Assessing the effectiveness of surrogates for conserving biodiversity in the Port Stephens-Great Lakes Marine Park

Vanessa Owen B Env Sc, B Sc (Hons)

School of the Environment

University of Technology Sydney

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Certificate of Original Authorship

I certify that the work in this thesis has not been previously submitted for a degree nor has it been submitted as part of requirements for a degree except as fully acknowledged within the text. I also certify that the thesis has been written by me. Any help that I have received in my research work and preparation of the thesis itself has been acknowledged. In addition, I certify that all information sources and literature used as indicated in the thesis.

Signature of Student:

Date:

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Abstract

The effectiveness of marine protected areas (MPAs) in conserving biodiversity depends, in part, on which areas are chosen for protection and how these areas represent the true biodiversity of the planning region. Advances in acoustic technology have enabled high resolution maps of seabed habitats to create habitat maps based on depth and sea bed characteristics, which is quicker and cheaper than sampling biota over similar spatial extents. These habitat classification schemes are often used as surrogates of biodiversity for fish and benthic assemblages in the absence of biodiversity inventories, to depict spatial variation in biodiversity and support conservation planning. However, the intra-habitat variability and precision of these biodiversity surrogates is largely unknown.

The aim of this thesis is to assess the effectiveness of habitat classification schemes as surrogates for biodiversity conservation in Port Stephens-Great Lakes Marine Park (PSGLMP). Fishes were sampled with baited remote underwater video stations (BRUVS) and sessile benthic assemblages were surveyed using an Autonomous Underwater Vehicle (AUV). The results of this study indicate that habitat mapping based on depth is a suitable surrogate for biodiversity of fish assemblages in unvegetated, unconsolidated habitats. Habitat mapping based on depth only categories is not a suitable surrogate for biodiversity of rocky reef sessile benthic assemblages, nor fish assemblages in sponge-dominated reef habitat. Multiple samples of sessile benthic assemblages and fish assemblages from a range of locations subject to differing environmental influences are required to adequately conserve representative samples of biodiversity within the PSGLMP. In the context of MPA planning, sessile benthic assemblages are not a suitable surrogate for biodiversity of fish assemblages. An examination of scales of autocorrelation in sessile benthic assemblages indicates a significant positive correlation between distance and dissimilarity, meaning that assemblages become more dissimilar as distance increases. Biodiversity sampling in this habitat is required at a fine scale (25 m) for the purposes of creating habitat maps for MPA planning.

The results of this study have important consequences for future MPA planning, indicating that representative samples of rocky reef fish and sessile benthic assemblages from a variety of locations within differing environmental domains are required to adequately conserve representative samples of biodiversity. More studies are required to effectively understand what additional information needs to be incorporated into habitat classification schemes so

that they can act as a surrogate for biodiversity for the range of assemblages conserved within PSGLMP.

Chapter 1 Overview of Thesis

1.1 Overall Aim

Temperate southeast Australia contains diverse marine and estuarine habitats that are valuable commercial and recreational assets. Eastern Australia supports almost half of Australia's population, and as a consequence considerable pressures are placed on the region's unique and diverse marine and estuarine environment (Edgar *et al.,* 1999; Birch, 2000; Zann, 2000; Edgar *et al.,* 2000; Lindegarth and Hoskin, 2001; Edgar *et al.,* 2005; Edgar *et al.,* 2014). Threats to marine and estuarine species in temperate Australia, in the form of climate change, coastal development, pollution, invasive species, loss of habitat and species, fisheries overexploitation and catchment discharges, are accelerating, fully encompass species ranges, and are of sufficient magnitude to cause species extinction (Dee Boersma and Parrish, 1999; Zann, 2000; Edgar *et al.,* 2005; Edgar *et al.,* 2014).

In Australia a National Representative System of Marine Protected Areas (MPAs) has been established with the aim of conserving marine biodiversity and maintaining ecological processes (IMCRA Technical Group, 1998; ANZECC TFMPA, 1999). The National Representative System of MPAs aims to be comprehensive, adequate, and representative (ANZECC TFMPA, 1998). In New South Wales (NSW) MPA planning has recently been revised and the NSW Marine Estate planning policy is to have a healthy coast and sea, managed for the greater well-being of the community, now and into the future (NSW Marine Estate Management Authority, 2013). Habitat classification schemes are often used as surrogates of biodiversity in the absence of biodiversity inventories, to depict spatial variation in biodiversity and support conservation planning (Ward *et al.,* 1999; Banks *et al.,* 2005; Winberg *et al.,* 2007; Lindsay *et al.,* 2008; Last *et al.,* 2010; Malcolm *et al.,* 2010; Malcolm *et al.,* 2011). This assumes that habitats are homogeneous, and therefore any area of that habitat type will represent the full spectrum of ecological diversity within that habitat (Winberg *et al.,* 2007; Smith *et al.,* 2008). The efficacy of habitat classification schemes as biodiversity surrogates in conservation planning is poorly understood (Ward *et al.,* 1999; Mumby *et al.,* 2008; Shokri and Gladstone, 2013). The suitability of these surrogates may be affected by unrecognised sources of variation in biodiversity, including environmental variation within the same habitat. The objective of this thesis is to assess the effectiveness of habitat classification schemes as surrogates for biodiversity conservation in Port Stephens-Great Lakes Marine Park (PSGLMP).

1.2 Study Approach

To achieve the above objective, the second chapter of the thesis reviews the literature reporting on patterns and processes of two subtidal habitat classes (sponge-dominated 'deep reef' habitat and subtidal unvegetated, unconsolidated habitat) used for marine park spatial planning in NSW. The need, framework and benefits of MPAs are then reviewed. Literature relating to the need for, and use of, biodiversity surrogates in the selection and design of MPAs is then examined. Specifically, studies that have used habitat mapping as surrogates for biodiversity in the selection and design of MPAs are detailed. The third chapter describes the study area where the field surveys were undertaken in PSGLMP.

The fourth chapter looks at intra-habitat variability in the biodiversity of sessile benthic assemblages within sponge-dominated deep reef habitat, and its implications for the development of surrogates for conservation planning. It firstly determines optimal sampling effort required for a representative description of sessile benthic assemblages in a single habitat class (sponge-dominated reef) surveyed remotely using an autonomous underwater vehicle. It then examines whether these assemblages varied in different environments (coastal headlands, offshore islands) where the habitat occurred, to assess if habitat mapping based on depth only categories is a suitable surrogate for biodiversity of rocky reef sessile benthic assemblages, or if multiple examples of sessile benthic assemblages from differing environmental influences are required to adequately conserve representative samples of biodiversity within the PSGLMP.

The existence of spatial autocorrelation in sessile benthic assemblages has implications for the scales of studies undertaken to describe patterns of spatial structure in benthic assemblages, the design of monitoring schemes, and decisions about the linear dimensions of areas selected to represent examples of assemblages in marine protected area planning. The fifth chapter builds on the results of the fourth chapter and reports on scales of autocorrelation in sessile benthic assemblages within sponge-dominated deep reef habitat to determine appropriate scales for biodiversity sampling for the purposes of creating habitat maps for MPA planning.

The sixth chapter quantifies spatial and temporal variability in the biodiversity of rocky reef fishes among locations in different environmental domains within the sponge-dominated deep reef habitat class, and discusses the implications for surrogacy schemes that use habitat mapping for conservation planning. This chapter assess if habitat mapping based on depth only categories is a suitable surrogate for biodiversity of rocky reef fish assemblages, or if

multiple examples of fish assemblages from differing environmental influences are required to adequately conserve representative samples of biodiversity within the PSGLMP.

The seventh chapter examines the influence of biogenic attributes of habitats on sources of variation in the biodiversity of rocky reef fishes. The relationship between fish and sessile benthic assemblages within sponge-dominated deep reef habitat is examined to determine the usefulness of these groups as surrogates of biodiversity in relation to MPA planning. The research tested whether there was a relationship in the spatial variation of biodiversity in both groups, and determined the most important features of benthic assemblages that influenced fish assemblages.

The eighth chapter reports on the effectiveness of a depth-based habitat classification scheme as a surrogate for offshore fish biodiversity within subtidal unvegetated unconsolidated habitat, to determine if habitat mapping based on depth only is a suitable surrogate for biodiversity of fish assemblages in this habitat. The ninth chapter draws conclusions as to the effectiveness of the examined habitat classification schemes as surrogates for fish and sessile benthic assemblage biodiversity conservation in PSGLMP.

Each of the data chapters (chapters four to eight) have been written as stand-alone manuscripts for submission to journals. Therefore there is some repetition in the content of the literature review and the introductions of each data chapter.

Chapter 2 Literature Review

This thesis chapter examines the literature reporting on patterns and processes of two subtidal habitat classes (sponge-dominated subtidal rocky reef and subtidal unvegetated unconsolidated habitat) used for marine park spatial planning in New South Wales (NSW). The need, framework and effects of marine protected areas (MPAs) are reviewed. Literature relating to the need for, and use of, biodiversity surrogates in the selection and design of MPAs is examined. Specifically, studies that have used habitat mapping as surrogates for biodiversity in the selection and design of MPAs are detailed.

2.1 Patterns and Processes in Australian Temperate Marine and Estuarine Habitats

Temperate Marine Habitats

Species and assemblages tend to occur within a particular set of environmental conditions suited to their biological needs (O'Hara, 2001). On shallow temperate subtidal reefs in NSW, habitats can be classified in a biologically meaningful way by the dominance or presence of major habitat-forming macroalgae species (Shears *et al.,* 2004). In a description of marine subtidal rocky reef assemblages in temperate NSW Underwood *et al.* (1991) described several distinctive habitats, the distribution of which related to physical forces including depth and wave exposure, and biological pressures, most notably herbivory by the sea urchin *Centrostephanus rodgersii*. Fringe habitat occurs just below low tide level to depths of approximately 3 m and is dominated by a diverse range of algae. Turf habitat is characterised by a variety of turfing coralline and filamentous algae and occurs within shallow (<10 m) water. Forests of kelp (*Ecklonia radiata*) occur at intermediate depths (approximately 2-25 m), and are interspersed with patches of sea urchin grazed crustose coralline algae (the 'barrens' habitat). Forests of *Phyllospora comosa* occur at nearshore reefs in the southern area of NSW at intermediate depths (approximately 2-25 m). Pyura habitat is dominated by the large solitary ascidians *Pyura gibbosa* and *P. stolinifera* and occurs at intermediate depths (approximately 2-25 m). Sponge-dominated 'deep reef habitat' occurs >9 m depth and is characterised by a significant density of sessile benthic animals, including a number of sponges, corals and bryozoans unique to the habitat (Underwood *et al.,* 1991; Smith *et al.,* 2010). Large gaps in knowledge still exist about spatial and temporal patterns in the distribution of subtidal habitats in temperate NSW, their associated assemblages, and the underlying ecological processes.

Deep Reef Habitat

Sponges are the dominant sessile animal of deep reef habitat in temperate NSW (Roberts *et al.,* 1994; Roberts, 1996; Roberts and Davis, 1996; Roberts *et al.,* 1998), but in general little is known about their biodiversity and factors that influence their distribution and abundance (Hooper and Kennedy, 2002). Sponge assemblages are highly variable at spatial scales of m, 100s m and 10s km (Roberts, 1996; Roberts and Davis, 1996; Owen, 2003; Roberts *et al.,* 2006). Generally, the abundance (Wilkinson and Evans, 1989; Underwood *et al.,* 1991) and taxonomic richness (Roberts and Davis, 1996) of sponges increase with depth, as do the number of upright or massive forms (Roberts and Davis, 1996). Depth influences a range of environmental parameters, including light, sedimentation, temperature and water movement which dictate the diversity and abundance of sponge assemblages (Garrabou *et al.,* 2002). Cover of sponges (particularly encrusting forms) decreases with depth, and a significant positive relationship occurs between species richness and cover (Roberts and Davis, 1996).

Studies on sessile benthic assemblages in temperate NSW have documented great spatial and temporal variability in shallow-water (~20 m) assemblages, challenging pre-conceived ideas that these assemblages are relatively stable through time (Roberts *et al.,* 1998). The composition of temperate deep reef sessile benthic assemblages (20-50 m depth) are highly variable within and between locations, depths and times (Roberts, 1996; Roberts and Davis, 1996), with greater temporal variation in abundance occurring in assemblages of shallow reefs (20 m) than those at 30 m and 50 m (Roberts and Davis, 1996). Exposure has a significant influence on sessile benthic assemblages, with upright sponges forms accounting for the majority of the species richness and cover of sponges on sheltered reefs, and encrusting species dominating exposed reefs (Roberts *et al.,* 2006a). Most variability is found at the smallest spatial scale (among replicate samples separated by metres) and this variability is generally greatest for taxa on exposed reefs compared with sheltered reefs (Roberts *et al.,* 2006a). Proximity to an estuary also has a significant influence on sessile benthic assemblages, with assemblages near estuaries differing to those at offshore reefs (Owen, 2003). Encrusting forms are more common at near-estuarine reefs and upright forms are more common at offshore reefs (Owen, 2003).

Assemblages of sessile benthic organisms in southern Australia are diverse, highly endemic and a commercially important part of Australia's marine diversity (Keough, 1999; O'Hara, 2002; Ponder *et al.,* 2002; Fromont *et al.,* 2006). There are currently ~7000 described species

of sponges worldwide, which is estimated to represent 50% of likely sponge diversity (Hooper, 2000). In Australia, knowledge of sponge biodiversity is poor, with approximately 1400 described species, representing approximately a quarter of the estimated biodiversity (Hooper, 2000). Descriptions of deep reef habitat on the NSW Central Coast revealed diverse fauna, with over 65% of sponges collected previously undescribed (Roberts and Davis, 1996). A recent description of the marine benthos in South Australia recorded over 350 sponge species (Sorokin *et al.,* 2008). A hindrance to the understanding of sponge-dominated assemblages stems from the poorly resolved systematic framework surrounding the phyla (Hooper and Kennedy, 2002). Also, environmental variability can significantly influence body form (Trammer, 1983; Palumbi, 1986) and tissue structure (McDonald *et al.,* 2002) of sponges.

Marine sponges have a significant and widespread influence on substrate, bentho-pelagic coupling and other organisms (Bell, 2008). Recent research indicates a positive linear relationship between sponges species and morphological richness in rocky reefs in Ireland (Bell and Barnes, 2001) and in Indonesian coral reefs (Bell, 2007a), however the generality of this has not been tested in different locations and habitats. The discovery of medicinal benefits of sponges has fuelled recent research into sponge identification and collection (Hooper, 2000). Recent research has also highlighted the diversity of sponge endofauna (crustaceans and fish) (Abdo, 2007). However, there is still a high degree of uncertainty regarding the magnitude of sponge diversity, the interactions and responses of sponge-dominated assemblages to environmental variables and the appropriate spatial and temporal scales at which they need to be described for effective conservation and management (Hooper and Kennedy, 2002; Worheide *et al.,* 2005).

Ascidians and cnidarians are minor contributors to macrobenthic assemblages in deep reef habitat in temperate Australia (Roberts, 1996; Roberts *et al.,* 1998). Ascidians are generally out-competed for space by sponges (Keough, 1999) but can replace sponges as the dominant faunal group when cover of sponges is significantly reduced following exposure to sewage outfalls (Roberts *et al.,* 1998). A description of ascidians on subtidal rocky reefs in temperate NSW indicated that assemblages were highly variable between sites (100s m), reef exposures and depths (Newton *et al.,* 2007). The highly variable spatial patterns exhibited in subtidal sessile benthic assemblages indicate that numerous subtidal reefs may need to be protected for the aim of adequate representation to be realised (Newton *et al.,* 2007).

Bryozoans are common in deep reef habitat (Roberts, 1996; Roberts *et al.,* 1998) and their distribution and abundance is determined by depth, current and food supply (Shepherd and Thomas, 1982). There are few descriptions of the diversity and abundance of macroalgae in deep reef habitat, despite southern Australia being the regional epicentre of macroalgae richness and endemism (Phillips, 2001). Crustose coralline algae is patchily distributed in deep reef habitat (Roberts, 1996; Roberts *et al.,* 1998), as is *Ecklonia radiata,* which can occur at high densities (Underwood *et al.,* 1991).

Species respond to resource gradients, whose distribution patterns are most accurately measured in multi-dimensional environmental space and only then translated to geographic space (Margules *et al.,* 2002). The resultant spatial patterns show high or dense populations in scattered locations, representing the most favourable habitat (or mix of environmental variables), and lower, more sparse populations in areas of less favourable habitat (Margules *et al.,* 2002). Thus, the geographic distribution patterns of species can be linked to variation in environmental domains (Margules *et al.,* 2002).

