

Ecological Role and Potential Value of Sponges to Torres Strait

Annual Report 2007

Alan Duckworth, Carsten Wolff, Rose Cobb and Nicole Webster
Australian Institute of Marine Science



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SUMMARY

Sponges are a dominant organism on coral reefs through-out Torres Strait and elsewhere have been shown to play an important ecological role by acting as a nursery or recruitment habitat for other species of economic importance. Sponges can also compete for food and space to the detriment of other sessile coral reef organisms. In addition to their ecological importance, sponges that have good quality spongin fibres have commercial value and may be sold as bath sponges. A recently completed three-year CRC Torres Strait study between AIMS and the Yorke Island Council developed farming procedures to commercially grow the common bath sponge *Coscinoderma* sp. around Masig (Yorke). To examine the sustainability of a bath sponge industry in Torres Strait, it is important to understand the dynamics and structure of bath sponge population(s) and explore the risks and threats to these populations. In November 2006, the waters around Ugar, Erub, Masig, Poruma and Warraber in central and eastern Torres Strait were surveyed for *Coscinoderma* sp. The bath sponge was found at all five island-groups; however it was most abundant at Masig with an average of 5.5 *Coscinoderma* sp. individuals per 30 m². Within island-groups, the abundance of *Coscinoderma* sp. varied significantly between locations (kilometres) and sites (200 m), probably resulting from the interaction of physical, biological and stochastic processes influencing the recruitment of juveniles and the survival of adults. This survey also provided information on the spatial patterns in Torres Strait of ecologically and economically important coral reef animals such as coral trout and crown-of-thorns-starfish. *Coscinoderma* sp. individuals were largest at Masig and Poruma, with sponges expected to grow to over 20 cm in size. Genetic and microbial analyses of sponges from each island-group found little variation in either genetic profiles or intra-sponge microbial populations across central and eastern Torres Strait, suggesting that only one large population of *Coscinoderma* sp. occurs in Torres Strait with transfer of larvae between island-groups. Of the 436 *Coscinoderma* sp. individuals recorded from the survey, only one was partially diseased, indicating a healthy sponge population. A smaller scale survey around Masig determined that *Coscinoderma* sp. is more common and grows larger at 12 m than at 6 m, possibly due to reduced levels of damaging water flow at greater depths. Substrate type also influences the abundance and size frequency patterns of *Coscinoderma* sp. A settlement plate experiment started in November 2006 is investigating the settlement of bath sponges and other sessile organisms across seasons, islands and depths. This experiment will run for 3 years and will provide vital information about when, where and how often bath sponges recruit onto coral reefs in Torres Strait. For all field work in Torres Strait, the Masig Islanders John Morris and Samson Lowatta are employed to help with the various experiments. This has achieved effective capacity building and contributes income directly into the local community. The findings of this MTSRF study and previous experiments indicate that for sustainable management of the *Coscinoderma* sp. population in Torres Strait, harvesting of sponges should occur on deep reef around Masig. To minimise any potential environmental impact, only 10% of the population should be harvested, with at least one-third of each sponge left behind and still attached to the substrate. In addition, only large sponges (>15 cm) should be harvested to maximise explant production. This MTSRF study also suggests that *Coscinoderma* sp. can be safely translocated from Masig to the other island-groups, to set-up bath sponge farms where *Coscinoderma* sp. is not naturally abundant.

1. INTRODUCTION

1.1 BACKGROUND

Sponges are an important component in many reef habitats in terms of biomass and diversity (Reiswig 1973; Dayton et al. 1974; Schmahl 1990) and they may interact with the wider community in several important ways. Sponges can provide food (Ayling 1981; Wulff 1994) or shelter (Costello & Myers 1987; Duffy 1992) for other organisms. They can also filter and extract much of the available phytoplankton (Reiswig 1971; Pile et al. 1996, 1997; Duckworth et al. 2006) to the possible detriment to other suspension feeding organisms. Sponges can compete for and dominate the substrate (Dayton et al. 1974) and thereby exclude other organisms from settling and recruiting into the community.

In addition to their ecological value in community dynamics, some sponges also have commercial value. Commercial bath sponges, species from the order Dictyoceratida that have a high quality spongin skeleton, have industrial and house-hold value. To supply global markets, commercial bath sponges have traditionally been harvested from natural populations in the Mediterranean Sea and around Florida, USA. Over-harvesting and periodic disease outbreaks have decimated these natural populations and severely limited the yield of bath sponges (Pronzato, 1999). In 2003, for example, global trade in natural sea sponges was 2127 metric tons but reported global production from harvesting was a mere 55 metric tons (FAO 2004). Because harvesting natural populations cannot meet demand, an opportunity exists to develop alternative supply methods. In-sea aquaculture has the potential to supply sufficient and sustainable quantities of bath sponges to meet market demand.

A Torres Strait wide survey in 2004 discovered a potential commercial bath sponge species, *Coscinoderma* sp. (Fig. 1.1), common to the central region, particularly around Masig (Yorke) Island (Duckworth et al. 2007). Market analysis on a conspecific population from central Great Barrier Reef determined that *Coscinoderma* sp. has commercial grade spongin.



Figure 1.1. Photo of the commercially important bath sponge, *Coscinoderma* sp., common to the central region of Torres Strait.

A recently completed farming study in Torres Strait (CRC Torres Strait Task 1.6) has identified good farming procedures, and coupled with the high growth rates of *Coscinoderma* sp., suggests that bath sponge aquaculture in Torres Strait will be a viable industry (Duckworth et al. 2007).

This current MTSRF project builds on the outputs of sponge aquaculture research in Torres Strait to help determine the sustainability of a sponge farming industry in Torres Strait. This will be achieved by gaining a greater understanding of the dynamics and structure of bath sponge population(s) and exploring the risks and threats to these populations. Given sponges play an important ecological role in tropical ecosystems, through acting as nursery or recruitment habitat for other species of economic or ecological importance (Butler et al. 1995), factors that influence dominant sponge species can have wider community effects. Sponges are useful indicator or sentinel species for environmental stress, and can provide relevant information of general habitat risk from pollution, disease, invasions or sedimentation (Carballo et al. 1996).

This MTSRF project will:

- Determine the size of the *Coscinoderma* sp. population in Torres Strait, and explore and identify the environmental factors that structure the abundance and size patterns of the bath sponge species;
- Determine the possible risks of translocating individuals of *Coscinoderma* sp. within Torres Strait, to possibly set-up bath sponge farms where it is not naturally abundant; and
- Determine when, where and how often sponges such as *Coscinoderma* (and other sessile organisms) recruit onto coral reefs in Torres Strait

1.2. OBJECTIVES

The specific objectives of this project are as follows:

1. Undertake an assessment of the distribution and abundance of wild commercial sponge species in Torres Strait, identifying elements of environmental risk (evidence of disease, sedimentation, invasives), and establish a sustainable strategy for seed stock harvest.
2. Determine connections between sponge populations and risks in translocation.
3. Determine patterns of sponge recruitment/mortality and the environmental risk of seed stock harvest leading to development of a sustainable seed collection strategy.

1.3. INVOLVEMENT OF TORRES STRAIT ISLANDERS

This MTSRF project involved much field and diving work in Torres Strait, particularly around Masig Island. For all field work, two Torres Strait Islanders from Masig, John Morris and Samson Lowatta (Fig. 1.2), were employed. For the diving work, a boat was hired daily from a Masig Islander, further contributing to the local economy. This was based on the good working model established from the previous CRC Torres Strait project. Stanley Lui (Fig. 1.2), a marine biologist from Erub Island, also helped out on the bath sponge survey in November 2006. Following this survey, a report was sent to communities on all surveyed islands in Torres Strait fully informing them of the results (Appendix 1). Permission was obtained from Traditional Owners prior to diving in their local waters.



Figure 1.2. Photos of Torres Strait Islanders: *(left)* John Morris attaching settlement plates to the coral reef around Masig to help determine when and where bath sponges recruit (Objective 3); *(top-right)* Samson Lowatta (right) and Carsten Wolff steaming to a dive site during the November 2006 sponge survey (Objective 1); *(below-right)* Stan Lui surveying the waters of Torres Strait for bath sponges (last two photos taken by Eric Matson).

2. DISTRIBUTION AND ABUNDANCE OF *COSCINODERMA SP.*

Objective 1. Undertake an assessment of the distribution and abundance of wild commercial sponge species in Torres Strait, identifying elements of environmental risk (evidence of disease, sedimentation, invasives), and establish a sustainable strategy for seed stock harvest.

2.1. INTRODUCTION

Distribution and size frequency patterns of sessile organisms such as sponges may vary among and within neighbouring islands and regions. Heterogeneity over both small and large spatial scales is the result of the interaction of physical, biological and stochastic factors influencing the distribution and abundance of individual species (Wilkinson and Cheshire 1989; Zea 2001). Sponges are an important component in many benthic communities and can dominate the benthos in some regions in terms of biomass and diversity (Schmahl 1990; Wilkinson and Cheshire 1990). Being efficient filter feeders of small particulate matter, sponges also represent an important energy coupling between the benthic and pelagic communities (Reiswig 1971; Pile *et al.* 1996; Duckworth *et al.* 2006).

The abundance and distribution patterns of sponges can be influenced by water flow and depth (Wilkinson and Evans 1989; Roberts and Davis 1996), larval dispersal and recruitment patterns (Maldonado and Young 1996), predation (Dunlap and Pawlik 1996), light intensity (Wilkinson and Trott 1985) as well as substrate and habitat type (Reiswig 1973; Adjeroud 1997). Environmental and biological factors such as disease can also generate randomness in sponge distribution (Zea 2001). The influence or impact of each factor varies between sponge species, often restricting species to a specific area or depth (Wilkinson and Evans 1989) and exacerbating heterogeneity in community structure between and within reefs or islands.

Structuring factors that promote patchy distributions may also influence size frequency patterns of sponges over short spatial scales. The effect of a physical or biological factor on size frequency patterns is often complex (Turon *et al.* 1998; Bell *et al.* 2002) and may have a positive or negative impact depending on its level of intensity. For example, sponge growth rates will generally increase as water flow increases because of the greater availability of suspended food (Wilkinson and Vacelet 1979; Duckworth and Battershill 2003), however, high water flow can also damage sponges, remove tissue, and decrease their size (Trautman *et al.* 2000)

Surveys at two spatial scales were done in Torres Strait examining the abundance and size frequency distributions of *Coscinoderma* sp. The first surveyed reefs around islands across central and eastern Torres Strait (scale over 100 km), to determine where *Coscinoderma* sp. is most abundant. This survey also collected information on the distribution and abundance of several commercially and ecologically important species such as coral trout, crown-of-thorn-starfish, sea cucumbers and snappers (These results are shown in Appendix 1 and will be submitted to ReefCheck). The second survey addressed a smaller spatial scale of kilometres and was based in the area where *Coscinoderma* sp. is most common, to further determine what factors influence its size and abundance at that location.

2.2. METHODS

2.2.1. Central and Eastern Torres Strait Survey

Study area and sampling strategy

The study area in Torres Strait is situated between Papua New Guinea and northern Queensland, Australia, and is bordered by the Warrior Reefs to the west and the edge of the continental shelf to the east (Fig. 2.1); this represents the known distribution of *Coscinoderma* sp. in Torres Strait (Duckworth et al. 2007). Surveys for *Coscinoderma* sp. were done at five island-groups: Ugar (Stephen Is) and Erub (Darnley Is) in eastern Torres Strait and Masig (Yorke Is), Poruma (Coconut Is) and Warraber (Sue Is) in central Torres Strait (Fig. 2.1). All five islands are inhabited, with populations in the low hundreds. The island-groups were, on average, 66 km (\pm SE = 11) km apart from each other. Ugar and Erub are both volcanic islands, rising above 30 m, while islands of the three central Torres Strait island-groups consist entirely of sand cays and are generally low-lying (<10 m in height). All surveyed islands are small in size (<10 km²) and are enclosed by coral reef. The reef slope generally starts at a depth of 5 m (mean low water) and stops at 15 m, descending at an angle ranging from 20 to 60°. Maximum depth between neighbouring islands and reefs is approximately 30 m, with the substrate consisting of muddy sand (Harris 1988). South-easterly trade winds are common from April to December, while monsoonal weather patterns with more northerly winds dominate in summer.

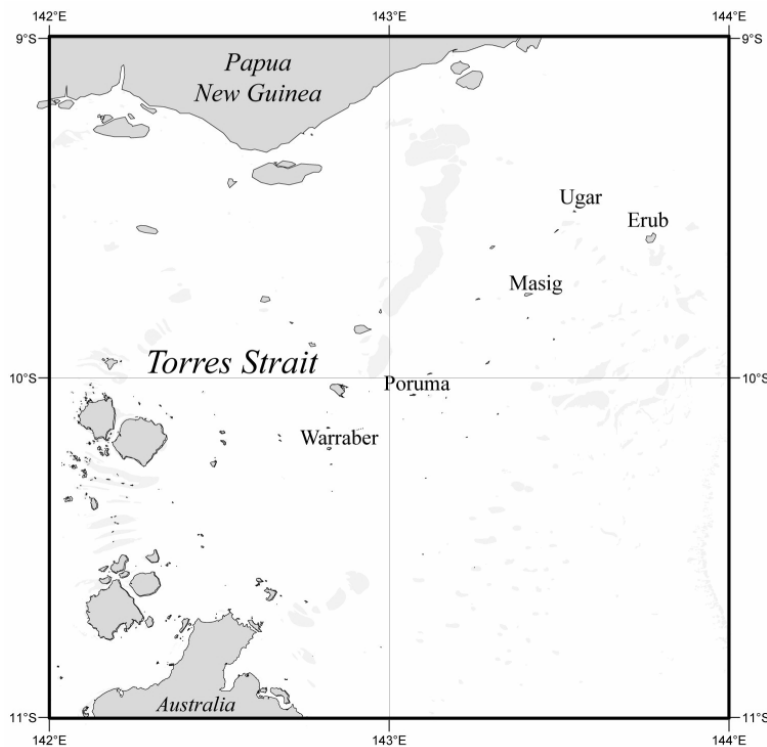


Figure 2.1. Map of Torres Strait showing the five island-groups surveyed for *Coscinoderma* sp.

Sponge surveys were done at 7 or 8 randomly selected locations in each island-group, with each location ≥ 2 km apart, averaging 8 km. The locations were situated around each main island (e.g. Ugar, Masig) and neighbouring islands and reefs in each island-group. Each location was divided into two sites, approximately 200 m apart. At each site, three 30 x 1 m strip transects were quantitatively surveyed for *Coscinoderma* sponges. Transects were separated by at least 20 m to retain independence and all were done between 7-11 m, a depth where *Coscinoderma* sp. is common in Torres Strait (Duckworth and Wolff 2007). Transect depth did not vary significantly between island-groups (Nested ANOVA: $F_{DF=4,32}=1.48$; $P=0.231$) nor between locations nested within island-groups (Nested ANOVA: $F_{DF=32,37}=1.53$; $P=0.105$).

To examine size frequency distributions patterns, the greatest dimension of every *Coscinoderma* sp. was measured by a ruler attached to the dive slate and recorded. For graphical interpretation, sponges were grouped into 2 or 5 cm size classes. For any diseased sponge, the percent of infected or necrotic pinacoderm was noted. All surveys were done in November 2006, thus preventing any possible temporal variation in sponge size and abundance influencing the results.

Environmental factors

For each transect we also recorded the angle of reef slope and the percentage of consolidated limestone rock (hereafter rock), dead coral rubble (rubble) and sand. These environmental variables were previously found to partially influence the distribution patterns of dictyoceratid sponges such as *Coscinoderma* sp. in Torres Strait (Duckworth et al. 2007). They are also quick to measure and so were able to be incorporated into the logistics of the survey.

