

3.6 Statistical analysis

3.6.1 Visualizing fish assemblage structures

The data consisted of many species and environmental conditions which made it difficult to test this with simple univariate analyses. Multivariate analyses are able to specify the occurrences of species in assemblage samples (Anderson and Millar 2004). A Bray-Curtis dissimilarity matrix, an abundance-weighted measure of how similar two assemblages are in terms of their species composition (Beals 1984), was used to generate a non-metric Multi-Dimensional Scaling (nMDS) ordination plot. nMDS is commonly regarded as the most robust unconstrained ordination method in community ecology (Minchin 1987). This test was performed to visually illustrate variation in reef fish assemblage structure across habitats and depths. The nMDS function automatically transformed the data with square-root transformation and solutions are based on the distance between samples in ordination space (Clark 1993). Samples of the fish assemblages from the no-fishing and fishing zone were also compared, as the impact of fisheries was expected to modify the structure of fish assemblages.

To assess species variation between the three treatments (defined by three habitat categorizations, depths and zones) and the interactions between them (Jackson and Somers 1991), we used Detrended Correspondence Analysis (DCA). Its performance provided a more specific look into species and sample ordinations that were being produced simultaneously. More information on DCA and its advantages compared to other ordination techniques can be found elsewhere (Hill and Gauch Jr 1980). The axes are scaled in standard deviation units with a definite meaning of the interaction between treatments and species. To identify the species that contribute most to the multivariate pattern, we isolated those species which had a strong correlation (>0.5) between the original data and the first DCA axis. Only the treatments that were most significant ($p \leq 0.05$) to correlate with those species were shown in the graph.

3.6.2 Fish biomass, density and species richness

The data consisted of many variables and large differences on the number and diversity of species recorded. Permutational Analysis of Variance (PERMANOVA) was used for allowing the analysis of multivariate data in the context of more complex sampling structures (Anderson 2001). The use of permutational techniques does not require parametric assumptions and used distance or dissimilarity between pairs of samples or variables. Two models were applied with one testing the explanatory variables habitat complexity, location, zone and interactions among these variables on differences of fish abundance, density and biomass. The other model consisted of the simpler habitat category, to compare for the different habitat categories. Both models were tested within depths and differences between depths were tested separately.

Species richness was measured from the total number of species (Nsp) observed per BRUV deployment. Relative abundance was calculated with the maximum number of individuals per species (MaxN). For this study area, certain species (i.e. *Thalassoma bifasciatum, Sparisoma aurofrenatum, Scarus taeniopterus*) occurred in relative high numbers not only for adult stages but as well as for juvenile and intermediate phases. When more life stages within a species were observed the MaxN was calculated as the sum of all life stages per species (sum of MaxN). The biomass per individual was calculated from the length-weight relationship equation $W = aL^b$ (Bohnsack et al. 1988) using the length measurement and length-weight parameters (www.fishbase.org). Then each individual biomass of the MaxN per species was summed which resulted in the total biomass per species per BRUV deployment. For individuals with missing lengths, we used the average biomass from lengths of other individuals that belonged to the MaxN of that species. If length-weight parameters in fork length were not available the values from a close relative or from a species within family-level was used (see Appendix 2). All species observed within depths were calculated for relative abundance and biomass (see Appendix 1,2). For some fish, only densities were given as we were unable to measure length of one individual from the MaxN or length-weight parameters were not available from that species and other species within that family. Species that were not considered as demersal fish species were excluded from further analysis. Other related studies also excluded certain species from analysing tropical demersal fish assemblages (Langlois, 2012). Species that were excluded were pelagic schooling fish (*Decapterus macarellus*, *Selar crumenophtalmus*), the larger pelagic species (*Scomberomorus regalis*) and

aggregations of eel species that were nestling in the sand bottom (*Heteroconger longissimus*) not able to measure lengths. Species of sharks were analyzed separately (*Carcharhinus falciformis*, *Carcharhinus limbatus, Carcharhinus perezii*, *Galeocerdo cuvier, Ginglymostoma cirratum*, *Sphyrna lewini*), due to disproportionally large biomass that even after severe transformation of the data it would have masked changes in the patterns of other demersal species. All statistics were performed using statistical program R V2.15.1 (for R scripts see appendix 6), and other programs when mentioned otherwise.

3.6.3 Species accumulation curves

Plotting the curve gives an estimate of the number of additional species that was recorded with further effort (Colwell, 2004). It also visualizes whether all species in the area were detected indicated by decreased values on the variation in observing new species. The sampled area in total, each depth and levels of habitat were tested on the number of species observed.

3.6.4 Power analysis

Statistical power is defined as the probability of correctly rejecting a null hypothesis and the power is defined as 1–B, where B is the probability of a type-II error (Fairweather 1991, Harvey et al. 2001). An example of a type-II error in environmental monitoring would be to conclude that no effect has occurred when one has. Power analysis determines the optimum size of samples to detect an effect of a particular change with a desired level of probability (Harvey et al. 2012). The limit was set for a number of samples that reached a statistical power of 0.8 (Cohen 1988). We used the program G*power 3 (Erdfelder et al. 1996) to calculate power and effect sizes with using the observed mean and variance estimates of species richness, biomass and number of fish. From the assumption that high variability of fish assemblages was detected through sampling a wide variety of habitats, a non-normal distribution of the data was applied with a non-parametric test. A two-sided, difference in means can be positive or negative, Wilcoxon-Mann-Whitney test was used to compute the required sample size.

First, the power and number of samples within depths were estimated to detect a change of 25 and 50% in species richness. Then each habitat categorization was examined on the sensitivity to detect changes on species richness, fish abundance and biomass, according to the following hypotheses. A simpler habitat model using

fewer levels of classifying habitat differences produce larger variances among fish population' s mean categorized into each of those levels. Larger variances reduce the probability to detect significant differences among the sampled fish assemblages and lowered the statistical power. A fine-scale habitat model using more levels generates more power of minimalizing variances on fish assemblages associated to finer-scale levels on habitat. In order to find an effect of a particular change increased, as smaller variations lowered the possibility of overlapping standard deviations. However, the number of samples used declines in categorizing these on levels of the finer-scale habitat complexity category, as the total amount of samples is now divided over more levels of habitat. When sample sizes are smaller, the standard errors become higher of certain variance values among the sampled means, what makes it more difficult to detect a significant difference. Finally, the habitat categorization most efficient in sampling statistical power to detect changes in fish assemblage data will be used for further analysis.

3.6.5 Trophic groups

In order to investigate trophic linkages, fish biomass of 5 different families ordered in 2 trophic group' s, e.g. herbivorous and carnivorous fish, is examined. This selection of species was chosen for the following reasons: (1) the species that were considered to be the most commonly exploited species in the SMP (Polunin and Roberts 1993), and/or (2) the species that were most abundant in present study. Biomass of species were shown across zones and where possible to be discussed with earlier derived data (Polunin and Roberts 1993, Roberts 1995, Noble et al. 2013). Hereby, only the effect of zones were tested and not controlled for other environmental conditions. This allows relative comparison of results from previous studies to determine temporal variability of fish biomass. Effects of protection from fishing on the lengths of targeted and non-targeted fish species were analyzed with length frequency distributions and the average fish length. Herbivores and carnivores were examined. It was hypothesized that targeted species would be larger, on average, in no-fishing compared to fishing zones. In general, families of carnivores were found to be more vulnerable to fishing impacts and are here described as targeted species (Roberts 1995). For non-targeted species, we predicted no differences in mean lengths of fish between protected and fished areas.

3.6.6 Distribution of sharks

The distributions of the two most common species of sharks were examined across zones and which type of habitat they were observed. In order to compare results with other study areas, sightings of the two most abundant shark species were expressed as the percentage of samples with shark sightings of the total number of BRUV samples used (Belize, Caribbean; Bond et al. 2012) as well as in the number of sharks per hour of the BRUVs recording time (Bahama' s, Caribbean; Brooks et al. 2011).

4. Results

4.1 Visualizing fish assemblage structures

Sample measures on fish assemblages were shown in ordination plots through species occurrence and relative abundance (MaxN). The nMDS ordination (Fig. 11A) showed a separation of samples ordered from low to higher complexities on habitat structures (habitat categorization according to Polunin ey al. 1993). Fish assemblages associated to lower habitat complexities were found at the upper part of dimensional scaling. Fish assemblages increased in similarity towards higher complexities of habitat and were more situated at the lower part of the ordination plot (point 3-5; Fig.11A). These fish assemblages were more abundant in shallow depths (Fig.11B), as shallow samples of fish assemblages were also shown at the lower part in the ordination plot. The stress value indicated how well the ordination summarizes the observed distances among the samples. From the use of a high number of samples and variables a stress value of 0.17 was a good representation of the visualized data. Stress values below 0.2 indicate a useful 2 dimensional picture and less than 0.1 corresponds to an ideal ordination with no real misinterpretations (CLARKE, 1993).

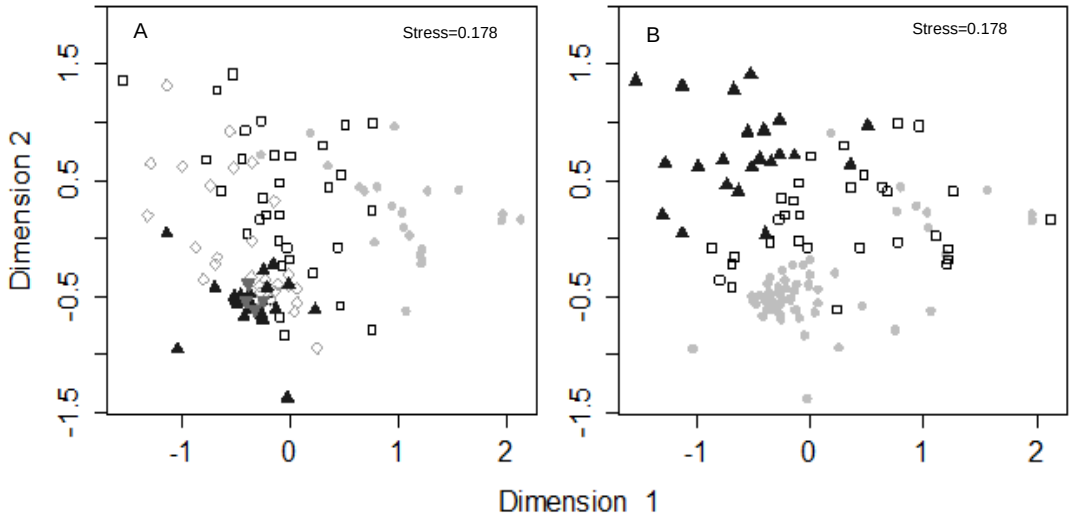


Figure 11. Non-metric Multi-Dimensional Scaling of fish species sample data: (A) on a scale of habitat complexity (0=filled circle grey, 1=square black, 2=diamond grey, 3=filled triangle point up black,

The distinction between habitat types was due to a prevalence of *Chromis cyanea*, *Lutjanus apodus* and *Halichoeres garnoti* (Fig.12) on reef areas, whereas *Mulloidichthys martinicus*, *Caranx ruber* and *Hemipteronotus martinicensis* were occurring mostly on sand areas. Species shown close to 0 from the values given by the dimension axes (Fig.12) were more abundant in shallow areas (*Cephalopholis fulva*, *Acanthurus coeruleus* and *Thalassoma bifasciatium*), and species (*Serranus tabacarius*, *Serranus tortugarum* and *Lutjanus bucanella*) with relative high to lower

values for both dimension axes indicated their occurrence in deeper areas. The variables depth and habitat category of Polunin et al. (1993) had the strongest dimension of correlation (> 0.5) with species that contributed most of the multivariate pattern (Fig.12). Factors zone and other habitat categories were not significant on the correlation with species abundance and not shown in the graph (Fig.12). Further, the nMDS plot of visualizing samples of fish assemblages across different zones showed no distinct separation (Fig.13).

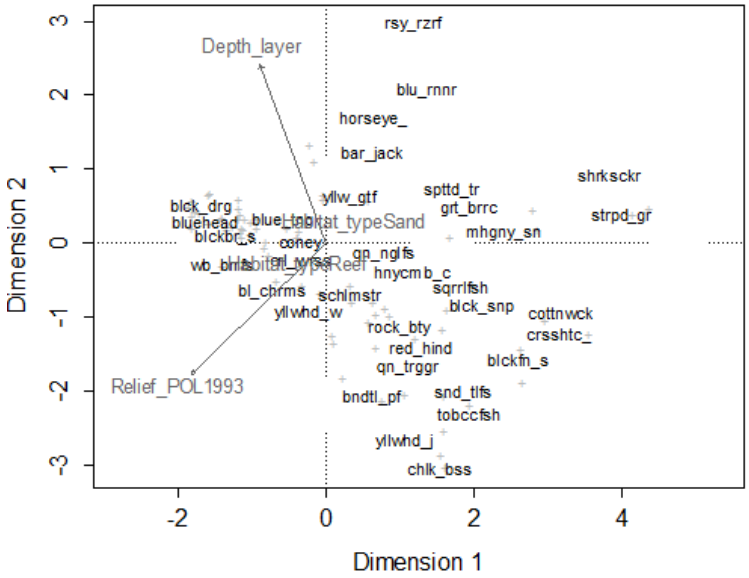


Figure 12. Detrended Correspondence Analysis showing the interaction between treatments and species (abbreviations of species names are shown in table 4).

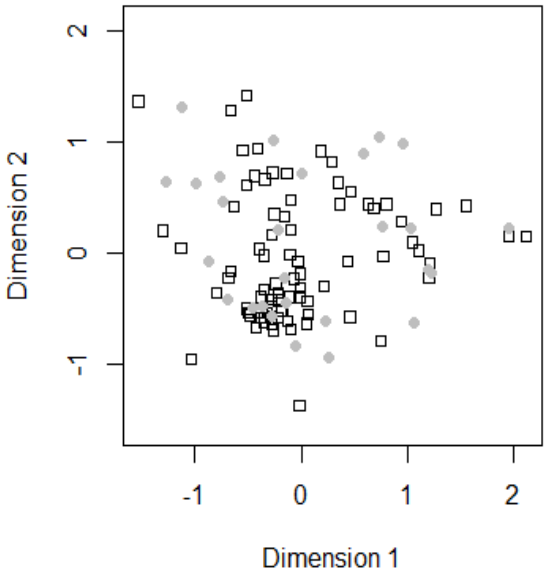


Figure 13. nMDS ordination of fish assemblages sampled across different zones: Fishing zone=square black, No-fishing zone=filled circle grey.

Table 3. Abbreviations of species codes translated from (1) short name, to (2) species code, and (3) family and species name. These species contributed most of the multivariate pattern in the DCA shown in figure 17.

1)	bndtl_pf	bar_jack	blckbr_s	blck_drg	blck_snp	bl_chrms
2)	bandtail puffer	bar jack	blackbar soldierfish	black durgeon	Blackfin snapper	Blue chromis
3)	*Sphoeroides spengleri*	*Caranx ruber*	*Myripristis jacobus*	*Melichthys niger*	*Lutjanus bucanella*	*Chromis cyanea*
1)	bluehead	blue_tng	blu_rnnr	chlk_bss	Coney	cottnwck
2)	bluehead wrasse	blue tang	blue runner	chalk bass	Coney	cottonwick
3)	*Thalassoma bifasciatum*	*Acunthurus coeruleus*	*Caranx crysos*	*Serranus tortugarum*	*Cephalopholis fulva*	*Haemulon melanurum*
1)	cl_wrss	crsshtc_	grt_brrc	hnycmb_c	horseye_	mhgny_sn
2)	creole wrasse	crosshatch bass	great barracuda	honeycomb cowfish	horse-eye jack	mahogany snapper
3)	*Clepticus parrae*	*Serranus luciopercanus*	*Sphyraena barracuda*	*Acanthostracion polygonia*	*Caranx latus*	*Lutjanus mahogoni*
1)	qn_nglfs	qn_trggr	red_hind	rock_bty	rsy_rzrf	snd_tlfs
2)	queen angelfish	queen triggerfish	red hind	rock beauty	rosy razorfish	sand tilefish
3)	*Holacanthus ciliaris*	*Balistes vetula*	*Epinephelus guttatus*	*Holacanthus tricolor*	*Hemipteronotus martinicensis*	*Malacanthus plumieri*
1)	schlmstr	Shrksckr	spttd_tr	sqrrlfsh	strpd_gr	tobccfsh
2)	schoolmaster	Sharksucker	spotted trunkfish	squirrelfish	striped grunt	tobaccofish
3)	*Lutjanus apodus*	*Echeneis naucrates*	*Lactophrys bicaudalis*	*Holocentrus adscensionis*	*Haemulon striatum*	*Serranus tabacarius*
1)	wb_brfs	yllw_gtf	yllwhd_j	yllwhd_w	strpd_gr	tobccfsh
2)	web burrfish	yellow goatfish	yellowhead jawfish	squirrelfish	striped grunt	tobaccofish
3)	*Chilomycterus antillarum*	*Mulloidichthys martinicus*	*Opistognathus aurifrons*	*Holocentrus adscensionis*	*Haemulon striatum*	*Serranus tabacarius*

4.2 Species richness

A graphical overview was given on the variability of species richness distributed along a gradient of depths, locations (Sites) and zones (Fig.14). Along the depth gradient was species richness higher in shallow areas. To deeper areas the number of species declined (Table 4) with lower variation among samples (Fig.14). The number of species unique to each depth decreased from shallow to deeper areas; with 7 species unique to the deeper depth range (see also Appendix 1 for those specific species). Among locations (Fig.14; "Sites"), sites East and South were sampled with relatively higher species richness than West and South. The fishing zone had higher values for species richness. The dispersion of data on species richness was low in the no-fishing zone compared to the fishing zone (Fig.14).

Table 4. Summary of parameters listed for fishing (F) and no fishing (NF) zones within depth ranges of 15, 50 and 100 meters.

	15m		50m		100m
	F zone (N=44)	NF zone (N=12)	F zone (N=23)	NF zone (N=8)	F zone (N=23)
Habitat (Reef vs. Sand)	31 vs. 13	6 vs. 6	5 vs. 18	3 vs. 5	9 vs. 14
Total # individuals	4378	3705	4424	3572	3383
Total # species	87	47	77	38	63
Total # families	33	22	29	18	27
# Unique for depth	24		12		7
Growth (K)	0.55	0.47	0.75	0.98	0.46
Lmax	406	377	495	493	526
Mean MaxN*	50	33	26	20	21
% # Carnivores	15	13	18	28	42
% # Herbivores	29	23	14	13	2
Mean Biomass*	11852	8105	12223	8569	7761
% Biomass Carnivores	35	33	39	25	56
% Biomass Herbivores	29	24	18	11	11
Top five species*					
(Mean MaxN)	*Thalassoma bifasciatum*	*Thalassoma bifasciatum*	*Caranx ruber*	*Lutjanus buccanella*	*Lutjanus buccanella*
	Melichthys niger	*Melichthys niger*	*Clepticus parrae*	*Caranx crysos*	*Haemulon striatum*
	Cephalopholis fulva	*Cephalopholis fulva*	*Caranx crysos*	*Haemulon melanurum*	*Lutjanus vivanus*
	Caranx ruber	*Chromis cyanea*	*Lutjanus buccanella*	*Clepticus parrae*	*Xanthichthys ringens*
	Acanthurus coeruleus	*Chromis multilineata*	*Sparisoma aurofrenatum*	*Scarus taeniopterus*	*Lutjanus mahogoni*
(Mean Biomass)	*Sphyraena barracuda*	*Dasyatis americana*	*Mycteroperca venenosa*	*Dasyatis americana*	*Sphyraena barracuda*
	Melichthys niger	*Sphyraena barracuda*	*Dasyatis americana*	*Lutjanus buccanella*	*Lutjanus buccanella*
	Caranx ruber	*Ocyurus chrysurus*	*Caranx ruber*	*Caranx lugubris*	*Pomacanthus paru*
	Dasyatis americana	*Epinephelus guttatus*	*Sphyraena barracuda*	*Haemulon album*	*Haemulon striatum*
	Cephalopholis fulva	*Megalops atlanticus*	*Caranx crysos*	*Ocyurus chrysurus*	*Lutjanus vivanus*

*Species that formed large pelagic schooling species not belonged to the demersal species (*Decapterus macarellus, Selar crumenophtalmus*)) or had disproportionally large biomass from body mass *(Scomberomorus regalis, Sphyrna lewini, Carcharhinus falciformis, Carcharhinus perezii, Ginglymostoma cirratum, Carcharhinus limbatus, Galeocerdo cuvier*) or through numbers (*Heteroconger longissimus*) were excluded from parameters calculated on fish densities (Mean MaxN, % # Trophic groups), biomass (Mean Biomass, % Biomass Trophic groups) and for the most dominant species in terms of abundance and biomass.