Deep reef habitat supports diverse fish assemblages that are highly variable at scales of 100s m (Curley *et al.,* 2002; Gladstone, 2007; Lindfield, 2007; Malcolm *et al.,* 2007). Often the combined influence of several environmental gradients must be considered in order to understand how the environment structures fish assemblages (Chatfield *et al.,* 2010). Rocky reef fish assemblages in temperate Australia are influenced by depth (Chatfield *et al.,* 2010; Malcolm *et al.,* 2011), distance from shore (Malcolm *et al.,* 2010), habitat type (Curley *et al.,* 2002; Chatfield *et al.,* 2010), exposure (Vanderklift *et al.,* 2009) and proximity to seagrass beds (Valesini *et al.,* 2004) The strong influence of environmental variables on the structure of fish assemblages suggests that assemblages may differ between environmental domains where environmental influences including depth, proximity to estuary, distance to coastline, and exposure differ.

Mobile macroinvertebrates (e.g. asteroid starfish, echinoids) are major contributors to the flux of materials on rocky reefs (Taylor, 1998). Density of small refuges is an important factor influencing mobile macroinvertebrates in shallow temperate rocky reefs (Alexander *et al.,* 2009). There is little published information on patterns in the abundance and diversity of these macroinvertebrates in the deep reef habitat, with the exception of Underwood *et al.* (1991) who noted a patchy distribution of the mollusc *Astralium tentoriformis* and the sea urchin *Centrostephanus rodgersii*.

Subtidal Unvegetated Unconsolidated Habitat

Subtidal unvegetated unconsolidated habitat is a dominant feature of coastlines and represents a significant component of the total marine habitat available to fauna (Morrison *et al.,* 2002). Brown and McLachlan (2006) classified fish assemblages of the surf zones of sandy beaches into two groups. The first group contains approximately 10% of the fish assemblage and comprise true residents such as flatfishes and elasmobranchs (Brown and McLachlan, 2006). The second group is comprised of non-residents, which occur in sandy beaches in large numbers, including juveniles of many species (Brown and McLachlan, 2006). The importance of sandy beach surf zones as habitat for larvae and juveniles of numerous fish species has been documented from studies overseas. In South Africa, seine net catches are dominated by juvenile fish, indicating the importance of this habitat for fisheries (Clark, 1997). In Japan, variation in surf-zone fish assemblages has been related to wave exposure, with mean density negatively correlated with wave exposure, and highest species richness and diversity recorded at intermediate levels of exposure (Inoue *et al.,* 2008). At the microhabitat scale, surf-zone fish assemblages in Japan are similar despite differences in abiotic and biotic variables, suggesting large-scale environmental variables have a greater role in structuring fish assemblages (Inoue *et al.,* 2008). Variation in surf-zone fish assemblages is also highly correlated with temperature (Clark *et al.,* 1996a; Suda *et al.,* 2002; Wilbur *et al.,* 2003; White and Potter, 2004), salinity (Pessanha and Araujo, 2003), turbidity (Clark *et al.,* 1996b), wave exposure (Clark *et al.,* 1996b) and time of day, with higher abundance and larger fishes recorded at night in the surf zone (Ross *et al.,* 1987; Gibson *et al.,* 1996).

One study has examined the role of wave activity in structuring sandy beach fish assemblages on the NSW Central Coast. Twelve species from nine families were recorded, with the stingaree (*Trygonoptera* spp.), fiddler ray (*Trygonorrhina fasciata*), sand flathead (*Platycephalus bassensis*) and six-spine leatherjacket (*Meuschenia freycineti*) the most common species recorded (Yona, 2008). There was no difference in the mean number of species, relative abundance or diversity of fishes between low energy, intermediate energy and high energy beaches (Yona, 2008). Multivariate analyses indicated that the low energy fish assemblage was different to the intermediate and high energy beaches (Yona, 2008). There is no information available comparing fish assemblages between unvegetated unconsolidated marine habitats with adjacent rocky reef habitat in temperate NSW, however a recent study from subtropical eastern Australia indicates that distance from reef is an important determining factor for fish assemblages in unconsolidated habitats (Schultz *et al.,*

2012). Studies from overseas indicate that abundance and species richness of fishes is higher in rocky reef habitat, and different from, adjacent unvegetated sand habitat (Ribeiro *et al.,* 2005).

The influence of environmental domains in structuring the fish assemblages of unvegetated unconsolidated marine habitats has not been widely studied in Australia. Gray and Otway (1994) recorded diverse and abundant fish at 30 m (42 species), 50 m (57 species) and 100 m (35 species), and found that assemblages of demersal fishes at 30 m and 60 m were most similar to each other and they consistently differed from assemblages at 100 m depth. A study in the Solitary Islands Marine Park used Baited Remote Underwater Videos (BRUVs) to survey fish assemblages of unconsolidated substrata and determined that fish assemblages were different across depths, distance from shore and spatial scales. Examples from other countries suggest that environmental domains are likely to be an important source of variation structuring shallow-water marine unvegetated unconsolidated fish assemblages. In USA (Ruiz *et al.,* 1993) and Scotland (Gibson *et al.,* 1996), depth-related patterns of distribution and abundance in unvegetated unconsolidated habitat have been demonstrated.

Temperate Estuarine Habitats

Estuaries are a common feature of south-east Australia, with more than twenty large estuaries discharging into the Tasman Sea (Roy *et al.,* 2001). Estuaries in NSW can be classified in terms of measurable geomorphic characteristics, and these geomorphic characteristics exert an influence on estuarine assemblages (Saintilan, 2004). Estuarine faunal species richness is influenced by the variety and area of habitats (in particular seagrass and mangroves), and conditions such as calmness of water, food, shelter, and protection from predators (Pollard, 1984; Gray *et al.,* 1996; Saintilan, 2004, Dixon-Bridges *et al.,* 2014).

Estuarine Unvegetated Unconsolidated Habitat

There is very little published information relating to spatial patterns of faunal assemblages and/or ecological processes in unvegetated unconsolidated estuarine habitat in Australia and overseas. Most studies that report results describing patterns of biodiversity and abundance of fauna in subtidal unvegetated unconsolidated estuarine habitats in temperate NSW are comparing the results to seagrass beds. Studies relating to benthic macroinvertebrates in temperate Australia indicate that diversity and abundance is lower in unvegetated unconsolidated habitat when compared to seagrass habitat, and that assemblages in

unvegetated unconsolidated subtidal sand habitat differ to those in seagrass and mangrove habitat (Ferrell and Bell, 1991; Connolly, 1994; Gray *et al.,* 1996; West and King, 1996; Jenkins and Wheatley, 1998; Travers and Potter, 2002; Heithaus, 2004; Hindell and Jenkins, 2004; White and Potter, 2004; Bloomfield and Gillanders, 2005; Smith *et al.,* 2008). However, as Hutchings (1999) noted, Australia has highly diverse marine invertebrate assemblages, which thrive in the sheltered protected waters of estuaries and the associated soft sediments.

A greater diversity and abundance of fishes, and distinctive assemblages, occur in seagrass than over unvegetated sand or mud (Gray *et al.,* 1996; Travers and Potter, 2002; Heithaus, 2004; Hindell and Jenkins, 2004; Bloomfield and Gillanders, 2005; Gladstone *et al.,* 2012). However, unvegetated unconsolidated habitat is a dominant feature of many estuaries, represents a significant component of the total estuarine habitat available to fauna, and is important habitat for many estuarine fauna (Morrison *et al.,* 2002; Dixon-Bridges *et al.,* 2014). For example, Jenkins and Wheatly (1998) found that in southern Australia the commercially important King George whiting (*Sillaginodes punctata*) showed a complex relationship with habitat, occurring in both seagrass and rocky reef habitat immediately after settlement. With growth, the species showed an increasing preference for rocky reef habitat before finally shifting to unvegetated sand habitat approximately four months after settlement (Jenkins and Wheatley, 1998). Ross *et al.* (2007) found that snapper (*Pagrus auratus*) were more abundant over sand flats adjacent to rocky reef habitats in New Zealand, a distribution that is hypothesised to balance the requirements of both food acquisition and predator avoidance. Additionally, studies in Chile have reported high biomass values of benthic fish assemblages in subtidal unvegetated unconsolidated habitat, in some cases higher than at adjacent seagrass habitat (Ortiz and Wolff, 2002).

Utilisation of sandy, unvegetated estuarine habitat by fishes in temperate Australia is very dynamic and highly variable through space and time (Miller and Skilleter, 2006). The clearest patterns observed are diurnal effects, where generally the abundance of fishes is greater at night than during the day (Gray *et al.,* 1998; Miller and Skilleter, 2006; Johnson *et al.,* 2008; Rotherdam *et al.,* 2008). At night estuarine unvegetated unconsolidated habitat is an important habitat for a wide range of estuarine fish and invertebrates on the NSW Central Coast (Rotherdam *et al.,* 2008) and south-western Australia (Travers and Potter, 2002). Travers and Potter (2002) showed the number of species and density of fishes over bare sand were greater at night than day, reflecting, in part, a tendency for species in move into unvegetated

unconsolidated areas to feed at night, where the likelihood of predation by visual predators is reduced. In south-eastern NSW, newly recruited juveniles of economically important species occur in both estuarine unvegetated unconsolidated and seagrass habitat (Gray *et al.,* 1998). Both seagrass and unvegetated unconsolidated estuarine habitat are therefore important habitat for fisheries resources (Gray *et al.,* 1998).

There are no studies comparing fish assemblages between estuarine unvegetated sand and marine unvegetated sand, however there is the potential for these assemblages to be different due to differing environmental characteristics of the two environmental domains. For example salinity, temperature and turbidity have been shown to be key environmental factors structuring temperate Australian fish assemblages (Loneragan *et al.,* 1987; Edgar *et al.,* 1999; Edgar *et al.,* 2000; West and Walford, 2000; Kanandjembo *et al.,* 2001; Kanou *et al.,* 2007) and these parameters, as well as exposure and proximity to seagrass beds, are likely to differ between estuarine unvegetated sand and marine unvegetated sand environmental domains.

2.2 Factors Influencing Marine and Estuarine Habitats and Assemblages

The forces that drive the spatial and temporal variation in estuarine habitats and assemblage structure (species composition and richness, relative species abundances, trophic organisation, size structure) can be both physical (topographic complexity, light and nutrient availability, currents and wave exposure), and biological (recruitment, predation, competition, mutualism, disturbance) (McGuinness, 1990; Garcia-Charton and Perez-Ruzafa, 1999; Dixon-Bridges *et al.,* 2014). The influence and interaction between these processes lead to natural spatial and temporal heterogeneity in habitats and assemblages. This section of the review addresses the roles of both environmental variables and biological processes in shaping spatial and temporal patterns in marine and estuarine habitats and assemblages.

Deep Reef Habitat

Large-scale environmental factors including depth, aspect, salinity, turbidity and light availability interact to shape the distribution and abundance of deep reef sessile benthos on temperate rocky reefs (Roberts, 1996; Roberts *et al.,* 1998; Smith and Witman, 1999; Cleary *et al.,* 2005; Fromont *et al.,* 2006) and strongly contribute to the heterogeneous, spatially patchy distribution patterns (Worheide *et al.,* 2005). Sites of moderate and high sedimentation have high sponge biodiversity (Bell and Barnes, 2000a; Bell, 2007b), and contain sponges with increased branching complexity, which prevents sediment settlement on

sponge surfaces (Bell *et al.,* 2002). Sites of high turbulence exhibit lower species and morphological diversity than sites of either high or low (relatively consistent) flow (Wilkinson and Cheshire, 1989; Bell and Barnes, 2000a; Bell and Barnes, 2000b). Sponge-dominated deep reef assemblages at estuarine mouths exposed to high sedimentation differ from assemblages at other reefs of similar depth (Roberts *et al.,* 1998; Hooper and Kennedy, 2002; Owen 2003).

Whilst research on the relationship between sessile benthic assemblages and environmental variables in deep reef habitat in temperate NSW has focused on sponges (the dominant taxa), results from studies examining the impact of sewer plumes on ascidians and bryozoans (Roberts *et al.,* 1998) indicate that the distribution and abundance of these faunal groups are closely related to environmental variables. The distribution and abundance of ascidians in southern Spain has also been correlated to a range of environmental variables including turbidity and organic matter (Naranjo *et al.,* 1996).

Depth can be considered an environmental stress gradient, as it modifies the extent to which abiotic factors (including light, temperature, water movement and sedimentation), influence sessile benthic assemblages (Garrabou *et al.,* 2002). Sponge species richness and the abundance of upright species increase with depth (Wilkinson and Cheshire, 1989; Roberts and Davis, 1996; Bell and Barnes, 2000b; Ginn *et al.,* 2000). Morphological diversity (Kaandorp, 1999) and taxonomic richness (Bell and Barnes, 2000b; Roberts, 2000) of sessile organisms is greatest on sheltered reefs, and highest cover is present on exposed reefs, consistent with greater turbulence at exposed locations. Depth and spatial heterogeneity of substrate type has also been highlighted as an important variable for sponge assemblages in deeper (>100 m) reefs in temperate Australia (Schlacher *et al.,* 2007).

The phototropic sponge *Cymastella concentrica* is one of the dominant species that occurs in shallow (20-50 m) deep reef habitat in temperate NSW. A study of processes influencing the abundance and reproductive ability of *C. concetrica* highlights the important role that environmental variables can have in influencing sessile benthic assemblages. The cover of *C. concentrica* declines in response to the discharge of sewer effluent (Roberts *et al.,* 1998). Experimental manipulation of shading, siltation, nutrients and salinity on the cover of *C. concentrica* found that shading and siltation caused a decline in growth, reproductive status and symbiotic algae (Roberts *et al.,* 2006b). A decrease in salinity also caused a decline in growth, reproductive status and symbiotic algae (Roberts *et al.,* 2006b).

Biological processes also contribute to spatial patterns of sessile benthic assemblages. Reproductive output, larval behaviour and recruitment influence spatial patterns of sponges (Uriz *et al.,* 1998). Once established, biological processes including competition (Keough, 1999), mutualism (Abdo *et al.,* 2008) and predation by the grazing sea urchin *Centrostephanus rodgersii* (Ayling, 1981; Wright *et al.,* 1997) continue to influence and shape sponge-dominated deep reef assemblages on temperate subtidal reefs.

At a broad-scale, fish assemblages in rocky reef habitat in temperate Australia differ in species composition between reef type (Williams and Bax, 2001; Harman *et al.,* 2003; Smith *et al.,* 2008), depth (Connoll and Lincoln-Smith, 1999; Williams and Bax, 2001; Travers *et al.,* 2006; Lindfield, 2007; Chatfield *et al.,* 2010; Malcolm *et al.,* 2011), headlands and offshore islands (Lindfield, 2007), distance from shore (Malcolm *et al.,* 2010), habitat type (Curley *et al.,* 2002; Chatfield *et al.,* 2010), exposed and sheltered sites and proximity to seagrass beds (Valesini *et al.,* 2004). Large-scale spatial patterns of fish assemblages in NSW vary with latitude and are highly variable at the site scale (Malcolm *et al.,* 2007). Depth and distance from shore have been highlighted as strong influences on rocky reef fishes in subtropical NSW, with distinct assemblages occurring in shallow (< 25 m), intermediate (25-50 m) and deep (> 50 m) reefs (Malcolm *et al.,* 2011), and inshore (< 1.5 km), mid-shelf (1.5-6 km) and offshore (> 6 km) reefs (Malcolm *et al.,* 2010). Furthermore, Malcolm *et al.* (2010) found species richness of reef fishes increased with increasing distance from shore. Fish assemblages also undergo consistent cyclic, seasonal changes, related to changes in temperature and salinity (Hydnes *et al.,* 1999).

At a smaller scale, habitat topographic complexity is a strong determinant of fish assemblage structure, with enhanced protection from predators considered one of the main benefits (Travers and Potter, 2002; Ruso and Bayle-Sempere, 2006; Airoldi *et al.,* 2008; Hunter and Sayer, 2009; Ordines and Massuti, 2009). Habitat topographic complexity is defined by one or more physical habitat variables including rugosity, vertical relief, reef type, topographic position and aspect (Wilson *et al.,* 2007). Smith *et al.* (2008) found reef type was a key predictor of patterns of diversity and abundance for rocky reef fish on the NSW north coast. There is little further information available regarding the importance of habitat topographic complexity or context for rocky reef fishes in temperate Australia, apart from Tuya *et al.* (2009) who correlated an increase in labrid fishes with increase in small topographic elements across temperate reefs in south-western Australia. However, results from studies on

rocky reef fishes in the Mediterranean indicate that habitat topographic complexity is likely to be an important variable structuring fish assemblages abundances.