Data analysis

Abundance of *Coscinoderma* sp. across spatial scales was analysed using a nested ANOVA, with island-group as a fixed factor, and location and site as nested factors. To meet assumptions of ANOVA, data was $\log(x+1)$ transformed and island-groups with less than 25 sponges were not included in the analysis to reduce the probability of a Type I error occurring due to different sample sizes (Zar 1999). The Tukey-Kramer Multiple Comparison (TKMC) Test was used to determine which island-group(s) differed from each other in sponge abundance (and size)

Sponge size was compared among island-groups using one-way ANOVA. Only island-groups with greater than 25 recorded sponges were analysed to reduce the probability of a Type I error occurring. Data was \log transformed. For each island-group, mean sponge size, standard-deviation, 95th percentile and coefficient of variation (CV) were calculated on raw, untransformed data. Because the maximum size of sessile invertebrates can be influenced by chance events, the 95th percentile is used instead to compare the upper size limit across space (Soong 1993; Meesters et al. 2001). The CV is a measure of the amount of variation in a population irrespective of mean size. Sponge size for each island-group was also analysed using single Kolmogorov-Smirnov tests with Lilliefors adjustment ($P>0.05$) to determine if the size data has a normal distribution. To ensure that each test had a similar statistical power, 50 *Coscinoderma* sp. individuals were randomly selected if sample number from an island group exceeded 60 recorded sponges. Skewness (g_1) values were also calculated, with a positive value indicating a greater proportion of small individuals and a negative value indicating that the population is dominated by large individuals. For each island-group, Kolmogorov-Smirnov and skewness tests were done on both raw and log-transformed data, to determine if a log-transformation can normalise the size data for a sponge as shown for many hard coral species (Bak and Meesters 1998; Vermeij and Bak 2003)

To investigate variation in size distribution over small spatial scales, sponge size was analysed in the island-group where *Coscinoderma* sp. was most abundant using a nested ANOVA with location as a fixed factor and site nested; data was log-transformed. Only locations where both sites had >10 individuals were analysed to reduce the likelihood of a Type I error. For each analysed site, mean sponge size, standard-deviation, 95th percentile and coefficient of variation (CV) were calculated.

Separate nested ANOVAs were applied to each environmental factor to test for differences among island-groups, locations and sites. All environmental factors were arcsine transformed.

2.2.2. Masig Island-group Survey

Study area and sampling strategy

This study was done around Keats, Kodall and Masig Islands, located in central Torres Strait and where *Coscinoderma* sp. is most abundant. Keats, Kodall and Masig are sand cays, low-lying (<10 m in height) and small in size (<5 km²). Coral reef surrounds all islands, with broken reef connecting Kodall and Masig. The coral reef slope generally starts at a depth of 6 m (MLW) and stops on sand at 15 m, descending at an angle ranging from 20 to 60°. South-easterly trade winds (15-20 knots) are common from April to December, while monsoonal weather patterns with more northerly winds dominate during summer.

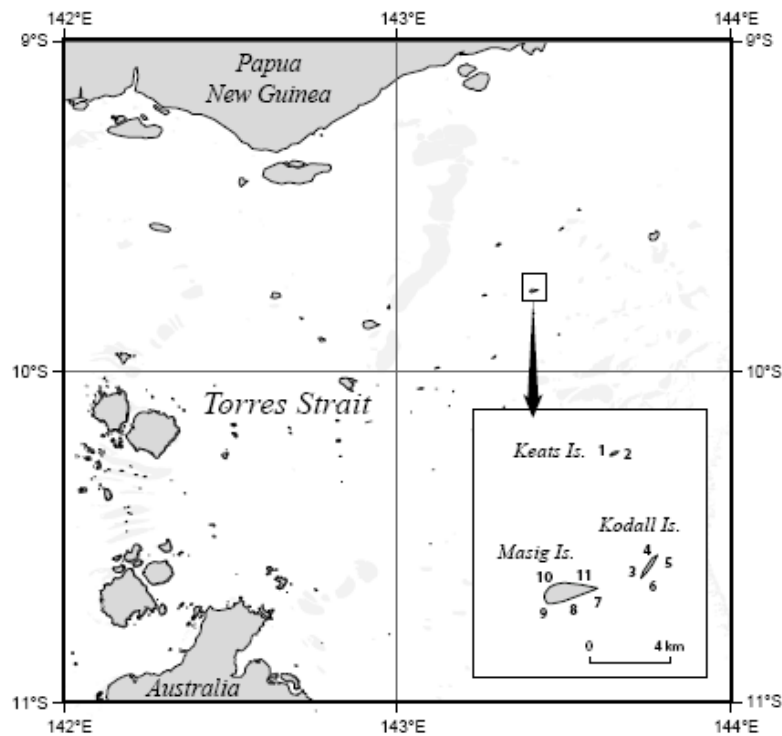


Figure 2.2. Map of Torres Strait showing the surveyed sites (1-11) around Keats, Kodall and Masig.

Abundance between depths and microhabitats

In March 2007, *Coscinoderma* sp. was surveyed at 11 sites on coral reef at Keats, Kodall and Masig, with locations at least 1 km apart. At each site, *Coscinoderma* sp. was surveyed at both shallow (4-6 m) and deep (10-12 m) depths, with the former generally on the reef flat. Three 20 x 1 m transects were examined at each depth, with transects separated by at least 20 m to retain independence. For each transect, divers recorded every *Coscinoderma* sponge found within 1 m of one side of the transect line. Basic environmental factors were also noted and for each transect we estimated the degree of reef slope and the percentage of dead coral rubble (rubble), sand and consolidated limestone rock (hereafter rock) free of living organisms.

For each sponge, we recorded the substrate type that it was attached to and growing on. Three types were identified: rock; rubble; and sand, with grain size ranging from 0.5-2 mm. These three substrate types vary in their level of stability for sponge attachment and growth, with rock providing a secure immobile base for sponges, while sand being easily moved by water currents is a relatively insecure and fluid substrate for attachment. Rubble provides an intermediate level of stability; a separate study at Masig has found that rubble pieces (with a sponge attached) can move several meters between monitoring events (3 months), at times causing the sponge to become partially buried by rubble or sand. For each sponge we also recorded whether it was living in an exposed microhabitat, such as on top of rock fully exposed to the ambient water flow, or in a sheltered microhabitat, such as under an overhang or protected between surrounding rocks.

To examine size frequency distributions patterns, the greatest length, width and height of every *Coscinoderma* sp. was measured by a ruler attached to the dive slate and recorded. For graphical interpretation, sponges were grouped into 2 cm size classes. Some individuals of *Coscinoderma* sp. in Torres Strait have a palmate morphology, where large lobes project upwards from the main sponge base. For each measured sponge, we also counted and recorded the number of lobes it possessed.

Data analysis

A MANOVA was done to examine the influence of site (random factor), depth (fixed factor) and their interaction on the four environmental factors (slope, %rock, %rubble and %sand), with factors arcsine transformed (Zar 1999). For all environmental factors (and size comparisons; see below), within-cell correlation analyses detected no multicollinearity problems (r -squared <0.99) while Bartlett-Box homogeneity tests determined that the covariance matrices are equal ($P > 0.05$). Wilks' lambda statistic was used to compute F-ratios and data was then analysed further by ANOVA.

The abundance of *Coscinoderma* sp. between sites and depth was analysed using a two-way ANOVA, with location and depth as a random and fixed factor, respectively. Data was log (x+1) transformed to meet the assumptions of ANOVA. Chi-Square analysis was used to compare observed and expected frequencies of sponges living on rock and rubble at 6 and 12 m. If a significant result was obtained, we subdivided the Chi-Square analysis (Zar 1999) to determine which substrate-depth treatment(s) primarily contributed to the nonconformity of the data.

Differences in sponge length, width, height and lobe number between depths and substrate types were analysed using MANOVA. To ensure similar sample sizes between treatments to reduce the probability of a Type I error (Zar 1999), 50 individuals were randomly selected if sample number from a treatment exceeded 50 sponges; data was log (x+1) transformed. Size frequency distributions for *Coscinoderma* sp. do not vary greatly over distances of km's (previous study), thus data in this study was pooled across sites. Wilks' lambda statistic was used to compute F-ratios and data was then analysed further by ANOVA.

For significant factors, mean size, standard deviation, 95th percentile and coefficient of variation (CV) were calculated on raw, untransformed data for sponge length, width and height. Because the maximum size of sessile invertebrates can be influenced by chance events, the 95th percentile is used instead to compare the upper size limit across space (Soong 1993; Meesters et al. 2001). The CV is a measure of the amount of variation in a population irrespective of mean size. Each depth-substrate class was also analysed using single Kolmogorov-Smirnov tests with Lilliefors adjustment ($P>0.05$) to determine if sponge length, width and height have a normal distribution. Sample numbers need to be similar between classes to ensure that each test has a similar statistical power. If need be, a minimum of 50 *Coscinoderma* sp. individuals were randomly selected to ensure similar sample numbers. Skewness (g_1) values were calculated as well, with a positive value indicating a greater proportion of small individuals and a negative value indicating that the population is dominated by large individuals. For each depth-substrate class, Kolmogorov-Smirnov and skewness tests were done on both raw and log-transformed data. Exposure (sheltered vs. exposed) was not included in this analysis because the sample number in some depth-substrate-exposure classes would be too small.

2.3. RESULTS

2.3.1. Central and Eastern Torres Strait Survey

Spatial variability of environmental factors

The degree of reef slope and percentage of rock and sand but not rubble varied significantly among the five island groups (Table 2.1). Reef slope was steepest at Masig where it averaged 46°; at the four other island-groups it averaged 23-30°. Reef slope also varied significantly between locations nested within island-groups (Table 2.1), ranging 10-56° at Erub for example. The percentage of rock was greatest at Ugar, Erub and Masig where consolidated limestone constituted about half of the reef substrate, while at Poruma and Warraber it averaged less than 35%. Approximately one-third of the rock substrate at each island-group was occupied by living organisms, predominantly Scleractinian and sponge species (unpublished data), leaving two-thirds as “free space”. The percentage of sand was highest at Warraber (>30%) and lowest at Ugar (<20%). At all island-groups, approximately 33% of the substrate consisted of dead coral rubble. All four environmental factors differed significantly among sites (Table 2.1), indicating variation over short spatial scales (~200 m).

Table 2.1. Summary of nested ANOVA's examining variation of the four environmental factors among island-groups, locations and sites. All factors were arcsine transformed. F-ratios shown. Probability: * = <0.05; **=<0.01; *** = <0.001.

Source	DF	Reef slope	% Rock	% Rubble	% Sand
Island-group	4	3.52*	4.25**	2.10	3.88*
Location (Island)	32	4.78***	0.91	1.47	0.72
Site (Location(Island))	37	2.10***	5.08***	5.58***	4.54***
Error	148				

Spatial variability in abundance

In total, 436 *Coscinoderma* sp. individuals were counted and measured during the survey, with the sponge species found at all five island-groups (Fig. 2.3). However, *Coscinoderma* sp. was uncommon at Warraber with only 19 sponges recorded and therefore Warraber was not included in the statistical analysis for abundance comparisons. The abundance of *Coscinoderma* sp. varied significantly among island-groups in Torres Strait (Nested ANOVA: $F_{DF=3,26}=9.94$; $P<0.001$), being most abundant at Masig with 5.5 sponges per 30 m² on average (Fig. 2.3). On coral reefs at Masig, *Coscinoderma* sp. is a dominate sponge species in both abundance and biomass; in this survey, 233 *Coscinoderma* sponges were recorded from Masig. In contrast, mean abundance (and total number) was similar according to the TKMC Test among Ugar, Erub and Poruma being 1.7 (81), 1.1 (53) and 1.2 (50) sponges per 30 m² respectively. At Warraber, mean abundance was 0.5 *Coscinoderma* per transect.

Sponge abundance varied significantly among locations within each island group (Nested ANOVA: $F_{DF=26,30}=1.93$; $P=0.042$). At Erub and Poruma, for example, *Coscinoderma* sp. was relatively common at some locations but not recorded at neighbouring locations a few kilometres away (Fig. 2.3). Among the seven locations at Masig, mean abundance ranged from 0.8 to 8.8 sponges per 30 m².

The abundance of *Coscinoderma* sp. also varied significantly among sites (Nested ANOVA: $F_{DF=30,120}=2.28$; $P<0.001$). In some locations at Ugar, Erub and Poruma, *Coscinoderma* sp. was found at one site but not recorded 200 m away (Fig. 2.3.). In locations where *Coscinoderma* sp. was recorded at both sites, density could vary by a factor of 10. Of the 24 locations with ≥ 5 *Coscinoderma* sp., almost half (11/24) had $>75\%$ of its individuals recorded from one site. Variation in *Coscinoderma* sp. abundance between neighbouring sites was therefore a common phenomenon in Torres Strait.

Of the 436 *Coscinoderma* sp. individuals recorded from Torres Strait, only one was diseased with approximately 20% of its pinacoderm necrotic. The diseased sponge was found at Erub, living within several meters of healthy, non-diseased *Coscinoderma* sp. individuals.

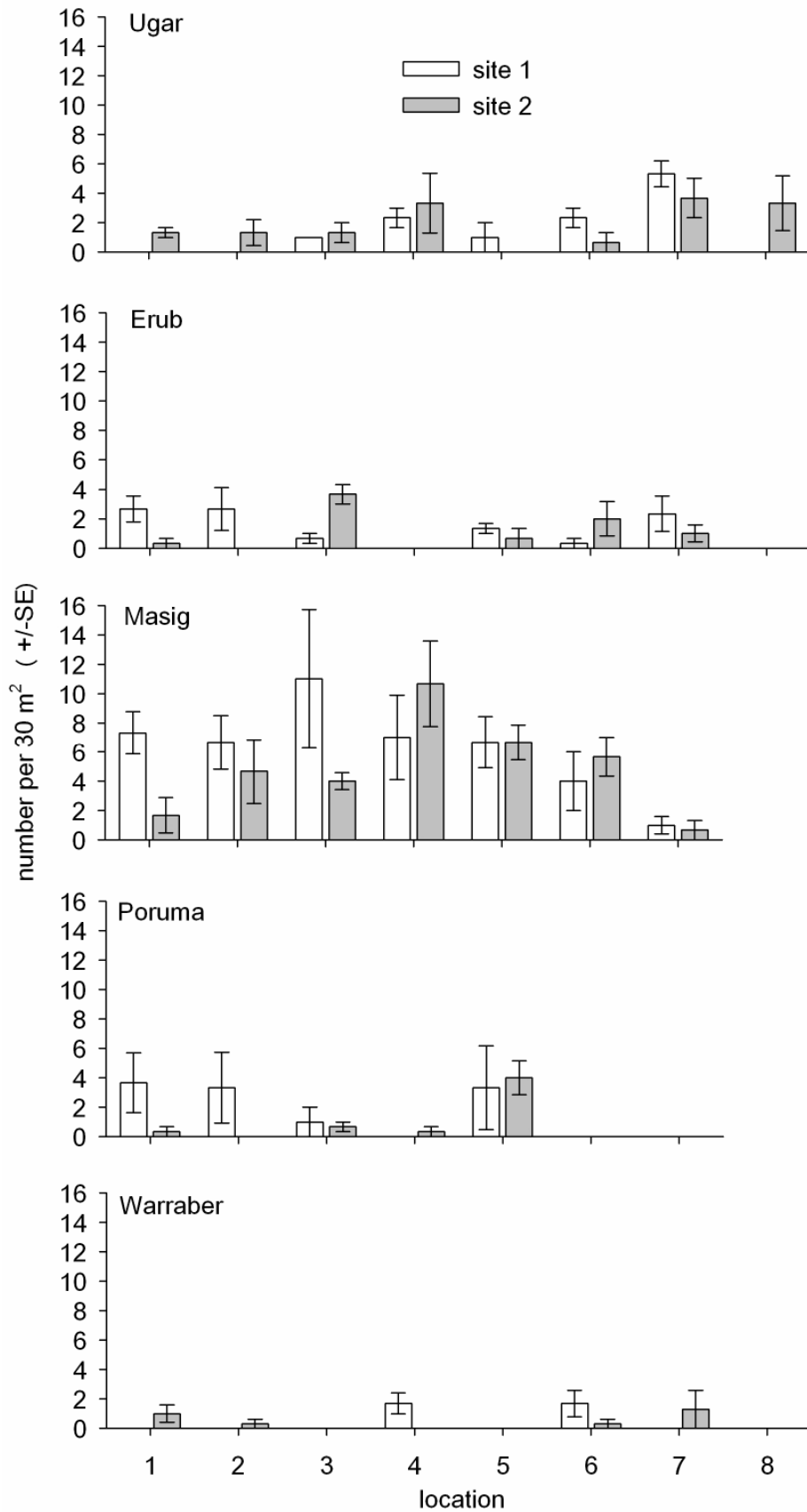


Figure 2.3. Mean abundance of *Coscinoderma* sp. at each island-group, with nested sites and locations.