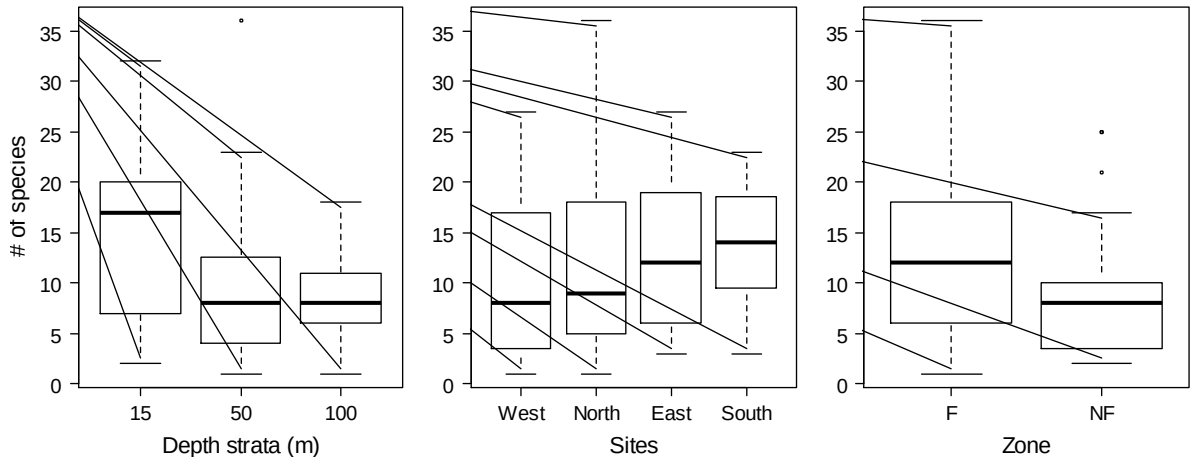


Figure 14. Graphical overview of species richness data, the number of species observed, on different depth ranges, sites and zones. The boxplots represent the median (black bar), interquartile range (central rectangle) and locations of minimum and maximum (whiskers).

The number of species found on different depths was significantly different (Table 5). Between locations and zones there was not a significant difference found. The opposite was only found for species richness ($P < 0.05$) from the effect of different zones with the interaction of habitat complexity in the deep area. Here, the outcome of the perMANOVA was not significantly different of species richness tested on the interaction of zone with relief as habitat category. A higher total number of species was recorded in the fishing zone (Total Nsp= 77, Table 4) compared to the no-fishing zone (Total Nsp= 38, Table 4). Factor habitat was in overall highly significant on differences found for species richness except for samples in the deeper area (Table 5). Location (Fig 14; Sites) was the less determining factor in explaining the observed variation on species richness.

Table 5. PERMANOVA results of the relative abundance (MaxN), species richness (Nsp) and biomass tested for significant differences (P(perm) < 0.05) on factors habitat by 2 treatments (Habitat complexity; Polunin et al. 1993 and Relief; Watson et al. 2005), location and zones, within and between depths separately.

Source	15m				50m				100m			
	df	MS	Pseudo-F	P(perm)	df	MS	Pseudo-F	P(perm)	df	MS	Pseudo-F	P(perm)
Habitat complexity												
MaxN	1	2.47	10.3	**0.001**	1	1.38	4.44	**0.001**	1	0.49	1.66	**0.049**
Nsp	1	3.97	5.78	**0.016**	1	12.0	22.0	**0.001**	1	0.01	0.01	0.923
Biomass	1	1.52	4.98	**0.001**	1	1.18	3.53	**0.001**	1	0.91	3.11	**0.003**
Location												
MaxN	3	0.41	1.74	**0.014**	3	0.56	1.79	**0.007**	3	0.28	0.96	0.550
Nsp	3	0.88	1.29	0.276	3	0.71	1.29	0.276	3	0.55	1.53	0.207
Biomass	3	0.50	1.66	**0.006**	3	0.58	1.71	**0.007**	3	0.24	0.85	0.696
Zone												
MaxN	1	0.25	1.06	0.360	1	0.37	1.20	0.237				
Nsp	1	1.18	1.73	0.188	1	1.74	3.19	0.075				
Biomass	1	0.50	1.66	0.053	1	0.43	1.30	0.177				
Habitat complexity × Location												
MaxN	3	0.35	1.46	0.056	3	0.25	0.80	0.873	3	0.42	1.44	**0.042**
Nsp	3	0.09	0.13	0.941	3	0.28	0.50	0.677	3	0.17	0.47	0.704
Biomass	3	0.37	1.21	0.145	3	0.36	1.09	0.269	3	0.46	1.57	**0.024**
Habitat complexity × Zone												
MaxN	1	0.44	1.86	**0.037**	1	0.36	1.16	0.287				
Nsp	1	2.34	3.41	0.065	1	2.47	4.53	**0.034**				
Biomass	1	0.55	1.83	**0.027**	1	0.41	1.25	0.207				
Relief × Zone												
MaxN	2	0.35	1.48	0.080	1	0.26	0.78	0.740				
Nsp	2	1.16	1.71	0.181	1	0.07	0.13	0.718				
Biomass	2	0.32	1.08	0.344	1	0.29	0.78	0.688				
Between depths												
MaxN	1	5.15	17.4	**0.001**								
Nsp	1	11.5	18.7	**0.001**								
Biomass	1	3.34	9.86	**0.001**								

4.3 Fish biomass and density

Fish biomass and density increased with habitat complexity (Fig.15). Overall, fish densities and biomass were significantly different across both habitats and depths, only less significant on differences of habitat at deeper areas (Table 5). The variation of data of fish biomass and density was less in the no-fishing zone, this may be due to fewer amount of samples collected from this zone (Fig. 15). The mean and variances of biomass and density of fish sampled in the no-fishing zone in shallow areas were especially lower (Fig.15). This resulted in the interaction between habitat complexity and zone to be significantly different on both MaxN (Table 5; 15 m: F = 1.86, P = 0.037) and biomass (Table 5; 15 m: F = 1.83, P = 0.027) in shallow areas. The difference between zones was evident from the mean MaxN (Table 4; F = 50, NF = 33) and mean biomass (Table 4; F =11852, NF = 8105) recorded in shallow areas. The effect of zone without the interaction of habitat was not significantly different on

both fish densities and biomass (Table 5). Moreover, the simpler habitat category with the interaction of zone (Relief × Zone) had not a significant effect on fish biomass and densities.

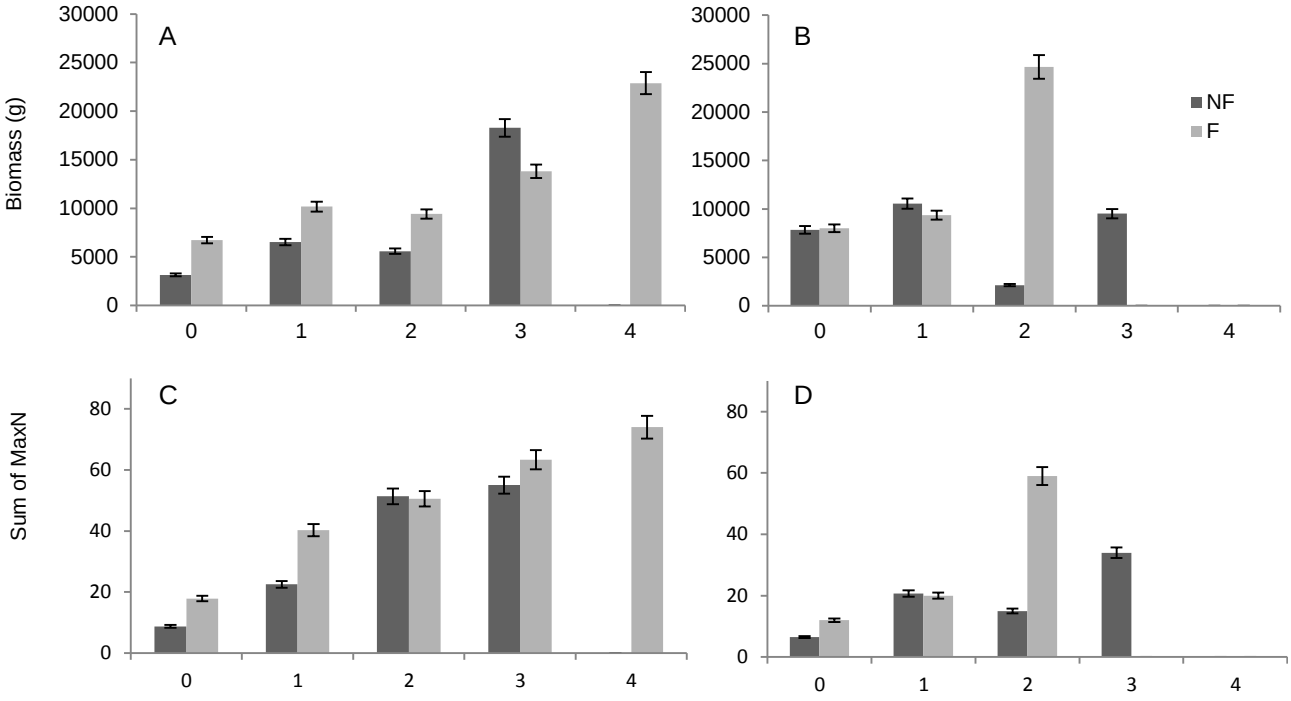


Figure 15. Barplots of fish biomass and abundance (sum of MaxN) in No-Fishing (NF) and Fishing (F) zones within levels of habitat complexity category (Polunin et al. 1993) and depths of 15 m; (A) and (C), and 50 m; (B) and (D). The barplots show means and 95% confidence interval bars.

4.4 Species accumulation curves

Accumulation curves estimated whether the total number of samples (N=108) used recorded all possible species over the sampled area (Ugland, 2003). At a cumulative number of 110 samples the standard deviation was almost zero from observing new species with increased effort (Fig.16). This was almost similar to the total number of samples used on each depth range (Fig.17). Here the rates of species accumulation also decreased levelled off with

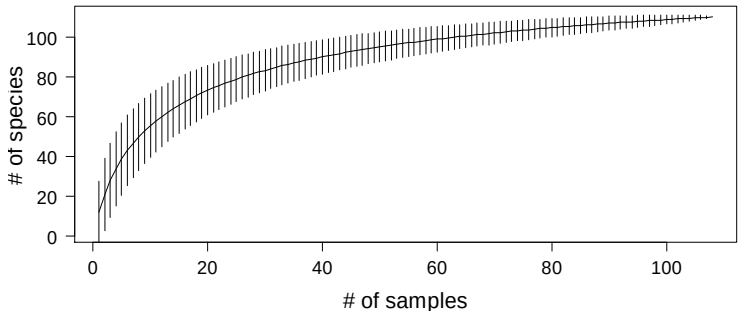


Figure.16. Species accumulation curve calculated for the total number of samples used. A cumulative number of species is recorded as a function of the number of samples used (N=108). The vertical lines represent the standard deviation of observing new species per extra sample.

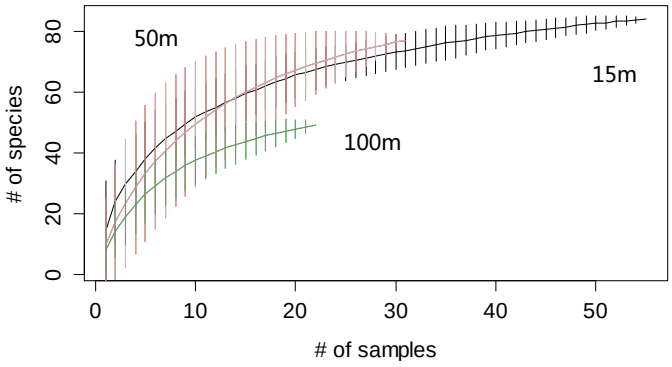


Figure 17. Species accumulation curves on a cumulative number of samples used per depth range; 15, 50 and 100 meters.

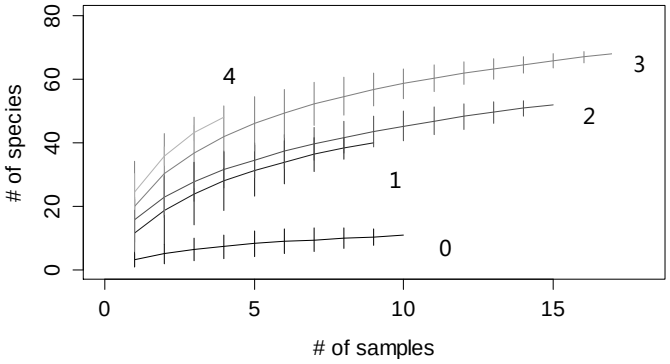


Figure 18. Species accumulation curves of samples from different levels on habitat complexity (0-4) measured on 15 meters depth.

increased sampling effort. However, standard deviations were higher for deeper depth range categories. The sampled area was also subdivided in different habitat complexities. The rate of increase in sampling new species was higher when samples were taken in more complex habitats (Fig.18). The highest rate of increase on the total number of samples used between levels of habitat was the curve represented 4 on the scale of habitat complexity. This sampled habitat was covered by the lowest amount of samples (N=4).

4.5 Power analyses

Species richness

First, samples were pooled per depth range category and determined on the sampling effort in reaching the required statistical power (p=0.8) of detecting changes in species richness. For each depth range 100 or more samples were needed to detect a small change (25%) in species richness (Fig.19A). The deeper area showed lower variation in species richness (Fig.14), which increased the probability to detect a similar change of fish population' s mean. Therefore, samples of deeper areas reached the required power faster than shallower areas (Fig.19A). Less number of samples were needed to detect a larger change (50%) compared to detect a smaller change (25%) in species richness (Fig.19B). In order to cover the required power of sampling each depth, relatively more samples has to be collected for the deep area (50m).

The number of samples linked to each habitat was low for categorizing these into high relief (Watson et al. 2005). The two categorizations habitat and relief showed the same pattern of values on species richness (Fig.20). Therefore we used only one, the habitat category of Colton (2010), of representing the simpler category on habitat in

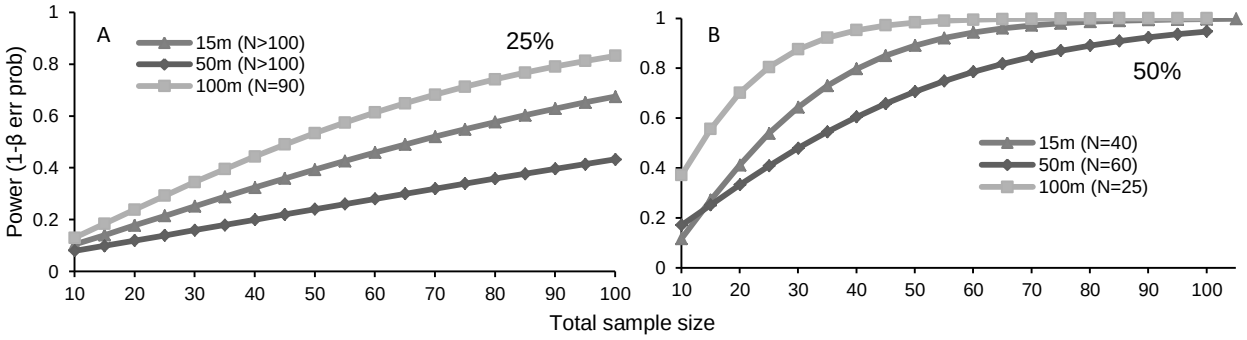


Figure 19. Power analysis. The required numbers (N) of samples were estimated and shown in the legend of reaching the statistical power (p=0.8) to detect a level of change, 25 (A) or 50% (B), in species richness for the sampled depth ranges.

order to make comparisons with the finer-scale category on habitat complexity. The deeper area (100m) was associated with low habitat variety as well as for species richness data (Fig.14). This depth range was therefore not included to reveal differences between habitat categories on the observed species richness.

The main difference between habitat categories was the degree on scaling (number of levels) in characterizing habitat types, e.g. sand and reef. The simpler habitat category (Fig. 20A,B) used 1 level and habitat complexity category (Fig.20C) used 2 levels per habitat type, not only to distinguish habitat types but as well as for habitat differences within habitat type. The variation around the observed mean on species richness to each habitat level declined within using more levels of categories (Fig.20A,C: 0 and 1 versus Sand).

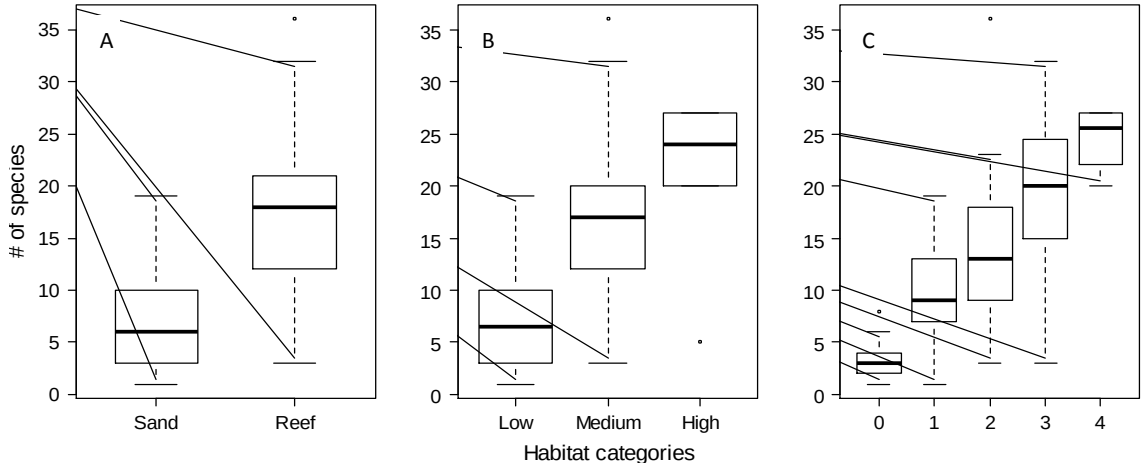


Figure 20. Boxplots on species richness recorded over different habitats. Different degree on habitat scaling can be used to associate the observed species richness on habitat characteristics. The different habitat categories are showed from low to higher degree on habitat scaling, respectively categorized on (A) habitat: Colton et al. 2010, (B) relief: Watson et al. 2005 and (C) habitat complexity: Polunin et al. 1993.

Category habitat generated different power between levels sand and reef, from the observed species richness at each depth (Fig.21). Reef samples reached the required power faster than sand habitat. Species richness derived from sand habitat had higher variation in shallow compared to deep sampled areas (Fig.14). Thus samples of sand in shallow areas had relatively low power of detecting a 50% change in the number of species observed (Fig.21). Further, the habitat complexity category (Polunin et al. 1993) was found to produce more statistical power within levels of 0-1 vs. sand of the "habitat" category in shallow areas whereas in deeper areas the habitat category method produced on average more statistical power (Table 6). Deeper samples (50m) of level reef of the category habitat generated more power. As from the number of samples used in this study, the required power was not reached for samples of sand habitat in both depths (Table 6). Further, reef habitat was scarce in deeper areas (50m) from which the required power was also not sampled.

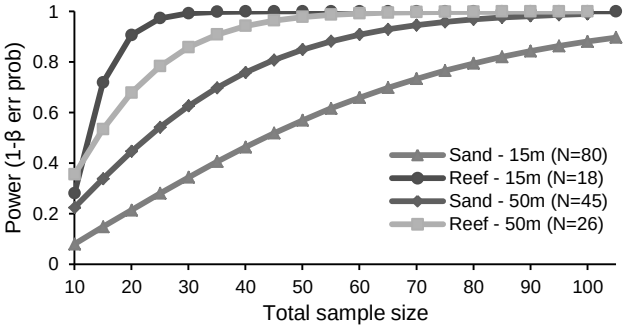


Figure 21. Power analysis to detect a change of 50% on the number of species observed and categorized into 2 levels of habitat, e.g. sand and reef, at 15 and 50 m depth ranges. The number (N) of samples equivalent to a power of 0.8 was shown for each level of habitat.

Table 6. The statistical power () to detect a 50% change in species richness, reached with a certain number of samples used and been categorized into levels of different habitat categories; Habitat (Colton et al. 2010), Relief (Watson et al. 2005) and Habitat complexity (Polunin et al. 1993). The average power reached with the total number of samples was also shown for each habitat category.

Habitat categories	15 m	50 m
Habitat		
Sand	19 (0.2)	23 (0.5)
Reef	37 (1)	8 (0.3)
	56 (0.6)	31 (0.4)
Relief		
Low	19	23
Medium	33	8
High	4	0
Habitat complexity		
0	10 (0.3)	10 (0.5)
1	9 (0.4)	13 (0.5)
2	15 (1)	6 (0.2)
3	18 (0.9)	2 (0.1)
4	4 (0.6)	0
	56 (0.65)	31 (0.33)

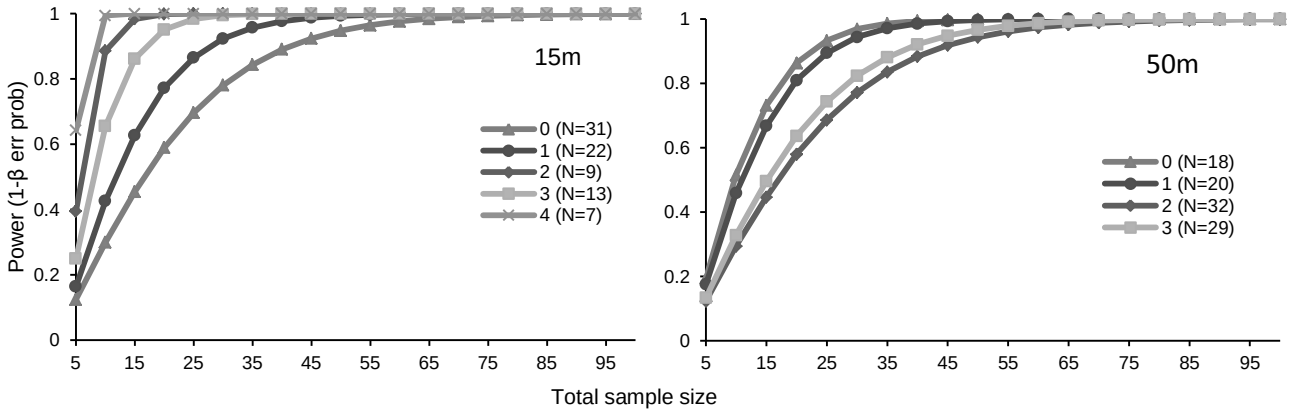


Figure 22. Power was calculated to detect a change of 50% in the number of species observed at 15 and 50 meters depth. The number of samples (N) in reaching the required power was estimated for habitat complexity levels on a scale of 5 and 4 points. Higher complexities of habitat than point 3 on the scale was not sampled in 50 meters.