At a large scale, bottom type and depth influence rocky reef fish assemblages in shallow-water Mediterranean rocky reef fishes (Tuneai *et al.,* 2006). At a smaller scale, habitat structure drives a large part of spatial variability in the distribution, species richness, biomass and abundance of Mediterranean rocky reef fishes, with higher habitat topographic complexity correlated to higher number of fish species and greater abundances (Garcia-Charton and Perez-Ruzafa, 2001; Garcia-Charton *et al.,* 2004; Ribeiro *et al.,* 2005). Particulate organic consumers (e.g. Muglidae) are more abundant at exposed rocky reef sites, whilst Labridae and Serranidae are more common at sheltered locations (Pais *et al.,* 2007). Direct effects, such as wave exposure, can affect the distribution patterns of rocky reef fish, depending on their swimming ability, while indirect effects, including changes in benthic cover (especially macroalgae), caused by wave action, also impact fish assemblages (Pais *et al.,* 2007).

Subtidal Unvegetated Habitat

There has been less research into the role that environmental variables and biological processes have in shaping subtidal unvegetated unconsolidated fish assemblages in temperate Australia. Depth (Gray and Otway, 1994) has been shown to be an important large-scale environmental factor that influences deep (> 30 m) offshore fish assemblages; however this has not been tested in shallower near shore habitats. Exposure (Yona, 2008) has been shown to be an important environmental factor that influences fish assemblages on the NSW Central Coast; however the generality of this result has not been tested in other regions. Studies from overseas also suggest that temperature (Clark *et al.,* 1996a; Suda *et al.,* 2002; Wilbur *et al.,* 2003; White and Potter, 2004), salinity (Pessanha and Araujo, 2003) and turbidity (Clark *et al.,* 1996b) are also important factors.

Estuarine Habitats and Assemblages

Estuarine faunal assemblages are distributed along gradients of diversity that reflect the scales of influence of environmental variables (Edgar and Barrett, 2002). Species richness and abundance of benthic macroinvertebrates and fishes in Tasmanian estuaries are related to geographical and environmental variables, including the presence of an entrance bar, salinity, seagrass biomass and tidal range (Edgar *et al.,* 1999; Edgar *et al.,* 2000). Estuarine plant and

animal assemblages are often described in terms of salinity, because this is the factor usually considered to most affect the distribution of species (Edgar, 2001). In addition to salinity, the abundance and species composition of benthic macroinvertebrates in temperate Australian estuaries are also influenced by sediment particle size and temperature (Coull, 1999; Hirst, 2004; Currie and Small 2005, Dixon-Bridges *et al.,* 2014). Studies in the USA (Hyland *et al.,* 2006), South Africa (Teske and Wooldridge, 2001) and Portugal (Rodrigues *et al.,* 2006) confirm the importance that grain size has in structuring estuarine benthic macrofaunal assemblages. There is a strong relationship between sediment type and benthic faunal assemblages in the Tropical Eastern Pacific, providing useful information to help inform the designation of marine protected areas (MPAs) (Mair *et al.,* 2009).

Salinity, temperature and turbidity are key environmental factors structuring temperate Australian estuarine fish assemblage species richness, abundance and biomass (Loneragan *et al.,* 1987; West and Walford, 2000; Kanandjembo *et al.,* 2001; Kanou *et al.,* 2007, Morton and Gladstone, 2014). These environmental influences vary seasonally, influencing the abundance and structure of fish assemblages (West and Walford, 2000). Temperature is particularly important for the growth rate of several species of juvenile fishes utilising seagrass beds as post-settlement habitat (Smith and Sinerchia, 2004). The abundance and structure of estuarine fish assemblages in England (Attrill and Power, 2004), South Africa (Childs *et al.,* 2008) and Portugal (Pombo *et al.,* 2005) are also strongly correlated with temperature. At a smaller scale, wave action (physical disturbance) significantly increases the abundance of some post-larval and planktonic fish species, and may facilitate secondary planktonic dispersal in some species (Moran *et al.,* 2003). Freshwater flows can have a great impact on physical and biological aspects of estuaries. Changes to freshwater input affect habitats and organisms, including mortality, movement of organisms and changes in growth and development (Gillanders and Kingsford, 2002).

Biological processes also influence the distribution and abundance of estuarine fish assemblages. For example, the distribution and abundance of prey is a significant determinant in patterns of habitat use and abundance of fishes in estuarine habitats in temperate Australia (Jenkins and Hamer, 2001). Fish and decapod abundance and biomass closely correspond to seagrass biomass and abundance of food organisms (Paperno *et al.,* 2001; Kwak and Klumpp, 2004).

2.3 The Need and Framework for Marine Protected Areas

The declining state of the world's oceans, and declining catches and/or collapse of many fisheries, has created the need for effective management of marine biodiversity and fisheries resources (National Centre for Ecological Analysis and Synthesis, 2001). MPAs have been established in many countries as a tool for habitat protection, biodiversity conservation and fisheries management (Dee Boersma and Parrish, 1999; Stelzenmuller *et al.,* 2007; Edgar *et al.,* 2014). It was estimated that in 2010, less than 1.0% of the world's sea surface was included within MPAs (Cullis-Suzuki and Pauly, 2010), with a much smaller proportion (probably <0.1 %) included within the fully protected 'no-take' zones within MPAs (Edgar, 2011). The International Union for Conservation of Nature (IUCN), backed by many ecologists and fishery scientists, recommended this area to be increased to 20-30% by 2012 in an effort to conserve fish stocks and marine biodiversity (Jones, 2006). The United Nations Convention on Biological Diversity has a Strategic Plan for Biodiversity 2011-2012 that urges party states to conserve, by 2020, 10% of their coastal and marine areas (Convention on Biological Diversity, 2010).

In Australia the goal for MPAs is the conservation of marine ecosystems and the protection of marine biodiversity (ANZECC TFMPA, 1999). These goals are recognised nationally and internationally as being best achieved through strategic regional planning that provides for the establishment and effective management of a representative system of MPAs, and the complementary sustainable management of adjoining waters (ANZECC TFMPA, 1999). Australia has a national program for the approach to design, declaration and reporting of MPAs, the National Representative System of Marine Protected Areas (NRSMPA). In 2011 the NRSMPA covered nearly 10% of Australia's marine waters (Department of Sustainability, Environment, Water, Populations and Communities (DSEWPaC), 2011). While the NRSMPA is intended to be underpinned by the 'CAR' principles of comprehensiveness, adequacy and representativeness, interpretation and implementation of these principles vary across state jurisdictions, and there is considerable concern about a lack of attention to CAR principles in the NRSMPA (Scientific Peer Review Panel for the NRSMPA, 2006). The lack of a cooperative and integrated approach to the planning and management of MPAs in Australian waters (particularly coastal shelf waters) has become a critical impediment to achieving an adequate level of conservation and effective management of representative elements of Australia's marine environment and biodiversity (DSEWPaC, 2011). A representative system of MPAs should include the complete range of environmental

gradients or habitat types, at any given scale, to maximise the protection of marine biodiversity (Banks *et al.,* 2005). The benefits of protecting representative samples of habitats include the protection of associated biological assemblages and species, a better understanding of marine systems through the establishment of long-term monitoring programs, improved non-consumptive opportunities (e.g education, tourism, research), and potential fisheries benefits (Banks *et al.,* 2005).

In NSW MPA planning has recently been revised and the NSW Marine Estate planning policy is have a healthy coast and sea, managed for the greater well-being of the community, now and into the future (NSW Marine Estate Management Authority, 2013). There are ten underpinning principles for managing the NSW Marine Estate, relating to community engagement, threat and risk assessment, values of the estate, access arrangements, precautionary principle, cost effectiveness and knowledge gaps (NSW Marine Estate Management Authority, 2013). In NSW, MPAs range from small, highly protected areas that focus on species or community protection, to large multiple-use areas that include complex linkages of ecosystems and habitats (NSW Marine Parks Authority, 2001). The NSW system of MPAs encompasses six multiple use marine parks, 12 aquatic reserves and 62 national parks and reserves with marine components. The marine parks in NSW are zoned for multiple activities, including recreational and commercial fishing, diving, boating, snorkelling and tourism (NSW Marine Park Authority, 2013).

2.4 Effects of Marine Protected Areas

Beneficial Effects of Marine Protected Areas: Fish

Research conducted within MPAs worldwide indicates substantial benefits for biodiversity conservation (Shears *et al.,* 2006; Edgar, 2011). Examples include MPAs that safeguard spawning populations of exploited threatened species, such as grouper (Sala *et al.,* 2001), MPAs that increase ecosystem heterogeneity at regional scales through addition of unfished community patches to the seascape mosaic (Edgar *et al.,* 2009), and MPAs where coral cover is maintained in the face of regional declines (McCook *et al.,* 2010; Selig and Bruno, 2010). There are clear benefits reported to using MPAs in conjunction with catch or effort control, with benefits expressed in terms of higher catch, increased catch rate and reduction of fishing effort (Russ *et al.,* 2004), increased long-term yield and recovery possibilities (Stefansson and Rosenberg, 2006). A continental-scale analysis on the effects of MPAs in Australia found that larger fish, and greater fish biomass, occurred within MPAs than at nearby fished

reference sites (Edgar and Stuart-Smith, 2009). At the scale of an individual MPA, benefits for biodiversity include maintenance of habitat diversity and species genetic variability, species recovery and enhanced population sizes (Babcock *et al.,* 1999; Edgar and Barrett, 1999; Roberts *et al.,* 2005). Increases in the abundance, size and biomass of fish within MPAs have been clearly demonstrated in a number of countries. For example, in a review of the success of MPAs, Halpern and Warner (2002) found that 63% of surveys for fish density, 90% of surveys for fish biomass, and 80% of surveys for fish size, recorded higher values inside MPAs than outside. Other examples of published meta-analyses consistently show substantial increases in fish numbers and biomass within MPAs (Claudet *et al.,* 2008; Lester *et al.,* 2009; Molloy *et al.,* 2009). Edgar *et al.* (2014) recently showed that the conservation benefits of 87 MPAs investigated worldwide increase exponentially with the accumulation of five key features: no take, well enforced, old (>10 years), large (>100 km^2), and isolated by deep water or sand. Below is a brief summary of the success of MPA for fish.

There is a lot of evidence available supporting the benefits of MPAs for fish in coral reef habitats, with benefits shown though increases in species richness and/or abundance, mean size and biomass of commercially and/or recreationally-targeted species, in Western Australia (Westera *et al.,* 2003), central Great Barrier Reef (Evans and Russ, 2004; Williamson *et al.,* 2004; McCook *et al.,* 2010), Hawaii (Friedlander *et al.,* 2003; Meyer 2007), Sulawesi (Unsworth *et al.,* 2007b), Philippines (Russ *et al.,* 2004), Egypt (Galal *et al.,* 2002), Tanzania (McClanahan *et al.,* 1999; McClanahan *et al.,* 2009; Kamukuru *et al.,* 2004;), St. Lucia, (Hawkins *et al.,* 2006), Seychelles (Jennings *et al.,* 1996), Kenya (McClanahan *et al.,* 2007; McClanahan *et al.,* 2009) and New Caledonia (Chateau and Wantiez, 2005).

In rocky reef habitats, there are examples of increases in species richness and/or abundance, egg production, mean size and biomass of commercially and/or recreationally-targeted species in southeast Australia (Edgar and Barrett, 1999; Gladstone, 2001; Pillans *et al.,* 2007; Kleczkowski *et al.,* 2008; Watson *et al.,* 2009), the Italian Adriatic Sea (Guidetti *et al.,* 2005; Michelie *et al.,* 2006), New Zealand (Willis *et al.,* 2003; Denny *et al.,* 2004), California (Paddack and Estes, 2000; Tetreault and Ambrose, 2007) and the Mediterranean Sea (Pipitone *et al.,* 2000; Jouvenel and Pollard, 2001; Lenfant *et al.,* 2003).

There are fewer published examples of the effects on MPA on estuarine fish assemblages. McKinley *et al.* (2011) found that highly protected sanctuary zones within MPAs in a

southeast Australian estuary increased the abundance of targeted fish. Ley *et al.* (2002), documented greater catch rate for commercially targeted species in MPAs in mangrove-dominated estuaries in north Queensland, and Johnson *et al.* (1999) reported greater abundance and size of estuarine fish in Florida, USA.

There is less information available for the benefits of MPA in temperate Australia than from studies overseas. MPAs in Tasmania resulted in an increase in the number of rocky reef fish species, the density of large (>325 mm length) fish, abundance and mean size of commercially targeted fish (Edgar and Barrett, 1999). Gladstone (2001) recorded greater species richness, abundance and mean size of commercially and/or recreationally targeted fishes within an MPA on the NSW Central Coast. Kleczkowski *et al.* (2008) reported significantly higher abundance and biomass of commercially targeted and non-target species in Western Australia. Watson *et al.* (2009) documented increased size-structure of target and some non-target species of warm temperate and tropical reef fishes in Western Australia.

The size of MPAs is important for fish conservation, with small MPA having limited value (Parnell *et al.,* 2005; Perez-Ruzafa *et al.,* 2008). Fishes with large home ranges, or fishes undertaking seasonal migrations for spawning, require large reserves (Meyer *et al.,* 2007; Martell *et al.,* 2000). An analysis of 58 datasets from 19 European marine reserves showed that increasing the size of no-take zones increased the density of commercial fishes within the reserve compared to outside (Claudet *et al.,* 2008). In Tasmania, the largest MPAs are the most effective at achieving species conservation and resource enhancement (Edgar and Barrett, 1999). Changes in species richness of fishes, invertebrates and plants were detected in a reserve ~ 7 km long, but the effects of protection were not statistically detected in reserves with coastlines < 2 km long, despite trends observed for increasing densities of large fishes and lobster, and increases in the mean size of lobster, abalone and exploited fishes (Edgar and Barrett, 1999). For mobile fish species, MPAs can only be effective if the species has small movement rates, high fecundity relative to fishing rates or large habitat sizes (Malvadkar and Hastings, 2008).

The effects of MPAs can vary with depth and increasing distance from the MPA boundary, reflecting patterns of fishing effort (Ashworth and Ormond, 2005). Studies have recorded the highest density and biomass of commercially targeted fish in the centre of an MPA and declining towards the boundaries of the MPA in Tasmania (Willis *et al.,* 2003) and the Philippines (Russ *et al.,* 2004), suggesting that species become increasingly vulnerable to

fishing towards the boundary. Furthermore, Stuart-Smith *et al.* (2008) linked spatial patterns in exploited fish species in Tasmania to distance from boat ramps, and concluded that greater fishing impacts occur at more accessible sites. The length of time since MPA declaration also impacts on its success, with positive effects on commercial fish species and species richness linked to the time elapsed since the establishment of MPAs in Europe (Claudet *et al.,* 2008).

Benefits of an MPA for fishes may also include protection of spawning sites, enhancement of spawning biomass and conservation of a proportion of the population, resulting in spillover effects, and increasing fish stocks in adjacent fished areas (Ashworth and Ormond, 2005; Perez-Ruzafa *et al.,* 2008; Harrison *et al.,* 2012). Patterns of spillover are strongly influenced by physical habitat barriers, topographic features such as channels, with MPAs that are physically connected by contiguous reef structures likely to provide more spillover to adjacent fished sites than those separated by habitat barriers (Tupper, 2007). Increased catches and/or increased catch per unit effort (CPUE) have been reported in areas adjacent to MPAs (McClanahan and Kaundra- Arara, 1996; MacClanahan and Mangi, 2000; Galal *et al.,* 2002; Domeier, 2004), suggesting export of adults and perhaps larvae from reserves to adjacent fisheries (MacClanahan and Mangi, 2000). In New Zealand, mean size and survivorship of blue cod (*Parapercis colias*) is greater within MPAs (Cole *et al.,* 2000), and a tagging study indicated that this species has limited dispersal, grows to larger sizes in MPAs, and via spillover becomes available to fishers in adjacent areas of contiguous coast (Cole *et al.,* 2000).