Spatial variability in size among island-groups

The size frequency distribution of *Coscinoderma* sp. varied significantly among island groups in Torres Strait (One-Way ANOVA: $F_{DF=3,414}=16.93$; $P<0.0001$). The TKMC Test determined that sponge size was similar between Masig and Poruma, and between Ugar and Erub (Table 2.2; Fig. 2.4). At Warraber, which was not included in the statistical analysis because of low sponge abundance, mean length was similar to Ugar and Erub (Table 2.2). Size results for the 95th percentile showed a similar pattern, being highest at Masig and Poruma and smallest at the three remaining island-groups. At Masig and Poruma, *Coscinoderma* sp. could be expected to grow to over 20 cm in length. The coefficient of variation varied little among the island-groups (Table 2.2), indicating that variation around the mean was similar throughout Torres Strait.

The Kolmogorov-Smirnov Normality test on raw size data was significant for Ugar, Erub and Masig (Table 2.2), indicating that the untransformed size structure of *Coscinoderma* sp. at three of the five island-groups did not have a normal distribution. After a log-transformation, the size structure at Ugar, Erub and Masig became normally distributed. The untransformed size distributions at all island-groups were positively skewed, indicating that small individuals dominant the *Coscinoderma* sp. population at each island-group. The proportion of small individuals was greatest at Ugar and Masig (Table 2.2), where *Coscinoderma* sp. was most abundant. Log-transforming the size data reduced the level of skewness (g_1 value closer to zero) at four of the five island-groups. The one exception was at Poruma, where the raw, untransformed size data had a normal distribution and was only slightly positively skewed (Table 2.2).

Table 2.2. Size distribution parameters for *Coscinoderma* sp. in each island-group giving sample number (N), mean size, standard deviation (SD), coefficient of variation (CV) and the 95th percentile (95th); all measurements in centimetres. Also shown are results from the single Kolmogorov-Smirnov Normality Test (KS) and skewness (g_1) tests for untransformed and log (+1) transformed data. Probability for KS either non-significant (n.s.) or significant (<0.05); *test done on 50 randomly chosen sponges.

Island-group	N	Mean	SD	CV	95 th	Untransformed data		Log-transformed data	
						KS	g_1	KS	g_1
Ugar	81	6.9	4.1	0.6	15.0	<0.05*	1.24*	n.s.*	-0.29*
Erub	53	7.6	5.2	0.7	18.4	<0.05	1.08	n.s.	0.09
Masig	233	10.3	6.1	0.6	22.0	<0.05*	1.22*	n.s.*	0.07*
Poruma	50	12.7	6.4	0.6	24.1	n.s.	0.34	n.s.	-0.42
Warraber	19	7.5	6.1	0.8	20.1	n.s.	0.96	n.s.	-0.01

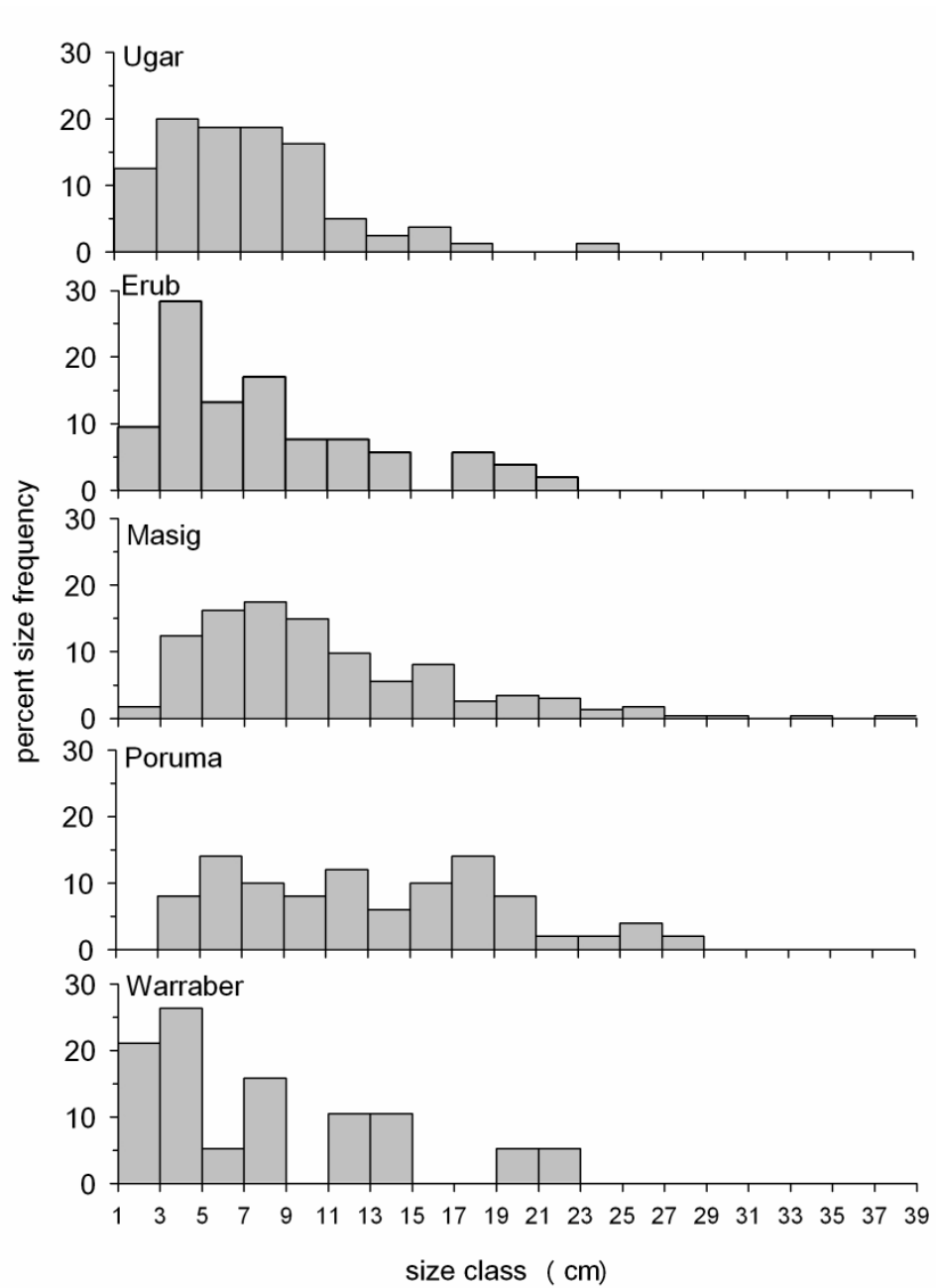


Figure 2.4. Size frequency distributions of *Coscinoderma* sp. between island-groups.

Spatial variability in size among locations and sites

At Masig, the size frequency distribution of *Coscinoderma* sp. was similar between locations (Nested ANOVA: $F_{DF=4,5}=0.93$; $P=0.515$); two Masig locations were not included in the analysis because <10 sponges were recorded from at least one site. *Coscinoderma* sp. size patterns varied significantly, however, between sites nested within locations (Nested ANOVA: $F_{DF=5,191}=4.27$; $P=0.001$), indicating that size frequency distributions can vary greatly over short spatial scales (~200 m). At location 2, for example, 60% of *Coscinoderma* sp. sponges at site 1 were larger than 10 cm while >90% of individuals at site 2 were smaller than 10 cm (Fig. 2.5). A greater proportion of large sponges at site 1 resulted in mean size and 95th percentile values double those recorded from site 2 (Table 2.3). Although the results shown in Table 2.3 have to be treated cautiously because of low sample number at several sites, some patterns emerge. The coefficients of variation were generally similar between neighbouring sites, which suggests the amount of variation around a mean was similar across short spatial scales. The mean size and 95th percentile value can vary greatly between sites at some but not all Masig locations.

Table 2.3. Size distribution parameters for *Coscinoderma* sp. between sites at Masig locations showing sample number (N), mean size, standard deviation (SD), coefficient of variation (CV) and the 95th percentile (95th); all measurements in centimetres. Only locations where both sites had ≥ 10 individuals were compared.

Location	Site	N	Mean	SD	CV	95 th
2	1	20	13.9	5.8	0.4	21.2
	2	14	6.4	3.3	0.5	10.7
3	1	33	8.5	4.9	0.6	18.0
	2	12	9.3	8.7	0.9	23.7
4	1	21	9.0	4.8	0.5	15.0
	2	32	12.3	7.8	0.6	25.0
5	1	20	9.9	5.6	0.6	18.3
	2	20	7.4	3.3	0.5	12.1
6	1	12	13.8	8.4	0.6	27.3
	2	17	12.5	4.6	0.4	18.8

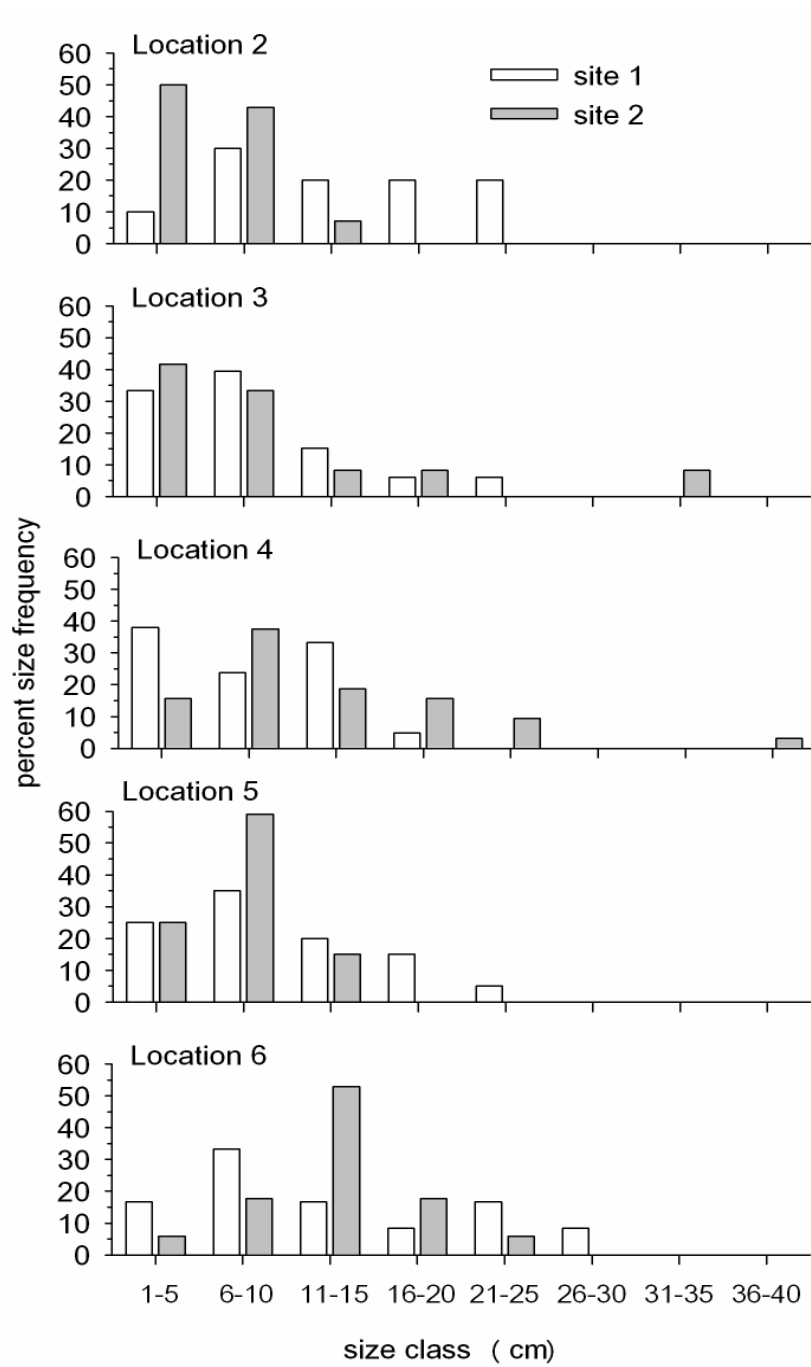


Figure 2.5. Size frequency distributions of *Coscinoderma* sp. between sites and locations at Masig.

2.3.2. Masig Island-group survey

Environmental factors

A MANOVA of the four environmental factors found a significant interaction between site and depth (Wilks' Lambda: $F_{df=10,157}=2.92$; $P<0.001$). Of the ANOVAs examining the four factors, the interaction term was significant for reef slope ($F_{df=10,44}=4.68$; $P<0.001$) and %rubble ($F_{df=10,44}=2.48$; $P=0.018$). Although the difference in reef slope between 6 and 12 m varied greatly across space (sites), deep reef at all sites was steeper (mean= 37°) than shallow reef (14°) (Fig. 2.6). Both shallow and deep reef had similar percentages of rubble (~30%), but rubble cover at 6 and 12 m varied greatly between neighbouring sites (Fig. 2.6). The percentage of rock was similar between depths and sites, and there was no interaction effect (all with $P>0.05$). On average, 18% of the substrate in the study area consisted of rock free of living organisms (Fig. 2.6). Percent sand did not have a significant interaction term but varied significantly between depths ($F_{df=1,10}=25.21$; $P<0.001$). On average, shallow reef had half the amount of sand (16%) as deep reef (33%) (Fig. 2.6), probably because sand is more easily swept away in the shallows. The percentage of sand also varied significantly between sites ($F_{df=10,44}=5.41$; $P<0.001$), ranging from 12% to 43% among neighbouring sites. In addition to rock, rubble and sand, living organisms occupied the remaining substrate cover on each transect. Living macro-organisms, dominated by scleractinian corals, occupied more space on shallow reef (39%) than deep reef (18%).

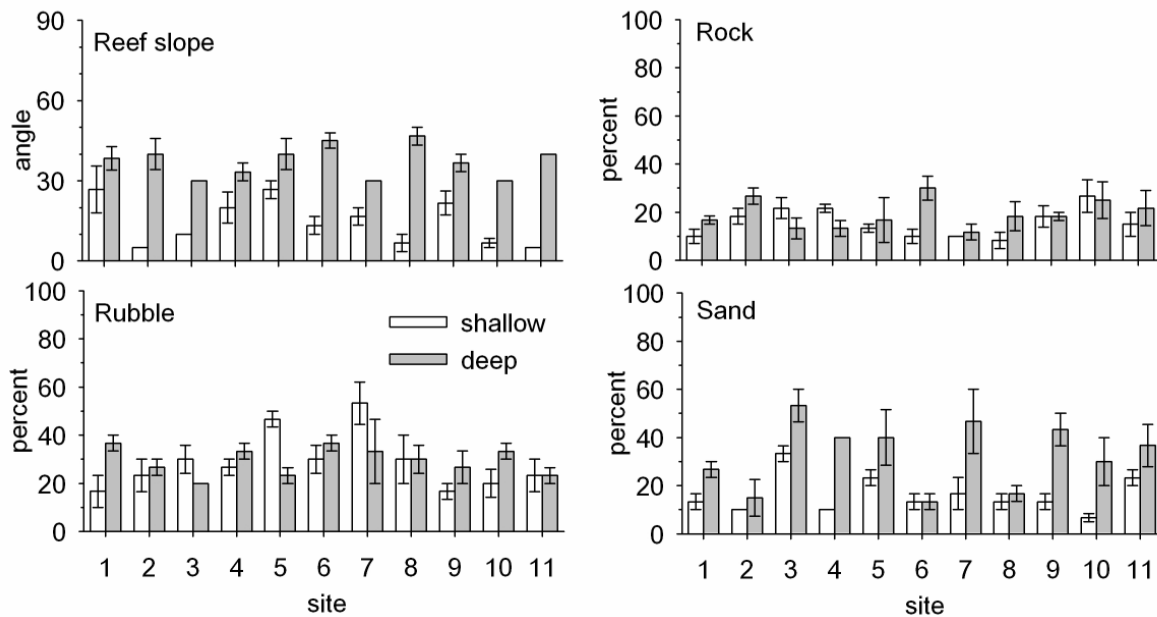


Figure 2.6. Mean values of reef slope, %rock, %rubble and %sand between depths at each surveyed site. Error bars represent variation (1 standard error) among transects.