Fish densities

If sample means on fish density were higher indifferent of standard deviation values, then the relative standard deviation became smaller. This was mainly observed of sampling reef relative to sand habitat in 15 meters depth (Table 7). To detect 50% changes on the observed fish densities, more than 50 samples on sand habitat are needed (Table 7; Sand, point 0-1). For this habitat type only the samples in deep area within habitat complexity level 1 reached the required power faster. Both averages and standard deviations on fish densities increased (Table 7; 50m) with higher levels of habitat complexity. From shallower (15m) and deeper (100m) areas a relative lower variation among the increased means of fish density was detected in relation with higher complexities on habitat which increased the statistical power.

Table 7. The number of samples equal to the required power (p=0.8) was calculated from a change of 50% and 100% on the observed average of the total number of individuals, recorded over shallow (15m), deep (50m) and deeper (100m) areas, and different habitats categorized into two categories (habitat: sand-reef vs. habitat complexity:0-4).

Habitat	15m		±50%	±100%	50m		±50%	±100%	100m		±50%	±100%
	Avg	Sd	N= p(0.8)	N= p(0.8)	Avg	Sd	N= p(0.8)	N= p(0.8)	Avg	Sd	N= p(0.8)	N= p(0.8)
Sand	24.7	25.6	>150	37	16.1	9.8	50	15	24.5	16.9	65	18
Reef	57.9	24.2	25	14	47.3	31.5	60	18	16.2	6.1	22	7
Total			>175	51			110	33			87	25
0	14.2	11.3	85	22	10.9	7.7	67	18	20.5	16.2	85	22
1	36.3	32.1	>100	17	20.1	9.5	32	10	25.2	17.6	65	18
2	50.6	17.5	18	7	51.6	34.5	60	17	16.2	6.4	22	7
3	60.4	29.1	33	10	34	22.6	60	17	16	NA	NA	NA
4	74	14.9	8	<5	NA	NA	NA	NA	NA	NA	NA	NA
Total			244	61			219	62			172	47

Table 8. Power estimated on detecting changes of 50% and 100% on the observed average MaxN (total number of individuals) and average biomass, from the number of samples (N) used in 15, 50 and 100 meters depth. The sampled habitats were categorized into two habitat categories, on a 2 (Sand-Reef, Colton 2010) and 5 (0-4, Polunin 1993) point scale.

Habitat	15 m	±50%		±100%		50 m	±50%		±100%		100m	±50%		±100%	
	N=56	p(MaxN)	p(biom)	p(MaxN)	p(biom)	N=31	p(MaxN)	p(biom)	p(MaxN)	p(biom)	N=23	p(MaxN)	p(biom)	p(MaxN)	p(biom)
Sand	19	0.17	0.25	0.5	0.74	23	0.41	0.3	0.95	0.84	14	0.22	0.32	0.6	0.82
Reef	36	0.91	0.64	1	0.99	8	0.15	0.1	0.5	0.28	9	0.35	0.3	0.8	0.8
Avg		0.54	0.44	0.75	0.86		0.28	0.2	0.73	0.56		0.28	0.31	0.7	0.81
0	10	0.13	0.16	0.4	0.5	10	0.16	0.1	0.45	0.26	2	0.1	0.8	0.25	1
1	9	0.12	0.15	0.5	0.45	13	0.4	0.3	0.9	0.8	12	0.19	0.25	0.57	0.7
2	15	0.7	0.35	1	0.89	6	0.15	0.1	0.5	0.3	8	0.35	0.3	0.8	0.8
3	18	0.52	0.43	1	0.92	2	0.1	0.4	0.4	0.85	1	NA	NA	NA	NA
4	4	0.5	0.5	0.9	0.56	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
Avg		0.4	0.32	0.76	0.66		0.2	0.23	0.56	0.55		0.21	0.45	0.54	0.83

The total number of samples covering all depths and habitat levels of the habitat complexity category was 635 samples as to be required to detect a 50% change in fish densities and less than 170 samples for a 100% change. Less samples are required with using habitat as category to reach the same power (p=0.8) (Table 7). As for comparing levels separately between categories, for example sand with point 0, the effort needed was less by using the habitat complexity category. However, this difference was more related with sampling fish biomass (Table 8). The significant differences in using different habitat categories for testing the effect of zones was smaller on fish densities (*P*) compared to fish biomass and species richness (Table 5).

Fish biomass

The shallow samples arranged in 1 level within reef habitat had higher statistical power on detecting changes of fish biomass than the use of more levels (habitat complexity:2-4) (Table 8). This was in contrast to samples taken in deeper areas. Reef habitat did not reach the required power in deeper areas of the habitat category, whereas habitat complexity level 3 had enough power to detect a 100% change on fish biomass. The deepest area was sampled with the power required to detect larger changes (100%) on fish biomass (Table 8). The effect of habitat complexity with zone as interaction on the fish biomass, compared with using habitat as category, was larger in shallow depths (Table 5).

Table 9. The number of samples equal to the required power (p=0.8) was calculated for a change of 50% and 100% on the observed average total biomass per depth (15, 50 and 100 meters) and between habitats and habitat categories (on a 2 and 5 point scale).

	15m		±50%	±100%	50m		±50%	±100%	100m		±50%	±100%
Habitat category	Avg	Sd	N = p(0.8)	N = p(0.8)	Avg	Sd	N = p(0.8)	N = p(0.8)	Avg	Sd	N = p(0.8)	N = p(0.8)
Habitat												
Sand	7228	5678	85	24	8923	6527	73	20	9600	5176	40	13
Reef	13043	7925	50	15	18058	15780	>100	28	5104	2206	28	9
Total			135	39			>173	48			68	14
Habitat complexity												
0	5302	3684	65	17	7984	8171	>100	36	11478	521	<5	<5
1	9369	6891	75	20	9646	5173	40	12	9259	5594	50	14
2	8654	4773	42	12	20905	17583	95	25	5201	2339	29	7
3	14600	7890	40	12	9519	1725	7	<5	4326	NA	NA	NA
4	22882	7439	17	7	NA	NA	NA	NA	NA	NA		
Total			239	68			242	78			84	26

In total, fewer samples were needed (Table 9) when those were subdivided into levels of the simpler habitat category. To compare each level separately, the habitat complexity category needed fewer samples. Standard deviations on the observed fish biomass were smaller within levels of the habitat complexity. In general, particular levels of habitat complexity within habitat types generated more power. This trend was different among the sampled depths (Table 9). For instance, the resulting power to detect changes on fish biomass was not that different from levels 2 and 3 in shallow areas, where the opposite was found in deep areas.

4.6 Trophic groups

Greater biomass in the fishing zone at shallow depths (15m) was found for the first three out of four herbivore fish species (Fig.23; A-D), except for the species *Sparisoma viride*. However, not a clear difference between zones for herbivore fish biomass was detected, as variation of biomass data overlapped. Also, at deeper depths the opposite was found where herbivore species *Acanthurus coeruleus* and *Sparisoma aurofrenatum* showed, on average, higher biomass in no-fishing zones (Fig.23; A and C). Among the herbivore species, *Sparisoma viride* was found with the highest biomass, especially to depths of 50 meters (Fig.23D). For the invertivore species (Fig. 23; E and F) there were also no marked differences among zones, and like other herbivore species did not occur in deeper depths (100m). From the carnivore species only the species of the Serranidae family *Epinephelus guttatus* in the shallow depth (Fig.23G, 15m) showed a strong correlation towards higher biomass in the no-fishing compared to the

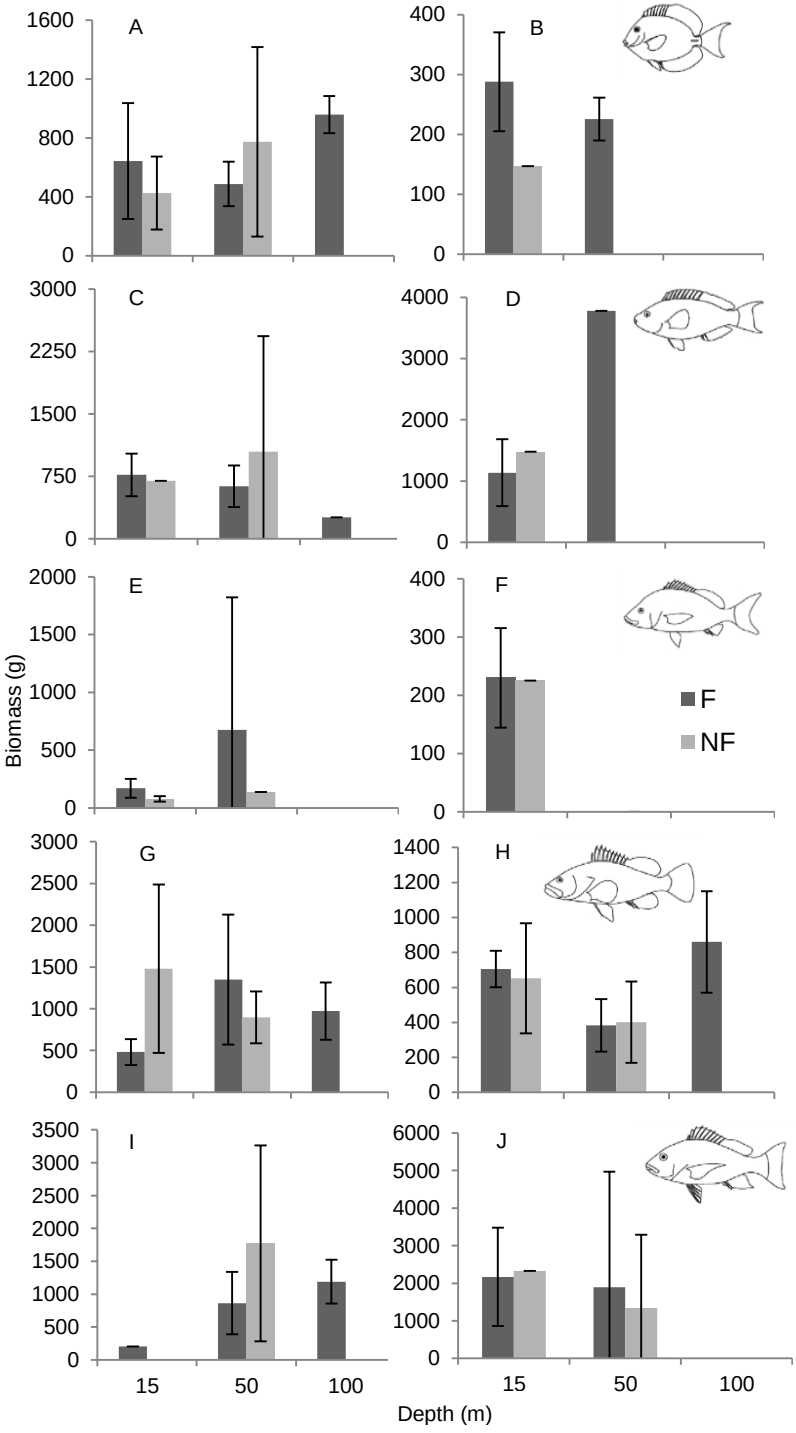


Figure 23. Barplots of fish species biomass, mean biomass in gram, among fishing (black bars) and no-fishing (grey bars) zones per depth range. The species are arranged in trophic groups and ascending trophic level, respectively: (A) *Acanthurus coeruleus* (herbivore, 2.0), (B) *Acanthurus tractus* (herbivore, 2.0), (C) *Sparisoma aurofrenatum* (herbivore, 2.0), (D) *Sparisoma viride* (herbivore, 2.0), (E) *Haemulon flavolineatum* (invertivore, 3.3), (F) *Haemulon carbonarium* (invertivore, 3.3), (G) *Epinephelus guttatus* (carnivore, 3.9), (H) *Cephalopholis fulva* (carnivore, 4.1), (I) *Lutjanus buccanella* (piscivores, 3.9), (J) *Ocyurus chrysurus* (piscivores, 4.0).

fishing zones. This was in accordance to the hypothesis of potentially targeted species having higher biomass in no-fishing zones. Both species of the Serranidae family were almost equally distributed, in terms of fish biomass, over the different depth ranges. The species *Lutjanus bucanella,* most abundant within the Lutjanidae family, showed higher biomass in deeper areas, and *Ocyurus chrysurus* had higher biomass in shallower areas. Also here, not a clear difference was detected between the different zones.

The total average fish biomass, for all fish measured, was almost significantly different between zones in shallow depths (Table 5), with a higher mean biomass in the fishing zone (Table 4). Although, the very common species in the area, *Epinephelus guttatus,* showed the opposite trend with higher biomass in the no-fishing zone in the shallow depth (15m). The deep (50m) and deeper (100m) areas were less different (*P*) on the total average fish biomass between zones, for all samples of fish assemblages (Table 5).

4.7 Fish length

For the herbivore species of the Acunthuridae family (Fig.24;A and B), it appears that larger fish were more abundant inside the no-fishing zone. This observation was mainly caused by a larger average length of the species *Acunthurus* coeruleus, measured in the no-fishing zone at depths of 15 meters (Table 10). Smaller individuals of Scaridae were not recorded in the no-fishing zone as

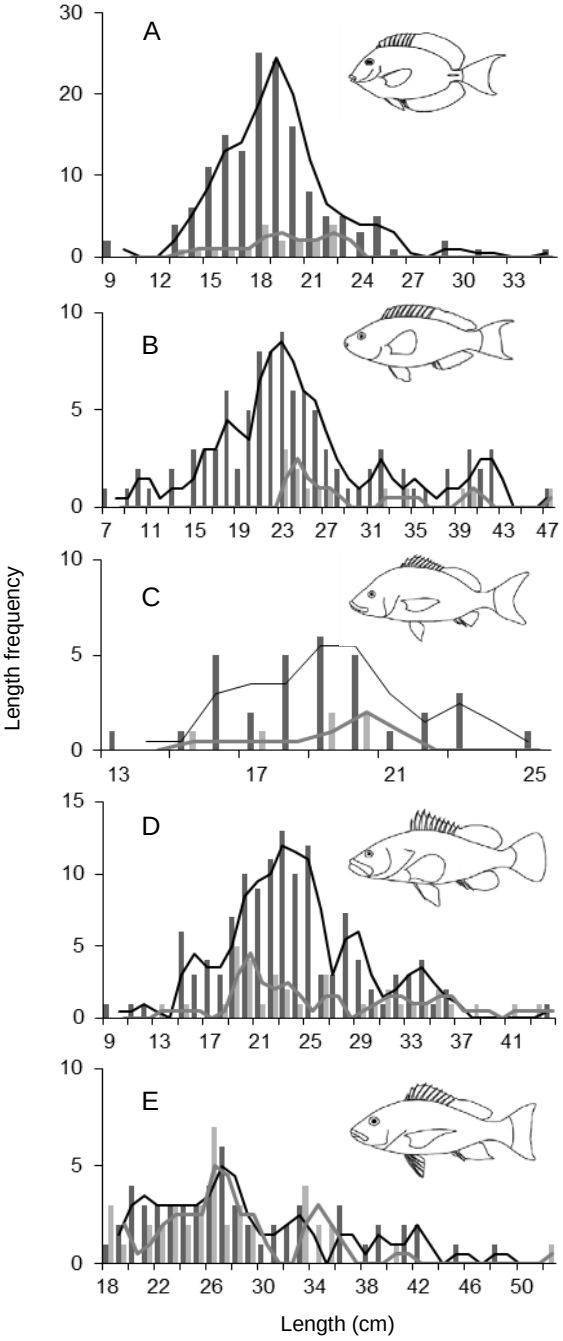


Figure 24. Length frequency histograms of the two most common species (see Fig.20) within families of Acanthuridae (A), Scaridae (B), Haemulidae (C), Serranidae (D) and Lutjanidae (E) sampled in fishing zones (dark bars and trendline) and the no-fishing zone (grey bars and trendline) are shown, pooled for depths (15 and 50 m) within the boundaries of the Saba Marine Park.

Table 10. Fish average lengths and standard deviations across different zones. The p-value showed the difference in fish average lengths between fishing (F) and no-fishing (NF) zone whereas two populations were significantly different when p-value was lower than 0.05, according to the test of Mann-Whitney U.

		Zone		15m	Zone		50m	100m
Fish family	Genus + Species	F	NF	*p*-value	F	NF	*p*-value	F
Acanthuridae	*Acanthurus coeruleus*	18.8 ± 2.8	19.7 ± 1.6	0.174	21.5 ± 4.2	21.6 ± 1.1	0.857	29 ± 5.7
	Acanthurus tractus	17.1 ± 3	17.1 ± 2.9	0.877	22.3 ± 2.9	NA	NA	NA
Scaridae	*Sparisoma aurofrenatum*	21.8 ± 6.7	25.8 ± 3.8	0.073	21.5 ± 2.9	24.8 ± 1.5	0.182	21.4
	Sparisoma viride	30.9 ± 9.2	39.8 ± 5.4	0.085	42.2 ± 0.2	NA	NA	NA
Haemulidae	*Haemulon flavolineatum*	17.8 ± 1.9	16.3 ± 1.3	0.182	19.3 ± 2.7	19.8	0.667	NA
	Haemulon carbonarium	20.2 ± 3.2	19.4 ± 0.7	1	NA	NA	NA	NA
Serranidae	*Epinephelus guttatus*	27.3 ± 5.9	37.8 ± 3.8	**0.014**	29.6 ± 6.9	30.2 ± 4.7	0.315	29.4 ± 3.7
	Cephalopholis fulva	20.8 ± 3.7	19.9 ± 3.4	0.217	24.7 ± 1.9	21.8 ± 2.7	0.383	27.9 ± 3.3
Lutjanidae	*Lutjanus buccanella*	NA	24.0 ± 4.2	NA	22.1 ± 3.8	26.2 ± 4.1	0.628	26.9 ± 5.5
	Ocyurus chrysurus	41.3 ± 2.1	36.4 ± 3.7	0.095	36.3 ± 3.4	40.2 ± 10.2	0.8	NA

referred to the overall mean lengths (23-25 cm) observed for both zones. Both species within the Scaridae family showed almost a significant difference on the average length between zones (Table 10). The length measurements obtained of species of Haemulidae were almost similar across zones and depths.

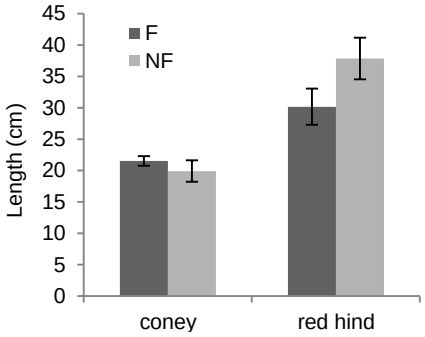


Figure 25. The average lengths with 95% confidence intervals are shown for the two most abundant carnivore species at 15 meter depths, respectively coney (*Cephalopholis fulva*) and red hind (*Epinephelus guttatus*).

The carnivore species of the Serranidae family showed the highest length frequency peak in the no-fishing zone for relative smaller individuals compared to the peak observed in the fishing zone (Fig.24D). However, the species *Epinephelus guttatus* within the same family showed on the average length a positive effect of the protected area, with a significant (Table 10; *p*-value: 0.014) higher average length in shallow areas (Fig.25). *Cephalopholis fulva* was found with a slightly smaller average length in the no-fishing zone. Other carnivorous species from the Lutjanidae family (Fig.24E) showed almost no differences on the average length (Table 10) and length frequency distributions of following the same pattern of the recorded fish lengths across zones.

4.8 Distribution of sharks

From the abundance data (MaxN-A), sightings of two species of sharks were more frequent (Appendix 1; *Carcharhinus perezii, Ginglymostoma cirratum*) than other shark species (*Carcharhinus falciformis, Carcharhinus limbatus, Sphyrna lewini*). The most common shark species were observed on 10 to 20% of all the BRUV samples used in shallow depths (Fig.25), and with an amount of 0.11 to 0.22 sharks per hour. In deep areas (50 m) was *Ginglymostoma cirratum* not recorded whereas number of *Carcharhinus perezii* sightings increased to 0.5 shark sighting per hour, equal to almost 40% of all samples used in the no-fishing zone.