There is evidence that partial protection of fishery resources is not an effective conservation tool. Fish assemblages, density, length and biomass of target species in a Mediterranean MPA did not differ between partially protected and unprotected areas (Di Franco *et al.,* 2009). Williams *et al.* (2006) investigated the effects of rotational closures of an MPA on coral reef fishes in Hawaii, and found that whilst fish biomass tended to increase during the 1 to 2 year closure periods, the scale of these increases was insufficient to compensate for the declines during open periods. The net effect was that total fish biomass declined by about two-thirds over 24 years, and large (> 40 cm) commercially targeted fish disappeared (Williams *et al.,* 2006). McClanahan *et al.* (2006) documented increased fish stocks and maintenance of ecological diversity within partially-protected MPAs when compared to fished zones. However when compared to permanently closed sanctuary areas, the partially-protected MPA had lower diversity, did not maintain diversity of fish and coral assemblages, and had lower

predation rates on sea urchins and hence lower herbivory rates which resulted in higher cover of algae.

Beneficial Effects of Marine Protected Areas: Invertebrates

There is less information available on the effects of MPAs for invertebrates than fish. Many MPAs that involve conservation of invertebrates are established primarily for the conservation of fish, and the conservation of commercially important invertebrates (e.g. shellfish, holothurians, lobsters) is an added benefit. A study in Tasmania found that the mean size and abundance of the rock lobster *Janus edwardsii* increased within a marine reserve when compared to fished reference sites (Barrett *et al.,* 2009). In Egypt, MPAs have resulted in significantly higher abundance, and significantly greater mean size, of targeted molluscs (Ashworth *et al.,* 2004). In an example from the USA, MPAs have enhanced the medium and large size classes of an exploited sea urchin population (Tuya *et al.,* 2000). In South Africa, populations of a targeted mollusc in a protected area were significantly larger, occurred at greater densities, and had higher biomass, survivorship and reproductive output than populations in unprotected areas (Branch and Odendaal, 2003). Lincoln Smith *et al.* (2006) documented an increase in abundance of some of the most valuable and heavily exploited Solomon Island invertebrate species (holothurians, shellfish) in protected areas. However, it is acknowledged that due to the less mobile or sedentary nature of the targeted invertebrates, there can be little or no spill over of adults from the no-take zones into fished areas, and any benefit to the mollusc fishery largely depends on greater larval production and export from the no-take zones (Ashworth *et al.,* 2004).

There is little published information available on the benefits of MPA for invertebrates in temperate rocky reefs in Australia, apart from Alexander and Gladstone (2013) who documented significantly larger commercially targeted rocky shore invertebrates within a protected area, and Barrett *et al.* (2009) who documented increased biomass of the commercially targeted lobster *Janus edwardsii* inside a Tasmanian MPA. Surveys examining the recovery of *J. edwardsii* in rocky reef habitat in New Zealand found that the abundance, size, biomass and reproductive output of this species was greater inside an MPA when compared to fished areas (Cole *et al.,* 1990; Kelly *et al.,* 2000). Examination of temporal patters based on data from four MPAs of differing ages indicated that for each year of protection, the mean size, biomass and density of the lobster population grew (Kelly *et al.,* 2000). Recent further survey work on long-term patterns of *J. edwardsii* provide an

unequivocal example of the recovery of lobster populations in a no-take MPA, and also clearly demonstrated that allowing recreational fishing (partially protecting the species) has little benefit to the species (Shears *et al.,* 2006).

The size of MPAs is important for invertebrate conservation. Edgar and Barrett (1999) documented an increased number of invertebrate species, increased abundance of commercially targeted abalone and lobster, increased mean size of abalone and biomass of lobster within a large Tasmanian MPA (~7 km coastline length), but not within smaller MPAs covering < 2 km coastline.

Indirect Effects, Cascade Effects and Tropic Interactions of Marine Protected Areas

Aside from the direct influence that protection can have on species, MPAs can have indirect effects, cascading effects, and effects on trophic interactions. Indirect effects of MPAs can benefit non-target fish species, entire assemblages, ecological processes and even entire ecosystems (Agardy, 2000). Sasal *et al.* (1996) investigated indirect benefits of an MPA on a goby population, a cryptic species of low economic importance, and found the population showed an indirect reserve effect, with higher mean length, longevity, biomass and density within the MPA (Sasal *et al.,* 1996). In contrast, Willis and Anderson (2003) and Harasti *et al.* (2014) demonstrated that sites within MPAs contained lower mean densities of cryptic fishes than sites outside MPAs, a trend attributed by the authors to the increased effects of predators within the MPA.

Fishing of shallow coastal reefs impacts the structure of marine assemblages by removing predators, grazers, and/or algae to support commercial industries (Edgar and Barrett 1999; Ceccherelli *et al.,* 2006). Recent long-term monitoring studies indicate that ecological changes to non-harvested species through secondary and tertiary trophic effects continue to develop over decades in well-protected MPAs (Edgar and Stuart-Smith, 2009; Babcock *et al.,* 2010). In temperate Australia, Edgar and Barrett (1999) found indirect effects of MPAs on shallow coastal reefs within Tasmanian MPAs. Accompanying an increase in abundance of commercially targeted fish, abalone and lobster, and species richness of fish, invertebrates and algae, was a change in the predominant plant species from *Cystophora retroflexa* to *Ecklonia radiata,* thought to be an interacting result of fishing protection and hydrological processes (Edgar and Barrett, 1999).

Trophic cascades are predatory interactions involving three or more trophic groups (Menge, 1995). An example of the key role that predators have in shaping the structure of subtidal rocky reef habitats is from New Zealand MPAs, where the abundance of sea urchin predators such as lobster (Kelly *et al.,* 2000), cod and snapper (Willis *et al.,* 2000), are significantly greater inside MPAs (Babcock *et al.,* 1999). This has led to a decline in sea urchins within MPAs due to increased predation from predators (Barrett *et al.,* 2009), which has then led to an associated change of rocky reef habitat from urchin grazed barrens habitat to kelp over a 20-year period (Babcock *et al.,* 1999; Shears and Babcock 2002; Shears and Babcock, 2003). In the Leigh Marine Reserve this large-scale habitat change has been mapped via acoustically positioned radio transects (Parsons *et al.,* 2004). The most obvious changes to subtidal reef habitats since protection from fishing have been the total disappearance of sea urchin barrens across all depths, and the recovery of kelp forest in water < 8 m, caused by a trophic cascade related to predator recovery (Parsons *et al.,* 2004). Further work on trophic cascades within New Zealand MPAs involving infaunal bivalves and their predators (snapper, lobster), has correlated the high density of upper-level predators within MPAs to high predation rates of infaunal bivalves (Langlois *et al.,* 2005; 2006). Long-term changes in benthic communities in New Zealand MPAs and the stability of differences between MPA and non-MPA sites over time are consistent with gradual declines of urchin densities due to increased predation on urchins, thus providing further evidence for a trophic cascade in this system (Shears and Babcock, 2003). Greater abundance of predatory fishes resulting in lower abundance of prey inside MPAs has been established by the use of prey tethering experiments (Diaz *et al.,* 2005). Similar cascading effects have been documented in shallow rocky reef habitats in Italy (Ceccherelli *et al.,* 2006), Galapagos Islands (Sonnenholzner *et al.,* 2007), eastern Atlantic (Tuya *et al.,* 2004), Canary Islands (Clemente *et al.,* 2009) and the Mediterranean Sea (Micheli *et al.,* 2005). In the example from the Mediterranean the structure of subtidal habitat (i.e. the extent of macroalgae and barrens habitat) within an MPA changed following protection from fishing, with decreased urchins and increased barrens areas inside the MPA, where large predatory fish are more abundant. More cascade effects are likely to be found in the soft-substratum habitats that are also crucial to many fisheries (Pinnegar *et al.,* 2000).

Trophic cascades are complex and not always so clearly defined. For example, in the northwestern Mediterranean, protection from fishing within MPAs was thought to return the former predation levels on sea urchins and to have an important indirect effect on the ecosystem through trophic cascades (Sala *et al.,* 1998). However, sea urchins exhibited

striking short-term fluctuations in abundance, with patterns of lower sea urchin density relative to unprotected areas not maintained over time (Sala *et al.,* 1999). This is an important lesson in the importance of long-term assessments and the risk of misinterpretation of large-scale temporal patterns. Furthermore, some studies report no trophic cascade effects. Again in the Mediterranean, abundance and biomass of invertebrate-feeding fish and sea urchins, and cover of upright algae, all increased within MPAs (Cardona *et al.,* 2007). Changes in the abundance of fish did not cascade to sea urchins, and changes in the abundance of sea urchins did not affect upright algae (Cardona *et al.,* 2007).

MPAs can influence different fish trophic groups in different ways. Fishing restrictions are expected to result in an increase in the abundance of targeted species; however changes to fishes that are not targeted depend on their role in the ecosystem and their relationship with the targeted species (Watson *et al.,* 2007). The removal of abundant targeted species from an ecosystem by fishing can indirectly impact untargeted species, and alter the trophic structure of fish assemblages (Watson *et al.,* 2007). Ashworth and Ormond (2005) found a significant increase in commercially targeted fish within an MPA in Egypt, and interestingly also found the abundance of two herbivorous fish families was significantly less within the MPA when compared to reference sites, an effect thought most likely due to reduced competition or predation from commercially targeted species in reference areas. Watson *et al.* (2007) also documented an increase in commercially-targeted fish within an MPA in Western Australia. However fish species not commercially targeted showed mixed results, with some species more abundant within the MPA, and some species less abundant, a result thought to be related to the trophic relationship of the non-target fish to the commercially targeted species (Watson *et al.,* 2007).

Mixed-results of Marine Protected Areas

Despite many examples of successful MPA implementation, MPA effects may be diverse in direction and magnitude (Claudet *et al.,* 2006). Habitat quality and heterogeneity, intensity of exploitation around an MPA, MPA size, species' dispersal patterns, natural spatial-temporal variations in faunal populations, proximity to other MPAs, species' life histories, history of exploitation, dispersal characteristics and boundary porosity all affect the success of MPAs (Roberts, 2000; Russell *et al.,* 2005; Carson and Hentschel, 2006; Ceccherelli *et al.,* 2006; Tuya *et al.,* 2006; Stelzenmuller *et al.,* 2007). Examples of MPAs that fail to increase the abundance of exploited species due to low quality habitats (Fernandes and Castilla, 2000;

Edgar *et al.,* 2004), or failure to include recruitment areas (Trexler and Travis, 2000) have been documented. Unintended consequences of MPAs that affected other fisheries include shifting fishing effort, which increased the vulnerability of additional fish populations (Coleman *et al.,* 2004).

Examination of the effects of partial marine reserves (areas closed to commercial fishing but open to recreational fishing) indicates that partial closures are ineffective as conservation tools. The abundance and size of commercially targeted fish within an area closed to commercial fishing but open to most forms of recreational fishing in New Zealand showed no difference between an area open to all fishing, indicating that fishing pressure within the partial marine reserve is at least as high as at other fished sites (Denny and Babcock, 2004).

Behavioural plasticity can also act as a barrier to generalisation of some ecological models (Crowe and Underwood, 1999), with fish behaviour able to affect reserve function. MPAs can protect fish species only if individuals restrict their movements to a localised home range during at least part of their lifecycle (Krammer and Chapman, 1999). Fish home ranges increase with body size. In small MPAs, a significant proportion of fish can be exposed to fishing mortality if their home ranges include non-MPA areas (Krammer and Chapman, 1999).

Spatial variability of indicators of success of protection measures (e.g. abundance, diversity) is very high, which can make it difficult to separate reserve effects from natural heterogeneity (Garcia-Charton *et al.,* 2004). The hierarchical patchiness of habitats imposes constraints when undertaking a study of ecological effects of protection in MPAs (Garcia-Charton and Perez-Ruzafa, 1999). The diversity and complexity of responses of species and assemblages to the effects of protection needs to be integrated into the design of monitoring programs for MPAs to allow for better management (Garcia-Charton and Perez-Ruzafa, 1999). Monitoring programs can also face problems identifying independent control sites because the spatial extent of fisheries export is unknown (Halpern *et al.,* 2004).

Another source of poor results for MPAs is noncompliance. The socio-economic aspects of conservation ultimately determine a MPA's success or failure (Stewart and Possingham, 2005; Voyer *et al.,* 2012; Voyer *et al.,* 2015). Studies examining the effects of MPAs rarely consider the potential for noncompliance, however this can have a large effect on the success of MPAs (Kritzer, 2004). Violation of MPAs typically occurs near boundaries, and if the MPAs are small, or dispersal largely localised, this can have a negative impact on the species

occurring within the MPA (Kritzer, 2004). Examples from the Adriatic Sea (Lipej *et al.,* 2003), Great Barrier Reef (McCook *et al.,* 2010) and Seychelles (Jennings *et al.,* 1996) showed that species composition and richness were comparable at protected and unprotected sites, a result attributed to a combination of noncompliance and partial protection.

The ability to generalise about the effects of MPAs has also been hampered by the use of poorly designed surveys with inadequate levels of replication or lack of baseline data (Garcia-Charton *et al.,* 2000; Halpern and Warner, 2002). Baseline information is critically important, and the use of an appropriate experimental design with adequate spatial and temporal replication (for example, the use of multiple before-after, control-impact data), is essential in understanding patterns of biodiversity (Underwood, 1992; Underwood *et al.,* 2000). The use of only a single protected and non-protected reference location can lead to the possibility that the observed differences were due to variability from location to location rather than protection effects (Kelly *et al.,* 2000). There are limited studies examining the effects of MPAs that include data from more than one protected area. The use of multiple protected areas can have a significant impact on conclusions drawn from the study. For example, MacDiarmid and Breen (1993) found that the lobster *Janus edwardsii* occurred at higher densities within one MPA, and lower densities at another MPA, than at unprotected areas. Investigations into habitat types within the two MPAs indicated that suitable habitat for the species was absent at the MPA site with low species density (MacDiarmid and Breen, 2003), highlighting the need for multiple MPA and unprotected areas to be used in sampling designs that aim to assess the impact of protection and the need for sampling designs to be well designed (for example sampling within the same habitat).

2.5 Selection and Design of Marine Protected Areas

On a global scale, MPAs can only be effective if they are substantially representative of all biogeographic zones, single reserves are networked within biogeographic zones, and the total amount of area reserved per zone is 20% or greater (Dee Boersma and Parrish, 1999). However, choosing the best areas for establishing MPAs is not simple, the process being confounded by competing demands for other resources (e.g. fisheries, minerals, oil), geopolitical issues, poor knowledge on species' distributions and the ecological processes that maintain genes, populations, species and ecosystems (Ward *et al.,* 1999). Roberts *et al.* (2003) described a framework to examine MPA options with respect to the distribution and sustainability of biodiversity and fisheries values, threats and ecosystem linkages.

Prerequisite criteria necessary for this framework to ensure the protection of biodiversity and productivity within a network of MPAs are the delineation of biogeographic regions and representation of habitat diversity and heterogeneity (Roberts *et al.,* 2003).

The location and site selection of MPAs is critically important. Monaco *et al.* (2007) undertook surveys of habitat and fishes inside and outside the US Virgin Islands Coral Reef National Monument, and found that areas outside the MPA had significantly more hard corals, greater habitat topographic complexity, and greater richness, abundance, and biomass of reef fishes than areas within the MPA. The administrative process used to delineate the boundaries of the MPA did not include a robust ecological characterisation of the area (Monaco *et al.,* 2007). Monaco *et al.* (2007) predicted that because of the reduced habitat topographic complexity within the MPA, the enhancement of the marine ecosystem may not be fully realised, or increases in economically important reef fishes may take longer to detect. History of disturbance is also important with coral reef MPAs. Studies on the Great Barrier Reef indicate that natural disturbance has a greater impact on benthic cover of hard corals than protection from fishing (Myers and Ambrose, 2009).

A necessary component of implementing a successful MPA is the quantification of the biological resources that fall under its protection (Kendall *et al.,* 2004). Without such an initial assessment, the future effects of the MPA on the local habitat and biotic community cannot be quantified and will remain the subject of debate (Kendall *et al.,* 2004). For example, in the US Virgin Islands, fish species richness, diversity and density were greater in hard-bottom habitats than sand and seagrass habitats, and fish assemblages were different between habitats (Kendall *et al.,* 2004). The results of assessments like this are useful for guiding selection of MPAs. In temperate Australia, the greatest variation in fish assemblages occurs at scales 2-6 km along-shore, with the most predictable differences in assemblages found among reef habitats (barrens, kelp forest and sponge-dominated deep reef), and among depths (Curley *et al.,* 2002). Adequate conservation of temperate reef fishes should ideally incorporate all available habitats over the entire depth range at which they occur. To adequately conserve reef fishes in temperate Australia, MPAs may need to be larger than 2-6 km, or there needs to be multiple MPAs that have been specifically located to include these features, as representation of habitats vary at scales of km to 10s of km along the shore (Curley *et al.,* 2002).