Abundance between sites and depths

In total, 269 *Coscinoderma* sponges were counted and measured during the survey. The abundance of *Coscinoderma* sp. varied significantly between sites (ANOVA: $F_{df=10,44}=3.09$; $P=0.005$), ranging from 1.2 to 7.0 individuals on average per 20 m² (Fig. 2.7). Depth also had a significant effect on abundance (ANOVA: $F_{df=1,10}=60.25$; $P<0.001$), with sponge density almost three times greater at 12 m (mean=5.9 sponges per 20 m²) than at 6 m (2.2) (Fig. 2.7). There was no significant interaction term (ANOVA: $F_{df=10,44}=0.71$; $P=0.713$). No diseased sponges were found.

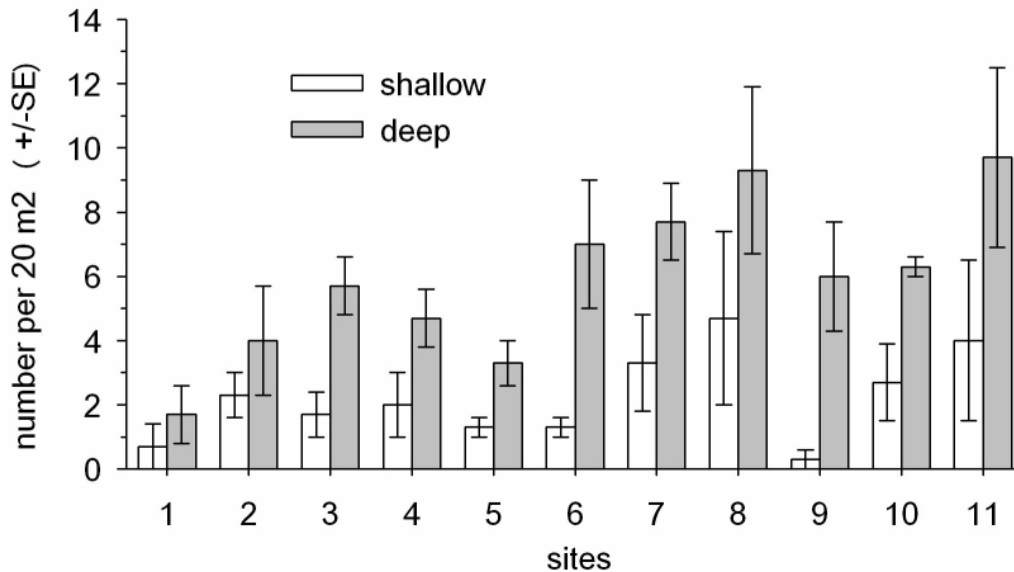


Figure 2.7. Mean abundance of *Coscinoderma* sp. between depths at each surveyed site. Error bars represent variation (1 standard error) among transects.

Abundance between depth, substrate types and exposures

All individuals of *Coscinoderma* sp. except two were found attached to and living on either rock or rubble. The exceptions included one sponge that was found growing on sand at a depth of 12 m in an exposed microhabitat. This sponge appeared healthy, was of average size, and had its base buried ~5 cm into sand; moving the sand away from the sponge's base determined that it was only attached to sand. The second sponge was found growing directly on coral (*Porites* sp.). This sponge was relatively small in size and appeared healthy. Because only one sponge each was found living in sand or on coral, the Chi Square test analysed frequencies of sponges recorded from rock and rubble substrate only.

Of the 267 individuals included in this analysis, the number of *Coscinoderma* sp. individuals found growing on rock and rubble at each depth is shown in Table 2.4. This table also shows the expected frequencies, calculated using the availability of rock and rubble at each depth. The Chi-Square analysis determined a difference between the observed and expected frequencies ($\chi^2_{df(3)}=33.0$, $P<0.0001$), indicating that *Coscinoderma* sp. individuals were found at one or more substrate-depth combinations at frequencies too different to be attributed to stochastic processes. Subdividing the Chi-Square analysis (Zar 1999) determined that the observed and expected frequencies were similar for sponges found in the treatments rock-shallow, rock-deep and rubble-deep ($\chi^2_{df(2)}=5.54$, $P=0.063$). When the frequency of sponges found in the rubble-shallow treatment is tested against the combined frequencies for the other three treatments, the Chi-Square analysis is highly significant ($\chi^2_{df(1)}=28.3$, $P<0.0001$).

This result indicates that nonconformity of sponge abundance data between substrates and depths results largely from significantly less *Coscinoderma* sp. found growing on rubble at shallow depths than expected considering the availability of rubble at 6 m (Table 2.4).

Table 2.4. Observed and expected frequencies of *Coscinoderma* sp. found growing on rock and rubble at shallow and deep depths.

Substrate, depth	Observed	Expected
Rock, shallow	40	46
Rock, deep	91	55
Rubble, shallow	33	83
Rubble, deep	103	83

Depth interacting with exposure also influences the abundance of *Coscinoderma* sp. (Fig. 2.8). *Coscinoderma* sp. is more common in sheltered microhabitats at shallow depths, but more abundant in exposed microhabitats on deeper reef. Similar findings between rock and rubble at each depth, suggests that substrate type does not influence this generalisation.

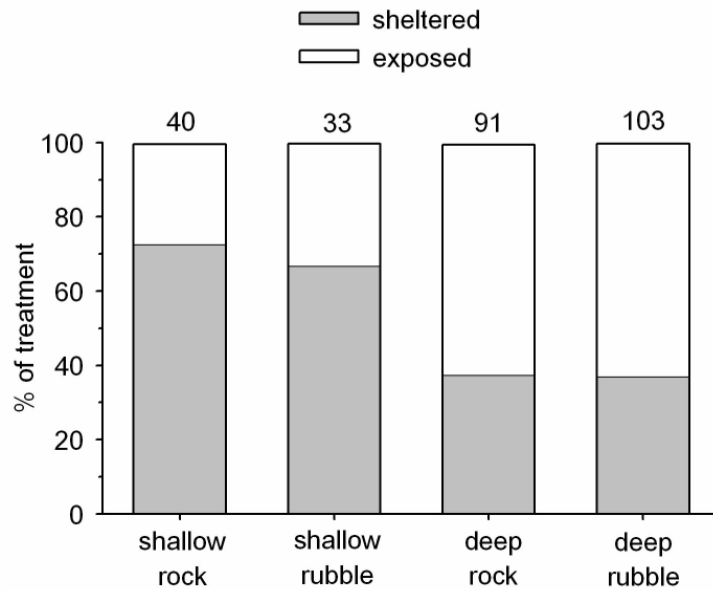


Figure 2.8. Percent of sponges found in sheltered and exposed microhabitats per depth-substrate treatment. The number on each scale represents the number of individuals per treatment.

Size frequency distributions between depths and substrates

A MANOVA of sponge length, width, height and lobe number found a significant effect of depth (Wilks' lambda $F_{df(4,166)}=9.13$; $P<0.0001$) and substrate (Wilks' lambda $F_{df(4,166)}=2.77$; $P=0.028$) and no significant depth*substrate interaction (Wilks' lambda $F_{df(4,166)}=0.88$; $P=0.479$). Subsequent ANOVA's determined that survey depth had a significant effect on all four sponge parameters: length ($F_{df=1,169}=6.90$; $P=0.009$); width ($F_{df=1,169}=5.46$; $P=0.021$); height ($F_{df=1,169}=7.47$; $P=0.007$); and lobe number ($F_{df=1,169}=32.3$; $P<0.0001$). ANOVA's also determined that substrate type influenced both sponge length ($F_{df=1,169}=8.97$; $P=0.003$) and width ($F_{df=1,169}=4.40$; $P=0.037$) but not height or lobe number ($P>0.05$).

For sponge length, individuals generally reached largest size when attached to rock and occurring on deeper reefs (Table 2.5; Fig. 2.9). The result of the TKMC test, showing most similarities between substrate types, indicates that depth had the greatest influence on sponge length. This is supported by the 95th percentile results, with sponges growing on rubble at 12 m expected to grow to twice the size of sponges on rubble at 6 m (Table 2.5). Further comparing maximum size between depths, only 1 individual was ≥ 30 cm in length at 6 m while 11 sponges were ≥ 30 cm in size on deep reef; in addition, 3 individuals were recorded from 12 m that were >40 cm in length (Fig. 2.9). The coefficient of variations were largest for sponges growing on deep reef (Table 2.5), indicating that sponges found at 12 m vary more in length regardless of substrate type. Although substrate type is comparatively less important to size structure compared with depth, it can influence sponge length. In shallow water, for example, mean length of individuals growing on rock was more than 1½ times the length of sponges living on rubble. For all depth*substrate classes, the length frequency distributions using raw, non-transformed data were positively skewed (Table 2.5), indicating a greater proportion of small sponges (Fig. 2.9). The skewness for each class was generally not improved after a log-transformation. The raw length data in the shallow*rubble, deep*rock and deep*rubble treatments produced significant Kolmogorov-Smirnoff tests (Table 2.5), indicating that the length structure of sponges in these three treatments did not have a normal distribution. A log-transformation "corrected" these distribution patterns.

Table 2.5. Length distribution statistics for *Coscinoderma* sp. growing on rock and rubble substrate at shallow and deep depths. Table gives sample number (N), mean size, standard deviation (SD), coefficient of variation (CV) and the 95th percentile (95th); all measurements in centimetres. For mean size, depth*substrate treatments with the same letter have similar sized sponges according to the TKMC test. Also shown are results from the single Kolmogorov-Smirnov Normality Test (KS) and skewness (g_1) tests for untransformed and log (+1) transformed data. Probability for KS either non-significant (n.s.) or significant (<0.05); *test done on 50 randomly chosen sponges.

Depth*substrate	N	Mean	SD	CV	95 th	Untransformed data		Log-transformed data	
						KS	g_1	KS	g_1
shallow, rock	40	12.0 ^B	7.2	0.6	26.2	n.s	0.75	n.s.	-1.22
Shallow, rubble	33	7.2 ^A	4.2	0.6	14.0	<0.05	1.01	n.s.	-0.66
Deep, rock	91	13.4 ^B	9.8	0.7	30.0	$<0.05^*$	0.83 [*]	n.s.*	-0.81 [*]
Deep, rubble	103	11.6 ^A _B	8.5	0.7	28.5	$<0.05^*$	1.25 [*]	n.s.*	-0.61 [*]

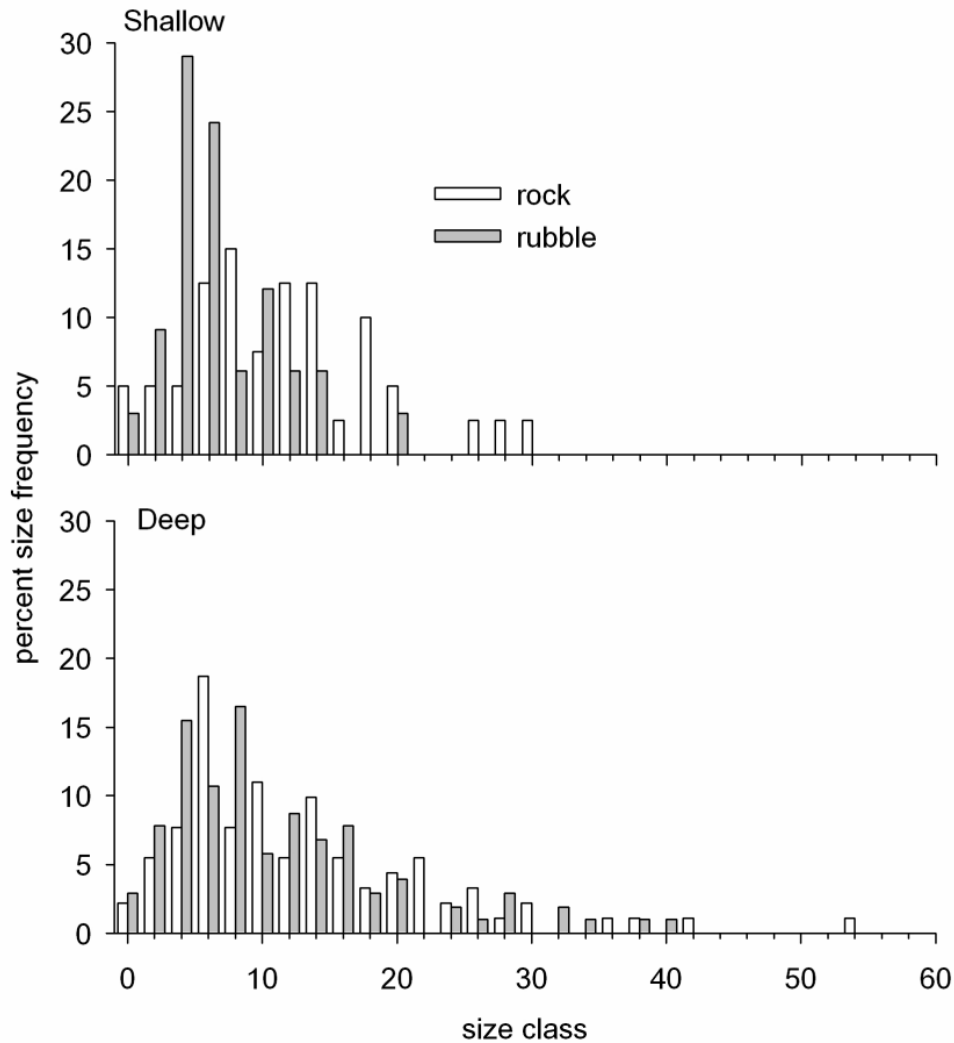


Figure 2.9. Length frequency distribution of *Coscinoderma* sp. between depths and substrate types.

Considering sponge width, individuals were generally widest when growing on rock and at deeper depths (Table 2.6; Fig 2.10). The TKMC test found that sponges growing on rubble at 6 m were significantly different in size to sponges attached to rock at 12m, with mean width of rubble*shallow sponges only two-thirds that found for rock*deep sponges. The 95th percentile results indicate that sponges attached to rock at 12 m are expected to grow to double the width of sponges growing on rubble at 6 m (Table 2.6). Sponges attached to rock at 12 m also have the highest coefficient of variation (Table 2.6), indicating that these sponges show the most variation in width among the *Coscinoderma* sp. population in the study area. The Kolmogorov-Smirnov tests on non-transformed width data for all depth*substrate treatments were significant, indicating that raw width data does not have a normal distribution regardless of depth or substrate type. Each Kolmogorov-Smirnov test was non-significant after a log-transformation (Table 2.6), indicating that the log-width frequency patterns are normally distributed. The raw width data for each depth*substrate treatment was positively skewed (Table 2.6), indicating more small than large sponges across depths and substrate types. Similar to sponge length, a log-transformation on width data did not generally improve the skewness values (Table 2.6).

Table 2.6. Width distribution statistics for *Coscinoderma* sp. growing on rock and rubble substrate at shallow and deep depths. See Table 2.5 for explanation of codes.