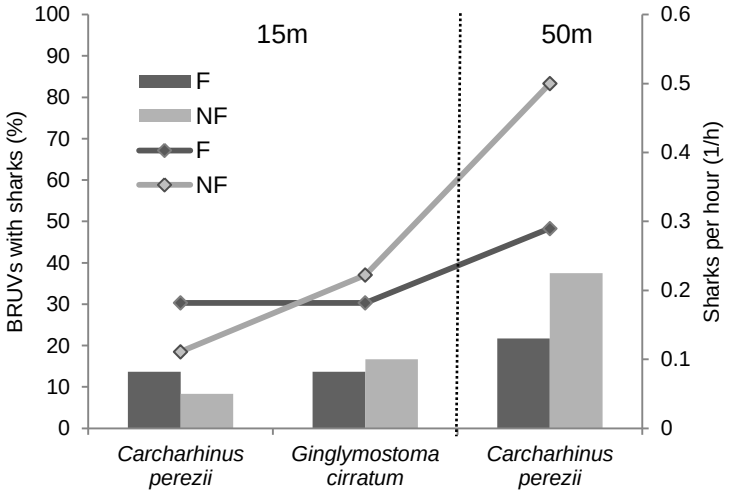


Figure 26. Shark sightings (*Carcharhinus perezii, Ginglymostoma cirratum*) shown in percentage (dark bars; Fishing zone, grey bars; No-Fishing zone) of BRUV samples of the total number of samples used per zone within depths and in the number of sharks per hour recording time (dark line; Fishing zone, grey line; No-Fishing zone)

Ginglymostoma cirratum was more observed in the shallow depth and only one individual was recorded in the deeper (100m) area (Fig.26). Both shark species were almost equally distributed over different levels of habitat complexity, independent of depths (Fig. 26). More individual sharks were, at time of recording, associated to moderate complexity of habitat (Fig.26; point 2). *Carcharhinus perezii* was observed on moderate complexity of habitat twice as much as in lower habitat complexities in deeper areas. For all other findings, the difference consisted of only one or two more sightings from that of lower or higher complexity on habitat structures.

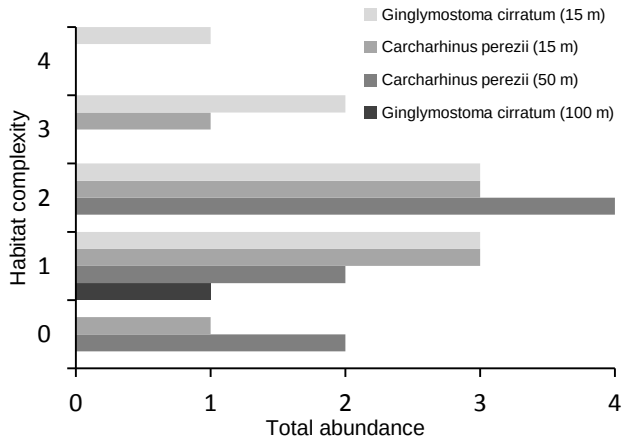


Figure 26. The number of shark sightings per habitat, on a scale of 0-4 on habitat complexity (habitat category of Polunin et al. 1993), recorded in depths of 15, 50 and 100 meters.

5 Discussion

Patterns of species richness and fish abundance

The total number of species recorded in shallow areas (15m) was 103, and gradually declined to 88 species in deep (50m) and 63 in deeper (100m) areas. The average number of species also declined along this depth gradient. In the deeper areas, higher similarities among samples of fish assemblages were found with distinct separation between fish assemblages sampled on the three different depths. This pattern was also observed by other studies, like a significant change on reef fish assemblages found between depth categories of shallow (<30m), and deeper areas (30-60m) in the Red Sea (Brokovich et al. 2008) and in New South Wales, Australia (Malcolm et al. 2011). Zintzen et al. (2012) studied reef fish assemblages in north-eastern New-Zealand at depths of 50 to 1200 meters, and found a peak in species richness in 50 meters depth from which the number of species gradually declined beyond 100 meters to 700 meters. Therefore, it is not surprising that depth was highly significant in explaining the variation of the observed fish assemblages. The clear change of fish assemblages between depths was due to a greater prevalence and/or abundance for some species with increasing depth, like the carnivore species *Lutjanus bucanella* and *Lutjanus vivanus*. Some of those species had not previously been recorded in the SMP as these studies did not record fish at deeper depths of 15 meters (Noble et al. 2013, Polunin et al. 1993, Roberts et al. 1995). Other species within families of Acanthuridae, Scaridae and Haemulidae showed the opposite trend and were more observed in shallow areas. Species of these families were relatively common in the shallow depth ranges, also previously observed in 5 meters depth (Noble et al. 2013). And a few species were found at all depths, including species (*Epinephelus guttatus, Cephalopholis fulva*) that are potentially targeted by fisheries in the area (Roberts 1995). However, through sampling only certain depth ranges, it is possible that not all species in the area have been recorded during this study. It can be that certain species occurred at depth ranges that have not been studied so far, or that the species observed were more abundant in other depth ranges than the depth categories used in this study (15, 50 and 100m). For instance, Malcolm et al. (2012) found a clearer change in fish assemblages at depths of 50 m rather than at 60 m. In other studies, fish assemblages observed at depths between 20 and 50 meters were found with the highest species richness (Malcolm et al. 2011, Zintzen et al. 2012).

Further, reef habitats supported higher species richness than sand habitats. There was a strong positive correlation between substratum complexity and the density and

diversity of fish assemblages. The species that contributed most to this correlation between habitat types were mainly herbivorous species particularly found on shallow reef areas, like species within families of Labridae, Pomacentridae and Scaridae. The common observed species *Caranx ruber* and *Lactophrys bicaudalis* were typical species to be found on sand habitats. Habitat complexity in terms of coral structures significantly declined with depth. The strong correlation of fish assemblage structures with depth and habitat is consistent with previous research that have examined demersal fish assemblages (Anderson et al. 2004, Ferreira et al. 2001, Harman et al. 2003, Toller et al. 2010).

Habitat categories

This study identified that within a zone and depth combination there was the need to minimize the variability of reef fish assemblages caused by sampling different habitats. Only a few other studies revealed the fine-scale variability on fish assemblage compositions between and within habitat types along a depth gradient (Moore et al. 2010, Malcolm et al. 2011, Zintzen et al. 2012). Moore et al. (2010) had access to a detailed habitat map over various depths (10-100 meters) which made it possible to link the structure of fish assemblages to very fine-scale habitat differences. This sampling approach allowed identification of environmental conditions that correlates with the distribution of fish assemblages. As in many other studies, specific information on environmental conditions was unavailable prior to sample reef fish assemblages with BRUV (Colton et al. 2010, Goetze et al. 2011, Harvey et al. 2007, Langlois et al. 2006, Ledlie et al. 2007, Newman et al. 2006, Watson et al. 2005, Willis et al. 2000). Some of those studies had to rely upon hierarchical classifications which combined factors depth and habitat into "habitat" types (Colton et al. 2010), "relief" (Watson et al. 2005) or "habitat complexities" (Polunin et al. 1993). The simpler habitat categories "habitat" and "relief" defined larger habitat differences, while "habitat complexities" was a finer-scale category using 6 levels of structuring habitats. It turned out that the spatial distribution of reef fish assemblages was significantly different among zones, when samples of fish assemblages were categorized into finer-scale on habitat complexity category. The finer-scale category defined smaller differences within habitat type's sand and reef, which resulted in smaller variation among fish assemblages to be associated with habitat differences. This increased the probability of finding a significant difference between two fish populations' mean, as smaller variations lowered the possibility of overlapping standard deviations.

Detecting changes on fish assemblages

It is necessary to test for statistical power in which significant differences were found on reef fish assemblages. To verify that a significant difference between fish populations' mean was actually true a certain statistical power is required (p=0.8). Only a few studies used power analysis to only compare sampling methods on the efficiency of sampling to reache that power (Langlois et al. 2010, Colton et al. 2010, Harvey et al. 2012). However, it is also relevant to detect changes of reef fish assemblages on the statistical power variable of sampling habitat differences. Habitats can be described in many ways to associate the observed fish assemblages with habitat differences. The required power of sampling depends on the variance among samples, sample size and difference between samples means (Cohen, 1988). In this study, the variance among samples of fish assemblages was larger when habitats were categorized into a simpler habitat category, which distinguished fish assemblages to larger changes on habitat, e.g. sand vs. reef. The variation between fish assemblages decreased when smaller habitat differences were described among samples of fish assemblages. It was expected that lowering the variability of reef fish assemblages should improve the statistical power to detect changes on fish biomass, diversity and species richness. Thus, when habitat was categorized into the finer-scale habitat complexity category the statistical power increased in detecting changes on fish assemblages compared to other simpler habitat categories. However, sample sizes were lower for habitat levels of the finer-scale habitat complexity category due to covering more levels of categories. The lower the sample size the larger are the standard errors of the means at certain variance values (Cohen, 1988). This is therefore likely that sampling effort between habitat categories not differ so much in reaching the required statistical power.

Some studies examined the relative sampling effort of BRUV to detect changes on species richness (Langlois et al. 2010), fish abundance (Taylor et al. 2013, Harvey et al. 2012) or only for a selection of species (Babcock et al. 2008). Here we showed that statistical power was not similar for sampling changes on species richness, fish density or biomass. More samples were required to generate the power of detecting changes on fish biomass. We detected lower values of mean and high variance on fish density and diversity on sand habitat, which made the effort higher of sampling this habitat type to reach the required power. Samples on reef habitat generated more statistical power with an equivalent number of samples. In deeper areas (50 and 100 m), the sampled habitat was often categorized as low complexity on habitat structures. Only here the variance of the observed species richness was lower than in

shallow areas. Thus, the power was reached faster for deeper areas than for shallow areas within the same habitat type.

In general, the present study shows that studies using finer-scale habitat categories are likely to find less variation in assemblage composition, greater mean values of species richness, fish density and biomass and in some cases greater power to detect change within habitats. Particular levels of the habitat complexity category generated relatively higher power than other levels of habitats. It is more efficient to concentrate the sampling design on these habitat complexity levels to generate less variation on fish assemblages observed within habitats. This is to prevent the drawing of false conclusions to describe significant differences on species richness, fish abundance and biomass to other explanatory variables, such as no-fishing versus fishing zone

Species composition in the Marine Park

In the Saba Marine Park area fish length, biomass, density and species richness was less driven by the impact of fisheries. There was not a clear pattern observed for targeted species being smaller within the no-fishing zone. Remarkably, on average we found higher values of species richness, fish density and biomass in the fishing zone. Earlier derived data also revealed a significant overall effect in shallow areas (15m) of lower species richness and habitat complexity in the no-fishing zone (Noble et al. 2013). More studies showed a decline in live hard coral across all zones of the SMP from the 1990s to 2008 (Polunin and Roberts 1993, Roberts et al. 1995, Nobel et al. 2013). It is therefore likely that habitat loss, in terms of coral structures, influenced the observed pattern on reef fish assemblages in the SMP area. Furthermore, the level of fishing pressure was relatively low what might be the reason to not find higher species richness, fish abundance and biomass in the no-fishing zone. Here, the fishing pressure was exerted by recreational line fishers only. However, other studies showed that recreational line fishing alone might, in some cases, be sufficient to alter the composition of targeted fish (Westera et al. 2003). The opposite in shallow depths (15m). This was also confirmed by the study of Noble et al (2013) that recorded lower species richness and percent cover of live coral in shallow areas within the no-fishing zone. On the contrary, they found that the protected area in depths of 5 meters had higher species richness and percent coral cover. The correlation between changes on species richness across zones and different depths was discussed to be driven by habitat influences rather than fishing pressure (Noble et al. 2013).

Previous studies within the SMP area were only focussed to detect changes in fish assemblages at depths of 5 and 15 meters, as sampling was conducted by divers not able to effectively monitor deeper located areas (Polunin and Roberts 1993, Roberts 1995, Noble et al. 2013). In our study we found that carnivorous species of the family Lutjanidae have significantly higher mean biomass in the no-fishing zone. These species are important to conservation programs and occurred in deeper located areas than 5 and 15 m depth ranges previously been studied within the SMP (Polunin and Roberts 1993, Roberts 1995, Noble et al. 2013). Other species were also observed in deeper located areas of 50 and 100 meters. Like the most abundant species in the area, *Epinephelus guttatus*, that was equally distributed over the different depth ranges. Furthermore, we found a relatively high abundance of the shark species *Carcharhinus perezii* in deep areas (50m) within the no-fishing zone. Their occurrence in deep areas was not previously been studied. The overall number of sharks present in this study was relatively high compared to other areas in the Caribbean (Newman et al. 2006). From our observations, we assumed that there was no shift in assemblage trophic structure, suggested by previous studies that recorded low abundance of carnivorous species at shallow depths (<15m) (Noble et al. 2013). We found that biomass and density of carnivorous species increased to deeper located areas, which might enhance the balance in community compositions relative to the abundance of other trophic groups in shallow areas (i.e., herbivorous species). Thus, ecological data on the spatial distribution of reef fish along a depth gradient were giving new insights of the reef fish assemblages at deeper depths within the SMP. However, since a particular depth category was used, recordings were not gradual, and might not be representative for all reef fish that can be detected. Future research should aim to first sample more different depth ranges to find out which depth ranges represents the clearest change in reef fish assemblages distribution and composition. Finally, a long-term monitoring program should increase the range to match those depths that can potentially be fished (0-60m) or where habitats might suffer from a decline of live coral.

Comparing methods

Except for the ability of BRUV to sample fish at greater depths than 40 meters, also a high diversity of fish were detected, including herbivorous fish that were passing through and/or attracted to the commotion of carnivorous species approaching the bait to feed. However, from comparative studies we know that other sampling methods can obtain different assemblage data, like diving transects are better able to detect territorial and cryptic species (Cappo et al. 2003). Previous data on reef fish

recorded with the use of diver point-count census (Polunin and Roberts 1993, Roberts 1995, Noble et al. 2013) indicated a decline of carnivorous species since the SMP was established. However, large carnivorous species may be repelled from divers (Chapman and Atkinson 1986), and this may influence the observation of a decline of these species (Willis and Babcock 2000). We used stereo-BRUV and detected a high abundance of larger carnivorous species. Furthermore, we observed a high number of a large predatory species, the Caribbean reef shark (*Carcharhinus perezii*), less observed from the research done by divers (Polunin and Roberts 1993, Roberts 1995, Noble et al. 2013). There is a need for further research using stereo-BRUV to detect temporal and spatial variability of reef fish assemblages which will remove biases of comparing sampling methods.

6 Conclusion

The use of stereo-BRUV has been proven to detect high number and diversity of both herbivorous and carnivorous species across different habitats and depths. This study presented a clear change of reef fish assemblages between categories of depths and habitats. The sampled habitats rather unknown prior of sampling were effectively represented by a finer-scale habitat complexity category. Other habitat categories defining larger habitat differences were less able to detect small-scale changes on the reef fish assemblages. Ideally, is to provide accurate habitat maps to link habitat characteristics on reef fish assemblages. When an accurate habitat map is unavialable, stereo-BRUV studies should use a finer-scale habitat complexity category. Finally, BRUV sampling designs were considered to include certain levels of categories on habitat generating more statistical power to detect changes on fish biomass, density and species richness. This in order to prevent drawing the false conclusions of explaining the variability of reef fish assemblages to other variables, such as the effect of a no-fishing zone in Marine Parks.

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8.1 Appendix 1

Fish densities. Species average and standard deviation was calculated from the total abundance (sum of MaxN) per depth and divided by the total number (N) of samples used. At the bottom, the total number of species per depth are shown.

Family	Genus species	Depth		N	Depth		N	Depth		N
		15m		56	50m		31	100m		23
Acanthuridae	*Acanthurus chirurgus*	0.39	±	0.83	0.12	±	0.42	0.08	±	0.28
	Acanthurus coeruleus	2.37	±	4.33	0.55	±	0.97	0.13	±	0.45
	Acanthurus tractus	2.12	±	2.02	0.33	±	0.65		–	
Aulostomidae	*Aulostomus maculatus*	0.15	±	0.36	0.06	±	0.24		–	
Balistidae	*Balistes vetula*	0.31	±	0.50	0.55	±	0.75	0.42	±	0.58
	Cantherhines macrocerus	0.27	±	0.55	0.15	±	0.51	0.04	±	0.20
	Melichthys niger	4.59	±	6.18	0.06	±	0.35		–	
	Xanthichthys ringens		–		0.27	±	1.07	1.25	±	1.87
Bothidae	*Bothus lunatus*	0.10	±	0.30	0.03	±	0.17		–	
Carangidae	*Caranx bartholomaei*	0.07	±	0.41	0.09	±	0.52		–	
	Caranx crysos	0.58	±	2.61	2.52	±	4.86	0.08	±	0.41
	Caranx latus	0.07	±	0.41	0.15	±	0.71		–	
	Caranx lugubris	0.02	±	0.13	0.03	±	0.17	0.29	±	0.62
	Caranx ruber	2.71	±	5.21	2.12	±	2.87	0.42	±	0.83
	Decapterus macarellus	2.46	±	14.70	9.61	±	24.43	3.17	±	12.49
	Selar crumenophtalmus	0.95	±	6.54		–			–	
	Seriola rivoliana		–		0.15	±	0.36	0.17	±	0.38
Carcharhinidae	*Carcharhinus falciformis*	0.02	±	0.13		–			–	
	Carcharhinus limbatus		–		0.03	±	0.17		–	
	Carcharhinus perezii	0.25	±	0.48	0.24	±	0.50		–	
Chaenopsidae	*Emblemaria pandionis*		–		0.09	±	0.29		–	
Chaetondontidae	*Chaetodon aculeatus*	0.05	±	0.22	0.15	±	0.44	0.25	±	0.53
	Chaetodon capistratus	1.08	±	1.16	0.18	±	0.53		–	
	Chaetodon ocellatus	0.05	±	0.29		–			–	
	Chaetodon sedentarius		–		0.30	±	0.68	0.29	±	0.69
	Chaetodon striatus	1.24	±	0.97	0.58	±	0.97	0.08	±	0.41
Cheloniidae	*Chelonia mydas*	0.08	±	0.28		–			–	
	Eretmochelys imbricata	0.07	±	0.25		–			–	
Congridae	*Heteroconger longissimmus*	11.98	±	44.02	25.00	±	48.97	1.50	±	6.55
Dasyatidae	*Dasyatis americana*	0.24	±	0.50	0.24	±	0.44	0.04	±	0.20
Diodontidae	*Chilomycterus antillarum*	0.02	±	0.13		–			–	
Echeneidae	*Echeneis naucrates*		–		0.06	±	0.24	0.08	±	0.41
	Echeneis neucratoides	0.05	±	0.22		–			–	
Gerreidae	*Eucinostomus jonesii*	0.02	±	0.13		–			–	
	Eucinostomus lefroyi	0.02	±	0.13		–			–	
Grammatidae	*Gramma loreto*	0.24	±	0.93	0.06	±	0.35	0.04	±	0.20
Haemulidae	*Anisotremus surinamensis*	0.14	±	0.47	0.06	±	0.24		–	
	Haemulon album		–		0.09	±	0.29		–	
	Haemulon aurolineatum	0.03	±	0.18		–			–	
	Haemulon carbonarium	0.36	±	1.03		–			–	
	Haemulon chrysargyreum	0.08	±	0.34	0.09	±	0.52		–	
	Haemulon flavolineatum	0.37	±	0.85	0.33	±	1.57		–	
	Haemulon melanurum	0.05	±	0.39	0.33	±	1.29	0.08	±	0.28
	Haemulon sciurus		–		0.03	±	0.17		–	
	Haemulon striatum		–			–		3.25	±	8.00
	Orthopristis chrysoptera		–			–		0.04	±	0.20
Holocentridae	*Holocentrus adscensionis*	0.10	±	0.36	0.12	±	0.33	0.29	±	0.46
	Holocentrus rufus	0.25	±	0.51	0.15	±	0.57	0.25	±	0.53
	Myripristis jacobus	0.03	±	0.18		–			–	
	Neonipheon marianus	0.02	±	0.13	0.03	±	0.17	0.04	±	0.20
Inermiidae	*Inermia vittata*	1.92	±	14.19		–			–	
Kyphosidae	*Kyphosus sectatrix-incisor*	0.64	±	1.59	0.03	±	0.17		–	
Labridae	*Bodianus rufus*	0.81	±	0.92	0.09	±	0.38	0.04	±	0.20
	Clepticus parrae	2.92	±	8.50	1.82	±	6.19		–	
	Decodon puellaris		–			–		0.25	±	0.61
	Halichoeres bivittatus	0.10	±	0.48		–			–	
	Halichoeres cyanocephalus	0.03	±	0.18	0.03	±	0.17	0.21	±	0.41
	Halichoeres garnoti	1.54	±	2.14	0.76	±	1.71	0.29	±	1.23
	Halichoeres maculipinna	0.03	±	0.26		–			–	
	Halichoeres radiatus	0.41	±	0.62	0.06	±	0.24		–	
	Hemipteronotus martinicensis	0.78	±	2.88	0.94	±	5.22		–	
	Thalassoma bifasciatum	12.92	±	17.77	0.21	±	0.78		–	
Lutjanidae	*Apsilus dentatus*		–		0.03	±	0.17	0.08	±	0.28
	Lutjanus apodus	0.15	±	0.41	0.27	±	1.10	0.08	±	0.28
	Lutjanus buccanella	0.02	±	0.13	1.39	±	3.12	3.46	±	3.23
	Lutjanus jocu		–		0.06	±	0.24		–	
	Lutjanus mahogoni	0.78	±	2.15	0.30	±	0.68	0.79	±	1.96
	Lutjanus synagris	0.24	±	1.39		–			–	
	Lutjanus vivanus		–		0.03	±	0.17	2.46	±	10.36
	Ocyurus chrysurus	0.42	±	0.65	0.45	±	1.48		–	
Malacanthidae	*Malacanthus plumieri*	0.32	±	0.65	0.82	±	1.01	0.71	±	0.81
Megalopidae	*Megalops atlanticus*	0.03	±	0.18		–			–	
Monacanthidae	*Aluterus scriptus*	0.05	±	0.22	0.06	±	0.24		–	
Mullidae	*Mulloidichthys martinicus*	1.81	±	7.50	0.61	±	2.66		–	
	Pseudupeneus maculatus	0.41	±	0.67	0.36	±	0.60	0.17	±	0.38
Muraenidae	*Enchelycore nigricans*	0.02	±	0.13		–			–	
	Gymnothorax funebris	0.05	±	0.29		–			–	
	Gymnothorax miliaris	0.15	±	0.36		–			–	
	Gymnothorax moringa	0.17	±	0.38	0.03	±	0.17	0.04	±	0.20