MPA planning can also include conservation requirements for specific species or assemblages. The design of MPAs for fishes involves examination of habitat preferences, short-term and long-term movement patters, location of spawning grounds and connections between habitats (Griffiths and Wilke, 2002). In NSW, conservation of fisheries resources is particularly important. Gladstone (2007) examined the conservation requirements for rocky reef fish in temperate NSW, by undertaking biodiversity surveys for fish and comparing the outcomes of this survey to alternative procedures for selecting MPAs. A high number of locations (92%) were required for representation of all species, and Gladstone (2007) concluded that MPAs selected without information on intra-habitat variation in species assemblages would be unrepresentative. Known correlations for spatial variability of fish assemblages such as wave exposure and depth can be applied to MPA design (Curley *et al.,* 2002). For example, Malcolm *et al.* (2010) found that for subtropical fish assemblages in NSW, distance-from-shore was strongly correlated with patterns of reef fish assemblages, and recommended that distance-from-shore be incorporated into existing habitat classification schemes to improve the ability of MPA to represent biological diversity. The upper range of currently promoted targets for MPA (30%) should be regarded as a minimum for biodiversity conservation of rocky reef fishes in temperate NSW, and MPAs selected for biodiversity conservation may not adequately protect fisheries-related species (Gladstone, 2007).

Ecological processes (such as reproduction, recruitment, dispersal, species interactions and disturbance) as well as evolutionary mechanisms underlie patterns of biodiversity, and consequently ecological processes need to be integrated into marine reserve design to ensure persistence of target populations, species and assemblages (Leslie *et al.,* 2005; Frid *et al.,* 2008). For example, the identification and protection of reproductive hotspots is a high priority for the conservation of marine biodiversity, and are more preferable locations for the establishment of MPAs as they are more likely to act as sources for recruitment and provide offspring for unprotected sites in the region (Benkendorff and Davis, 2004; Leslie *et al.,* 2005). The results from studies in other countries indicates great potential for the incorporation of information on ecological processes in MPA planning, coupled with information regarding species richness 'hotspots' that can be related to ecological process such as upwelling zones (Edgar and Barrett, 2010).

One study linked inputs from large-scale oceanographic processes (e.g. nutrient cycling, particulates and propagules) with marine assemblage structure and dynamics. Menge *et al.*

(2003) established that larval transport and recruitment on rocky shores in New Zealand were driven by coastal oceanography. Propagule delivery determined the abundance of prey, which drove how quickly space was colonised and probably how intensely organisms competed for space (Menge *et al.,* 2003). Propagule delivery rates influenced growth of sessile invertebrates, which in turn influenced assemblage structure, prey availability and ultimately the growth and survival of prey (Menge *et al.,* 2003). Leslie *et al.* (2005) established links between greater larval production of an ecologically important barnacle, with higher primary productivity in the adjacent nearshore ocean. The importance of spatial heterogeneity in ecological processes in the marine environment was highlighted, and provides a basis for evaluating the relative contributions of different sites when designing marine reserves (Leslie *et al.,* 2005).

Some MPAs aim to protect areas of high reproductive output by conserving key sources of larval production that may replenish non-protected areas through larval export (Sanford and Menge, 2007). However, identifying sources of larval production is difficult due to variation in the quality of reproductive output (Sanford and Menge, 2007). Sanford and Menge (2007) tested the spatial and temporal consistency of a source population of a sea star in California, and found that whilst the location's source populations were spatially consistent, identifying sources of larval production may be more complex than just targeting areas of high quality habitat and strong bottom-up influences. Predicting patters of reproductive output may require a more detailed understanding of the causes of spatial variation in relation to maintenance, growth and reproduction (Sanford and Menge, 2007). The principles of comprehensiveness, adequacy and representativeness used in the NRSMPA framework do not capture directly the need to conserve ecological processes.

MPAs have historically been designed either on an *ad hoc* basis or opportunistically due to limitations in time, resources, taxonomy, biological distributions or socio-economic influences (Pressey, 1994; Winberg *et al.,* 2007). This approach can be expensive and lead to ineffective or inadequate conservation (Pressey, 1995; Stewart *et al.,* 2003), as the establishment of an MPA without detailed biodiversity studies can lead to exclusion of species before understanding their role in ecology (Giangrande, 2003). The *ad hoc* approach to selecting MPAs appears to favour those habitats that are at least risk because of a lower demand for commercial extraction, while habitats that are threatened continue to be over-exploited (Pressey *et al.,* 2000). Many MPAs have been established in the absence of detailed information on biodiversity and ecological processes, or in response to local pressures, and

may be inappropriately placed, inefficient and inadequate for conservation goals (DeVantier *et al.,* 1998; Alexander and Gladstone, 2013). In particular, precise placement of an MPA may be necessary to encompass migration patterns and nursery areas (Roberts, 2000).

In response to the problems of *ad hoc* selection, the science of MPA design and management has been examined globally in detail, and advances in planning policies have been adopted by many Governments. The conservation value of sites for a proposed representative system of MPAs is maximised by undertaking systematic quantitative surveys at an appropriate scale for management (Edgar *et al.,* 1996). Systematic approaches to selecting MPAs avoid the inefficiencies that arise from inappropriate site selection or application of generalised targets (Margules *et al.,* 2002; Gladstone, 2007). Relevant selection criteria include habitat availability, degree of connectivity, productivity, presence of spawning aggregations, and density of exploitable species (Roberts *et al.,* 2003). For instance, it is now established that networks of MPAs provide greater protection for marine ecosystems than a single reserve, and a stable platform for the long-term persistence of marine ecosystems (National Centre for Ecological Analysis and Synthesis, 2001). An example of an advance in MPA planning in Australia is the marine park zoning for the Great Barrier Reef, which implemented many of the theoretical design principles discussed in the literature (Fernandes *et al.,* 2005). These include 20% protection per bioregion, minimum levels of protection for all known habitats and special or unique features, and minimum sizes for no-take areas of at least 10 or 20 km across at the smallest diameter (Fernandes *et al.,* 2005). Overall, more than 33% of the Great Barrier Reef was zoned no-take areas (increased from 4.5 % previously).

Australia has developed a hierarchical bioregionalisation of its marine environment at large (state) and regional (bioregion) scales. The bioregionalisation was based on the limits of distribution of a range of biota (primarily fishes) in conjunction with physical environment variables (IMCRA, 1998). However, biological assemblages exist and are exploited at a much more local scale, which are cumulative at the population level in marine fisheries, and therefore effective spatial protection of marine biodiversity needs to consider ecological patterns and conservation requirements at both local and regional scales (Williams and Bax, 2001).

In Australia, the current practice of MPA planning is based on comprehensiveness, adequacy and representativeness, and MPAs must contain multiple representative samples of all ecosystems, habitats and associated taxa within bioregions (ANZECC TFMPA, 1998). The

primary goal of the national representative system of MPAs is to establish and manage a comprehensive, adequate and representative system of MPAs to contribute to the long-term ecological viability of marine and estuarine systems, maintain ecological processes and systems, and protect Australia's biological diversity at all levels (ANZECC TFMPA, 1999).

NSW previously adopted the ANZECC (1999) 'Guidelines for Establishing the National Representative System of Marine Protected Areas' and IMCRA bioregions (IMCRA Technical Group, 1998) as the basis for establishing and managing the NSW Representative System of Marine Protected Areas (NSW Marine Parks Authority, 2001) (note current management of marine parks under the NSW Marine Estate no longer encompasses these principles). Bioregions were defined based on physical factors (Pollard *et al.,* 1998), and each bioregion would, in most instances, be represented by at least one large marine park declared under the *Marine Parks Act* 1997, and be representative of the ecosystems and habitats found in the bioregion (NSW Marine Parks Authority, 2001). In NSW MPA planning has recently been revised and the NSW Marine Estate planning policy is have a healthy coast and sea, managed for the grated well-being of the community, now and into the future (NSW Marine Estate Management Authority, 2013).

In NSW, an integrated system of MPAs is currently being developed, using marine parks, aquatic reserves, national parks and nature reserves to achieve the optimum conservation of biodiversity and habitat protection (NSW Marine Parks Authority, 2001). This is achieved through bioregional assessments that use ecological criteria to describe the conservation values of the bioregion, and site assessments, that describe site-specific conservation values in relation to habitats and species at smaller spatial scales (NSW Marine Parks Authority, 2001). The type, location and size of MPAs are guided by the nature of protection required to effectively conserve the species, habitats or ecological processes for which the site was identified (NSW Marine Parks Authority, 2001). The recent NSW Marine Parks Audit (Beeton *et al.,* 2012) recommended the current system of NSW marine parks should be maintained and to improve the management of biodiversity and threats in the identified gaps (Hawkesbury and Twofold Shelf marine bioregions) in the NSW marine park system. Other key recommendations included the establishment of the NSW Marine Estate, defined as the sea enclosed within the three-nautical-mile limit including all marine related bays, rivers under a detectable tidal influence, mangrove systems, islands, wetlands and lakes that are intermittently connected to the sea. It also includes coastal systems such as dune systems and headlands that are strongly influenced by the oceanic processes even though they are not

episodically inundated (Beeton *et al.,* 2012) The NSW Marine Parks Audit also recommended the formation of a Scientific Committee, which is independent of government agencies and established to oversee strategic research in the Marine Estate in NSW to synthesise MPA research, particularly the social impacts, of the establishment of MPAs.

2.6 The Need for, and Use of, Biodiversity Surrogates in the Selection and Design of Marine Protected Areas

The need to rapidly and accurately identify areas for protection and conservation in the marine environment is critically important (Campbell and Hewitt, 2006). Establishing a balance between adequate and appropriate survey design and practical constraints is important when selecting MPAs (Gladstone and Davis, 2003). Networks of reserves selected on the basis of complementarity and irreplaceability are more effective at representing biodiversity than an *ad hoc* approach (Margules and Pressey, 2000). However, large time and resource commitments are involved in the collection of detailed biodiversity data to undertake this procedure. The comprehensive, adequate and representativeness model of MPA design requires conservation of examples of all marine and estuarine habitats, however the distribution of habitats at a scale required for conservation planning is poorly known. Additionally, the identification of MPA sites is further complicated by incomplete taxonomy, lack of information on distribution and abundance of marine biodiversity, the patchy distribution of habitats, the coarse-scale of existing mapping and poor understanding of the role of ecological processes in the role of maintaining biodiversity (Gladstone and Alexander, 2005).

The ability to predict the distribution of biodiversity using surrogate measures enables decisions about the locations of MPAs to be made in the absence of detailed data on the distribution of species (Roberts *et al.,* 2003). Simple species-level approaches (such as identifying hotspots of species richness, or the distribution of species richness), may not be useful as the sole basis for establishing an MPA (Conroy and Noon, 1996). Research into the effects of reduced intensity of biodiversity surveys on intertidal rocky shores in southeast Australia found that a reduction in survey intensity led to increases in the size of reserve networks, the irreplaceability value of locations and the number of irreplaceable locations (Gladstone and Davis, 2003). Reduced survey intensity was therefore not considered to be a suitable alternative to detailed assessments of biodiversity. The use of surrogates to describe biodiversity (for example higher-taxon approaches, indicator groups, ecological processes,

habitat type) is a potentially useful approach that is more easily and quickly measured, and yet is still representative of species-level biodiversity.

Higher-taxon Approach

One of the aims of biodiversity conservation is the representation of species diversity (Vanderklift *et al.,* 1998). An alternative to species-level identification when undertaking biodiversity assessments and selecting MPAs is the higher-taxon approach, which is an effective surrogate of marine biodiversity (Mellin *et al.,* 2011). The use of higher taxa (i.e. genus or family-level data instead of species-level data) was examined for intertidal molluscs and rocky reef fishes in temperate NSW (Gladstone and Alexander, 2005). The study concluded that genus- and family- level data for intertidal molluscs, and genus-level data for rocky reef fishes, were suitable surrogates for species-level identification in the selection of candidate sites for MPAs (Gladstone and Alexander, 2005). Irreplaceability values of locations for species, genera and families of intertidal molluscs, and genus-level data for rocky reef fishes were highly correlated (Gladstone and Alexander, 2005). Shokri and Gladstone (2009a) found that the richness of higher taxa of macroinvertebrates, as a surrogate for species richness, was an accurate and effective method of selecting conservation reserves in an estuary in south-east Australia. Spatial patterns of richness and assemblage variation for species were significantly correlated with patterns defined using genera, family, order, class and phyla data (Shokri and Gladstone, 2009a). Goldberg *et al.* (2006) reported that genus-level data for marine macroalgae was strongly related to species-level diversity in shallow subtidal reefs in temperate Australia. Furthermore, Vanderklift *et al.* (1998) found that the use of genus-level assemblages resulted in selection of candidate MPA areas with a similar number of fish, invertebrates and plants, to those obtained by using species-level assemblages in temperate NSW. However, the spatial scales and identity of taxonomic groups may differ amongst geographic locations, and the use of higher taxa to select MPA candidate sites should be investigated at specific locations and through time prior to their use as a planning tool (Vanderklift *et al.,* 1998).

Indicator Groups

Indicator groups that effectively represent other elements of biodiversity can be used for the management and conservation of natural resources, on the assumption that the presence or abundance of a focal species, or group of species, is a means to understanding the biodiversity of the assemblage (Zacharias and Roff, 2001b). Indicator species or groups are

taxonomically and ecologically well known, are easily surveyed, and have distributions that are well documented (Gladstone, 2002). Indicator species or groups which can be related to habitat types can be spatially mapped (Zacharias and Roff, 2001b), which is a fundamental prerequisite for conservation initiatives based on representativeness (Roff and Taylor, 2000).

Most research on indicator groups has examined indicator groups for species richness and species diversity, and has focused on identifying a subset of taxa as a surrogate for total assemblage richness or diversity (Magierowski and Johnson, 2006). This spatial approach compares a range of taxonomic groups for their degree of spatial correspondence in hotspots for richness, rarity, endemism or conservation status, and has generally found low levels of correspondence (Gladstone, 2002). However, the potential value of indicator groups selected by determining the percentage of total species included in simulated MPA networks by complementarity analysis is high (Gladstone, 2002). Gladstone (2002) found that molluscs were a reliable indicator of intertidal biodiversity and areas for reservation in temperate NSW. Smith (2005) found that molluscs in subtropical NSW showed high levels of correlation with overall intertidal species richness and closely related patterns in the community data. Shokri *et al.* (2009a) found that annelids, arthropods and molluscs were each suitable as indicator groups for all estuarine macroinvertebrates when selecting conservation reserves in an estuary in temperate NSW. Shokri *et al.* (2009b) also found that synganthids (seahorses and pipefish) were a useful indicator group for all other fishes for conservation planning in estuarine seagrass beds. Malcolm and Smith (2010) found that species richness of two families of fishes, Labridae and Pomacentridae, was highly correlated with species richness of the entire reef fish assemblage in subtropical NSW. The usefulness of indicator groups as surrogates to estimate assemblage structure and the components of biodiversity in temperate Australia is further demonstrated by Goldberg *et al.* (2006) who found that dominant marine macroalgae (*Cystophora* sp., *Sargassum* sp., *Ecklonia radiata*) at offshore islands were effective at predicting species diversity across locations, depths and exposures to ocean swell.

In adopting an indicator group as surrogate, it is assumed that the relationship between the surrogates is consistent through space and time, a hypothesis tested by Magierowski and Johnson (2006) for macrofaunal assemblages inhabiting artificial kelp holdfasts. Magierowski and Johnson (2006) found that polychaetes, molluscs and echinoderms were well correlated within total familial richness for assemblages, however the strength of the correlation for molluscs and echinoderms declined through time, highlighting the need for

careful selection of indicators groups to ensure that they perform consistently across different-aged groups and are temporally consistent.