Depth*substrate	N	Mean	SD	CV	95 th	Untransformed data		Log-transformed data	
						KS	g ₁	KS	g ₁
shallow, rock	40	6.4 ^{AB}	3.7	0.6	13.1	<0.05	1.01	n.s.	-0.67
Shallow, rubble	33	4.9 ^A	2.6	0.5	10.0	<0.05	0.63	n.s.	-0.68
Deep, rock	91	7.7 ^B	5.3	0.7	20.0	<0.05*	1.04*	n.s.*	-0.15*
Deep, rubble	103	6.7 ^{AB}	4.2	0.6	14.5	<0.05*	0.54*	n.s.*	-0.72*

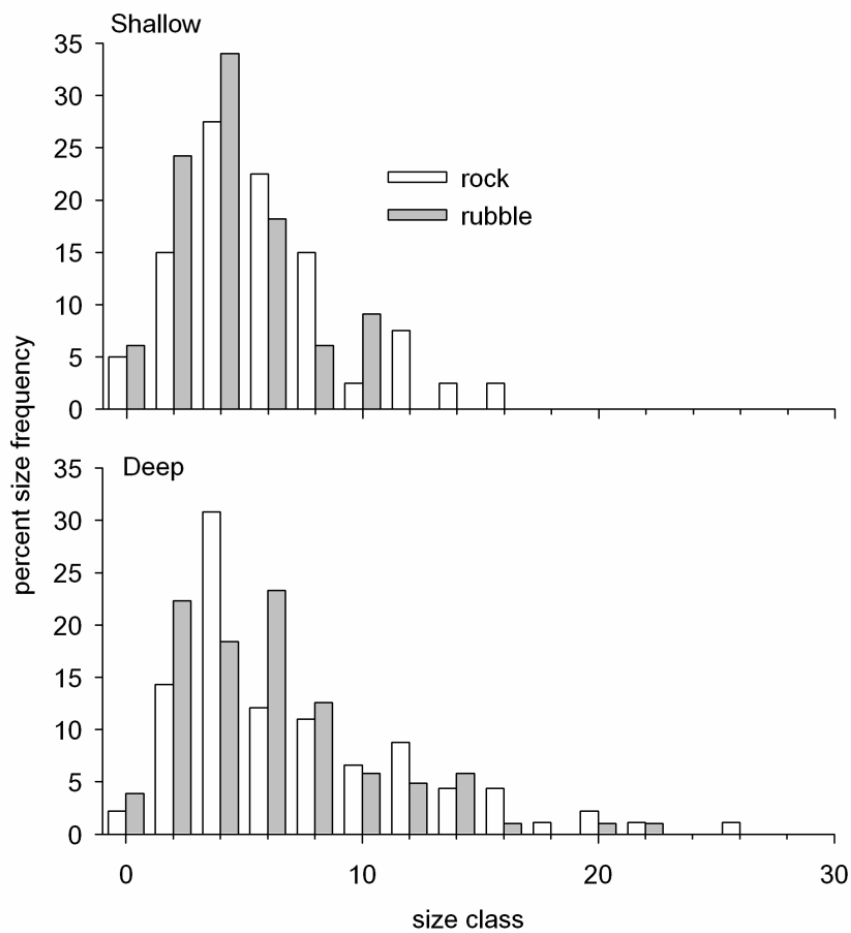


Figure 2.10. Width frequency distribution of *Coscinoderma* sp. between depths and substrate types.

Height of *Coscinoderma* sp. varied between depths only, with mean height of individuals at 6 m approximately three-quarters the height of sponges at 12 m (Table 2.7). The 95th percentile results were more similar between depths (Table 2.7) however, showing that *Coscinoderma* sp. in shallow water has only a slightly smaller maximum height than sponges living on deeper reef (Fig. 2.11). These differences in mean size and 95th percentile results explain the high coefficient of variation and the high positive skewness value for sponges found at 6 m (Table 2.7). A log-transformation did help normalise the skewness of shallow-water sponges. In contrast, a log-transformation did not fully normalise the height data according to the Kolmogorov-Smirnoff test, although it did improve the overall size structure (Table 2.7). Positive skewness values for sponges at 6 and 12 m indicates that *Coscinoderma* sp. in the study area have a greater proportion of short than tall individuals (Fig. 2.11).

Table 2.7. Height distribution statistics for *Coscinoderma* sp. growing at shallow and deep depths. See Table 2 for explanation of codes. *test done on 73 randomly chosen sponges.

Depth	N	Mean	SD	CV	95 th	Untransformed data		Log-transformed data	
						KS	g ₁	KS	g ₁
Shallow	73	6.5	5.1	0.8	17.2	<0.05	2.16	<0.05	0.29
Deep	194	8.6	5.7	0.7	19.4	<0.05*	0.95*	n.s.*	-0.47*

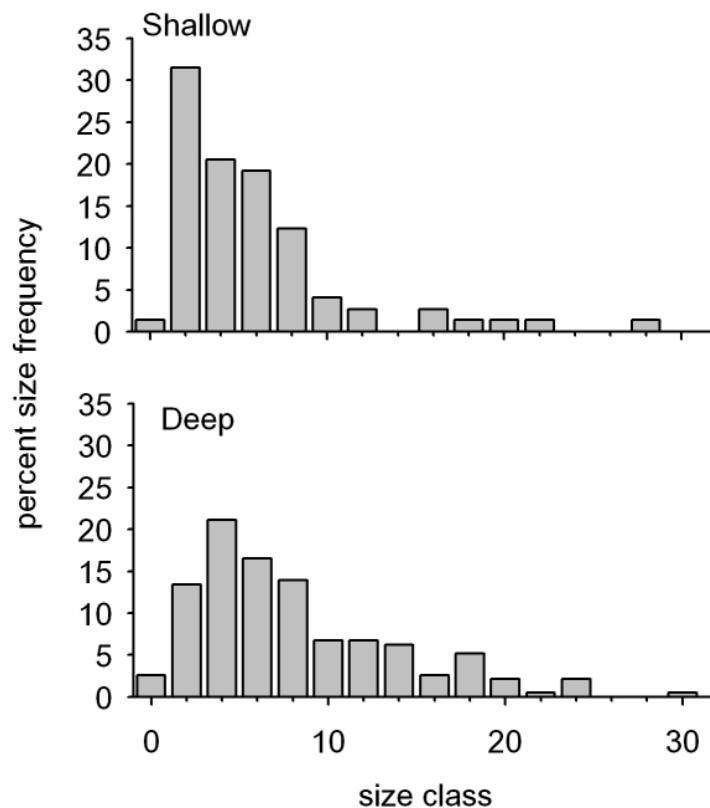


Figure 2.11. Height frequency distribution of *Coscinoderma* sp. between depths.

Individuals of *Coscinoderma* sp. living at 6 and 12 m also varied greatly in lobe number. Almost 75% of shallow-water sponges had no lobes, while most (62%) deep-water individuals had one or more lobes (Fig. 8). In addition, sponges with 5 of more lobes were rare at 6 m (1%) but reasonably common at 12 m (17%).

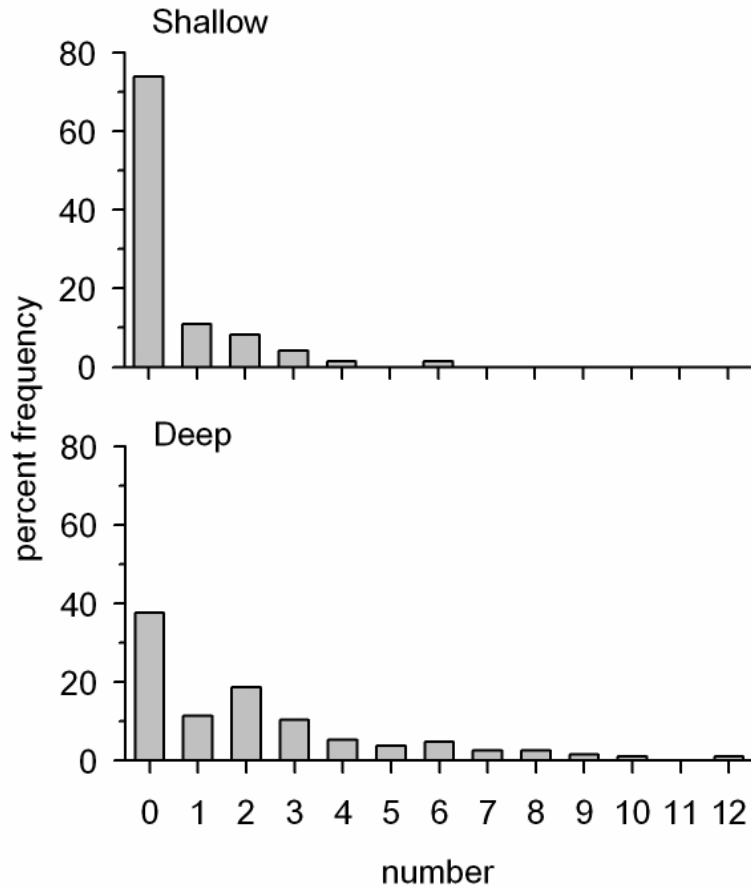


Figure 2.12. Lobe frequency distribution of *Coscinoderma* sp. between depths.

2.4. DISCUSSION

Of the central and eastern Torres Strait reefs surveyed in this study, *Coscinoderma* sp. is most abundant around Masig, supporting the findings from a Torres Strait wide survey in 2004 (Duckworth et al. 2007). Mean abundances per 100 m² of *Coscinoderma* sp. at Masig were higher in this study (18.5, S.E.=2.2) than recorded in 2004 (9.3, S.E.=3.4). *Coscinoderma* sp. has not been found in western Torres Strait. High abundance of the bath sponge at Masig is due to the interaction of physical, biological and stochastic processes (Duckworth and Wolff 2007). One physical factor that can have a significant effect on distribution patterns of sponges is reef slope (Bell and Barnes 2000), with some species excluded from flat habitats due to high sedimentation levels clogging their inhalant canals preventing them filtering efficiently. In the present study, reef slope was greatest at Masig. Perhaps *Coscinoderma* sp. in Torres Strait prefers steep habitats to reduce the smothering effects of fine sediments and detritus, which are common throughout the region. Masig also has relatively high levels of rock substrate, which the second smaller scale survey in that area determined to be an important requirement for both high abundance and large size of *Coscinoderma* sp. Rock substrate provides a secure substrate for attachment and subsequent high growth.

The *Coscinoderma* sp. populations at Ugar, Erub, Masig, Poruma and Warraber were dominated by small individuals, with the size frequency distributions positively skewed at each island-group. The proportion of small sponges varied between island-groups, however, with a higher proportion of small individuals at Ugar and Masig than at Poruma. Several factors could cause these size differences between island-groups, with one major factor likely to be that successful sponge recruitment varies across space in Torres Strait. One reason for the relatively low recruitment of *Coscinoderma* sp. to Poruma could be due to the lower levels of secure substrate (rock) for settlement. Objective 3, investigating the recruitment of bath sponges between island, depth and seasons, will help explain what factors and processes influence the recruitment of *Coscinoderma* sp. to Torres Strait coral reefs.

Water movement greatly affects sponge recruitment and distribution patterns, through influencing larval transport and settlement. Dictyoceratid sponges such as *Coscinoderma* sp. typically produce well developed larvae with poor swimming abilities that settle within a few hours or days (Bergquist and Sinclair 1968; Maldonado and Young 1996). While currents between islands in central and eastern Torres Strait can exceed 50 cm s⁻¹ (Wolanski and Ruddick 1981), eddies may form around islands (Wolanski *et al.* 1984), which could potentially trap larvae and promote high settlement and abundance of dictyoceratids in one localised area. This may explain why sponge abundance is patchy and can vary significantly between neighbouring locations or sites within a location. Asexual reproduction through budding or fragment production by storms could also promote patchy distribution patterns for *Coscinoderma* sp.

Differences in water flow across depth helps explain the variation in abundance and patterns of size frequency and shape of *Coscinoderma* sp. between 6 and 12 m on reefs at Masig. Ambient water flow generally decreases with depth which can greatly influence the abundance and diversity of coral reef organisms, and also their shape (Wilkinson and Evans 1989; Vermeij and Bak 2003; Duckworth and Wolff 2007; Penin et al. 2007). A separate study at Masig using an Acoustic Doppler Current Profiler has determined that average current speeds at 6 and 12 m are 0.25 and 0.11 ms⁻¹ (unpublished data). Sessile organisms such as sponges at 6 m would therefore experience ambient water flows twice as high as organisms living on reef at 12 m. Differences in water flow between depths would be even greater during storms, when most of the wave energy is concentrated in the shallows.

The lower water flow conditions experienced on deeper reef are probably more ideal for sponge settlement, growth and survival, which may explain why Masig sponges were larger in all three dimensions and more abundant at 12 m than at 6 m. The interaction between depth and substrate also shows that the availability of solid, rock substrate can at least partially compensate for higher water flow, by providing a firm foothold. The generally lower physical stresses due to water movement in deeper habitats may also explain why *Coscinoderma* sp. at 12 m produced more lobes. Protrusions such as lobes increase the surface area to volume ration, which would greatly increase feeding opportunities for a given surface area of attachment. However, such lobes would be constantly damaged and difficult to maintain in a higher energy, shallow environment. A full analysis of the environmental factors that interact to influence the size frequency and abundance patterns of *Coscinoderma* sp. in central and eastern Torres Strait will be undertaken in the future and presented in the second annual report of this MTSRF project.

The previous CRC Torres Strait project found that *Coscinoderma* sp. will survive and regrow after two-thirds of an individual's biomass is removed or harvested (Duckworth et al. 2007). The high abundance and large size of *Coscinoderma* sp. at Masig suggests that this island-group could be harvested with minimal environmental impact to supply sponge cuttings or explants to support the initial stage of a sponge farm. Any potential environmental impact could be further minimised by harvesting only a small proportion of the bath sponge population, such as 10% of sponges from any one site. In addition, if explant production is restricted to larger sponges greater than 15 cm in length, the number of donor sponges impacted could be kept to a minimum. Once a farm is established and producing sponge biomass, new explants could be obtained from harvesting farmed sponges that have grown to a large size. The sponge farm would be therefore largely self-sufficient, although some sponges may have to be harvested from wild populations at times. The large abundance of sponges around Masig also indicates that this population could act as a base stock for harvesting explants for sponge farms at other islands. The results of research to address the connectedness between populations indicate that the translocation risk (of genetic dilution or introduction of foreign microbes) is minimal. This is discussed further under Objective 2.

The results of this project will soon receive a commercial reality-check through the development of a business plan for a Masig Island sponge farm that will hopefully identify a commercially viable business model and determine how many and how often wild sponges would need to be harvested.

3. POPULATION GENETICS AND MICROBIAL ANALYSIS

Objective 2. Determine connections between sponge populations and risks in translocation.

3.1. INTRODUCTION

Genetic markers are a powerful tool for population structure analyses in sponges and other taxa, and different categories of molecular markers have already been applied to these types of investigations for sponges (Duran et al., 2004a). In the past, the most commonly used markers for sponge population studies were allozymes. However, these markers can mask genetic divergence, especially within populations (Klautau et al., 1999). Increasingly, population structures have been examined with DNA sequence analyses, which are considered more powerful as cryptic changes in genetic loci can be identified (Shearer et al., 2002; Duran et al., 2004a; Duran et al., 2004b).

For fine-scale population structure studies, the ribosomal internal transcribed spacer region (ITS) is the predominantly used marker (Nichols & Barnes, 2005). Sequences from the ribosomal subunits (5.8S rDNA, 18S rDNA and 28S rDNA) have also been useful in determining the genetic structure of sponge populations (Worheide et al., 2002; Watkins & Beckenbach, 1999). Microsatellites are very useful markers for describing population structures (Duran et al., 2004a), as subtle divergences have been detected when other markers failed to show genetic heterogeneity (Hughes and Queller, 1993; Jarne et al., 1994). Duran et al. (2004b) examined mitochondrial DNA (mtDNA) sequence data of *Crambe crambe* but found very low levels of intraspecific variation, and therefore mtDNA markers may not be useful for population-level studies of sponges.

Many sponge species are host to a huge density and diversity of microorganisms with bacterial cells comprising 40-60% of the tissue volume in some species (Hentschel et al., 2006). A variety of sponge-microbe associations have been described in tropical, temperate and Antarctic regions and these involve a diverse range of heterotrophic bacteria (including facultative anaerobes), cyanobacteria, unicellular algae, fungi and archaea (Wilkinson, 1980; Preston et al., 1996; Holler et al., 2000; Webster and Hill, 2001; Webster et al., 2001; Hentschel et al., 2002; Taylor et al., 2004; Webster et al., 2004).

There are numerous descriptions of specific sponge-microbe relationships in which the host may benefit from: the provision of nutrition (Wilkinson and Garrone, 1980); transportation of waste products or active metabolites (Wilkinson, 1978a; Wilkinson, 1983; Borowitzka et al., 1988); chemical defence (Unson et al., 1994); or contribution to mechanical structure (Wilkinson, 1978b). Presumably the microorganisms benefit from the provision of a protective supporting medium and nutrient flow, although little evidence has been published to support this. Sponge-associated microbial communities have a phylogenetic signature distinctly different from that of microorganisms residing within the marine plankton and sediments (Webster and Hill, 2001; Hentschel et al., 2002; Taylor et al., 2004; Webster et al., 2004; Taylor et al., 2005) with some evidence for uniformity in sponge microbial communities between oceans and species (Hentschel et al., 2002). Sponges however, can filter large quantities of seawater (Bell et al., 1998), hence a proportion of microbes residing within the tissue may be transient components of the ambient seawater. Even with the assistance of molecular techniques it can be extremely difficult to distinguish between true 'sponge-associated bacteria' and seawater-derived contaminants.