Opistognathidae	*Opistognathus aurifrons*		–		0.15	±	0.71		–	
Ostraciidae	*Acanthostracion polygonia*	0.17	±	0.42		–		0.08	±	0.28
	Acanthostracion quadricornis	0.02	±	0.13		–			–	
	Lactophrys bicaudalis	0.05	±	0.29		–		0.08	±	0.28
	Lactophrys trigonus	0.07	±	0.25	0.06	±	0.24	0.21	±	0.41
	Rhinesomus triqueter	0.27	±	0.45	0.27	±	0.57	0.17	±	0.64
Pomacanthidae	*Holacanthus ciliaris*	0.07	±	0.25	0.24	±	0.66	0.21	±	0.51
	Holacanthus tricolor	0.25	±	0.48	0.39	±	0.83	0.29	±	0.55
	Pomacanthus arcuatus	0.19	±	0.43	0.42	±	0.75		–	
	Pomacanthus paru	0.15	±	0.36	0.30	±	0.77	0.33	±	0.76
Pomacentridae	*Abudefduf saxatilis*	1.71	±	6.72		–			–	
	Chromis cyanea	3.78	±	7.47	0.45	±	1.37	0.54	±	2.45
	Chromis enchrysurus		–			–		0.04	±	0.20
	Chromis insolata		–		0.24	±	1.39	0.25	±	0.85
	Chromis multilineata	1.51	±	5.29	0.06	±	0.35	0.17	±	0.64
	Microspathodon chrysurus	0.39	±	0.53		–			–	
	Stegastes partitus	2.71	±	3.80	0.61	±	1.41	0.08	±	0.41
	Stegastes planifrons		–		0.03	±	0.17		–	
Rhincodontidae	*Ginglymostoma cirratum*	0.20	±	0.45		–		0.04	±	0.20
Scaridae	*Scarus iseri*	0.10	±	0.36		–			–	
	Scarus taeniopterus	2.66	±	3.25	1.18	±	2.72		–	
	Scarus vetula	0.05	±	0.22		–			–	
	Sparisoma aurofrenatum	1.54	±	1.96	1.06	±	1.97	0.04	±	0.20
	Sparisoma chrysopterum	0.15	±	0.36		–			–	
	Sparisoma rubripinne	0.22	±	0.49		–			–	
	Sparisoma viride	0.73	±	1.50	0.18	±	1.04		–	
Sciaenidae	*Equetus lanceolatus*		–			–		0.04	±	0.20
	Equetus punctatus	0.02	±	0.13		–			–	
Scombridae	*Scomberomorus regalis*	0.08	±	0.28	0.03	±	0.17		–	
Scorpaenidae	*Pterois volitans*	0.03	±	0.26	0.18	±	0.58	0.25	±	0.53
Serranidae	*Bullisichthys caribbaeus*		–			–		0.04	±	0.20
	Cephalopholis cruentata	0.22	±	0.62	0.21	±	0.65	0.25	±	0.68
	Cephalopholis fulva	3.14	±	2.23	0.48	±	0.83	0.50	±	1.10
	Epinephelus guttatus	0.41	±	0.67	0.79	±	1.17	0.67	±	0.96
	Epinephelus striatus	0.02	±	0.13		–			–	
	Hypoplectrus puella	0.02	±	0.13	0.06	±	0.24		–	
	Liopropoma mowbrayi		–			–		0.08	±	0.28
	Mycteroperca venenosa	0.03	±	0.18	0.06	±	0.24		–	
	Paranthias furcifer	0.19	±	0.90	0.33	±	1.74	0.08	±	0.28
	Rypticus saponaceus		–		0.09	±	0.38		–	
	Serranus baldwini		–		0.15	±	0.44		–	
	Serranus luciopercanus		–			–		0.46	±	0.66
	Serranus pheobe		–			–		0.04	±	0.20
	Serranus tabacarius		–		0.36	±	0.99	0.29	±	0.62
	Serranus tigrinus	0.19	±	0.57		–			–	
	Serranus tortugarum		–		0.82	±	2.89	0.08	±	0.41
Sparidae	*Calamus bajonado*		–		0.03	±	0.17		–	
	Calamus calamus	0.03	±	0.26		–			–	
Sphymidae	*Sphyrna lewini*		–		0.03	±	0.17		–	
Sphyraenidae	*Sphyraena barracuda*	0.32	±	0.51	0.15	±	0.36	0.25	±	0.44
Tetraodontidae	*Canthigaster rostrata*	0.07	±	0.25	0.15	±	0.44		–	
	Diodon hystrix	0.02	±	0.13		–			–	
	Sphoeroides spengleri	0.03	±	0.18	0.03	±	0.17		–	
	Total Nsp	103			88			63		

8.2 Appendix 2

Fish biomass. Biomass of each species was calculated through the biomass parameters derived from fishbase.org (see Appendix 3).The average and standard deviation of species biomass was calculated by total biomass divided by the total number (N) of samples used within depths. At the bottom, the average total biomass per sample is shown.

Family	Genus species	Depth		N	Depth		N	Depth		N
		15m		56.0	50m		31.0	100m		23.0
Acanthuridae	*Acanthurus chirurgus*	31.3	±	89.1	14.0	±	43.8	14.7	±	68.7
	Acanthurus coeruleus	428.8	±	915.1	133.0	±	275.2	87.2	±	282.9
	Acanthurus tractus	162.6	±	210.1	37.6	±	86.8		–	
Aulostomidae	*Aulostomus maculatus*	139.7	±	742.9	65.3	±	357.5		–	
Balistidae	*Balistes vetula*	281.7	±	281.7	578.4	±	925.7	363.5	±	638.4
	Cantherhines macrocerus	65.5	±	65.5	29.2	±	118.4		NA	
	Melichthys niger	726.1	±	1155.1	21.8	±	119.5		–	
	Xanthichthys ringens		–		13.1	±	65.0	69.9	±	105.1
Bothidae	*Bothus lunatus*	26.7	±	135.5	16.4	±	89.8		–	
Carangidae	*Caranx bartholomaei*	990.4	±	1789.2	74.9	±	410.2		–	
	Caranx crysos	142.6	±	505.0	656.7	±	1184.4		NA	
	Caranx latus	6.0	±	34.2	419.0	±	1810.0		–	
	Caranx lugubris	122.8	±	910.5	147.2	±	806.5	366.4	±	901.3
	Caranx ruber	690.5	±	1536.0	773.8	±	1255.6	146.2	±	318.8
	Decapterus macarellus	618.1	±	3498.7	2432.1	±	7244.5	1139.3	±	3903.6
	Selar crumenophtalmus	397.2	±	2591.4		–			–	
	Seriola rivoliana		–		444.9	±	1490.8	69.3	±	153.3
Carcharhinidae	*Carcharhinus falciformis*	303.7	±	2252.6		–			–	
	Carcharhinus limbatus		–		537.5	±	2992.6		–	
	Carcharhinus perezii	2929.8	±	15206.2	2869.1	±	6148.7		–	
Chaenopsidae	*Emblemaria pandionis*		–		0.0	±	0.1		–	
Chaetondontidae	*Chaetodon aculeatus*	0.8	±	3.9	2.3	±	10.7	1.9	±	4.5
	Chaetodon capistratus	56.7	±	69.6	12.2	±	38.4		–	
	Chaetodon ocellatus	7.5	±	44.9		–			–	
	Chaetodon sedentarius		–		17.3	±	43.4	15.9	±	36.1
	Chaetodon striatus	98.9	±	95.5	56.5	±	110.5	8.8	±	41.3
Cheloniidae	*Chelonia mydas*		NA			–			–	
	Eretmochelys imbricata		NA			–			–	
Congridae	*Heteroconger longissimmus*		NA			NA			NA	
Dasyatidae	*Dasyatis americana*	799.1	±	2495.9	1481.0	±	4106.2	355.9	±	1669.2
Diodontidae	*Chilomycterus antillarum*		NA			–			–	
Echeneidae	*Echeneis naucrates*		–			NA		37.9	±	177.6
	Echeneis neucratoides	0.6	±	4.7		–			–	
Gerreidae	*Eucinostomus jonesii*		NA			–			–	
	Eucinostomus lefroyi		NA			–			–	
Grammatidae	*Gramma loreto*		NA			NA			NA	
Haemulidae	*Anisotremus surinamensis*	26.5	±	105.1	19.4	±	106.4		–	
	Haemulon album		–		397.3	±	1218.5		–	
	Haemulon aurolineatum	3.3	±	17.4		–			–	
	Haemulon carbonarium	25.0	±	76.8		–			–	
	Haemulon chrysargyreum	12.6	±	54.9	12.9	±	70.9		–	
	Haemulon flavolineatum	33.8	±	85.6	49.5	±	230.4		–	
	Haemulon melanurum		NA		86.8	±	328.9	42.4	±	144.2
	Haemulon sciurus		–		12.9	±	70.9		–	
	Haemulon striatum		–			–		494.1	±	1112.0
	Orthopristis chrysoptera		–			–		6.4	±	30.1
Holocentridae	*Holocentrus adscensionis*	14.7	±	65.1	8.9	±	28.6	8.9	±	29.5
	Holocentrus rufus	32.8	±	84.6	24.8	±	84.4	24.3	±	78.8
	Myripristis jacobus	1.6	±	11.8		–			–	
	Neonipheon marianus	1.1	±	8.1		NA		2.8	±	13.4
Inermiidae	*Inermia vittata*		NA			–			–	
Kyphosidae	*Kyphosus sectatrix-incisor*	153.5	±	438.0		NA			–	
Labridae	*Bodianus rufus*	246.6	±	445.7	15.8	±	65.4	19.9	±	93.6
	Clepticus parrae	87.4	±	393.0	78.8	±	273.8		–	
	Decodon puellaris		–			–		17.1	±	43.4
	Halichoeres bivittatus	3.6	±	15.7		–			–	
	Halichoeres cyanocephalus	23.1	±	125.5	10.4	±	56.8	47.2	±	102.9
	Halichoeres garnoti	218.1	±	321.9	47.4	±	137.6	41.7	±	193.8
	Halichoeres maculipinna	11.6	±	86.2		–			–	
	Halichoeres radiatus	121.9	±	385.7	16.0	±	62.5		–	
	Hemipteronotus martinicensis	11.8	±	50.7	14.6	±	74.9		–	
	Thalassoma bifasciatum	20.9	±	26.9	0.7	±	3.0		–	
Lutjanidae	*Apsilus dentatus*		–		12.1	±	66.2	41.5	±	134.5
	Lutjanus apodus	164.8	±	489.9	193.6	±	739.7	79.4	±	257.1
	Lutjanus buccanella	3.7	±	27.5	292.5	±	695.4	1082.4	±	807.0
	Lutjanus jocu		–		226.1	±	914.7		–	
	Lutjanus mahogoni	77.6	±	192.6	47.0	±	105.7	80.7	±	200.2
	Lutjanus synagris	50.4	±	267.1		–			–	
	Lutjanus vivanus		–		11.4	±	62.3	491.5	±	1904.0
	Ocyurus chrysurus	363.7	±	978.2	260.6	±	859.1		–	
Malacanthidae	*Malacanthus plumieri*	45.5	±	109.1	123.2	±	185.5	114.7	±	193.7
Megalopidae	*Megalops atlanticus*	215.3	±	1118.5		–			–	
Monacanthidae	*Aluterus scriptus*	0.7	±	4.9	4.1	±	16.1		–	
Mullidae	*Mulloidichthys martinicus*	461.8	±	2204.5	211.6	±	1021.3		–	
	Pseudupeneus maculatus	24.9	±	144.1	17.2	±	94.1		NA	
Muraenidae	*Enchelycore nigricans*	5.5	±	40.6		–			–	
	Gymnothorax funebris	4.3	±	32.1		–			–	

	Gymnothorax miliaris	2.6	±	11.2		–			–	
	Gymnothorax moringa	34.9	±	158.4	8.8	±	48.1		NA	
Opistognathidae	*Opistognathus aurifrons*		–			NA			–	
Ostraciidae	*Acanthostracion polygonia*	35.3	±	140.6		–		61.3	±	228.6
	Acanthostracion quadricornis		NA			–			–	
	Lactophrys bicaudalis	8.8	±	46.2		–		32.7	±	118.3
	Lactophrys trigonus	17.0	±	88.8	36.8	±	151.4	95.2	±	247.0
	Rhinesomus triqueter	4.8	±	10.6	11.6	±	29.8	8.5	±	40.0
Pomacanthidae	*Holacanthus ciliaris*	61.1	±	233.0	103.9	±	274.3	88.6	±	286.7
	Holacanthus tricolor	19.8	±	94.7	77.6	±	185.5	53.2	±	134.7
	Pomacanthus arcuatus	192.8	±	621.6	504.4	±	1011.0		–	
	Pomacanthus paru	242.6	±	768.0	574.0	±	1672.7	721.4	±	1922.0
Pomacentridae	*Abudefduf saxatilis*	216.9	±	972.9		–			–	
	Chromis cyanea	86.4	±	406.0	5.2	±	16.8	3.9	±	18.2
	Chromis enchrysurus		–			–		2.6	±	12.4
	Chromis insolata		–		2.8	±	15.1	5.5	±	19.0
	Chromis multilineata	35.9	±	111.7	0.8	±	4.2	1.7	±	5.9
	Microspathodon chrysurus	29.0	±	54.4		–			–	
	Stegastes partitus	0.2	±	1.5	0.0	±	0.1		NA	
	Stegastes planifrons		–		0.0	±	0.1		–	
Rhincodontidae	*Ginglymostoma cirratum*	279.8	±	759.4		–		241.9	±	1134.5
Scaridae	*Scarus iseri*	8.9	±	53.6		–			–	
	Scarus taeniopterus	344.9	±	521.4	193.8	±	414.9		–	
	Scarus vetula	9.8	±	72.4		–			–	
	Sparisoma aurofrenatum	468.6	±	650.2	279.9	±	465.4	11.6	±	54.4
	Sparisoma chrysopterum	114.4	±	407.0		–			–	
	Sparisoma rubripinne	214.1	±	563.2		–			–	
	Sparisoma viride	411.2	±	835.8	126.1	±	690.6		–	
Sciaenidae	*Equetus lanceolatus*		–			–			NA	
	Equetus punctatus	0.2	±	1.7		–			–	
Scombridae	*Scomberomorus regalis*	316.6	±	1934.9	61.3	±	341.3		–	
Scorpaenidae	*Pterois volitans*		NA			NA			NA	
Serranidae	*Bullisichthys caribbaeus*		–			–			NA	
	Cephalopholis cruentata	54.0	±	188.0	62.8	±	218.2	35.2	±	115.3
	Cephalopholis fulva	531.8	±	415.9	129.7	±	215.1	195.5	±	396.1
	Epinephelus guttatus	195.1	±	485.4	434.0	±	770.7	353.5	±	557.4
	Epinephelus striatus	131.2	±	999.5		–			–	
	Hypoplectrus puella		NA		0.6	±	3.3		–	
	Liopropoma mowbrayi		–			–		0.3	±	1.5
	Mycteroperca venenosa	255.2	±	1364.7	1076.1	±	4692.7		–	
	Paranthias furcifer	22.4	±	105.0	53.2	±	277.7	5.1	±	23.9
	Rypticus saponaceus		–			NA			–	
	Serranus baldwini		–		0.3	±	1.3		–	
	Serranus luciopercanus		–			–		19.2	±	30.5
	Serranus pheobe		–			–			NA	
	Serranus tabacarius		–		5.4	±	15.5	20.0	±	45.6
	Serranus tigrinus	1.9	±	9.3		–			–	
	Serranus tortugarum		–		0.5	±	1.9		NA	
Sparidae	*Calamus bajonado*		–		45.1	±	247.1		–	
	Calamus calamus		NA			–			–	
Sphymidae	*Sphyrna lewini*		–		1816.3	±	10112.5		–	
Sphyraenidae	*Sphyraena barracuda*	1546.9	±	2852.7	674.1	±	2108.8	1913.5	±	3543.0
Tetraodontidae	*Canthigaster rostrata*	0.3	±	1.5	1.7	±	7.9		–	
	Diodon hystrix	12.5	±	92.4		–			–	
	Sphoeroides spengleri	1.4	±	8.8	1.0	±	5.5		–	
	Total Biomass / Sample	15596			18997			25628		

*Some species were visualized as Not Available (NA), meaning that their abundance was recorded but length measurements were missing (*Haemulon melanurum, Kyphosus sectatrix-incisor, Echeneis naucrates, Stegastes partitus, Serranus tortugarum, Hypoplectrus puella, Neonipheon marianus, Serranus pheobe, Pseudupeneus maculatus, Bullisichthys caribbaeus Eucinostomus jonesii, Equetus lanceolatus, Inermia vittata, Calamus calamus, Eucinostomus lefroyi, Acanthostracion quadricornis*) or biomass parameters were not available (*Chelonia mydas, Heteroconger longissimmus, Eretmochelys imbricata, Chilomycterus antillarum, Pterois volitans, Gramma loreto, Rypticus saponaceus, Opistognathus aurifrons*).

8.3 Appendix 3

Life history, length ("FL") -weight relationships, trophic level and groups of each species are shown. Parameters are derived from fishbase.org. Life history (K=growth rate, Lmax=maximum length, L50=length at first maturity), length-weight relationships (a and b) and trophic level were based on the average of all studies providing the specific parameters. Classification of trophic groups was based on former studies within areas of the Dutch Caribbean; Saba (Noble et al. 2013), Saba bank (Toller et al. 2010) and Sint Eustatius (McClellan et al. 2009).