Modelling

The application of species distribution modelling is relatively rare in marine conservation planning and mostly confined to a single species or assemblages of one taxa (e.g. fishes) (Berger and Possingham, 2008). Remotely measured environmental factors have been utilised to determine the distribution of coral reef fish species on a regional scale in Papua New Guinea (Berger and Possingham, 2008). Depth and exposure, as well as depth and distance from the nearest estuary, were the most prevalent predictors of fish distributions (Berger and Possingham, 2008). Modelling occurrence data can also highlight species with specific habitat requirements, which are of greater conservation concern than more generalist species because threats affect them more severely if the threats are selectivity affecting their habitat (Berger and Possingham, 2008). Species distribution modelling using remotely determined environmental data may be an efficient method to build models for habitat-specific species and inform the design of MPAs (Berger and Possingham, 2008).

Environmental Domains

Different environmental domains support different sets of species, and may be used to represent environmental heterogeneity and therefore act as biodiversity surrogates (Margules *et al.,* 2002).

Environmental domains have been shown to be an important predictor of biodiversity if habitat is to be used as a surrogate for fish diversity in the management and conservation of demersal fish assemblages in the USA (Anderson *et al.,* 2009) and seagrass habitat types in south western Australia (Carruthers *et al.,* 2007). In temperate NSW, studies on sponge-dominated deep reef habitat indicate that species and assemblages differ between depth (Roberts and Davis, 1996) and exposure gradients (Roberts *et al.,* 2006a). Lindfield (2007) found that rocky reef fish assemblages differed between depths, and representation of reef fish biodiversity required that multiple samples of reefs that covered a range of depths at different locations. However, the influence of other environmental factors as a source of variation within this habitat has not been examined, nor has the influence of any environmental domains for most subtidal marine and estuarine habitats been examined in the context for selection and design of comprehensive, adequate and representative MPAs.

Mapping of Seabed Habitats using Autonomous Underwater Vehicles

The habitat classification and mapping needed to incorporate considerations of representativeness into MPA planning must be carried out at the same scale at which management occurs, and is essential for assessment of, and design for, representation (Stevens, 2002; Stevens and Connolly, 2004). Remote videography, in some cases linked with acoustic discrimination sensors, can provide quantitative data on real biological distributions (Kloser *et al.,* 2001; Stevens, 2002; Jordan *et al.,* 2005; Rigby *et al.,* 2010). Such data lend themselves well to robust multivariate analyses in deriving habitat maps at scales relevant to managers, and as a basis for assessing and planning for representation in MPA design (Stevens, 2002).

Mapping of seabed habitats at a range of spatial scales is being recognised as an increasingly important component of the overall research required to identify the distribution and structure of marine ecosystems, and identification of representative habitat types, and is fundamental information for the future management of marine resources (Bax and Williams, 2001; Pickrill and Todd, 2003; Roff *et al.,* 2003). In order to maximise the comprehensive, adequate and representative goals for the design of MPAs, it is important to include biological information at the largest scale practical in the planning process (Jordan *et al.,* 2005). For example, at a large scale, seabed bathymetry can produce geomorphic features maps, which can be used in conjunction with biodiversity information to derive biologically unique areas (Harris *et al.,* 2008). At the scale of an individual MPA, Jordan *et al.* (2005) used a colour echosounder, differential global positioning system and an underwater digital colour video camera to map seabed habitats in Tasmania. A hierarchical classification scheme for subtidal seabed habitats was based on abiotic or biotic structuring variables, or a combination of the two (Jordan *et al.,* 2005). Different habitat types (continuous reef, patchy reef, sand, sponge, seagrass) and seabed profiles (low, medium high profile reef, and sand hills) were identified via visual differences in the echosounder and variations in the echogram (Jordan *et al.,* 2005). Extensive transects at several hierarchical levels provided an estimate of the broad-scale spatial distribution of seabed habitats and information on the cover of dominant benthic species (Jordan *et al.,* 2005). Seabed habitat mapping has the capacity to define the boundary and size of potential MPA zones and can be used as a step in the planning and design of comprehensive, adequate and representative MPAs (Jordan *et al.,* 2005).

Surveys of sessile benthic assemblages in subtidal reefs have previously included *in situ* diver surveys (Owen, 2003) and drop cameras (Roberts *et al.,* 1994; Roberts, 1996; Roberts and Davis, 1996; Roberts, 2006a), both of which are unable to collect large amounts of field data quickly and have a limited spatial coverage. The use of Autonomous Underwater Vehicles (AUVs) to survey sessile benthic assemblages can overcome the limitations of diver-based surveys and drop cameras, as AUVs can collect large numbers of high quality images suitable for biodiversity assessment, collect additional information on physical parameters such as depth and temperature, and survey pathways can be directed and linked with GPS (Jordan *et al.,* 2005; Rigby *et al.,* 2010).

Habitat Classification Schemes

Habitat can be defined as a combination of structural, biological and environmental conditions that can be mapped (O'Hara, 2001). The classification of habitats into mappable areas allows for physical demarcation of areas that contain reasonably consistent assemblages, represent biological conditions on a map, and provide a framework for experimental and descriptive studies (Underwood *et al.,* 1991). Within the hierarchical framework for classifying biodiversity within Australia, MPA planners commonly use maps of habitat types when selecting candidate areas for conservation at the scale of individual MPAs (Zacharias and Roff, 2000; Winberg *et al.,* 2007; Last *et al.,* 2010). These habitat types are mapped on the assumption that environments that have similar biophysical properties and environmental conditions predict, or at least correlate with, patterns of biological distributions (Stevens and Connolly, 2004; Banks *et al.,* 2005). This also assumes that habitats are homogeneous in biodiversity, and therefore that any area of habitat chosen as an area for conservation will reflect the full range of biodiversity within that habitat (Winberg *et al.,* 2007).

Although consistent assemblages occur within habitats, species variability within habitats on temperate subtidal rocky reefs can be high and assemblages can grade into one another (O'Hara, 2001). Evidence of intertidal (Underwood and Chapman, 1998a; Underwood and Chapman, 1998b; Underwood and Chapman, 2000), subtidal rocky reef (Underwood *et al.,* 1991; Andrew, 1993; Roberts *et al.,* 1996; Andrew and O'Neill, 2000; Roberts *et al.,* 2006a) and seagrass (Rotherham and West, 2002; Jelbart *et al.,* 2007) habitat heterogeneity has been shown within temperate NSW. The consequences for biodiversity conservation of habitat heterogeneity were demonstrated by Branch and Odendaal (2003) who found that size,

density, survivorship, biomass and reproductive output of intertidal molluscs were greater in sheltered than exposed locations on rocky shores, and that although MPAs had been established in both sheltered and exposed locations, beneficial effects for the species were only recorded at sheltered locations. Furthermore, Winberg *et al.* (2007) reported that macrobenthic assemblages in tidal flat habitats in temperate NSW were spatially heterogeneous in terms of taxonomic turnover, abundance, richness and diversity. Patterns of heterogeneity were scale dependant, with assemblages within tidal flats differing at scales of 100s m, yet more homogeneous at the 20 m scale (Winberg *et al.,* 2007). This research showed that although tidal flats in different estuaries are compositionally similar for dominant taxa, rarer taxa and high heterogeneity in abundance should influence the choice and number of tidal flats conserved in MPAs, and conservation of the whole tidal mudflat habitat, rather than sections of the habitat, is essential to represent taxonomic diversity (Winberg *et al.,* 2007).

The increasing amount of information regarding the distribution of species in relation to habitats and physical properties improves the chance that MPAs designed on this basis would benefit the protection of representative samples of biodiversity (Banks *et al.,* 2005). In the Solitary Islands Marine Park, the habitat classification scheme has been refined so that is it closely aligned with biological patterns of rocky reef fish diversity to improve the likelihood that the habitat classification will represent biodiversity in planning the arrangement of zones (Malcolm *et al.* 2010). More recently, (Schultz *et al.,* 2014) found that the pre-existing abiotic habitat classification scheme only partially represented the range of fish assemblages of unconsolidated habitats in the region. Banks and Skilleter (2002) described intertidal habitats along the Queensland coast and evaluated the effectiveness of existing protection of multiple-use reserves. This demonstrated that the existing system of MPAs failed to protect the full range of habitats, with implications for biodiversity conservation if these habitats support different assemblages and species (Banks and Skilleter, 2002). Confirmation that the different habitat types are biologically different would further increase the accuracy of this method for MPA planning.

However, classification and mapping of marine habitats at the local scale has not been widely done, generally due to lack of available information and the expense associated with subtidal surveys (Stevens and Connolly, 2004). Most habitat mapping studies therefore rely solely or in part on abiotic surrogates for patterns of biodiversity rather than directly reflecting biological distributions (Stevens and Connolly, 2004; Stevens, 2003). At the regional scale,

abiotic variables can be good predictors of biodiversity. For example, Zacharias and Roff (2001a) found that a combination of salinity, temperature and fetch predicted intertidal species richness in Canada. Edgar *et al.* (2000) classified Tasmanian estuaries using physical groups (salinity, tidal range, runoff etc.) as surrogates for biological patterns, which correlated with fish and macroinvertebrate distribution and abundance data. However, a study examining the utility of abiotic variables (depth, mud fraction, current velocity, distance to river, distance to ocean, fetch) in predicting biological soft-bottom assemblages at the local scale (10s of km) in Queensland indicated that abiotic variables did not discriminate sufficiently between different soft-bottom assemblages to be a reliable basis for mapping (Stevens and Connolly, 2004; Stevens, 2003). Stevens and Connolly (2004) suggested that little confidence can be placed in marine habitat classifications based solely or largely on abiotic surrogates without confirmation via rigorous biological surveys at an appropriate scale, and that MPAs designed solely on the use of abiotic surrogates for marine habitat mapping have questionable benefits for conservation (Stevens and Connolly, 2004; Dixon-Bridges *et al.,* 2014).

In temperate Australia, there is conflicting evidence that habitats may act as effective surrogates for initial identification of high-priority areas to manage marine diversity of coastal ecosystems (Ward *et al.,* 1999). Shokri and Glandstone (2013) found habitat classification schemes were inefficient in designing representative networks of estuarine protected areas. In contrast to this, Ward *et al.* (1999) reported that habitat-level surrogates can be used affectively to delineate reserves for conserving marine species in coastal waters, when developing a detailed inventory of species-level biodiversity would be prohibitively expensive. However, it should be noted that habitat classes used in this study were designated based on thorough baseline surveys, which is not always available (Lindsay *et al.,* 2008).

Although the design of MPA in NSW includes habitat maps as a surrogate for diversity, their precision is rarely tested. Surrogates must be ground-truthed in order to provide tarted protection at species or community levels (Last *et al.,* 2010). Several studies have examined the effectiveness of habitat mapping as a surrogate of biodiversity for rocky reef fish in NSW. Lindsay *et al.* (2008) tested the precision of habitat in predicting reef fish assemblage structure on subtropical coral reefs in NSW. Variations in fish assemblage were moderately correlated with habitat variations, and a combination of habitat and geographical data resulted in greater surrogate precision that habitat alone (Lindsay *et al.,* 2008). Malcolm *et al.* (2010) found that for subtropical fish assemblages in NSW, distance-from-shore was strongly

correlated with patterns of reef fish assemblages, and recommended that distance-from-shore be incorporated into habitat classification to improve the ability of MPA to represent biological diversity. Williams *et al.* (2009) found that depth, size, complexity, configuration and anthropogenic impact all needed to be added to geomorphic features when used as surrogates of biodiversity within Australia's deep-water reserve network. In an example from overseas, Mumby *et al.* (2008) examined the efficacy of surrogates in the Caribbean costal MPA and found that fish species were an appropriate surrogate for benthic species, but benthic species were not an appropriate surrogate for fish species. In an example from PSGLMP, Dixon-Bridges *et al.* (2014) found that a habitat classification scheme was not an effective surrogate for spatial variation of polychaete biodiversity. There are no studies evaluating the effectiveness of habitat mapping as surrogates for biodiversity for sessile benthic assemblages in sponge-dominated rocky reef, fish assemblages in sponge-dominated rocky reef, or subtidal unvegetated unconsolidated fish assemblages.

2.7 Conclusions

Managing marine ecosystems is largely guesswork without better knowledge of the components of biodiversity, and their relationship with environmental variables and biological processes (Ponder *et al.,* 2002). There are numerous gaps in knowledge regarding patterns and processes within sponge-dominated rocky reef fish and sessile benthic assemblages, and fish assemblages in subtidal unvegetated unconsolidated habitat.

The degree to which patterns in marine biodiversity can be explained by environmental pressures and biological processes has implications for conservation (Harriott *et al.,* 1999; Zacharias and Roff, 2001a). Areas of high biodiversity (Hooper *et al.,* 2002) and endemism (Phillips, 2001) may be related to the influence of environmental parameters, enabling identification of priority areas for conservation. In addition, if habitats and assemblages in different environmental domains represent distinct assemblages, this needs to be factored into the design of stratified surveys and addressed in plans to conserve representative samples of marine biodiversity (Zacharias and Roff 2001a; Benkendorff, 2005). Loss of habitats that support distinctive assemblages could result in loss of species richness and abundance, especially for organisms that that are not found in other habitats (Bloomfield and Gillanders, 2005). The influence of environmental domains on sponge-dominated rocky reef fish and sessile benthic assemblages, and fish assemblages in subtidal unvegetated unconsolidated habitat is largely unknown.

Habitat classification schemes are often used as surrogates of biodiversity for the selection and design of MPAs, however the precision of these surrogates is rarely tested, and the efficacy of habitat classification schemes as biodiversity surrogates in conservation planning is poorly understood (Ward *et al.,* 1999; Mumby *et al.,* 2008; Shokri and Gladstone, 2013).The use of habitat classification schemes in the selection and design of MPAs in NSW assumes that habitats are homogeneous, and therefore assumes that any area of that habitat type will represent the full spectrum of ecological diversity within that habitat. However, in temperate southeast Australia, high heterogeneity has been documented for marine and estuarine habitats and assemblages, including sponge-dominated rocky reef fish and sessile benthic assemblages, and fish assemblages in subtidal unvegetated unconsolidated habitat. Critics of the untested use of biodiversity surrogates of biodiversity for MPA design state that this approach lacks systematically surveyed biological data (Ward *et al.,* 1999; Banks and Skilleter 2002; Ponder *et al.,* 2002), and in particular there is limited information on the spatial scales at which faunal assemblages change in taxonomic composition within a habitat type (Winberg *et al.,* 2007). There is further need for more studies examining the effectiveness of habitat classification schemes as biodiversity surrogates for MPA planning, particularly as it is the method currently used in the section and design of MPAs in NSW and Australia.

Chapter 3 Study Area

There are currently six marine protected areas (MPAs) in New South Wales (NSW): Batemans, Cape Bryon, Jervis Bay, Lord Howe, Port Stephens-Great Lakes and Solitary Islands Marine Parks. Port Stephens-Great Lakes Marine Park (PSGLMP) was established by the NSW Government in December 2006, and is approximately 98 000 ha. The PSGLMP extends from Cape Hawke Surf Life Saving Club near Forster south to Birubi Beach Life Saving Club near Anna Bay and includes offshore waters to the 3 nautical mile limit of state waters (Fig. 3.1). It includes Port Stephens and the Karuah River, the Myall River, Myall and Smiths Lakes and all their creeks and tributaries to the tidal limit. The marine park includes:

- General use zones (for sustainable recreational and commercial activities)
- Habitat protection zones (that offer a high level of protection but allow a range of recreational activities, including recreational fishing, and some commercial fishing)
- Special purpose zones (that are set aside for specific purposes, for example, oyster leases)
- Sanctuary zones (that provide the highest level of environmental protection, where neither recreational nor commercial fishing are allowed, however recreational activities that don't harm plants, animals or habitat are permitted) (NSW Marine Parks Authority, 2014).

The NSW Marine Parks Authority used bioregional assessments to map scientific and ecological information about the marine environment and identify possible sites for marine parks. Breen *et al.* (2004) used broad-scale (10's km^2) and fine-scale (1 km^2) planning units to assess potential locations for MPAs within the Manning Shelf bioregion against more than 50 specific criteria derived from state and national guidelines. Assessments were assisted by mapped displays in a Geographic Information System, irreplaceability analysis in C-Plan reserve selection software, and multiple criteria decision analysis. The area where PSGLMP was established was identified for the many outstanding ecosystems, habitats and species occurring within one region (Breen *et al.,* 2004). It met criteria for comprehensiveness and representativeness for all mapped ecosystem and habitat units, with a high degree of naturalness and catchment protection (Breen *et al.,* 2004). It consistently scored highest in quantitative analyses for a range of criteria and complemented existing MPAs and other conservation management strategies (Breen *et al.,* 2004).