The bath sponge *Coscinoderma* sp. will soon be farmed in Torres Strait, with the first commercial venture located at Masig. If this farm proves commercially viable it is likely that

additional island communities will want to establish sponge farms in their local waters. This may require *Coscinoderma* sp. individuals to be moved from regions or islands where they are abundant (e.g. Masig) to regions where they are not. A potential problem of sponge translocations across large areas such as in Torres Strait rises if the transfer is between genetically distinct populations, which would result in a decrease in the genetic diversity of wild populations (Cognetti et al., 2006). Translocation may also have the potential to introduce new sponge-associated microbe types into a region. Because of these concerns, we examine and compare the genetic structure and microbial populations of *Coscinoderma* sp. populations from central and eastern Torres Strait.

3.2. METHODS

3.2.1. Genetic Analysis

Specimen collection and preservation

During the central and eastern Torres Strait survey in November 2006, tissue samples from 10 individuals of *Coscinoderma* sp. were collected from each island-group (Table 3.1). In addition, 10 sponges were collected from each of two sites at Masig (Table 3.1). All sponge samples were placed in separate cryo-tubes and preserved in liquid nitrogen until they could be stored at -80°C.

Table 3.1. Sample numbers (representing individual sponges) collected from each island-group.

Island-group	Site	Sample number codes
Masig	1, Kodall Is	1-10
Masig	2, Keats Is	11-20
Erub	1	21-30
Ugar	1	31-40
Poruma	1	41-50
Warraber	1	51-60

DNA extraction, amplification and sequencing

Approximately 2 g of tissue from each sample was homogenised in liquid nitrogen and 750 µl of lysis buffer [100 mM Tris pH 9, 100 mM EDTA, 1% SDS, 100 mM NaCl, 0.5 mg/ml Proteinase K], and subsequently it was incubated at 65°C for 1 hour with gentle agitation. KoAc was added to a final concentration of 1 M, followed by incubation on ice for 30 minutes. The samples were centrifuged at 8000 rpm for 15 minutes, and the supernatant was reserved for DNA precipitation with isopropanol using the standard protocol.

A fragment of nuclear DNA containing part of the 28S rRNA gene was amplified for all individuals using RD3A (5'-GACCCGCTTTGAAACACGA) and RD5B2 (5'-ACACACTCCTTAGCGGA) primers. Recombinant Pfu Polymerase (Fermentas) was used for the PCR. A total of 50 µl of reaction mixture were prepared for each sample according to the protocol. PCR was performed under the following conditions: initial denaturation at 95°C for 3 minutes; 35 cycles of 95°C for 30 seconds, 50°C for 20 seconds, 72°C for 1 minute; a final extension step of 72°C for 10 minutes. Products were purified with QIAquick (Qiagen)

columns according to protocol. Sequencing was performed at MacroGen Inc. with a 3730xl DNA analyser using both forward and reverse primers.

Data analysis

Sequences were edited and formed into contigs using Vector NTI (Invitrogen), then aligned in Sequencia and trimmed using MacClade. A BLAST search of GenBank was used to confirm the taxonomic origin of the sequences. The final length of the sequences was 690 bp. Two of the sequences (one each from Poruma and Warraber) were removed from the analysis due to poor sequence data. The data was analysed with MEGA3.1. To determine nucleotide differences, the following calculations were done:

Mean Diversity within Subpopulations

In a subpopulation, the mean diversity is defined as

$$\alpha_i = \frac{q}{q-1} \sum_{i=1}^q \sum_{j=1}^q \chi_i \chi_j d_{ij}$$

where χ_i is the frequency of i-th sequence in the sample from subpopulation i, and q is the number of different sequences in this subpopulation.

Mean Diversity for Entire Population

For the entire population, the mean diversity is defined as

$$\alpha_T = \frac{q}{q-1} \sum_{i=1}^q \sum_{j=1}^q \chi_i \chi_j d_{ij}$$

where χ_i is the estimate of average frequency of the i-th allele in the entire population, and q is the number of different sequences in the entire sample.

Mean Interpopulational Diversity

The estimate of interpopulational diversity is given by

$$\bar{d}_{ST} = \chi_T - \chi_S$$

Coefficient of Differentiation

The estimate of the proportion of interpopulational diversity is given by

$$N_{ST} = \bar{d}_{ST} / \chi_T$$

3.2.2. Microbial Analysis

For microbial analysis, a DNA fingerprinting technique (denaturing gradient gel electrophoresis – DGGE) was used to determine the stability of bacterial associations within *Coscinoderma* sp. across wide spatial scales.

DNA Extraction

Four replicate sponges were analysed from sites 1 and 2 at Masig and three replicate sponges were analysed from Erub, Ugar, Poruma and Warraber. DNA was extracted from individual sponges by homogenising approx 1g of tissue from each individual in 0.5 ml of grinding buffer (2 ml 1 M Tris, 4 ml 0.5M EDTA, 2 ml 10% SDS, 400 μ l 5 M NaCl and 11.6 ml distilled water). Tubes were immersed in liquid nitrogen and ground with plastic pestles. Samples were incubated at 65°C for 60 min prior to addition of 187 μ l 5 M potassium acetate. Samples were incubated on ice for 30 min and centrifuged at 8000 x g for 15 min. The supernatants were transferred to fresh tubes and DNA was precipitated with 0.8 vol of isopropanol.

3.2.2.2. DGGE

The 16S rDNA from each sample was amplified by PCR with universal bacterial primers 1055f: 5'-ATG GCT GTC GTC AGC T-3' and 1406r: 5'-ACG GGC GGT GTG TAC-3', (Ferris et al., 1996). The reverse primer was modified to incorporate a 40 bp GC clamp (Muyzer et al., 1993). Primers 1055f and 1406r match over 56,000 and 62,800 sequences respectively in the Ribosomal Database Project. PCR reactions were performed as described by (Ferris et al., 1996). Products from triplicate PCR reactions were combined and 15 µl applied to duplicate 40% wt/vol polyacrylamide (37:5:1) gels containing a 50-70% denaturing gradient of formamide and urea. Gels were electrophoresed at 60°C for 17 h in 1 x TAE buffer at 50V using the Ingeny D-Code system. Gels were stained with 1 x Sybr Gold for 30 min, visualised under UV illumination and photographed.

3.3. RESULTS

3.3.1. Genetic Analysis

The 690 bp sequence was analysed for all 58 individuals. The mean interpopulation diversity was 0.000 with a standard error of 0.000 when analysed with the Kimura 2-parameter model. However, there was variation observed in the sequences, and Table 3.2 shows that this was mostly within populations. Furthermore, after constructing a maximum parsimony tree with 500 bootstrap replicates, there were 293 equally probably trees indicating that there was no group structure, and this was supported by low bootstrap values (Fig. 3.1).

Table 3.2. Number of nucleotide differences (distance).

	Distance	Standard Error
Within Kodall (Masig)	1.578	0.579
Within Keats (Masig)	1.556	0.543
Within Erub	0.956	0.630
Within Ugar	0.528	0.273
Within Poruma	0.400	0.272
Within Warraber	2.833	0.773
Mean diversity within subpopulations	1.308	0.295
Mean diversity for the entire population	1.390	0.315
Mean interpopulational diversity	0.082	0.057
Coefficient of Differentiation	0.059	0.036

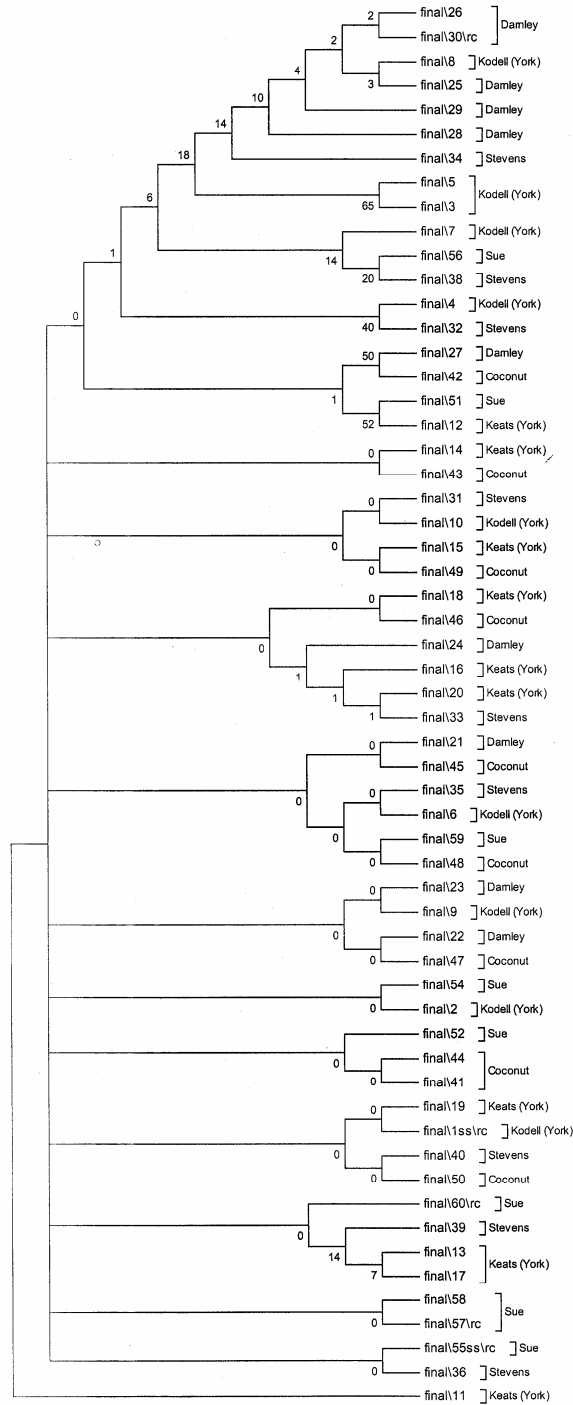


Figure 3.1. Maximum parsimony tree of the 6 sponge populations with 500 bootstrap replicates. The five island-groups are: Ugar=Stephens, Erub=Darnley, Masig=Yorke, Poruma=Coconut, and Warraber=Sue.

3.3.2. Microbial Analysis

DGGE analysis for replicate *Coscinoderma* sp. samples at each site revealed 5 predominant bands in all replicate sponges (Fig. 3.2). This indicates that a major component of the microbial community is conserved in all individuals across a wide spatial scale. Some intersponge variability in banding patterns was observed. For example, sponge 15 from Masig site 2 and sponge 41 from Poruma both contained a larger number of bands indicating a more diverse microbial community than other samples.

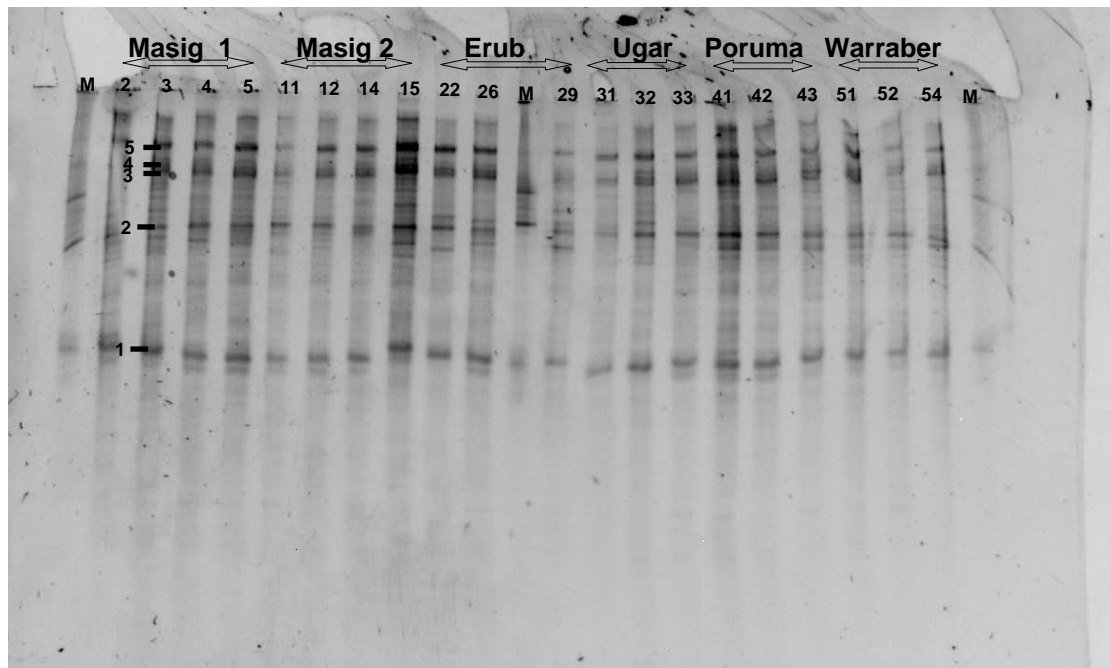


Figure 3.2. DGGE profile of 16S rRNA-defined bacterial populations from replicate *Coscinoderma* sp. individuals from each island-group. Masig had two sites. M = Marker and predominant bands are labelled 1-5.

3.4. DISCUSSION

The results of the genetic analysis revealed similar partial 28S sequences across all individuals from the six sample areas. There was little to no variation observed between island-groups but some variation was detected within a sample area. The lack of genetic variation of sponges from different island-groups is probably due to gene flow across the region, as the sample areas were separated by ~60 km. In fact, it has been argued that sponge larvae may travel greater distances than expected from their poor swimming capabilities by currents (Mariani et al., 2006). This would be further facilitated in central and eastern Torres Strait where currents between islands can exceed 50 cm s^{-1} (Wolanski and Ruddick 1981). Such strong water flow suggests that some sponge larvae could be quickly transported large distances among neighbouring islands-groups. The variation that was observed within a sample area may have been a result of intragenomic variation rather than variation between individuals as it has been determined that sponges have multiple copies of rRNA genes within a single genome (Wörheide et al., 2004).

While some sponge studies have shown high genetic heterogeneity over very small spatial scales, presumably due to reliance on asexual reproduction (Whalan et al. 2005), many studies have also shown sponge populations with greater separating distances than those

reported here with low levels of variation. Duran et al. (2004b) described one single polymorphic nucleotide in mtDNA sequences of *Crambe crambe* populations over 3000km in the western Mediterranean and Atlantic range, but in later studies based on ribosomal ITS sequences (Duran et al., 2004c) and on microsatellite sequence data (Duran et al., 2004a) it was found that these populations were genetically distinct. Identical mtDNA sequences were also found across four species and two genera (*Lubomirskia* and *Baikalospongia*) of Lake Baikal freshwater sponges (Schroder et al., 2003, cited in Erpenbeck et al., 2005). In contrast, Wörheide et al. (2002) identified four different clades of *Leucetta 'chagosensis'* over the western Pacific region with rDNA sequence data, although the geographical distances between the genotypes were relatively large. Two distinct clades of *Clavelina lepadiformis* (Asciacea) were found over short distances (<10 km) in different environments from mtDNA sequences, a result attributed to the species' short larval life-span (Tarjuelo et al., 2001).

Gene flow may be responsible for the homogeneity found in this study, however, slow evolution could be another explanation. The lack of variation observed in the mtDNA sequences of *Crambe crambe* was attributed to high conservation of this sequence rather than high levels of gene flow (Duran et al., 2004b). Shearer et al. (2002) suggested that slow evolution may occur in primitive metazoans after finding almost identical mitochondrial sequences among conspecific anthozoans. Also, historical events may account for the lack of variation, including a founder event or a selection-driven population bottleneck.