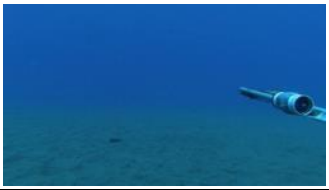
Family	Genus	Species	Code	K	Lmax	L50	Biomass a	Biomass b	Trophic level	Trophic group
Acanthuridae	Acanthurus	chirurgus	doctorfish	0.25	350	170	0.0204	2.9200	2.0	herbivores
Acanthuridae	Acanthurus	coeruleus	blue tang	0.11	369	130	0.0324	2.9500	2.0	herbivores
Acanthuridae	Acanthurus	sp	NA	0.25	321	151	0.0300	2.9200	2.0	herbivores
Acanthuridae	Acanthurus	tractus	ocean surgeonfish	0.40	246	155	0.0257	2.9000	2.0	herbivores
Aulostomidae	Aulostomus	maculatus	atlantic trumpetfish	NA	1000	NA	0.0040	2.8650	4.3	carnivores
Balistidae	Balistes	vetula	queen triggerfish	**0.60**	450	**235**	0.0398	2.8800	3.4	invertebrate feeders
Balistidae	Cantherhines	macrocerus	whitespotted filefish	0.60	460	235	**0.0561**	**2.6530**	3.0	invertebrate feeders
Balistidae	Melichthys	niger	black durgeon	0.60	500	235	0.0561	2.6530	2.4	herbivores
Balistidae	Xanthichthys	ringens	sargassum triggerfish	0.60	250	125	0.0561	2.6530	3.1	invertebrate feeders
Bothidae	Bothus	lunatus	peacock flounder	0.40	460	NA	0.0098	3.1890	4.5	carnivores
Carangidae	Caranx	bartholomaei	yellow jack	0.10	1000	450	0.0398	2.8000	4.5	carnivores
Carangidae	Caranx	crysos	blue runner	0.30	700	274	0.0200	2.9600	4.4	planktivores
Carangidae	Caranx	latus	horse-eye jack	0.10	1010	370	0.0417	2.7900	4.4	carnivores
Carangidae	Caranx	lugubris	black jack	**0.10**	**1000**	**450**	0.0240	2.9100	4.5	carnivores
Carangidae	Caranx	ruber	bar jack	0.10	590	310	0.0151	3.0200	4.4	planktivores
Carangidae	Caranx	sp	NA	0.10	1003	410	0.0400	2.8300	4.4	carnivores
Carangidae	Decapterus	macarellus	mackerel scad	**1.80**	**460**	**110**	**0.0087**	**3.1400**	**3.4**	**planktivores**
Carangidae	Decapterus	sp	NA	1.80	460	110	0.0087	3.1400	3.4	planktivores
Carangidae	Selar	crumenophtalmus	bigeye scad	2.00	300	110	0.0098	3.1800	4.1	planktivores
Carangidae	Seriola	rivoliana	almaco jack	0.10	1600	450	0.0186	2.9400	4.5	carnivores
Carcharhinidae	Carcharhinus	falciformis	silky shark	0.10	3500	2280	0.0079	3.0400	4.5	piscivores
Carcharhinidae	Carcharhinus	limbatus	blacktip shark	**0.20**	**2750**	**1570**	**0.0087**	**2.9600**	4.2	piscivores
Carcharhinidae	Carcharhinus	perezii	reef shark	0.20	3000	1570	0.0087	2.9600	4.5	piscivores
Chaenopsidae	Emblemaria	pandionis	sailfin blenny	NA	50	14	0.0077	2.9620	3.4	planktivores
Chaetondontidae	Chaetodon	aculeatus	longsnout butterflyfish	1.10	100	60	0.0252	3.0760	3.2	omnivores
Chaetondontidae	Chaetodon	capistratus	foureye butterflyfish	1.10	150	**90**	0.0234	3.1900	3.0	omnivores
Chaetondontidae	Chaetodon	ocellatus	spotfin butterflyfish	1.10	200	140	0.0318	2.9840	3.2	omnivores
Chaetondontidae	Chaetodon	sedentarius	reef butterflyfish	**1.10**	150	90	**0.0252**	**3.0760**	2.8	omnivores
Chaetondontidae	Chaetodon	striatus	banded butterflyfish	1.10	160	120	0.0222	3.1400	3.2	omnivores
Cheloniidae	Chelonia	mydas	green turtle	NA	NA	NA	NA	NA	NA	NA
Cheloniidae	Eretmochelys	imbricata	hawksbill	NA	NA	NA	NA	NA	NA	NA
Cheloniidae	NA	sp	NA	NA	NA	NA	NA	NA	NA	NA
Congridae	Heteroconger	longissimmus	brown garden eel	NA	510	NA	NA	NA	3.1	planktivores
Dasyatidae	Dasyatis	americana	southern stingray	NA	2000	800	0.0739	2.8100	3.5	omnivores
Diodontidae	Chilomycterus	antillarum	web burrfish	NA	300	na	NA	NA	3.4	omnivores
Echeneidae	Echeneis	naucrates	sharksucker	NA	1100	750	**0.0009**	**3.3200**	3.4	omnivores
Echeneidae	Echeneis	neucratoides	whitefin sharksucker	NA	750	NA	0.0009	3.3200	3.3	omnivores
Gerreidae	Eucinostomus	jonesii	slender mojarra	NA	200	NA	**0.0923**	**2.6500**	**3.2**	omnivores
Gerreidae	Eucinostomus	lefroyi	mottled mojarra	NA	230	NA	0.0923	2.6500	3.2	omnivores
Gobiidae	NA	sp	NA	1.60	66	38	0.0008	3.5300	3.1	planktivores
Grammatidae	Gramma	loreto	fairy basslet	NA	80	30	NA	NA	3.3	invertebrate feeders
Haemulidae	Anisotremus	surinamensis	black margate	0.17	760	428	0.0148	2.9600	3.3	omnivores
Haemulidae	Haemulon	album	white margate	**0.17**	753	**428**	0.0151	3.0600	3.2	invertebrate feeders
Haemulidae	Haemulon	aurolineatum	tomtate	0.20	250	140	0.0138	3.0000	3.2	omnivores
Haemulidae	Haemulon	carbonarium	caesar grunt	0.18	360	177	0.0404	2.7400	3.3	invertebrate feeders
Haemulidae	Haemulon	chrysargyreum	smallmouth grunt	0.30	230	177	0.0166	3.0400	3.3	planktivores
Haemulidae	Haemulon	flavolineatum	french grunt	**0.18**	294	**177**	0.0186	2.9900	3.3	invertebrate feeders
Haemulidae	Haemulon	melanurum	cottonwick	0.30	330	190	0.0331	2.8500	2.2	omnivores
Haemulidae	Haemulon	sciurus	bluestriped grunt	**0.30**	413	205	0.0245	2.9200	3.4	invertebrate feeders
Haemulidae	Haemulon	sp	NA	0.23	363	228	0.0200	2.9600	3.1	omnivores
Haemulidae	Haemulon	striatum	striped grunt	0.30	280	177	0.0175	3.0990	3.4	planktivores
Haemulidae	Orthopristis	chrysoptera	pigfish	0.30	460	205	0.0149	3.1890	3.4	invertebrate feeders
Holocentridae	Holocentrus	adscensionis	squirrelfish	1.18	504	145	0.0229	2.8600	3.5	omnivores
Holocentridae	Holocentrus	rufus	longspine squirrelfish	**0.90**	350	**135**	0.0186	2.8900	3.5	invertebrate feeders
Holocentridae	Myripristis	jacobus	blackbar soldierfish	0.90	250	135	**0.1110**	**2.7200**	3.6	omnivores
Holocentridae	Neonipheon	marianus	longjaw squirrelfish	0.90	180	135	0.1110	2.7200	3.6	invertebrate feeders
Inermiidae	Inermia	vittata	boga	1.80	230	110	0.0087	3.1400	3.2	planktivores
Kyphosidae	Kyphosus	sectatrix-incisor	bermuda-yellow chub	0.10	NA	NA	0.0083	2.9600	4.5	carnivores
Labridae	Bodianus	rufus	spanish hogfish	0.60	400	NA	**0.0144**	**3.0530**	3.4	invertebrate feeders
Labridae	Clepticus	parrae	creole wrasse	0.60	300	NA	0.0144	3.0530	3.3	planktivores
Labridae	Decodon	puellaris	red hogfish	0.60	300	NA	0.0144	3.0530	3.4	invertebrate feeders
Labridae	Halichoeres	bivittatus	slippery dick	0.60	350	NA	0.0112	3.0500	3.3	carnivores
Labridae	Halichoeres	cyanocephalus	yellowcheek wrasse	0.60	300	NA	0.0052	3.3750	3.4	invertebrate feeders
Labridae	Halichoeres	garnoti	yellowhead wrasse	0.60	193	NA	**0.0052**	**3.3750**	3.5	invertebrate feeders
Labridae	Halichoeres	maculipinna	clown wrasse	0.60	180	NA	0.0028	3.6930	3.3	invertebrate feeders
Labridae	Halichoeres	radiatus	puddingwife	**0.60**	510	NA	0.0131	3.0380	3.4	invertebrate feeders
Labridae	Hemipteronotus	martinicensis	rosy razorfish	0.60	150	NA	0.0180	3.0780	3.5	invertebrate feeders
Labridae	Thalassoma	bifasciatum	bluehead	0.80	250	NA	0.0110	2.9700	3.3	planktivores
Lutjanidae	Apsilus	dentatus	black snapper	0.70	650	400	0.0148	3.0000	4.1	carnivores
Lutjanidae	Lutjanus	apodus	schoolmaster	0.18	570	145	0.0182	3.0000	4.2	carnivores
Lutjanidae	Lutjanus	buccanella	blackfin snapper	0.08	730	310	0.0209	2.9400	3.9	carnivores
Lutjanidae	Lutjanus	jocu	dog snapper	0.10	854	229	0.0240	2.9500	4.3	carnivores
Lutjanidae	Lutjanus	mahogoni	mahogany snapper	0.10	618	130	0.0617	2.6500	4.4	carnivores
Lutjanidae	Lutjanus	synagris	lane snapper	0.10	618	206	0.0234	2.9100	3.8	carnivores
Lutjanidae	Lutjanus	vivanus	silk snapper	0.09	781	304	0.0219	2.9400	3.1	carnivores

Lutjanidae	Ocyurus	chrysurus	yellowtail snapper	0.17	484	199	0.0295	2.7900	4.0	carnivores
Malacanthidae	Malacanthus	plumieri	sand tilefish	0.10	700	NA	0.0158	2.7800	3.6	invertebrate feeders
Megalopidae	Megalops	atlanticus	tarpon	0.10	2500	1600	0.0083	2.9600	4.5	carnivores
Monacanthidae	Aluterus	scriptus	scrawled filefish	0.90	1100	NA	0.8230	1.8140	2.8	invertebrate feeders
Mullidae	Mulloidichthys	martinicus	yellow goatfish	0.40	394	170	0.0123	3.1100	3.2	invertebrate feeders
Mullidae	Pseudupeneus	maculatus	spotted goatfish	0.70	300	180	0.0158	3.0500	3.5	invertebrate feeders
Muraenidae	Enchelycore	nigricans	viper moray	NA	1000	NA	0.0017	3.0000	4.5	carnivores
Muraenidae	Gymnothorax	funebris	green moray	NA	2500	NA	0.0041	2.8560	4.1	carnivores
Muraenidae	Gymnothorax	miliaris	goldentail moray	NA	700	NA	0.0109	2.5740	3.9	carnivores
Muraenidae	Gymnothorax	moringa	spotted moray	NA	2000	NA	0.0005	3.3000	4.5	carnivores
Opistognathidae	Opistognathus	aurifrons	yellowhead jawfish	NA	100	NA	NA	NA	3.1	planktivores
Opistognathidae	Opistognathus	sp	NA	NA	100	NA	NA	NA	3.1	planktivores
Ostraciidae	Acanthostracion	polygonia	honeycomb cowfish	NA	500	198	**0.0269**	**2.9300**	2.0	invertebrate feeders
Ostraciidae	Lactophrys	bicaudalis	spotted trunkfish	NA	480	198	0.0589	2.8200	3.0	invertebrate feeders
Ostraciidae	Lactophrys	quadricornis	scrawled cowfish	NA	500	**198**	0.0269	2.9300	2.0	invertebrate feeders
Ostraciidae	Lactophrys	trigonus	trunkfish	NA	550	198	0.0178	3.0000	3.1	invertebrate feeders
Ostraciidae	Rhinesomus	triqueter	smooth trunkfish	NA	470	198	0.3090	2.2300	3.1	invertebrate feeders
Pomacanthidae	Holacanthus	ciliaris	queen angelfish	0.20	450	**220**	0.0336	2.9000	3.0	invertebrate feeders
Pomacanthidae	Holacanthus	tricolor	rock beauty	0.20	350	158	0.0331	2.9500	3.0	invertebrate feeders
Pomacanthidae	Pomacanthus	arcuatus	gray angelfish	0.20	600	226	0.0344	2.9680	2.9	herbivores
Pomacanthidae	Pomacanthus	paru	french angelfish	**0.20**	411	220	0.0203	3.1260	2.8	herbivores
Pomacentridae	Abudefduf	saxatilis	sergeant major	**0.30**	229	NA	**0.0200**	**3.1300**	3.4	invertebrate feeders
Pomacentridae	Chromis	cyanea	blue chromis	0.30	150	NA	0.0200	3.1300	3.1	planktivores
Pomacentridae	Chromis	enchrysurus	yellowtail reeffish	0.30	100	NA	0.0200	3.1300	3.4	planktivores
Pomacentridae	Chromis	insolata	sunshinefish	0.30	160	NA	0.0200	3.1300	3.4	planktivores
Pomacentridae	Chromis	multilineata	brown chromis	0.30	200	NA	0.0200	3.1300	3.0	planktivores
Pomacentridae	Chromis	sp	NA	0.30	152	NA	0.0200	3.1300	3.2	planktivores
Pomacentridae	Chromis	sp1	NA	0.30	152	NA	0.0200	3.1300	3.2	planktivores
Pomacentridae	Microspathodon	chrysurus	yellowtail damselfish	0.30	210	NA	0.0239	3.0820	2.1	omnivores
Pomacentridae	Stegastes	partitus	bicolor damselfish	0.30	100	NA	0.0182	3.1520	2.0	herbivores
Pomacentridae	Stegastes	planifrons	threespot damselfish	**0.30**	130	NA	0.0379	2.8570	2.6	omnivores
Ptereleotridae	Ptereleotris	sp	NA	NA	120	NA	NA	NA	3.4	planktivores
Rhincodontidae	Ginglymostoma	cirratum	nurse shark	0.10	4300	NA	0.0055	2.8800	3.8	invertebrate feeders
Scaridae	Scarus	iseri	striped parrotfish	0.60	350	150	0.0158	3.0200	2.0	herbivores
Scaridae	Scarus	taeniopterus	princess parrotfish	0.60	350	**150**	**0.0135**	**3.0000**	2.0	herbivores
Scaridae	Scarus	vetula	queen parrotfish	**0.60**	610	NA	0.0135	3.0000	2.0	invertebrate feeders
Scaridae	Sparisoma	aurofrenatum	redband parrotfish	0.20	280	150	0.0117	3.1500	2.0	herbivores
Scaridae	Sparisoma	chrysopterum	redtail parrotfish	0.80	460	150	0.0129	3.1000	2.0	herbivores
Scaridae	Sparisoma	rubripinne	redfin parrotfish	0.60	478	150	0.0178	3.0200	2.0	herbivores
Scaridae	Sparisoma	viride	stoplight parrotfish	0.60	640	163	0.0257	2.9300	2.0	herbivores
Sciaenidae	Equetus	lanceolatus	jackknife fish	NA	250	NA	**0.0011**	**3.8440**	3.4	invertebrate feeders
Sciaenidae	Equetus	punctatus	spotted drum	NA	270	NA	0.0011	3.8440	3.5	invertebrate feeders
Scombridae	Scomberomorus	regalis	cero	0.20	1830	350	0.0202	2.8000	4.5	carnivores
Scorpaenidae	Pterois	volitans	lionfish	NA	380	NA	NA	NA	4.5	carnivores
Serranidae	Bullisichthys	caribbaeus	pugnose bass	NA	60	NA	0.0129	3.0360	3.4	omnivores
Serranidae	Cephalopholis	cruentata	graysby	0.13	415	165	0.0110	3.1100	4.2	carnivores
Serranidae	Cephalopholis	fulva	coney	0.15	699	185	0.0162	3.0100	4.1	carnivores
Serranidae	Epinephelus	guttatus	red hind	0.20	471	341	0.0132	3.0500	3.9	invertebrate feeders
Serranidae	Epinephelus	striatus	nassau grouper	0.15	938	483	0.0091	3.1600	4.1	carnivores
Serranidae	Hypoplectrus	puella	barred hamlet	NA	NA	NA	**0.0129**	**3.0360**	3.4	omnivores
Serranidae	Liopropoma	mowbrayi	cave bass	NA	90	NA	0.0129	3.0360	3.4	omnivores
Serranidae	Mycteroperca	venenosa	yellowfin grouper	0.09	895	529	0.0148	3.0300	4.5	carnivores
Serranidae	Paranthias	furcifer	creolefish	0.20	300	NA	0.0135	3.0430	3.1	planktivores
Serranidae	Rypticus	saponaceus	greater soapfish	NA	350	NA	NA	NA	4.1	carnivores
Serranidae	Serranus	baldwini	lantern bass	NA	120	NA	**0.0129**	**3.0360**	4.1	carnivores
Serranidae	Serranus	luciopercanus	crosshatch bass	NA	120	NA	0.0129	3.0360	3.2	omnivores
Serranidae	Serranus	pheobe	tattler bass	NA	200	NA	0.0129	3.0360	3.5	invertebrate feeders
Serranidae	Serranus	tabacarius	tobaccofish	NA	220	NA	0.0129	3.0360	4.2	invertebrate feeders
Serranidae	Serranus	tigrinus	harlequin bass	NA	290	NA	**0.0145**	**3.0480**	3.7	invertebrate feeders
Serranidae	Serranus	tortugarum	chalk bass	NA	80	NA	0.0145	3.0480	3.1	planktivores
Sparidae	Calamus	bajonado	jolthead porgy	**0.20**	760	**300**	0.0398	2.8200	3.2	invertebrate feeders
Sparidae	Calamus	calamus	saucereye porgy	0.20	560	300	0.0269	2.9400	3.3	invertebrate feeders
Sphymidae	Sphyrna	lewini	scalloped hammerhead	0.20	4300	2100	0.0048	3.0700	4.1	carnivores
Sphyraenidae	Sphyraena	barracuda	great barracuda	0.10	2000	660	0.0095	2.9500	4.5	carnivores
Tetraodontidae	Canthigaster	rostrata	sharpnose puffer	NA	120	50	0.0224	2.9600	3.0	omnivores
Tetraodontidae	Diodon	hystrix	porcupinefish	NA	600	NA	0.5320	2.2760	3.4	invertebrate feeders
Tetraodontidae	Sphoeroides	spengleri	bandtail puffer	NA	300	NA	**0.0224**	**2.9600**	3.2	invertebrate feeders

* Life-history parameters, shown with underline, were not known for that species (fishbase.org) and the available parameters (shown in bold) of other species within family-level was referred to.

8.4 Appendix 4

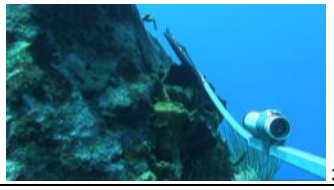
Zone	Habitat image +Habitat complexity category 0-5	Low, Medium or High Relief	Sand vs. Reef (in % coral, >20% of coral = Reef)	Position of cameras	Range of view (meters)	Visibility	Acceptable footage	MaxN by Stage	Presence of Sharks and/or Lionfish
West APR1	 1	Low	40	Straight	>8	Good	Yes	24	Perezii
APR2	 3	Medium	80	Straight	>8	Very good	Yes	28	0
APR3	 2	Medium	100	Straight	>8	Medium	Yes	28	Perezii
APR4	 0	Low	Sand	Straight	>8	Medium	Yes	3	0
APR5	 4	High	80	Straight	>8m=40% 4-6m=60%	Good	Yes	39	0
APR6	 4	High	80	Straight	4-6m=80% >8m=20%	Good	Yes	35	Cirratum
APR7	 2	Medium	100	Upwards	>8	Low	Yes	35	0
APR8	 0	Low	Sand	Straight	>8	Medium	Yes	2	0

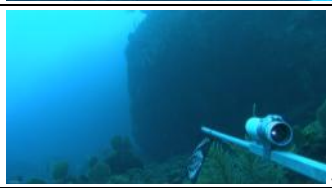
AZ1	 0	Low	Sand	Straight	>8	Good	Yes	5	0
AZ2	 3	Medium	60	Straight	>8	Good	Yes	25	0
RD1	 0	Low	Sand	Straight	>8	Medium	Yes	7	0
RD2	 1	Low	20	Upwards	>8	Low	No	10	0
ReRD2	 1	Low	20	Straight	>8	Medium	Yes	9	0
RD3	 3	Medium	100	Straight	>8m=40% 4-6m=60%	Very good	Yes	38	0
RD4							No: on his side		
ReRD4	 3	Medium	80	Straight	4m=80% >8m=20%	Very good	Yes	34	0
RD5	 0	Low	Sand	Straight	>8	Medium	Yes	5	0
RD6	 3	Medium	60	Straight	2-4m=40% >8m=60%	Good	Yes	26	Cirratum

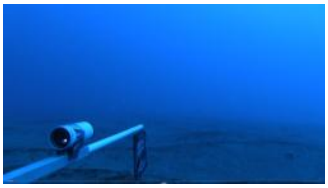
RD7	 2	Medium	100	Straight	>8	Medium	Yes	26	Perezii
RD8	 2	Medium	100	Upwards	>8	Low	Yes	20	0
RD9	 1	Low	60	Straight	>8	Good	Yes	21	Cirratum (2)
RD10	 2	Medium	100	Straight	>8	Medium	Yes	20	Perezii
RD11				Upwards			No		
RD12	 0	Low	Sand	Straight	>8	Medium	Yes	3	0
RD13	 0	Low	Sand	Straight	>8	Medium	Yes	4	0
South S1	 1	Low	30	Straight	>8	Very good	Yes	22	0
S2	 1	Low	20	Straight	>8	Good	Yes	15	0
S3	 0	Low	Sand	Straight	>8	Good	Yes	4	0

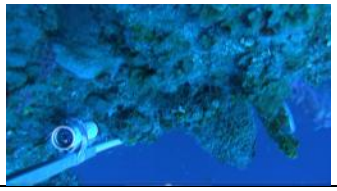
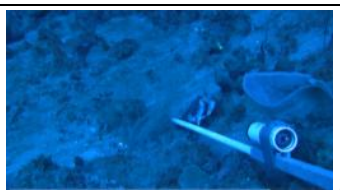
S4			0	Upwards			No		
ReS4	 2	Medium	100	Upwards	>8	Good	Yes	23	0
S5	 1	Low	20	Downwards	2m=50% >8m=50%	Very good	Y/N	6	Perezii
S6	 1	Low	60	Straight	>8	Very good	Yes	23	0
S7				Upwards			No		
ReS7	 2	Medium	100	Straight	>8	Very good	Yes	27	0
S8	 2	Medium	100	Straight	>8	Very good	Yes	24	0
S9	 2	Medium	60	Straight	>8	Very good	Yes	25	0
S10	 1	Low	40	Straight	>8	Very good	Yes	29	0