Figure 3.1: Port Stephens-Great Lakes Marine Park extends from Cape Hawke Surf Life Saving Club near Forster south to Birubi Beach Life Saving Club near Anna Bay.

The PSGLMP habitat map was developed by the New South Wales Marine Park Authority (2006) (Fig. 3.2) using broad abiotic categories such as depth, and habitat data derived from swath mapping in the region. The habitat classification scheme was developed during the establishment of the PSGLMP zoning plan (Fig. 3.3) with the goal of achieving comprehensive, adequate and representative areas of habitats being conserved in line with (at the time) NSW and Australian policy. The PSGLMP habitat classification scheme categorises habitats according to bottom type (unconsolidated, consolidated), depth (shallow 0-25 m, intermediate 25-60 m, deep 60-200 m), sediment type (mud, muddy sand, sand), and vegetation type if applicable (seagrass, mangroves, saltmarsh, macrophytes) (Malcolm *et al.,* 2010).

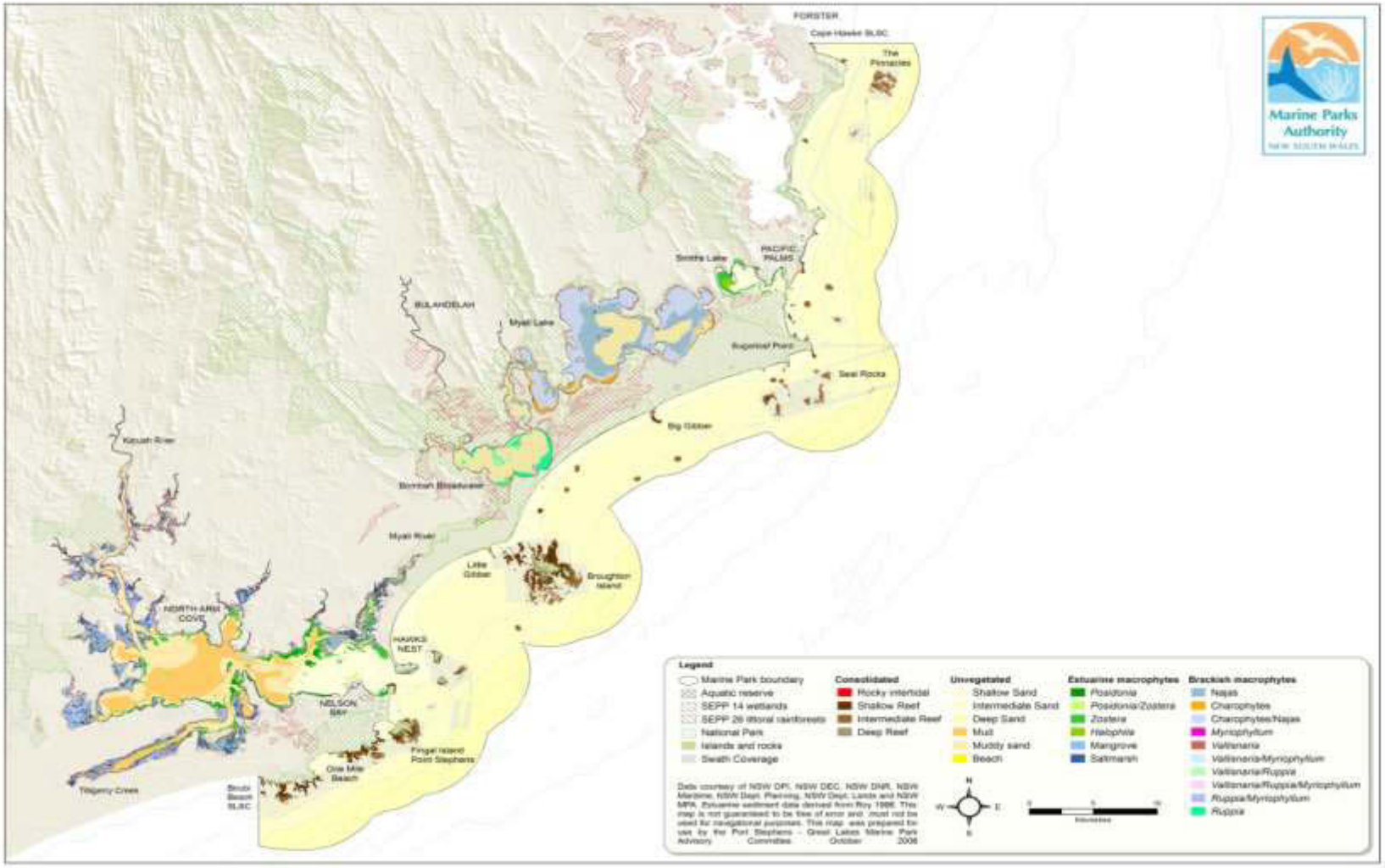

Figure 3.2: Port Stephens-Great Lakes Marine Park habitat map (New South Wales Marine Park Authority, 2006).

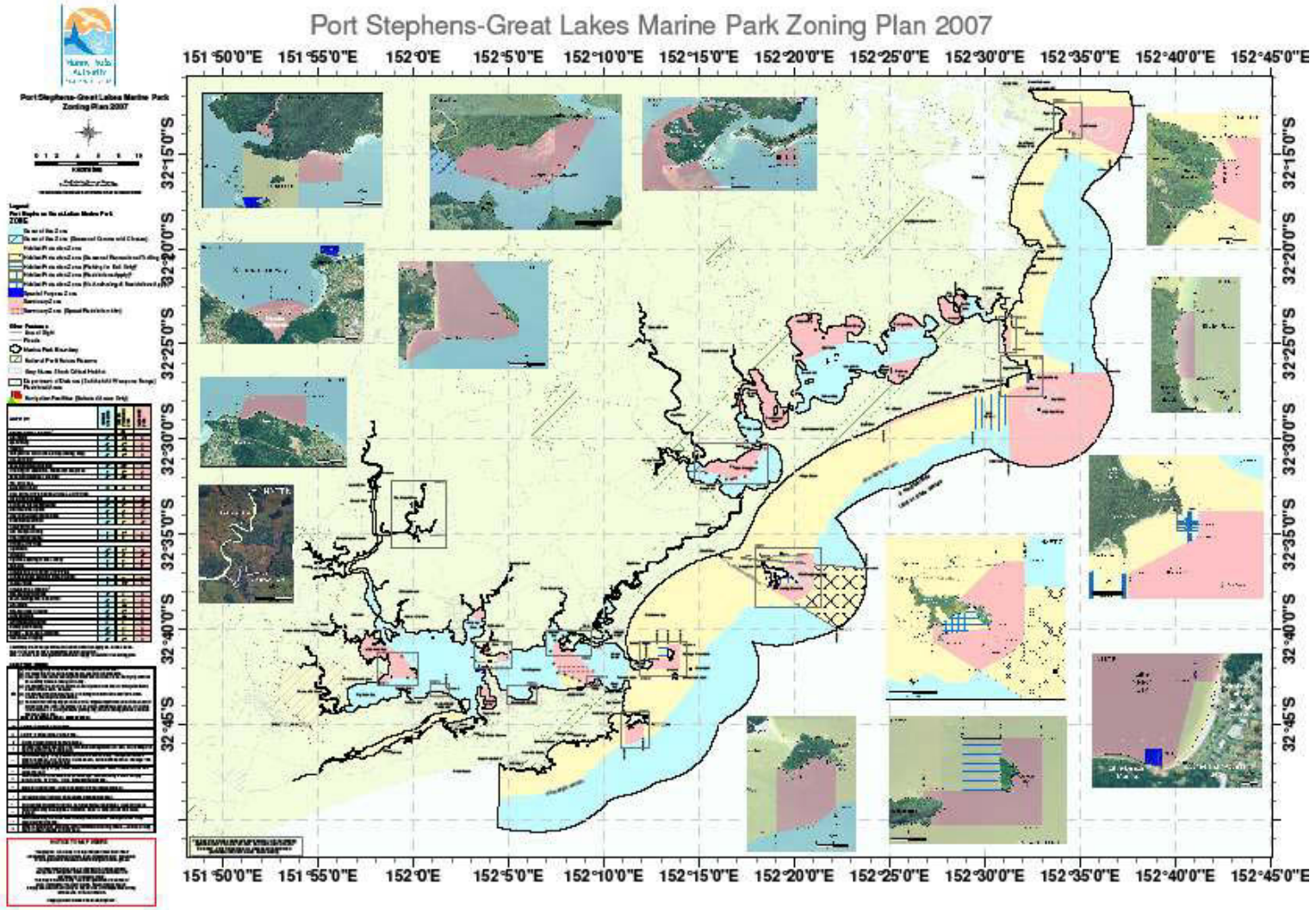

Figure 3.3: Port Stephens-Great Lakes Marine Park zoning plan (New South Wales Marine Park Authority, 2007).

The PSGLMP's diverse marine life includes many species of dolphins, turtles, fish, invertebrates, seabirds and seaweeds (NSW Marine Parks Authority, 2007). Humpback whales (*Megaptera novaeangliae*) travel along the marine park coastline during their annual migration north to breeding grounds (NSW Marine Parks Authority, 2007). The PSGLMP encompasses a range of habitats and environmental variation. This includes Broughton Island, the second largest island in NSW, which provides important habitat for the threatened grey nurse shark (*Carcharias taurus*) and black cod (*Epinephelus daemelii*), and Cabbage Tree Island (John Gould Nature Reserve), the primary breeding site for the threatened seabird Gould's petrel (*Pterodroma leucoptera leucoptera)* (New South Wales Marine Park Authority, 2014). The PSGLMP includes the majority of islands, reefs, beaches and rocky intertidal areas in the bioregion, providing significant habitats for the diverse fauna and flora, with five areas identified as major habitat sites for the grey nurse shark (New South Wales Marine Park Authority, 2014). Important oceanic islands, major estuarine wetlands and lake systems feature among a variety of habitats within PSGLMP, including the largest areas of mangrove and saltmarsh in the state, five percent of the seagrass area in NSW, the largest drowned river valley in NSW (Port Stephens), the largest brackish barrier lake system in NSW (Myall Lakes), and the largest intermittently open and closed lake in NSW (Smiths Lake) (NSW Marine Parks Authority, 2007; New South Wales Marine Park Authority, 2014). The PSGLMP includes important socio-economic values including quality recreational fishing and productive commercial fishing grounds, aquaculture, many popular scuba diving sites, and regionally significant tourism activities such as whale and dolphin watching (New South Wales Marine Park Authority, 2014). Additionally, many significant Indigenous cultural and spiritual sites are located within or adjacent to the marine park including middens, burial sites and traditional campsites (NSW Marine Parks Authority, 2007).

There has been a considerable amount of research undertaken within PSGLMP rocky reef habitats, including mapping and classifying nearshore marine habitats using large-scale physical and biological attributes (Jordan *et al.,* 2010). Rocky reefs are characterised by several distinctive habitats, the distribution of which are related to physical forces including depth, wave exposure and biological pressures, most notably herbivory by the sea urchin *Centrostephanus rodgersii* (Underwood *et al.,* 1991). Fringe habitat occurs just below low tide level to depths of approximately three metres and is dominated by a diverse range of algae. Turf habitat occurs is characterised a variety of turfing coralline and filamentous algae and occurs within shallow (less than ten metre) water. Forests of *Ecklonia radiata* occurs at

intermediate depths (approximately 2-25 m), and are interspersed with patches of sea urchin grazed crustose coralline algae (the 'barrens' habitat). Forests of *Phyllospora comosa* occur at nearshore reefs in the southern area of New South Wales (NSW) at intermediate depths (approximately 2-25 m). Pyura habitat is dominated by the large solitary ascidians *Pyura gibbosa* and *P. stolinifera* and occurs at intermediate depths (approximately 2-25 m). Sponge-dominated 'deep reef habitat' occurs >9 m depth and is characterised by a significant density of sessile benthic animals, including a number of sponges, corals and bryozoans unique to the habitat (Underwood *et al.,* 1991; Smith *et al.,* 2010).

Chapter 4 Intra-habitat variability in biodiversity of temperate rocky reefs and its implications for the development of surrogates for conservation planning

Abstract

Marine protected areas aim to conserve representative samples of the range of biological diversity. Habitat classification schemes are often used as surrogates in the absence of biodiversity inventories, to depict spatial variation in biodiversity and support conservation planning. However, the suitability of these surrogates may be affected by unrecognised sources of variation in biodiversity, including environmental variation within the same habitat. This study (1) determined optimal sampling effort required for a representative description of sessile benthic assemblages in a single habitat class (sponge-dominated reef) surveyed remotely using an autonomous underwater vehicle, and (2) tested whether these assemblages varied in different environments (coastal headlands, offshore islands) where the habitat occurred. The study was undertaken in the Port Stephens-Great Lakes Marine Park, south-east Australia. Twenty-one species of encrusting benthic organisms, 10 sponge morphological types, and 2 substrate variables (silt and sand) were recorded. Sessile benthic assemblages, life form richness, and cover of other taxa did not differ between offshore island and coastal headlands, although there was significant spatial variation (at the scale of km) in each variable within each environment. A subset of the sessile benthic assemblage, the sponge assemblage (the dominant fauna) differed between offshore island and coastal headlands. Cover of arborescent sponges was also greater at offshore islands than coastal headlands. Environmental variation within a habitat (attributed here to coastal headlands and offshore islands) was therefore a significant source of variation for only a minority of the components of the biodiversity of sessile benthic assemblages. In contrast, assemblages varied substantially at relatively small spatial scales (10s km). Conservation of a representative sample of the biodiversity of sessile benthic assemblages requires protection of multiple examples of this habitat.

4.1 Introduction

Subtidal rocky reefs in temperate southeast Australia support diverse, highly endemic and commercially important habitats, assemblages and species (Ponder *et al.,* 2002; Malcolm *et al.,* 2007). These reefs are characterised by several distinctive habitats, the distribution of which are related to physical forces including depth, wave exposure and biological pressures, most notably herbivory by the sea urchin *Centrostephanus rodgersii* (Underwood *et al.,*

1991). Fringe habitat occurs just below low tide level to depths of approximately three metres and is dominated by a diverse range of algae. Turf habitat occurs is characterised a variety of turfing coralline and filamentous algae and occurs within shallow (less than ten metre) water. Forests of *Ecklonia radiata* occurs at intermediate depths (approximately 2-25 m), and are interspersed with patches of sea urchin grazed crustose coralline algae (the 'barrens' habitat). Forests of *Phyllospora comosa* occur at nearshore reefs in the southern area of New South Wales (NSW) at intermediate depths (approximately 2-25 m). Pyura habitat is dominated by the large solitary ascidians *Pyura gibbosa* and *P. stolinifera* and occurs at intermediate depths (approximately 2-25 m). Sponge-dominated 'deep reef habitat' occurs at >9 m depth and is characterised by a significant density of sessile benthic animals, including a number of sponges, corals and bryozoans unique to the habitat (Underwood *et al.,* 1991; Smith *et al.,* 2010). There has been a considerable amount of research in these rocky reef habitats, including mapping and classifying NSW nearshore marine habitats using large-scale physical and biological attributes (such as depth categories shallow 0-25 m, intermediate 25-60 m and deep 60-200 m) (Jordan *et al.,* 2010). However, large gaps in knowledge occur regarding spatial and temporal patterns within sponge-dominated reefs in temperate NSW, their associated assemblages and underlying ecological processes (Davis *et al.,* 2010).

Australia is increasingly recognised as a global hotspot for sponge biodiversity (Schonberg and Fromont, 2012; Przeslawski *et al.,* 2014). In southeast Australia sponge-dominated reef assemblages are dynamic, with the structure and diversity of assemblages reflecting the influences of differing environmental variables (Roberts and Davis, 1996; Roberts, 2000; Roberts *et al.,* 2006). Sponge assemblages are highly variable at scales of m, 100s m and 10s km (Roberts, 1996; Roberts and Davis, 1996; Owen, 2003; Roberts *et al.,* 2006), but generally the abundance of massive and upright forms and taxonomic richness increase with depth (Roberts and Davis, 1996). Sponge cover has been found to be higher on reefs <20 m depth than deeper reefs, consistent with low sedimentation and high turbulence on these shallower reefs (Roberts and Davis, 1996). Sponge-dominated reef assemblages differ between reefs near estuaries and those further offshore reefs, due to relative differences in encrusting forms of sponges which are more common at near estuarine reefs and upright forms more common at offshore reefs (Owen, 2003). Patterns of sponge morphological diversity also reflect other environmental influences, with upright sponges accounting for the majority of the species richness and cover of sponges on sheltered reefs, and encrusting species dominating exposed reefs (Roberts *et al.,* 2006). Although sponge assemblages in

southern Australia are diverse, highly endemic and a commercially important part of Australia's marine diversity (Keough, 1999; O'Hara, 2002; Ponder *et al.,* 2002; Fromont *et al.,* 2006), there is still relatively little information available regarding the magnitude of sponge diversity, the interactions and responses of sponge-dominated assemblages to environmental variables, and the appropriate spatial and temporal scales at which they need to be described for effective conservation and management (Hooper and Kennedy, 2002; Worheide *et al.,* 2005).