The genetic analysis experiment indicates that there is little reason for concern regarding the impact of sponge translocations between island-groups, as there appears to be homogeneity across the sampled region. However, the sample sizes from each island-group or site may have been insufficient to accurately assess population structure of these sponges. It should also be noted that other DNA markers such as microsatellite (Duran et al., 2004a) or other ribosomal or ITS markers (Duran et al., 2004c) may be more variable, and could also be used to assess the risks involved with sponge translocation within Torres Strait. Such analysis is not possible within the current levels of MTSRF funding to the project.

The results (and conclusions) for the microbial analysis were similar to the genetic analysis. No microbial bands were exclusively present (or absent) in sponge samples collected at any particular island-group or site. This indicates that no site specific variability exists in microbial communities associated with *Coscinoderma* sp. from central and eastern Torres Strait. These results are in accordance with previous studies of tropical (Webster and Hill, 2001) and Antarctic (Webster et al., 2004) sponge-associated microbial communities which demonstrated highly conserved microbial assemblages across wide spatial scales.

The combined results from the genetic and microbial analysis, identifying great similarity between sponges and their microbial populations from Ugar, Erub, Masig, Poruma and Warraber, suggest that there is little risk in translocating *Coscinoderma* sp. between island-groups within central and Eastern Torres Strait. These are promising findings for the sustainability and commercial development of bath sponge aquaculture in Torres Strait. These results suggest that bath sponges could be harvested and transplanted from Masig, where they are common and large, to other island-groups for farming with no decrease in genetic diversity or introduction of new microbe types into an area.

4. SPONGE RECRUITMENT

Objective 3. Determine patterns of sponge recruitment/mortality and the environmental risk of seed stock harvest leading to development of a sustainable seed collection strategy.

4.1. INTRODUCTION

The recruitment of sessile invertebrates to the benthic habitat can vary greatly across time and space (Watson and Barnes 2004; Adjeroud et al. 2007; Rule and Smith 2007). Variation in the recruitment of larva between species greatly influences the composition and diversity of the benthic community (Smith and Witman 1999), and can explain much of the difference in community structure between regions, and across seasons and years. Variable recruitment of sponge and coral species that are community determiners — whose abundance or biomass contribute greatly to the benthic community — could have significant and wide-ranging effects on the health of the marine environment in Torres Strait.

The recruitment of coral species to reefs in Torres Strait has been investigated. In a large study done over the full length of the Great Barrier Reef including Torres Strait, Hughes et al. (1999) found that the recruitment of coral brooders (which release fertilised larvae similar to Dictyoceratid sponges) varied more within reefs than between reefs. In contrast, the recruitment patterns of sponges to coral reefs in Torres Strait are unknown. For a commercial species such as *Coscinoderma* sp. to be properly managed in Torres Strait it is important to know when, where and how often it recruits to the coral reef habitat. A three year long study at Masig is currently determining the recruitment patterns of bath sponges and other sessile organisms to Torres Strait coral reefs.

4.2. METHODS

Study site and plate deployment

This study is being done at Marsden and Masig Islands, located in central Torres Strait (Fig. 4.1). Both islands are sand cays with fringing coral reefs, low-lying (<10 m in height) and small in size (<5 km²). Marsden and Masig are separated by 5 km of open water; maximum depth between the islands is ~30 m, with the substrate consisting of muddy sand (Harris 1988). The coral reef slope generally starts at a depth of 6 m (MLW) and stops on sand at 15 m, descending at an angle ranging from 20 to 60°.

Settlement plates are deployed at 3 locations on the northern side of each island, with locations 200 m apart. The northern side was chosen as it allows greater access and safer diving during most weather conditions. Each location is further divided into 3 sites, each 20 m apart. At each site, 5 plates are deployed at 6 m and at 12 m using the direct-attachment method developed by Mundy (2000). In this method the settlement plate is securely attached to a stainless steel base plate, which is anchored to the reef. The settlement plate rests approximately 1 cm above the reef allowing the settlement and recruitment of organisms on both sides of each plate. At each site-depth, plates were ~1 m apart. Terracotta plates 11 x 11 cm in size with pitted surfaces were used in the study, as they have found to be a good and reliable substrate for recruitment studies (e.g. Mundy 2000)

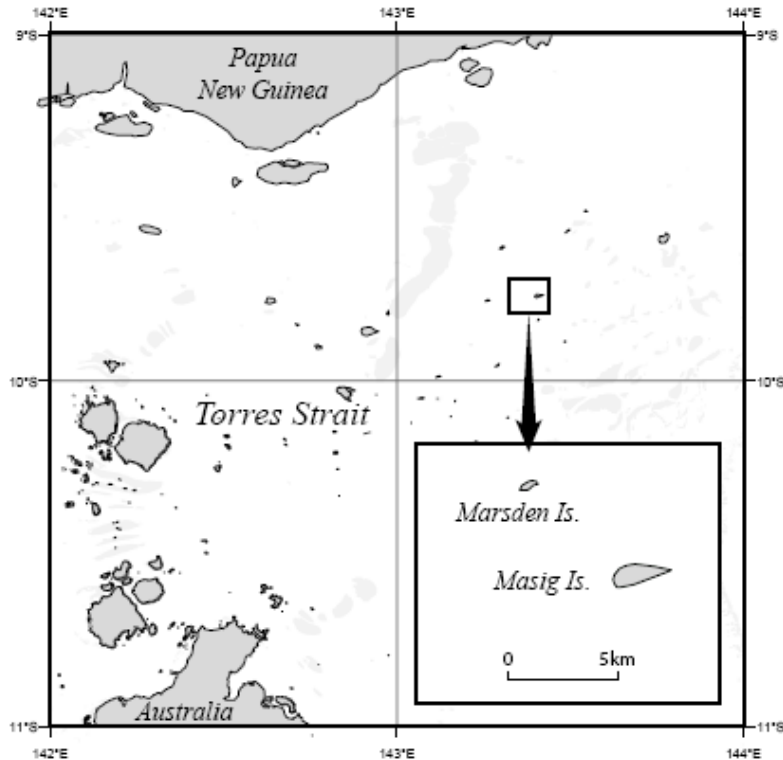


Figure 4.1. Map of Torres Strait showing the location of Marsden and Masig Islands.

This study is also investigating the recruitment of benthic organisms across seasons and years. Terracotta plates are deployed in November, at the start of summer, and in May, at the start of winter. Plates are left attached to reef at Marsden and Masig for 6 months, thus comparing the recruitment of organisms over summer and winter respectively. This study will run for 3 years, from November 2006 to November 2009. Each season, 180 plates will be deployed at Marsden and Masig, 30 plates per location. Each plate will be only used one, to prevent any confounding effects. At the end of each season, the top- and underside of each plate are photographed *in situ*. A new plate is then deployed onto the basal plate. Each plate has a small numbered-tag on both sides on one corner, clearly identifying the plate in the photographs.

During the first summer period, plates were deployed in November 2006, photographed *in situ* in March 2007, and photographed and replaced in May 2007. Analysis of this time series of settled species and their abundance will provide information about the recruitment of benthic organisms within a season.

Photographic analysis

An underwater close-up frame was constructed to photograph settlement tiles at a fixed distance and to record site and tile information on its frame (Fig. 4.2.). As the aspect ratio of the digital images allowed for the recording of extra information on each image, due to the tiles being square, a 4-digit code wheel was built into one side of the frame. The framer was adapted to accommodate either an Olympus C-7070 or Canon IXUS 850IS camera in underwater housings. Both these cameras have identical lenses and sensor-resolution and images produced are comparable in quality and view.

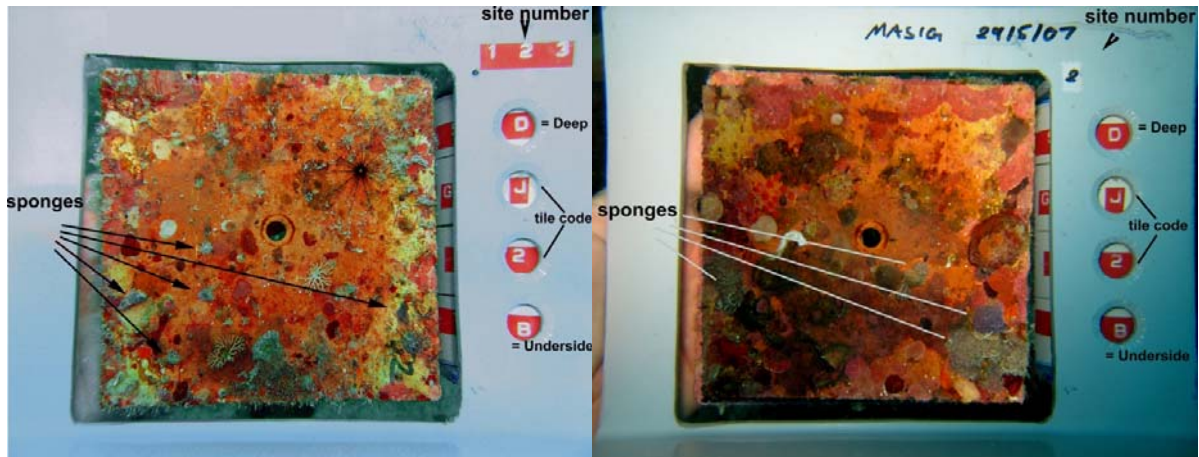


Figure 4.2. Photos showing sponges on the underside of settlement plate J2 taken in March 2007 (left) and May 2007 (right). Also shown is the frame used for each photograph, with site and plate information.

The recruitment of sponges and sessile organisms was determined for both abundance and percent cover. To determine the abundance or number of each taxa, an overhead transparency marked with a 132x132 mm square was overlaid on a PC-screen. The tiles are 115x115 mm square, but appear slightly magnified (to about 173x173 mm) on-screen to aid identification. All images of tiles were displayed by Microsoft Windows XP "Picture and Fax Viewer™" and enlarged by clicking the zoom-in button twice, which thus yielded an approximate 1.5:1 scale of each tile screen image. The square was reduced by 20 mm margin to minimise any edge effects being counted. To measure surface area occupied by the taxa identified, a 100 point grid was overlaid on the PC-screen image. The points were evenly spaced at a scaled distance in a 10x10 point grid which occupied the same area as the square in the abundance analysis.

4.3. RESULTS

Although this experiment is still ongoing, some preliminary results are available for the settlement plates deployed at Masig and monitored in March 2007; 4 months after the settlement plates were deployed. Over a dozen taxonomic groups settled and recruited to the plates at Masig, with the dominant groups shown in Figure 4.3. Among these groups, polychaete worms had the highest recruitment, followed by algae, hydroids, ascidians and sponges. In contrast, few hard or soft coral had recruited to the Masig plates. For most taxonomic groups, recruitment was higher at 12 m than at 6 m (Fig. 4.3.).

Considering sponges, mean number was approximately 1 sponge per plate at 12 m and 0.5 sponges per plate at 6 m. The main sponge recruits to Masig were *Dysidea*, *Callyspongia* and *Iotrochota* species and *Coscinoderma* sp. In total, 7 individuals of *Coscinoderma* sp. had recruited to Masig plates after 4 months, with 3 and 4 individuals recorded from shallow and deep reef, respectively.

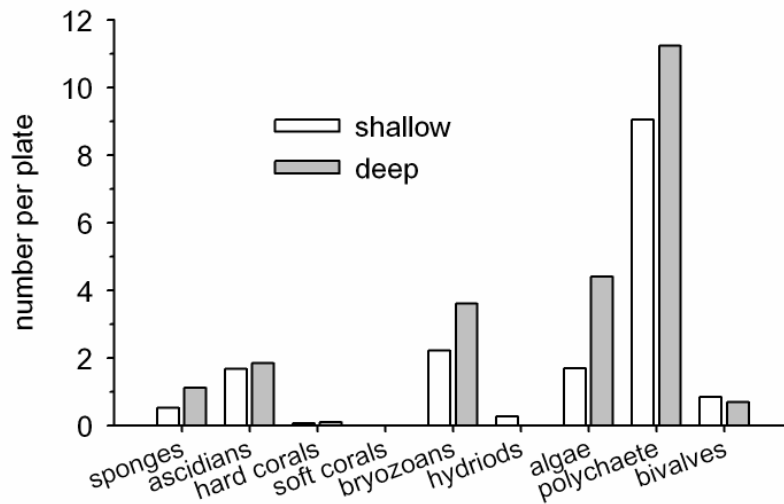


Figure 4.3. Recruitment after 4 months of major taxonomic groups to the underside of plates at shallow and deep reef at Masig.

4.4. DISCUSSION

Although at a very early stage, this study suggests that levels of recruitment in central Torres Strait varies greatly between taxonomic groups such as polychaete worms and corals. Recruitment variation between groups may result from differences in spawning times or survival of settling larvae. Depth is also clearly important, with generally higher recruitment at 12 m than at 6 m. However, the importance of depth in influencing recruitment appears to vary between taxonomic groups. Only after 3 years, when sufficient data has been obtained, will this study provide a clearer picture of the recruitment differences between taxonomic groups, and how they may vary between depths, seasons and islands.

The recruitment of *Coscinoderma* sp. to some plates at Masig is a very promising finding, indicating that new bath sponges are successfully recruiting to coral reefs in Torres Strait. After 4 months, a similar number of *Coscinoderma* sp individuals had recruited to plates at 6 and 12 m. Further monitoring will determine if this trend is real. Interestingly, adult sponges of *Coscinoderma* sp. are considerably more abundant on deeper reef. Possible differences in abundance across depth of juveniles (recruits) and adult *Coscinoderma* sp. may indicate a higher mortality of sponge recruits in the shallows.

A full analysis of recruitment from year 1, showing patterns across seasons, depth and islands will be given in the annual report for the second year of this MTSRF project.

5. SPONGE ASSETS AND ECOSYSTEM HEALTH

Although the bath sponge *Coscinoderma* sp. is found throughout central and eastern Torres Strait, it is most abundant and reaches a larger size in the Masig island-group. Its abundance varies however around Masig, with sponge density differing between locations (km's) and between sites (200 m). Variation in abundance between and within island-groups probably results from the interaction of physical, biological and stochastic processes. There was a difference in the abundance of *Coscinoderma* sp between 2004 (CRC Torres Strait project) and 2007 (MTSRF project), and further surveys over the next 3 years around Masig will determine how the abundance of *Coscinoderma* sp. varies across time.

The size frequency patterns of *Coscinoderma* sp. suggest a good recruitment of bath sponges to Torres Strait coral reefs, which is a promising sign. The sponge recruitment experiment will continue for the next 3 years and determine when, where and how many bath sponges recruit onto coral reefs in central Torres Strait. The size frequency results coupled with information on the sponge's natural growth rates (determined from the CRC Torres Strait project) suggest that *Coscinoderma* sp. is a long-lived species with individuals probably living >10 years. The very low incidence of sponge disease in Torres Strait is also a very promising finding. Similarities in the genetic profiles and microbial communities of sponges between island-groups suggest that bath sponges can be safely transplanted within central and eastern Torres Strait.

The results from the various experiments carried out in the first year of this MTSRF project suggests that Torres Strait has a large and healthy bath sponge asset, sufficient in size and other characteristics to provide the base stock for sponge farming. This will be ground-truthed further in the near future, with the development of a business plan for a sponge farm at Masig.

The preliminary results, examining ecologically and economically important coral reefs species (Appendix 1), show that some reef species vary in abundance between island-groups. These patterns probably reflect different levels or intensity of fishing pressure and/or recruitment. Variation in habitat characteristics such as reef slope or %sand could also promote differences in abundance across space.

6. FIELD WORK CONDUCTED

AIMS scientists visited Torres Strait three times during the first year of the MTSRF project, diving the waters in and around several island communities in central and eastern Torres Strait (Table 5.1.). During all field trips we worked alongside and dived with Torres Strait Islanders. This promoted the transfer of knowledge and experience between the project, Torres Strait Islanders and the local communities. During the November field trip when central and eastern islands were surveyed for bath sponges and sponges were collected for genetic and microbial analysis, three Torres Strait islanders worked on the project: Stanley Lui from Erub, and John Morris and Samson Lowatta both from Masig (Fig. 5.1.). John Morris and Samson Lowatta also participated in the subsequent two field trips to Masig. Both John Morris and Samson Lowatta were formally employed for each day that they worked on the project, with a wage that was agreed and accepted to be fair by John Morris, Samson Lowatta, AIMS and Torres Strait Regional Authority.