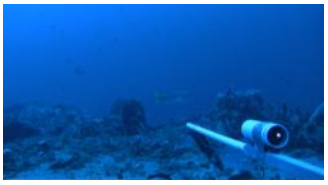
S11	 3	Medium	100	Upwards	2m=40% >8m=60%	Very good	Y/N	25	0
S12	 3	Medium	100	Upwards	2m=90% >8m=10%	Good	Yes	29	0
North N1	 0	Low	Sand	Straight	>8m	Medium	Yes	4	0
N2	 2	Medium	100	Upwards	2m=40% >8m=60%	Very good	Yes	29	Perezii
N3	 2	Medium	100	Downwards	2m=80% >8m=20%	Very good	Yes	28	Cirratum Perezii
N4	 2	Medium	100	Straight	>8	Medium	Yes	24	0
N5	 3	Medium	100	Straight, A bit on his side	>8	Medium	Yes	28	Perezii
N6			0	Upwards			No	5	Perezii
ReN6	 2	Medium	100	Straight	>8	Low	Yes	16	Cirratum

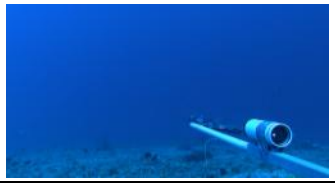
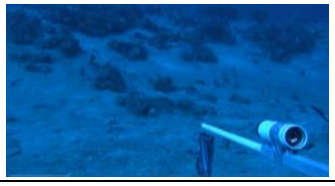
N7	 3	Medium	90	Straight	2m	Good	Yes	11	0
N8	 1	Low	20	Straight	>8	Medium	Yes	22	Perezii (2), Cirratum
N9	 3	Medium	60	Straight	>8	Good	Yes	44	0
N10	 3	Medium	100	Upwards	2m=40% >8m=60%	Good	Yes	34	0
N11	 2	Medium	100	Upwards	>8	Low	No	23	Perezii, Cirratum
ReN11	 4	High	60	Straight	2m=40% >8=60%	Very good	Yes	44	0
N12	 3	Medium	100	Upwards	2m=50% >8m=50%	Very good	Y/N	27	0
East E1	 3	Medium	100	Straight	4m=50% >8m=50%	Good	Yes	38	Perezii
E2	 3	Medium	100	Straight	4m=30% >8m=70%	Good	Yes	29	Cirratum

E3	 3	Medium	100	Upwards	2m=80% >8m=20%	Very good	Yes	24	Cirratum
E4	 3	High	100	Straight	2m=90% >8m=10%	Medium	Yes	31	0
E5	 4	High	100	Straight	>8	Good	Yes	26	0
E6	 3	Medium	100	Straight	2m=90% >8m=10%	Very good	Yes	35	0
E7	 2	Medium	100	Straight	>8	Good	Yes	34	Cirratum
E8	 2	Medium	80	Straight	>8	Medium	Yes	22	Falciformis
E9	 0	Low	Sand	Straight	>8	Good	Yes	9	Perezii
E10	 3	Medium	50	Straight	2m=20% >8m=80%	Very good	Yes	54	Perezii, Cirratum, Lionfish
50 METERS N1	 2	Medium	100	Straight	>8	Good	Yes	44	Lionfish
N2	 0	Low	Sand	Straight	>8	Good	Yes	7	0

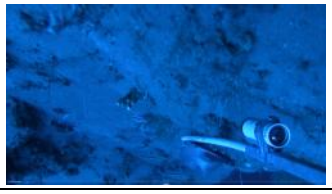
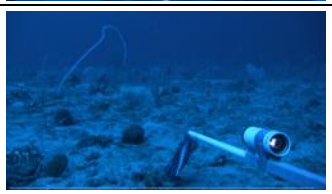
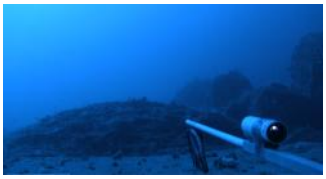
N4	 0	Low	Sand	Straight	>8	Medium	Yes	4	0
N5	 0	Low	Sand	Straight	>8	Medium	Yes	4	0
N6	 0	Low	Sand	Straight	>8	Medium	Yes	8	Perezii
N8	 1	Low	20	Straight	>8	Good	Yes	11	0
N9	 0	Low	Sand	Straight	>8	Medium	Yes	6	0
N10	 1	Low	20	Straight	>8	Good	Yes	13	0
APR3	 0	Low	Sand	Straight	>8	Medium	Yes	2	0
AZ1	 1	Low	40	Straight	>8	Good	Yes	25	Limbatus
AZ2	 1	Low	40	Straight	>8	Good	Yes	14	0
AZ4	 1	Low	40	Straight	>8	Low	Yes	9	0

AZ5	 0	Low	Sand	Straight	>8	Good	Yes	4	0
RD1			100	Upside down	Deleted		No		
ReRD1	 3	Medium	80	Straight	2m=50%, >8=50%	Good	Yes	27	0
RD2	 3	Medium	50	Straight	>8	Good	Yes	16	0
RD3	 2	Medium	40	Downwards	2m	Medium	Yes	10	0
RD4	 1	Low	20	Straight	>8	Medium	Yes	6	Perezii
RD5	 0	Low	Sand	Straight	>8	Good	Yes	4	0
RD6	 1	Low	10	Straight	>8	Good	Yes	10	Perezii
RD7	 1	Low	40	Straight	>8	Very good	Yes	15	0

RD8	 1	Low	20	Straight	>8	Good	Yes	8	0
RD9		NA	NA	Upwards	>8	Good	No	1	0
RD10	 0	Low	Sand	Straight	>8	Good	Yes	6	Perezii
S1	 2	Medium	80	Straight	>8	Good	Yes	29	Perezii
S2	 2	Medium	100	Straight	>8	Good	Yes	22	Perezii (2)
S4	 2	Medium	100	Upwards	>8	Good	Yes	36	Perezii
S5	 0	Low	Sand	Upwards	>8	Low	No	4	0
S6	 2	Medium	60	Straight	>8	Good	Yes	17	0
S8	 1	Low	20	Straight	>8	Medium	Yes	11	0

E1	 0	Low	Sand	Straight	>8	Medium	Yes	7	0
E2	 1	Low	20	Straight	>8	Good	Yes	10	0
E3	 1	Low	60	Straight	>8	Medium	Yes	19	Lewini
E7	 1	Low	50	Straight	>8	Good	Yes	20	0
E8	 1	Low	40	Straight	>8	Good	Yes	18	0
100 meters AZ1							No		
ReAZ1	 1	Low	20	Straight	>8	Good	Yes	13	lionfish
AZ2							No		
ReAZ2	 1	Low	20	Straight	>8	Good	Yes	13	Cirratum, lionfish
AZ3		Low	NA	Straight	2m	Low	No		

RD1	 2	Medium	80	Upwards	>8	Medium	Yes	10	0
RD2	 1	Low	50	Straight	>8	Good	Yes	10	0
RD3	 2	Medium	80	Straight	>8	Medium	Yes	11	0
RD4	 2	Medium	80	Straight	>8	Good	Yes	7	0
RD5	 2	Medium	60	Upwards	>8	Good	Yes	6	0
RD6	 1	Low	10	Straight	>8	Good	Yes	4	0
RD7	 1	Low	20	Straight	>8	Good	Yes	8	0
N1	 0	Low	100	Upwards	>8	Low	Yes	11	0
N2	 0	Low	Sand	Straight	>8	Medium	Yes	7	0
N3	 1	Low	40	Straight	>8	Low	Yes	5	0

N4	 3	Medium	100	Straight	2m=60%, >8=40%	Very good	Yes	12	0
N5	 2	Medium	40	Upside down	2m=80%, >8=20%	Very good	Yes	15	Lionfish (2)
E1	 2	Medium	60	Straight	>8	Good	Yes	9	0
E2	 1	Low	20	Straight	>8	Good	Yes	19	0
E3	 1	Low	50	Straight	>8	Good	Yes	8	Tiger shark
E4	 1	Low	20	Straight	>8	Good	Yes	12	0
E5	 1	Low	40	Straight	>8	Good	Yes	11	lionfish
S2	 1	Low	20	Straight	>8	Low	No	2	0
S3	 1	Low	60	Straight	>8	Medium	Yes	9	0

S4	 2	Low	80	Straight	>8	Good	Yes	17	Lionfish
S5	 2	Low	60	Straight	>8	Medium	Yes	17	0

8.5 Appendix 5

R scripts:

```
# Permutational Anova tests
# For Biomass, commsh stands for fish communities in shallow depth range, opcode for factors
# Upload data sheets
commsh<-read.csv("I:/BRUV/Video Analysis/Statistical Analysis/0. Raw data
(Drop,Species,Habitat)/Biomass_comm_shallow.csv",header=T, row.names=1)
attach(commsh)
names(commsh)
str(commsh)
opcodesh<-read.csv("I:/BRUV/Video Analysis/Statistical Analysis/0. Raw data
(Drop,Species,Habitat)/Factors_Shallow.csv",header=T, row.names=1)
attach(opcodesh)
names(opcodesh)
str(opcodesh)

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

# Select for deep fish communities and drops
commdeep<-read.csv("H:/BRUV/Video Analysis/Statistical Analysis/0. Raw data
(Drop,Species,Habitat)/Biomass_comm_deep.csv",header=T, row.names=1)
opcodedeep<-read.csv("H:/BRUV/Video Analysis/Statistical Analysis/0. Raw data
(Drop,Species,Habitat)/Factors_Deep.csv",header=T, row.names=1)
abundeep<-read.csv("H:/BRUV/Video Analysis/Statistical Analysis/0. Raw data
(Drop,Species,Habitat)/Relabun_deep.csv",header=T, row.names=1)
adonis(commdeep ~ Relief_WAT2005 * Zone, opcodedeep)
adonis(abundeep ~ Relief_WAT2005 * Zone, opcodedeep)

# And deeper areas
commdeeper<-read.csv("I:/BRUV/Video Analysis/Statistical Analysis/0. Raw data
(Drop,Species,Habitat)/Biomass_comm_deeper.csv",header=T, row.names=1)
opcodedeeper<-read.csv("I:/BRUV/Video Analysis/Statistical Analysis/0. Raw data
(Drop,Species,Habitat)/Factors_Deeper.csv",header=T, row.names=1)
abundeeper<-read.csv("I:/BRUV/Video Analysis/Statistical Analysis/0. Raw data
(Drop,Species,Habitat)/Relabun_deeper.csv",header=T, row.names=1)
adonis(commdeeper ~ Site * Relief_POL1993 * Zone, opcodedeeper)
adonis(abundeeper ~ Site * Relief_POL1993 * 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
detach(comm)
detach(data)
rm(list = ls())

# Upload data sheets
comm<-read.csv("I:/BRUV/Video Analysis/Statistical Analysis/0. Raw data
(Drop,Species,Habitat)/Relabun_comm.csv",header=T, row.names=1)
opcode<-read.csv("I:/BRUV/Video Analysis/Statistical Analysis/0. Raw data
(Drop,Species,Habitat)/Relabun_comm.csv",header=T, row.names=1)
attach(comm)
names(comm)
str(comm)

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

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

data<-read.csv("I:/BRUV/Video Analysis/Statistical Analysis/0. Raw data (Drop,Species,Habitat)/Factors.csv",header=T,
row.names=1)
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=1,cex.axis=1,cex.lab=1.2)
sp.comm <- specaccum(comm, xlab = "# of samples", ylab = "# of species",las=1,cex.axis=1,cex.lab=1.2)
plot(sp.comm)
spi<-specaccum(BCI, method="rarefaction")
plot(spi)

Now, add the species accumulation curve for area you did before, spa:

plot(spa, add=TRUE, col=4) #color number 4 is blue

# spec acc for each depth in one graph
#factors
shallow<-read.csv("I:/BRUV/Video Analysis/Statistical Analysis/0. Raw data
(Drop,Species,Habitat)/Factors_Shallow.csv",header=T, row.names=1)
deep<-read.csv("I:/BRUV/Video Analysis/Statistical Analysis/0. Raw data (Drop,Species,Habitat)/Factors_Deep.csv",header=T,
row.names=1)
deeper<-read.csv("I:/BRUV/Video Analysis/Statistical Analysis/0. Raw data
(Drop,Species,Habitat)/Factors_Deeper.csv",header=T, row.names=1)
#species
comm_sh<-read.csv("I:/BRUV/Video Analysis/Statistical Analysis/0. Raw data
(Drop,Species,Habitat)/Relabun_sh.csv",header=T, row.names=1)
comm_deep<-read.csv("I:/BRUV/Video Analysis/Statistical Analysis/0. Raw data
(Drop,Species,Habitat)/Relabun_deep.csv",header=T, row.names=1)
comm_deeper<-read.csv("I:/BRUV/Video Analysis/Statistical Analysis/0. Raw data
(Drop,Species,Habitat)/Relabun_deeper.csv",header=T, row.names=1)

plot(specaccum(comm_sh, method="random"), xlab="# of samples", ylab="# of species")
plot(specaccum(comm_deep),col="gray", add=T)
plot(specaccum(comm_deeper), col="gray52",add=T)

# spec acc for each level of habitat in one graph #
comm_0<-read.csv("I:/BRUV/Video Analysis/Statistical Analysis/0. Raw data (Drop,Species,Habitat)/Relabun_0.csv",header=T,
row.names=1)
comm_1<-read.csv("I:/BRUV/Video Analysis/Statistical Analysis/0. Raw data (Drop,Species,Habitat)/Relabun_1.csv",header=T,
row.names=1)
comm_2<-read.csv("I:/BRUV/Video Analysis/Statistical Analysis/0. Raw data (Drop,Species,Habitat)/Relabun_2.csv",header=T,
row.names=1)
comm_3<-read.csv("I:/BRUV/Video Analysis/Statistical Analysis/0. Raw data (Drop,Species,Habitat)/Relabun_3.csv",header=T,
row.names=1)
comm_4<-read.csv("I:/BRUV/Video Analysis/Statistical Analysis/0. Raw data (Drop,Species,Habitat)/Relabun_4.csv",header=T,
row.names=1)

plot(specaccum(comm_0, method="random"), xlab="# of samples", ylab="# of species",xlim=c(0,18), ylim=c(0,80))
plot(specaccum(comm_1),col="gray10", add=T)
plot(specaccum(comm_2), col="gray30",add=T)
plot(specaccum(comm_3),col="gray50", add=T)
plot(specaccum(comm_4), col="gray70",add=T)

ls()

# 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(1,3,1,0))
par(oma=c(0,0,0,0))
boxplot(specnumber(comm) ~ data$Habitat_type, ylab = "# of species",las=1)
boxplot(specnumber(comm) ~ data$Relief_WAT2005, ylab = "# of species",las=1)
boxplot(specnumber(comm) ~ data$Relief_POL1993, ylab = "# of species",las=1)

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

# 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
```

```
comm.bc.dist <- vegdist(comm, method = "bray",data=data)
# 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")

# 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)
# Names are opcodes
ordiplot(comm.bc.mds, display = "sites", 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)
# plot just the samples, colour by habitat, pch=19 means plot a circle
points(mds.fig, "sites", pch = 19, col = "yellow", select = data$Habitat_type ==  "Sand")
points(mds.fig, "sites", pch = 19, col = "Blue", select = data$Habitat_type ==  "Reef")
# add confidence ellipses around habitat types
ordiellipse(comm.bc.mds, opcode$Depth_layer, conf = 0.95, label = TRUE)
# overlay the cluster results we calculated earlier

# For Polunin category
str(opcode)
# ordination plots are highly customizable set up the plotting area but don't plot anything yet
par(mfrow=c(1,2))
#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 = 21, col = "gray", bg="gray", select = opcode$Relief_POL1993 ==  "0")
points(mds.fig, "sites", pch = 22, col = "black", select = opcode$Relief_POL1993 ==   "1")
points(mds.fig, "sites", pch = 23, col = "gray62", select = opcode$Relief_POL1993 ==  "2")
points(mds.fig, "sites", pch = 24, col = "gray11",bg = "gray11",select = opcode$Relief_POL1993 == "3")
points(mds.fig, "sites", pch = 25, col = "dimgray",bg="dimgray", select = opcode$Relief_POL1993 ==  "4")
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 = 21, col = "gray", bg="gray", select = opcode$Depth_layer == "15")
points(mds.fig, "sites", pch = 22, col = "black", select = opcode$Depth_layer ==  "50")
points(mds.fig, "sites", pch = 24, col = "gray11", bg="gray11", select = opcode$Depth_layer ==  "100")
savefont <- par(font=1)
par(savefont)

# add confidence ellipses around habitat types
ordiellipse(comm.bc.mds, opcode$Relief_POL1993, conf = 0.95, label = TRUE)
# overlay the cluster results we calculated earlier
ordicluster(comm.bc.mds, comm.bc.clust, col = "gray")

# 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 = 19, col = "green", select = opcode$Relief_WAT2005 ==  "High")
points(mds.fig, "sites", pch = 19, col = "yellow", select = opcode$Relief_WAT2005 == "Low")
points(mds.fig, "sites", pch = 19, col = "blue", select = opcode$Relief_WAT2005 ==  "Medium")
# add confidence ellipses around habitat types
ordiellipse(comm.bc.mds, opcode$Relief_WAT2005, conf = 0.95, label = TRUE)
# 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[, 1:3]))

opcode$Zone <- factor(opcode$Zone, levels = c("RD", "MU"),
                      labels = c("Closed","Open"))
# For Zone
str(opcode)
opcode$Zone <- factor(opcode$Zone, levels = c("RD", "MU"))
mds.fig <- ordiplot(comm.bc.mds, type = "none",xlab="Dimension 1",ylab="Dimension 2")
points(mds.fig, "sites", pch = 22, col = "black", select = data$Zone == "MU")
points(mds.fig, "sites", pch = 21, col = "gray", bg="gray", select = data$Zone ==   "RD")
# add confidence ellipses around zones
ordiellipse(comm.bc.mds, opcode$Zone, conf = 0.95, label = TRUE)
# overlay the cluster results we calculated earlier

# For site
mds.fig <- ordiplot(comm.bc.mds, type = "none")
points(mds.fig, "sites", pch = 19, col = "green", select = opcode$Site == "East")
points(mds.fig, "sites", pch = 19, col = "red", select = opcode$Site ==  "North")
points(mds.fig, "sites", pch = 19, col = "blue", select = opcode$Site ==   "West")
points(mds.fig, "sites", pch = 19, col = "yellow", select = opcode$Site ==   "South")
# add confidence ellipses around cluster of  sites
ordiellipse(comm.bc.mds, opcode$Site, conf = 0.95, label = TRUE)

# Ordination plot for species
library(vegan)
modsp <- decorana(abun)
?decorana
plot(modsp)
names(abun)[1:5]
# abbreaviation of names
shnam <- make.cepnames(names(abun))
shnam[1:5]
pl <- plot(modsp, dis="sp")
identify(pl, "sp", labels=shnam)
stems <- colSums(abun)
plot(modsp, dis="sp", type="n")
sel <- orditorp(modsp, dis="sp", lab=shnam, priority=stems, pcol = "gray", pch="+")
plot(modsp, dis="sp", type="n")
ordilabel(modsp, dis="sp", lab=shnam, priority = stems)
# Now add variables to the species graph
library(picante)
habitat<-factor(opcode$Relief_POL1993)
str(opcode)
#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="sp", type="n",xlab="Dimension 1",ylab="Dimension 2")
sel <- orditorp(modsp, dis="sp", lab=shnam, priority=stems, pcol = "gray", pch="+")
plot(envfit(comm.bc.mds, opcode[, 1:5]),col= "gray40",p.max=0.05, cex=0.8)


# Barplots of species biomass, select for most abundant herbivores and carnivores
detach(comm)
detach(abun)
rm(list = ls())

comm<-read.csv("I:/BRUV/Video Analysis/Statistical Analysis/0. Raw data
(Drop,Species,Habitat)/Biomass_comm.csv",header=T, row.names=1)
attach(comm)
names(comm)
str(comm)
opcode<-read.csv("I:/BRUV/Video Analysis/Statistical Analysis/0. Raw data (Drop,Species,Habitat)/Factors.csv",header=T,
row.names=1)
attach(opcode)
names(opcode)
str(opcode)

Depth_layer<-factor(Depth_layer)
Rel<-factor(Relief_POL1993)

## barplots with error bars are calculated with 95% confidence limits
#### Create multiple graphs in one window for herbivores
```

```
### biomass for blue_tang->y, x is depth_layer
#c(bottom, left, top, right)
par(mfrow=c(1,1))
par(mar=c(1,3,1,0))
par(oma=c(0,0,0,0))
y<-comm$blue_tang
x<-opcode$Zone
error.bar <- function(x, y, upper, lower=upper, length=0.1){
       if(length(x) != length(y) | length(y) !=length(lower) | length(lower) != length(upper))
         stop("vectors must be same length")
       arrows(x,y+upper, x, y-lower, angle=90, code=3, length=length)}

barb <- barplot(tapply(comm$blue_tang,list(opcode$Zone,opcode$Depth_layer),mean),
                  beside=T, axis.lty=1, ylim=c(0,800), las=1, cex.axis=0.7, cex.lab=0.8)
y.mean <- tapply(comm$blue_tang,list(opcode$Zone,opcode$Depth_layer),mean)
y.sd <- tapply(comm$blue_tang,list(opcode$Zone,opcode$Depth_layer),sd)
     error.bar(barb,y.mean, 1.96*y.sd/10)

### biomass for ocean_surgeonfish->y, x is depth_layer
par(mfrow=c(1,1))
par(mar=c(1,1,1,0))
par(oma=c(0,0,0,0))
str(comm)
y1<-comm$ocean_surgeonfish
x1<-opcode$Zone
error.bar <- function(x1, y1, upper, lower=upper, length=0.1){
       if(length(x1) != length(y1) | length(y1) !=length(lower) | length(lower) != length(upper))
         stop("vectors must be same length")
       arrows(x1,y1+upper, x1, y1-lower, angle=90, code=3, length=length)}

barb1 <- barplot(tapply(comm$ocean_surgeonfish,list(opcode$Zone,opcode$Depth_layer),mean),
                  beside=T, axis.lty=1,ylim=c(0,800), cex.axis=0.7,las=1,cex.lab=0.8)
y1.mean <- tapply(comm$ocean_surgeonfish,list(opcode$Zone,opcode$Depth_layer),mean)
y1.sd <- tapply(comm$ocean_surgeonfish,list(opcode$Zone,opcode$Depth_layer),sd)
error.bar(barb1,y1.mean, 1.96*y1.sd/10)

### biomass for redband_parrotfish->y3, x3 is depth_layer
par(mfrow=c(1,1))
par(mar=c(1,3,1,0))
par(oma=c(0,0,0,0))
str(comm)
y3<-comm$redband_parrotfish
x3<-opcode$Zone
error.bar <- function(x3, y3, upper, lower=upper, length=0.1){
       if(length(x3) != length(y3) | length(y3) !=length(lower) | length(lower) != length(upper))
         stop("vectors must be same length")
       arrows(x3,y3+upper, x3, y3-lower, angle=90, code=3, length=length)}

barb3 <- barplot(tapply(comm$redband_parrotfish,list(opcode$Zone,opcode$Depth_layer),mean),
                   beside=T, axis.lty=1,las=1, ylim=c(0,800), cex.axis=0.7, cex.lab=0.8)
y3.mean <- tapply(comm$redband_parrotfish,list(opcode$Zone,opcode$Depth_layer),mean)
y3.sd <- tapply(comm$redband_parrotfish,list(opcode$Zone,opcode$Depth_layer),sd)
error.bar(barb3,y3.mean, 1.96*y3.sd/10)

### biomass for stoplight_parrotfish->y4, x4 is depth_layer
par(mfrow=c(1,1))
par(mar=c(1,1,1,0))
par(oma=c(0,0,0,0))
str(comm)
y4<-comm$stoplight_parrotfish
x4<-opcode$Zone
error.bar <- function(x4, y4, upper, lower=upper, length=0.1){
       if(length(x4) != length(y4) | length(y4) !=length(lower) | length(lower) != length(upper))
         stop("vectors must be same length")
       arrows(x4,y4+upper, x4, y4-lower, angle=90, code=3, length=length)}

barb4 <- barplot(tapply(comm$stoplight_parrotfish,list(opcode$Zone,opcode$Depth_layer),mean),
                   beside=T, axis.lty=1,las=1, ylim=c(0,800), cex.axis=1, cex.lab=0.8)
y4.mean <- tapply(comm$stoplight_parrotfish,list(opcode$Zone,opcode$Depth_layer),mean)
y4.sd <- tapply(comm$stoplight_parrotfish,list(opcode$Zone,opcode$Depth_layer),sd)
error.bar(barb4,y4.mean, 1.96*y4.sd/10)

### biomass for french_grunt->y6, x6 is depth_layer
par(mfrow=c(1,1))
par(mar=c(1,4,1,0))
par(oma=c(0,0,0,0))
```