Table 5.1. Field trips dates and island visited during the first year of the MTSRF funding. Also shown is the Objective researched during the field trip.

Dates	Island visited	Objective
14-23 November 2006	Ugar	1 and 2
	Erub	1 and 2
	Masig	1, 2 and 3
	Poruma	1 and 2
	Warraber	1 and 2
26 February-12 March 2007	Masig	1 and 3
28 May-4 June 2007	Masig	3



Figure 5.1. Photos taken during the November field trip to Torres Strait showing: (left) Samson Lowatta; and (right) (taken by Eric Matson), John Morris (grey wetsuit) and Stan Lui

7. COMMUNICATION ACTIVITIES

Effective community extension has been a high priority of this project and the CRC funded project that preceded it. Besides actually involving community members in the research, steps were taken to fully inform the relevant Island councils and communities of the planned field work, before the work took place.

Before the first field trip (November 2006 survey) permission was first obtained from the chairman or council member of Ugar, Erub, Masig, Poruma and Warraber for their local waters to be surveyed for bath sponges. To inform the wider community at each island, a community flyer (Appendix 2) was posted to each council for public display. It fully explained the survey, the work that was planned, and included a photo of the RV Cape Ferguson so that all would know what the large vessel was doing in their local waters. Following the November 2006 survey, a non-technical report was sent to all island communities informing them of the results (Appendix 1).

For the subsequent two field works to Masig, the project built on the excellent working arrangement between the Yorke Island Community Council and AIMS which was established during the previous CRC Torres Strait project based at Masig. After each field trip, Torres Strait Regional Authority was informed of activities and interactions with island communities.

The distribution and abundance studies are currently being written up as manuscripts and will be submitted shortly. The recruitment study is still on-going and will be submitted to a science journal once finished.

8. PLANNED ACTIVITIES FOR 2007/2008

Due to the significantly reduced funding for the second year of this MTSRF project (47% of year 1 funds), the field work to Torres Strait and planned research has had to be reduced considerably. Two field trips are planned to Masig, one in November 2007 and the second in May 2008. Both field trips will concentrate on Objective 3, which examines the recruitment of bath sponges and other sessile organisms to coral reefs around Masig. In addition, benthic surveys in the waters around Masig will further investigate the occurrence of disease, abundance and size frequency patterns of the bath sponge *Coscinoderma* sp. (Objective 1). These surveys will also collect information on the health of coral reefs in central Torres Strait, including the spread of invasive species and the possible changing levels of sedimentation.

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APPENDIX 1

DISTRIBUTION AND ABUNDANCE OF THE BATH SPONGE COSCINODERMA IN CENTRAL AND EASTERN TORRES STRAIT

MTSRF Project 1.3.2: Ecological role and potential economic value of sponges to Torres Strait

Alan Duckworth, Carsten Wolff, John Morris, Samson Lowatta, Stanley Lui, Heidi Luter, Eric Matson and Tim Hyndes

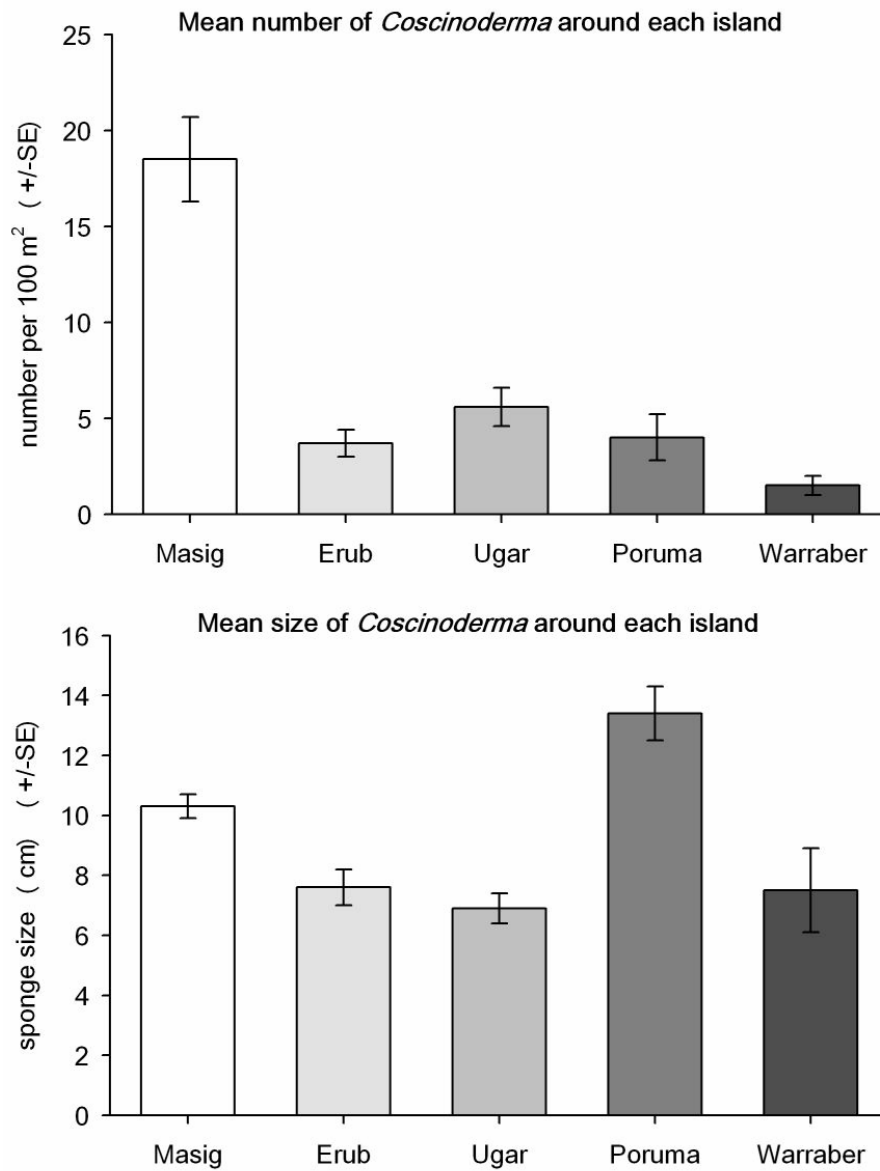
2007



- There is a worldwide shortage of bath sponges, used in cleaning, painting and cosmetics.
- AIMS researchers and Masig Island divers have found large numbers of the bath sponge *Coscinoderma* around Masig, and have worked out good methods of farming it.
- Masig Island may soon set up a commercial bath sponge farm, employing and managed by Torres Strait Islanders.
- Neighbouring islands and reefs in central and eastern Torres Strait may also have high numbers of *Coscinoderma*.
- In November 2006, AIMS and Torres Strait divers surveyed reefs for bath sponges around Masig, Erub, Ugar, Poruma and Warraber.
- We measured the size of each *Coscinoderma* we found.
- We also counted other commercially or environmentally important species such as coral trout, crown of thorn starfish, sea cucumbers and snappers.
- This project is funded by the Australian Institute of Marine Science, Torres Strait Regional Authority and the Australian Government's Marine and Tropical Sciences Research Facility.

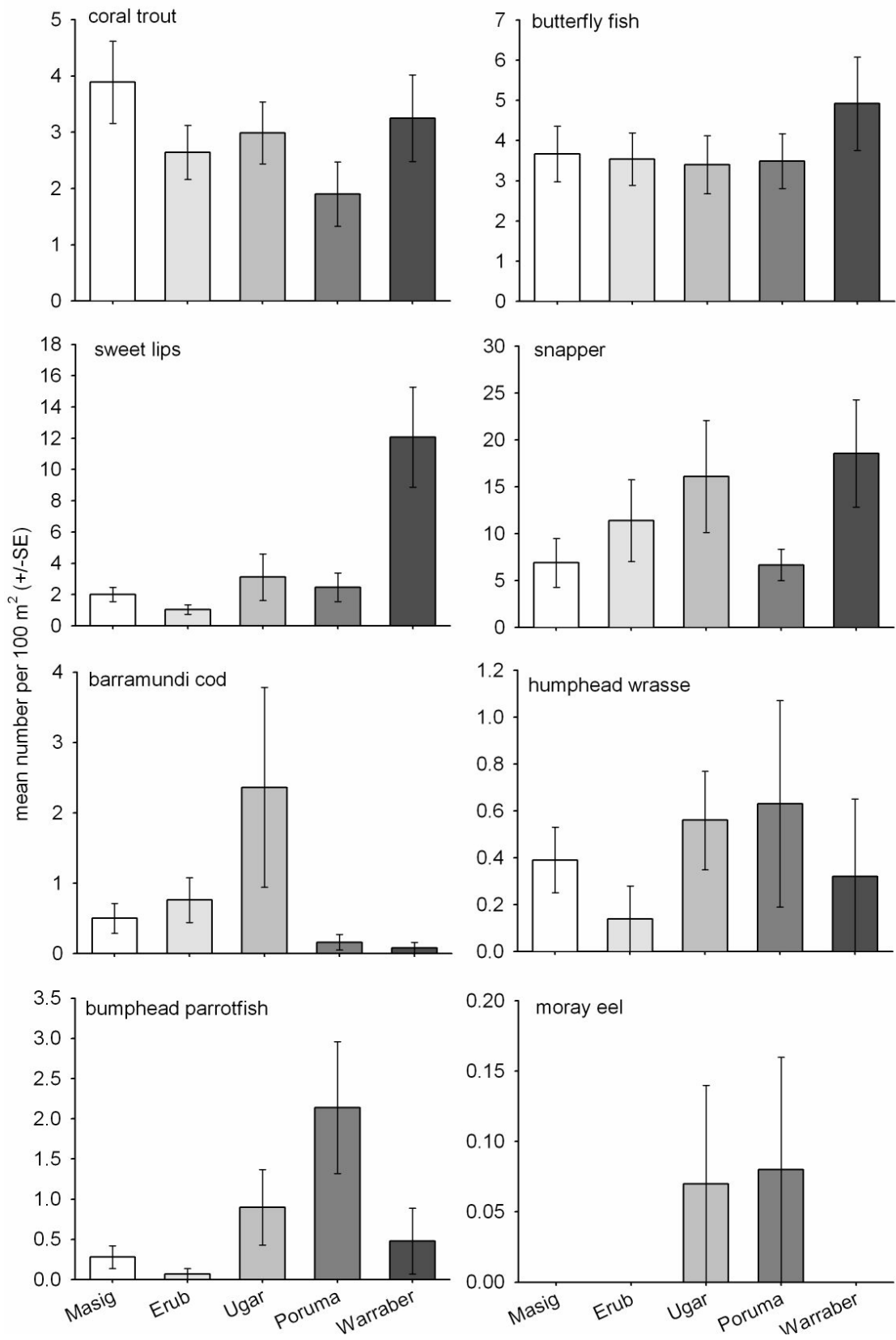


Stanley Lui surveying for sponges (photo by E. Matson).

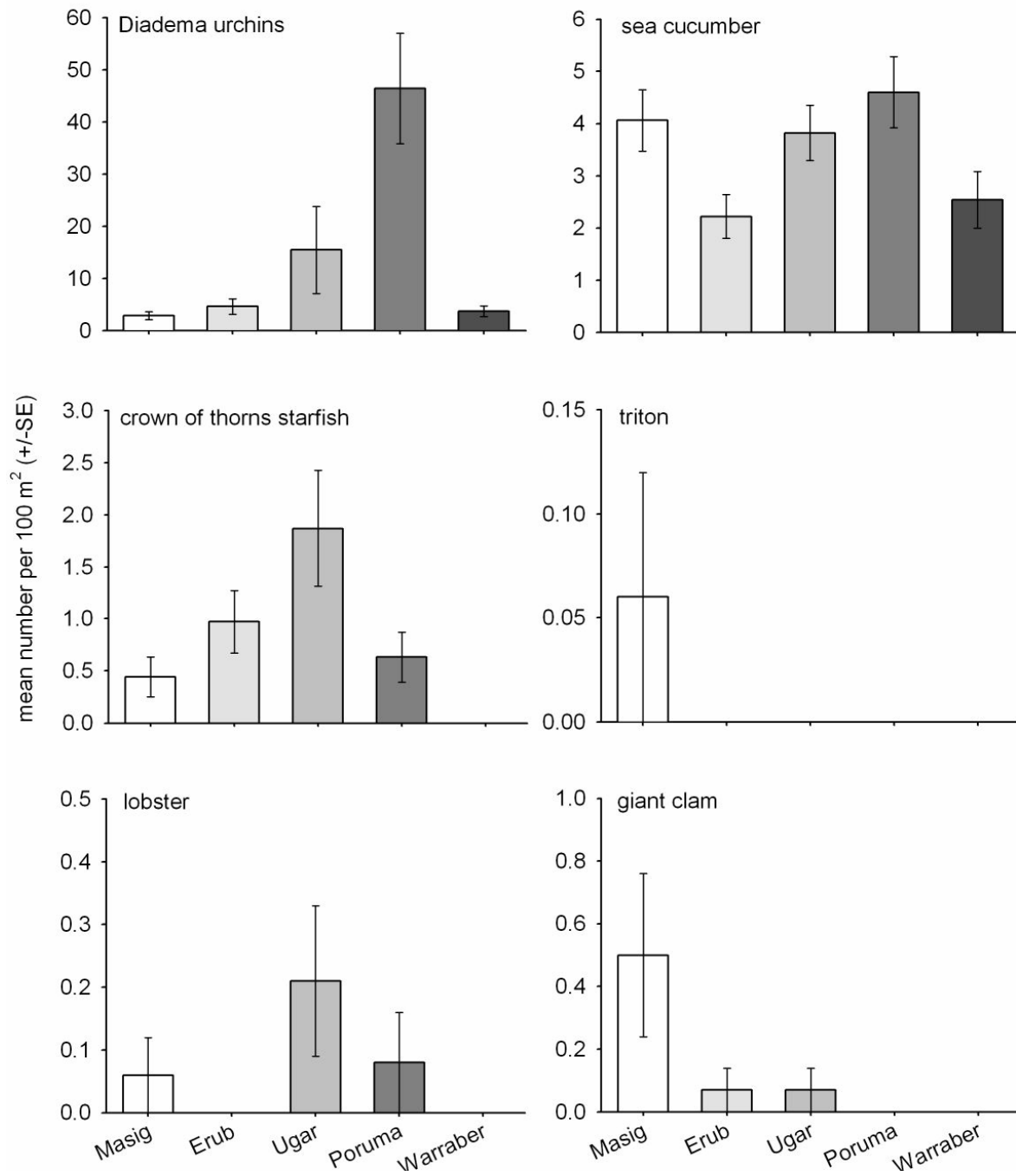


- *Coscinoderma* is very common at Masig and uncommon around Erub, Ugar, Poruma and Warraber.
- *Coscinoderma* is largest at Masig and Poruma.

Mean number of reef fish around each island



Mean number of reef invertebrates around each island





Sponge divers from top: Tim Hyndes, John Morris, Eric Matson, Carsten Wolff, Samson Lowatta, Heidi Luter, Alan Duckworth and Stanley Lui

For further information contact:
Alan Duckworth
Australian Institute of Marine Science
Townsville, QLD 4810
Phone: (07) 4753 4444
Email: a.duckworth@aims.gov.au

APPENDIX 2

BATH SPONGE RESEARCH IN TORRES STRAIT

- There is a worldwide shortage of bath sponges, used in cleaning, painting and cosmetics.
- AIMS researchers and Masig Island divers have found large numbers of bath sponges around Masig, and have worked out good methods of farming them.
- Masig Island may soon set up a commercial bath sponge farm, employing and managed by Yorke Islanders.
- Neighbouring islands and reefs in central and eastern Torres Strait may also have high numbers of bath sponges.
- From 12-24 November 2006, AIMS and Torres Strait divers will survey reefs for bath sponges around Erub, Ugar, Poruma, Masig and Warraber.
- We will work off the AIMS Research Vessel Cape Ferguson.
- Feel free to come and see us.



Samson Lowatta with farmed sponges

Cape Ferguson

For further information contact:
Alan Duckworth
Australian Institute of Marine Science
PMB No. 3
Townsville, QLD 4810
Phone: (07) 4753 4171
Email: a.duckworth@aims.gov.au

Cape Ferguson CDMA 0429 680 920