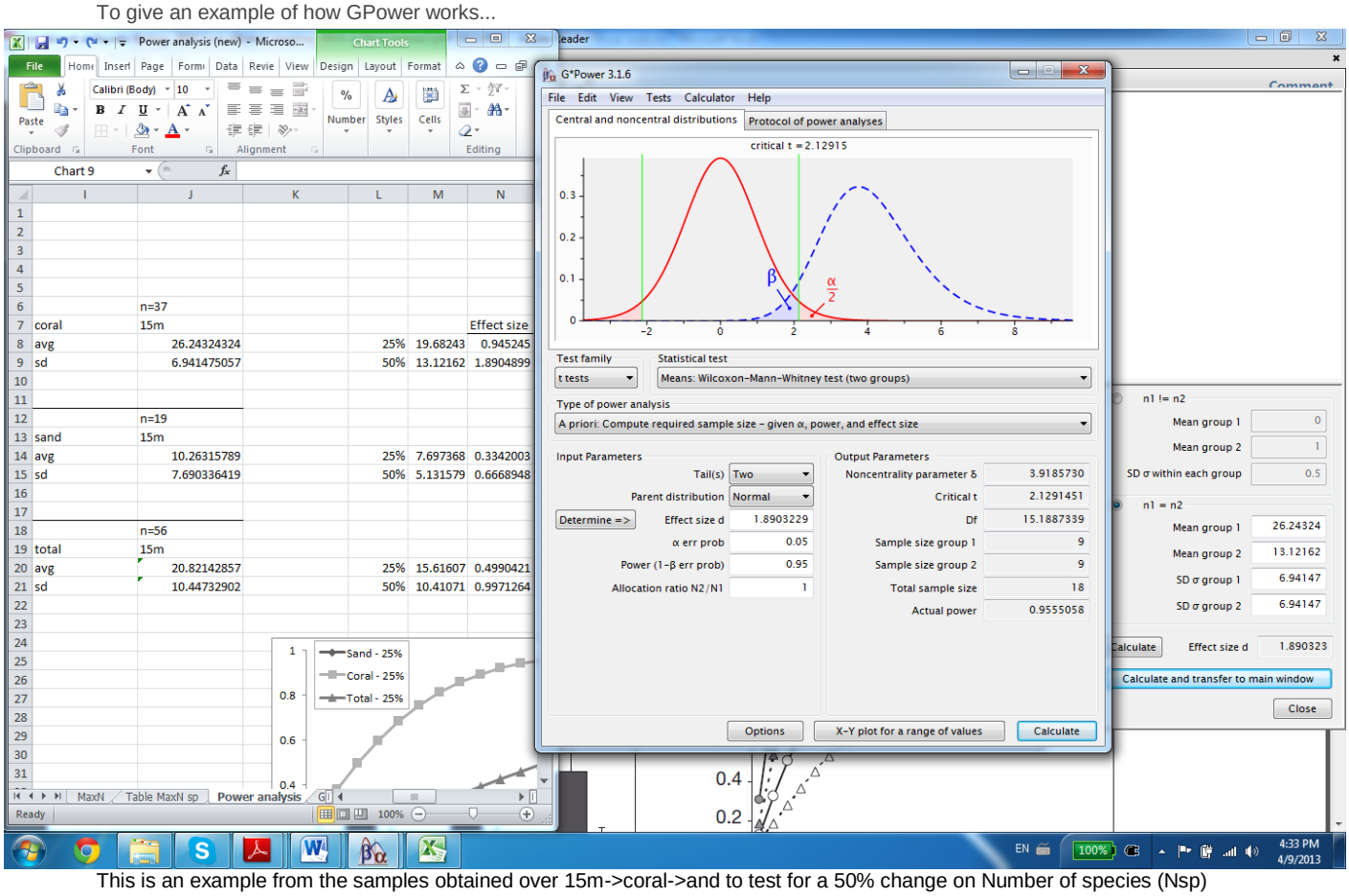
```
str(comm)
y6<-comm$french_grunt
x6<-opcode$Zone
error.bar <- function(x6, y6, upper, lower=upper, length=0.1){
  if(length(x6) != length(y6) | length(y6) !=length(lower) | length(lower) != length(upper))
    stop("vectors must be same length")
  arrows(x6,y6+upper, x6, y6-lower, angle=90, code=3, length=length)}

barb6 <- barplot(tapply(comm$french_grunt,list(opcode$Zone,opcode$Depth_layer),mean),
                 beside=T, axis.lty=1,las=1, ylim=c(0,200), cex.axis=0.7, cex.lab=0.9,ylab="Average of Total Biomass")
y6.mean <- tapply(comm$french_grunt,list(opcode$Zone,opcode$Depth_layer),mean)
y6.sd <- tapply(comm$french_grunt,list(opcode$Zone,opcode$Depth_layer),sd)
error.bar(barb6,y6.mean, 1.96*y6.sd/10)

### biomass for caesar_grunt->y7, x7 is depth_layer
par(mfrow=c(1,1))
par(mar=c(1,1,1,0))
par(oma=c(0,0,0,0))
str(comm)
y7<-comm$caesar_grunt
x7<-opcode$Zone
error.bar <- function(x7, y7, upper, lower=upper, length=0.1){
       if(length(x7) != length(y7) | length(y7) !=length(lower) | length(lower) != length(upper))
         stop("vectors must be same length")
       arrows(x7,y7+upper, x7, y7-lower, angle=90, code=3, length=length)}

barb7 <- barplot(tapply(comm$caesar_grunt,list(opcode$Zone,opcode$Depth_layer),mean),
                 beside=T, axis.lty=1, ylim=c(0,200),las=1, cex.axis=1, cex.lab=0.8)
y7.mean <- tapply(comm$caesar_grunt,list(opcode$Zone,opcode$Depth_layer),mean)
y7.sd <- tapply(comm$caesar_grunt,list(opcode$Zone,opcode$Depth_layer),sd)
     error.bar(barb7,y7.mean, 1.96*y7.sd/10)

### biomass for red_hind->y14, x14 is depth_layer
par(mfrow=c(1,1))
par(mar=c(1,3,1,0))
par(oma=c(0,0,0,0))
str(comm)
y14<-comm$red_hind
x14<-opcode$Zone
error.bar <- function(x14, y14, upper, lower=upper, length=0.1){
  if(length(x14) != length(y14) | length(y14) !=length(lower) | length(lower) != length(upper))
    stop("vectors must be same length")
       arrows(x14,y14+upper, x14, y14-lower, angle=90, code=3, length=length)}

barb14 <- barplot(tapply(comm$red_hind,list(opcode$Zone,opcode$Depth_layer),mean),
                  beside=T, axis.lty=1,las=1, ylim=c(0,800), cex.axis=0.7, cex.lab=0.8 )
y14.mean <- tapply(comm$red_hind,list(opcode$Zone,opcode$Depth_layer),mean)
y14.sd <- tapply(comm$red_hind,list(opcode$Zone,opcode$Depth_layer),sd)
error.bar(barb14,y14.mean, 1.96*y14.sd/14)


### biomass for coney->y8, x8 is depth_layer
par(mfrow=c(1,1))
par(mar=c(1,1,1,0))
par(oma=c(0,0,0,0))
str(comm)
y8<-comm$coney
x8<-opcode$Zone
error.bar <- function(x8, y8, upper, lower=upper, length=0.1){
       if(length(x8) != length(y8) | length(y8) !=length(lower) | length(lower) != length(upper))
    stop("vectors must be same length")
  arrows(x8,y8+upper, x8, y8-lower, angle=90, code=3, length=length)}

barb8 <- barplot(tapply(comm$coney,list(opcode$Zone,opcode$Depth_layer),mean),
              beside=T, axis.lty=1, ylim=c(0,800), las=1, cex.axis=0.7, cex.lab=0.6 )
y8.mean <- tapply(comm$coney,list(opcode$Zone,opcode$Depth_layer),mean)y8.sd <-
tapply(comm$coney,list(opcode$Zone,opcode$Depth_layer),sd)
error.bar(barb8,y8.mean, 1.96*y8.sd/10)

### biomass for blackfin_snapper->y12, x12 is depth_layer
par(mfrow=c(1,1))
par(mar=c(2,3,0,0))
par(oma=c(0,0,0,0))
str(comm)
y12<-comm$blackfin_snapper
x12<-opcode$Zone
```

```
error.bar <- function(x12, y12, upper, lower=upper, length=0.1){
  if(length(x12) != length(y12) | length(y12) !=length(lower) | length(lower) != length(upper))
         stop("vectors must be same length")
       arrows(x12,y12+upper, x12, y12-lower, angle=90, code=3, length=length)}

barb12 <- barplot(tapply(comm$blackfin_snapper,list(opcode$Zone,opcode$Depth_layer),mean),
                beside=T, axis.lty=1, las=1, ylim=c(0,1600), cex.axis=0.7)
y12.mean <- tapply(comm$blackfin_snapper,list(opcode$Zone,opcode$Depth_layer),mean)
y12.sd <- tapply(comm$blackfin_snapper,list(opcode$Zone,opcode$Depth_layer),sd)
error.bar(barb12,y12.mean, 1.96*y12.sd/12)
??cex.axis
### biomass for yellowtail_snapper->y13, x13 is depth_layer

par(mfrow=c(1,1))
par(mar=c(2,1,0,0))
par(oma=c(0,0,0,0))
str(comm)
y13<-comm$yellowtail_snapper
x13<-opcode$Zone
error.bar <- function(x13, y13, upper, lower=upper, length=0.1){
  if(length(x13) != length(y13) | length(y13) !=length(lower) | length(lower) != length(upper))
    stop("vectors must be same length")
  arrows(x13,y13+upper, x13, y13-lower, angle=90, code=3, length=length)}

barb13 <- barplot(tapply(comm$yellowtail_snapper,list(opcode$Zone,opcode$Depth_layer),mean),
                beside=T, axis.lty=1, las=1, ylim=c(0,1600), cex.axis=0.7, cex.lab=0.8 )
y13.mean <- tapply(comm$yellowtail_snapper,list(opcode$Zone,opcode$Depth_layer),mean)
y13.sd <- tapply(comm$yellowtail_snapper,list(opcode$Zone,opcode$Depth_layer),sd)
error.bar(barb13,y13.mean, 1.96*y13.sd/13)

### biomass for great_barracuda->y15, x15 is depth_layer
str(comm)
y15<-comm$great_barracuda
x15<-opcode$Zone
error.bar <- function(x15, y15, upper, lower=upper, length=0.1){
  if(length(x15) != length(y15) | length(y15) !=length(lower) | length(lower) != length(upper))
    stop("vectors must be same length")
  arrows(x15,y15+upper, x15, y15-lower, angle=90, code=3, length=length)}

barb15 <- barplot(tapply(comm$great_barracuda,list(opcode$Zone,opcode$Depth_layer),mean),
                beside=T, axis.lty=1, ylim=c(0,2600), cex.axis=0.8, cex.lab=0.8 )
y15.mean <- tapply(comm$great_barracuda,list(opcode$Zone,opcode$Depth_layer),mean)
y15.sd <- tapply(comm$great_barracuda,list(opcode$Zone,opcode$Depth_layer),sd)
error.bar(barb15,y15.mean, 1.96*y15.sd/15)

### biomass for black_durgeon->y2, x2 is depth_layer
str(comm)
y2<-comm$black_durgeon
x2<-opcode$Zone
error.bar <- function(x2, y2, upper, lower=upper, length=0.1){
  if(length(x2) != length(y2) | length(y2) !=length(lower) | length(lower) != length(upper))
    stop("vectors must be same length")
  arrows(x2,y2+upper, x2, y2-lower, angle=90, code=3, length=length)}

barb2 <- barplot(tapply(comm$black_durgeon,list(opcode$Zone,opcode$Depth_layer),mean),
               beside=T, axis.lty=1, ylim=c(0,800), cex.axis=1, cex.lab=1.2)
y2.mean <- tapply(comm$black_durgeon,list(opcode$Zone,opcode$Depth_layer),mean)y2.sd <-
tapply(comm$black_durgeon,list(opcode$Zone,opcode$Depth_layer),sd
      error.bar(barb2,y2.mean, 1.96*y2.sd/10)


### biomass for princess_parrotfish->y5, x5 is depth_layer
str(comm)
y5<-comm$princess_parrotfish
x5<-opcode$Zone
error.bar <- function(x5, y5, upper, lower=upper, length=0.1){
  if(length(x5) != length(y5) | length(y5) !=length(lower) | length(lower) != length(upper))
    stop("vectors must be same length")
  arrows(x5,y5+upper, x5, y5-lower, angle=90, code=3, length=length)}
barb5 <- barplot(tapply(comm$princess_parrotfish,list(opcode$Zone,opcode$Depth_layer),mean),
                beside=T, axis.lty=1, las=1, ylim=c(0,800), cex.axis=1, cex.lab=1.2 )
y5.mean <- tapply(comm$princess_parrotfish,list(opcode$Zone,opcode$Depth_layer),mean)
y5.sd <- tapply(comm$princess_parrotfish,list(opcode$Zone,opcode$Depth_layer),sd)
error.bar(barb5,y5.mean, 1.96*y5.sd/10)
```

```
### biomass for graysby->y9, x9 is depth_layer
str(comm)
y9<-comm$graysby
x9<-opcode$Zone
error.bar <- function(x9, y9, upper, lower=upper, length=0.1){
  if(length(x9) != length(y9) | length(y9) !=length(lower) | length(lower) != length(upper))
    stop("vectors must be same length")
  arrows(x9,y9+upper, x9, y9-lower, angle=90, code=3, length=length)}

barb9 <- barplot(tapply(comm$graysby,list(opcode$Zone,opcode$Depth_layer),mean),
                 beside=T, axis.lty=1, ylim=c(0,1000), cex.axis=0.8, cex.lab=0.8 )
y9.mean <- tapply(comm$graysby,list(opcode$Zone,opcode$Depth_layer),mean)
y9.sd <- tapply(comm$graysby,list(opcode$Zone,opcode$Depth_layer),sd)
error.bar(barb9,y9.mean, 1.96*y9.sd/10)

## biomass for schoolmaster->y10, x10 is depth_layer
str(comm)
y10<-comm$schoolmaster
x10<-opcode$Zone
error.bar <- function(x10, y10, upper, lower=upper, length=0.1){
  if(length(x10) != length(y10) | length(y10) !=length(lower) | length(lower) != length(upper))
    stop("vectors must be same length")
  arrows(x10,y10+upper, x10, y10-lower, angle=90, code=3, length=length)}

barb10 <- barplot(tapply(comm$schoolmaster,list(opcode$Zone,opcode$Depth_layer),mean),
                  beside=T, axis.lty=1, ylim=c(0,600), cex.axis=0.8, cex.lab=0.8 )
y10.mean <- tapply(comm$schoolmaster,list(opcode$Zone,opcode$Depth_layer),mean)
y10.sd <- tapply(comm$schoolmaster,list(opcode$Zone,opcode$Depth_layer),sd)
error.bar(barb10,y10.mean, 1.96*y10.sd/10)

### biomass for mahogany_snapper->y11, x11 is depth_layer
str(comm)
y11<-comm$mahogany_snapper
x11<-opcode$Zone
error.bar <- function(x11, y11, upper, lower=upper, length=0.1){
  if(length(x11) != length(y11) | length(y11) !=length(lower) | length(lower) != length(upper))
    stop("vectors must be same length")
  arrows(x11,y11+upper, x11, y11-lower, angle=90, code=3, length=length)}

barb11 <- barplot(tapply(comm$mahogany_snapper,list(opcode$Zone,opcode$Depth_layer),mean),
                  beside=T, axis.lty=1, ylim=c(0,600), cex.axis=0.8, cex.lab=0.8 )
y11.mean <- tapply(comm$mahogany_snapper,list(opcode$Zone,opcode$Depth_layer),mean)
y11.sd<tapply(comm$mahogany_snapper,list(opcode$Zone,opcode$Depth_layer),sd)error.bar(barb1,y11.mean,
1.96*y11.sd/11
```

8.6 Appendix 6

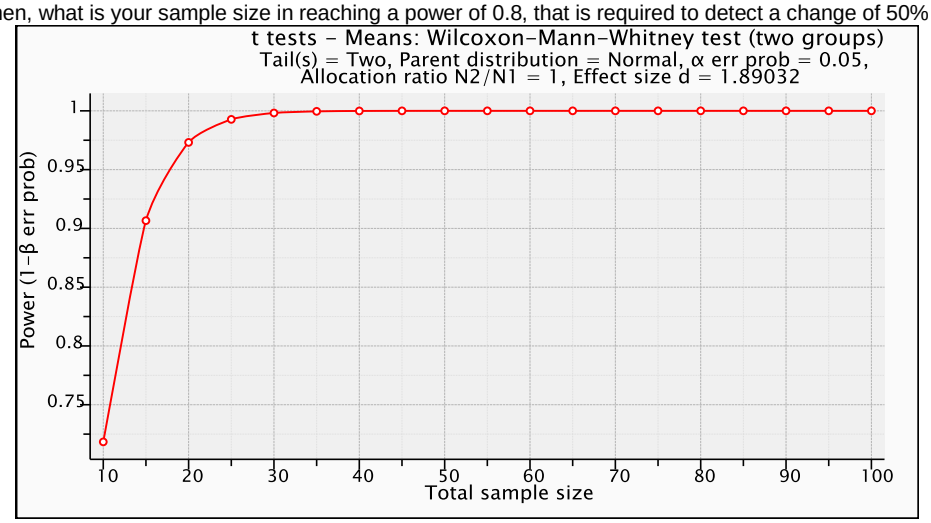
To give an example of how GPower works...



This is an example from the samples obtained over 15m->coral->and to test for a 50% change on Number of species (Nsp)

1) Mean group 1 is the average Nsp
2) Mean group 2 is the average Nsp – 50% of that average
3) Sd group 1 and 2 is the standard deviation sampled
4) Calculate the power for each drop and press on “X-Y plot” to see the graph and table of the number of samples equal to a certain statistical power..

Then, what is your sample size in reaching a power of 0.8, that is required to detect a change of 50% in species richness?



In this case, you need a sample size of 12 to reach the required statistical power