Despite the economic importance of marine resources in NSW, there is relatively little known about the biodiversity of habitats, assemblages and species (Ponder *et al.,* 2002). The development of habitat-based biodiversity surrogates has an important role in the identification of sites that will contribute to a representative system of marine protected areas (MPAs), on the basis that this increases the likelihood that the system will adequately achieve biodiversity objectives by ensuring protection of a greater range of habitats and species (Banks and Skilleter, 2002). In temperate Australia, there is some evidence that habitats may act as effective surrogates for species diversity for initial identification of high-priority areas to manage marine diversity of coastal ecosystems (Ward *et al.,* 1999). Therefore, mapping of seabed habitats may be a cost effective method of biodiversity assessment for MPA planning (Jordan *et al.,* 2005).

Habitat classification schemes have been used for MPA planning in Australia (Ward *et al.,* 1999; Banks *et al.,* 2005; Winberg *et al.,* 2007; Lindsay *et al.,* 2008; Last *et al.,* 2010; Malcolm *et al.,* 2010; Malcolm *et al.,* 2011) and New Zealand (New Zealand Department of Conservation and Ministry of Fisheries (2011). The use of habitat types assumes that they predict, or at least correlate with, patterns of biological distributions (Stevens and Connolly, 2004; Banks *et al.,* 2005). This also assumes that habitats are homogeneous in biodiversity, and therefore that any area of habitat chosen as an area for conservation will reflect the full range of biodiversity within that habitat (Gladstone 2007; Winberg *et al.,* 2007). Winberg *et al.* (2007) demonstrated that this is not always the case, reporting that macrobenthic assemblages in tidal flat habitats in temperate NSW were spatially heterogeneous in terms of taxonomic turnover, abundance, richness and diversity. Their research showed that although tidal flats in different estuaries are compositionally similar for dominant taxa, rarer taxa and high heterogeneity in abundance should influence the choice and number of tidal flats conserved in MPAs, and that conservation of the whole tidal mudflat habitat, rather than

sections of the habitat, is essential for this habitat type to be used to represent taxonomic diversity (Winberg *et al.,* 2007).

The hierarchical habitat classification scheme used in NSW MPA is nested at several levels and categorises habitats according to dominant substrate type (unconsolidated, consolidated), depth (shallow, intermediate, deep), sediment type (mud, muddy sand, sand), and vegetation type (seagrass, mangroves, saltmarsh, macrophytes). Modifications to this scheme may be needed when the habitat classes do not adequately represent variation in biodiversity. For example, Malcolm *et al.* (2010) found that for subtropical fish assemblages within the Solitary Islands Marine Park region in northern NSW, distance-from-shore was strongly correlated with patterns of variation of reef fish assemblages and species richness due to the presence of offshore islands and strong subtropical influence, and recommended that distance-from-shore be incorporated at the local level into habitat classification to improve the ability of the MPA to represent biological diversity. Within the Port Stephens-Great Lakes Marine Park (PSGLMP) the habitat class 'intermediate reef (25-60 m)' is largely sponge-dominated reef (Jordan *et al.,* 2010). The variability within sponge-dominated reefs occurring elsewhere in response to differing environmental influences (Roberts, 1996; Roberts and Davis, 1996; Owen, 2003; Roberts, 2006) has implications for MPA planning. If assemblages of the same habitat type differ among different environmental domains, this needs to be considered when planning to conserve the biodiversity of this habitat in representative areas. Two of the major features of the PSGLMP are the extensive areas of coastal headlands and several offshore islands (Breen *et al.,* 2004; Jordan *et al.,* 2010). Reefs adjacent to coastal headlands and offshore islands are considered different environmental domains due to perceived differences in exposure and/or distance from shore. Different environmental domains support different sets of species, and may be used to represent environmental heterogeneity and therefore act as biodiversity surrogates (Margules *et al.,* 2002). Previous research has documented differences between fish assemblages within PSGLMP at reefs adjacent to coastal headlands and offshore islands (Lindfield, 2007; Malcolm *et al.,* 2007).

A major challenge in describing the biodiversity of subtidal rocky reefs involves the collection of sufficient data from depth, and determining an adequate sampling regime. Methods of data collection in this habitat have previously included *in situ* diver surveys (Owen, 2003) and drop cameras (Roberts *et al.,* 1994; Roberts, 1996; Roberts and Davis, 1996; Roberts, 2006), both of which are unable to collect large amounts of field data quickly.

Most recently Autonomous Underwater Vehicles (AUV) have been utilised to map and describe sponge-dominated assemblages (Meyer *et al.,* 2011; Smale *et al.,* 2012). The ability of an AUV to collect large numbers of high quality images suitable for biodiversity assessment, when coupled with logistical constraints on image processing (especially time), requires an analysis of the image processing effort required to adequately describe the variables of interest. This has not been done before for AUV-collected images of rocky reef sessile assemblages where the variables of interest are both univariate and multivariate in nature. Techniques to measure accuracy and precision of univariate data (e.g. standard deviations, species accumulation curves, coefficients of variation) are either insufficient or invalid for assessing the quality of data describing entire assemblages (Cao *et al.,* 2003). The approach required to measure accuracy and precision for multivariate data sets are only partly answered by a species accumulation curve. Similarity-based approaches for comparing multiple pairs of replicate samples can be used to effectively measure and control the quality of assemblage survey data in freshwater benthic macroinvertebrates (Cao *et al.,* 2003). Only one study has compared the precision and accuracy of standard methods commonly used to estimate percent cover of sessile benthic organisms. This was undertaken in shallow (~5 m) turfing algae habitat and found that techniques that permit the greatest replication are likely to produce the most accurate and precise estimates of precent cover of univariate data sets describing sessile benthic organisms (Drummond and Connell, 2005). Variation in precision and accuracy of the entire assemblage was not examined.

The aim of this study was to determine whether environmental variation is a source of intra-habitat variation in biodiversity. The study used sponge-dominated sessile benthic assemblages within the intermediate reef habitat class in the PSGLMP and tested the a priori assumption that reefs adjacent to coastal headlands and offshore islands represent significant sources of variation for these assemblages within a habitat. If true, this variation would need to be considered in refinements of the current habitat classification scheme that may define further hierarchical levels on a more quantitative basis. The approach taken to examine this question utilised high resolution remote sampling of biodiversity within replicate and spatially separate examples of each environment by an AUV. A pilot study was first undertaken to determine the optimal sampling effort for number of replicates and intensity of image processing for the goal of describing sessile benthic assemblages. The combination of high resolution remote imagery and high intensity sampling is unique within this habitat.

4.2 Methods

Study Area

PSGLMP is situated on the mid-north coast of NSW (Fig. 3.1), and includes estuaries, open coast and islands covering approximately 98,000 ha. (see detailed description in Chapter 3). Subtidal rocky reef habitat is generally associated with rocky shore adjacent to both coastal and island headlands (Jordan *et al.,* 2010), represents approximately 3% of the PSGLMP and is classified by depth for planning purposes (New South Wales Marine Park Authority, 2006). In this study the coastal headland (Fingal) and offshore island (Broughton Island) environmental domains differed in exposure and distance from the mainland coast. Fingal is a tombolo connected to the mainland via a sand spit and can be classified as nearshore reef in the context of the PSGLMP habitat classification scheme. Broughton Island can be classified as mid-shelf in the context of the PSGLMP habitat classification scheme, with the island ranging from approximately 2.5 to 6.0 km offshore.

Experimental Design and Field Sampling

Sampling occurred in intermediate rocky reef class (25-60 m depth) within sponge-dominated assemblages. This habitat is inherently patchy, containing areas of sessile benthic assemblages as well as barrens and kelp. All images were analysed as this is representative of this habitat. Sessile benthic assemblages were remotely surveyed using the University of Sydney's Australian Centre for Field Robotics (ACFR) AUV (Rigby *et al.,* 2010; Williams *et. al.*, 2012). The AUV is equipped with high resolution stereo camera pair and strobes, multibeam sonar, depth and conductivity/temperature sensors, Doppler Velocity Log (DVL) including a compass with integrated roll and pitch sensors, Ultra Short Baseline Acoustic Positioning System (USBL) and forward looking obstacle avoidance sonar. Ten 25 m x 25 m photo sampling grids were surveyed in six coastal headland locations and four offshore island locations grouped into two environmental domains: offshore island and coastal headland (Fig.4.1). Locations occurred within both sanctuary zones and habitat protection zones within the PSGLMP, were separated by at least 200 m, and corresponded to locations where fish assemblages were surveyed using Baited Remote Underwater Video (see detailed description in Chapter 6). The mean depth of each location varied between 21.7 m and 32.0 m.

Figure 4.1: Location of study sites in Port Stephens-Great Lakes Marine Park. Symbols represent offshore island locations (square) and coastal headland locations (circle).

The number of images collected by the AUV varied between 975 and 1975 per location (n=18750 total images). There was often overlap between images (generally every 3rd to 5th image was a 'new' image without any overlap from the previous image), and when the AUV turned back to complete a loop every ~12th image contained no overlap. Prior to analysis each image was opened in Arc GIS to detect its location and ensure it was not overlapping with the last selected image. Images captured approximately 2.1 m^2 (1.6 m x 1.3 m) of the reef (a quadrat).

This amount of high resolution data has not been available for previous studies undertaken in this habitat, which were based on a limited number of photo-quadrats (Roberts and Davis, 1996; Roberts *et al.,* 1998; Roberts, 2000; Owen, 2003; Roberts *et al.,* 2006). A pilot study was therefore undertaken to determine optimal sampling effort and image processing. We defined 'sampling effort' as the number of images processed from the total pool of images available for a location, and 'sampling intensity' as the number of grid points overlaid on an image to quantify species present and estimate % cover. Increasing levels of sampling effort

were compared using groups of 5, 10, 15, 20, 25 and 30 replicate images. Images were randomly selected from the pool of available images to form each group. Each set of increasing number of images was independent of the previous set of images (i.e. the set of ten images did not include the set of five images). The process was repeated five times for each image group size. Sampling intensity was varied by applying varying numbers (25, 50 and 100) of random points over the top of each image, with the category under each point recorded. The cover and species richness of sessile benthic organisms were determined using Coral Point Count with Excel extensions (CPCe) (Kohler and Gill, 2006), a program developed for the determination of benthic substrate coverage.

A mixture of classification schemes was used to identify organisms in the selected images. Sponges were classified into broad morphological groups (arborescent, cup, encrusting, fan, globular, lumpy, massive, papillate, repent and tubular) developed by the Commonwealth Environment Research Facility (CERF) Marine Biodiversity Hub: Surrogates Program (Meyer *et al.,* 2011), as sponge species identification is not possible without tissue samples for examination. Other sessile benthic organisms were identified to species-level where possible (using Shepherd and Thomas, 1982; Edgar, 1997; Huisman, 2000; Veron, 2000; Gowlett-Holmes, 2008) and to morpho-species when identification was not possible.

Statistical Analyses to Determine Optimal Sampling Effort

Multivariate analyses were undertaken using PRIMER 6 software (PRIMER-E Ltd, Plymouth) (Clarke and Warwick, 2001) to test the hypothesis of no difference in the precision of assemblages identified using differing numbers of replicate images. Random images from one offshore island location and one coastal headland location were analysed in groups of 5, 10, 15, 20, 25 and 30 replicate images to mimic differing image sampling effort (the locations were analysed separately). An estimate of a pseudo standard error for the multivariate data was used as an estimate of sampling 'precision' because of the lack of an otherwise suitable measure for multivariate data using the approach of Anderson (2001) and Anderson *et al.* (2001). Bray Curtis similarity matrices were created for each data set, the similarity values were converted to dissimilarity and squared. The sum of squared inter-point dissimilarities was divided by sample size (n) to give a pseudo measure of multivariate variability (q_n). The pseudo standard error (SE mult) was calculated as $\sqrt{(q_n/n)}$ and used as a measure of precision for the multivariate data set. This was repeated 5 times for each data set with differing number of replicates (5, 10, 15, 20, 25, 30 images) and the mean +/- SE of the

five repetitions plotted vs number of images (n) to determine optimal sample effort. Multivariate analyses were repeated for data sets based on 25, 50 and 100 grid-point analysis. The decision on optimal sampling effort was based on an examination of the curves, and determination of the point at which additional sampling effort did not lead to increased precision.

Life form accumulation curves, that included sponge morphological groups and species from all other phyla, were created by plotting life form richness vs n to determine the asymptote at which increases in n did not result in higher life form richness. Life form accumulation curves were repeated for data sets based on 25, 50 and 100 grid-point analysis.

Statistical Analyses to Examine Variability Between Environmental Domains

Multivariate analyses were undertaken using PRIMER 6 and PERMANOVA+ software (PRIMER-E Ltd, Plymouth) (Clarke and Warwick, 2001) to test the hypothesis that assemblages differed between offshore islands and coastal headlands. Two-factor permutational multivariate analysis of variance (PERMANOVA) (Anderson, 2001) was used to test the hypothesis that benthic assemblages differed between environmental domains (offshore islands and coastal headlands). Environmental domain was analysed as a fixed orthogonal factor with two levels (coastal headland and offshore island), location was analysed as a random factor nested in habitat with n=6 levels for coastal headland and n=4 levels for offshore island. PERMANOVA was done on a Bray-Curtis similarity matrix of untransformed data. This PERMANOVA design was also used to test for differences between assemblages based on broad taxonomic groups (brown algae, red algae, sponges, ascidians, bryozoans, cnidarians, silt and sand), and between assemblages based only on sponge life forms (the dominant fauna group). Relative differences in sessile benthic assemblages were visualised by non-metric multidimensional scaling ordination plots, using the average cover from each location in each environmental domain.

The similarity percentages (SIMPER) procedure was used to identify taxa responsible for differences in assemblages between habitats and to select a subset of variables for univariate analysis. Large values (i.e.>1) of the ratio $\overline{\delta}_i$/SD($\overline{\delta}_i$) (where $\overline{\delta}_i$ is the average contribution of the *i*th species to the overall dissimilarity ($\overline{\delta}_i$) between 2 groups and SD is standard deviation); and values of $\%\overline{\delta}_i$ > 3% were used to indicate species that were important contributors to dissimilarity between habitats (Clarke 1993; Terlizzi *et al.,* 2005; Malcolm *et*

al., 2007). Finally, the role of distance between locations as a source of variation was examined using the RELATE test, which tested correlation between Bray-Curtis similarity matrix benthic assemblages and distance between locations, to check if locations that were further apart were less similar than locations closer together. The distance between locations was determined in ArcGIS.

Univariate PERMANOVA was used to test the hypothesis that single variables differed between environmental domains using the same design as the multivariate analyses. Homogeneity of variances was first tested by Cochran's C test using GMAV software (Institute of Marine Science, University of Sydney), and data were transformed using ArcSin% where necessary to eliminate heterogeneous variances. When heterogeneous variances could not be eliminated by transformation the raw data were used and a modified significance level of P=0.01 was used (Underwood, 1981). The life form richness, and covers of silt, filamentous algae, encrusting coralline algae, encrusting sponge and arborescent sponge were tested for differences between environmental domains, utilising the dataset containing n=25 images. The variables tested represented life forms that were most abundant or showed a pattern of difference between environmental domains.

4.3 Results

Precision in Sampling Multivariate Assemblage

Precision values increased with increasing levels of replication at both Fingal and Broughton Island (Fig. 4.2). An asymptote in precision is apparent at n=25 images for image processing based on 25, 50 and 100 grid points at both locations. There was very little difference in the precision of datasets analysed using 50 and 100 grid points for datasets of 25 images (6.48 and 6.85 at Fingal, 5.98 and 5.90 at Broughton Island).

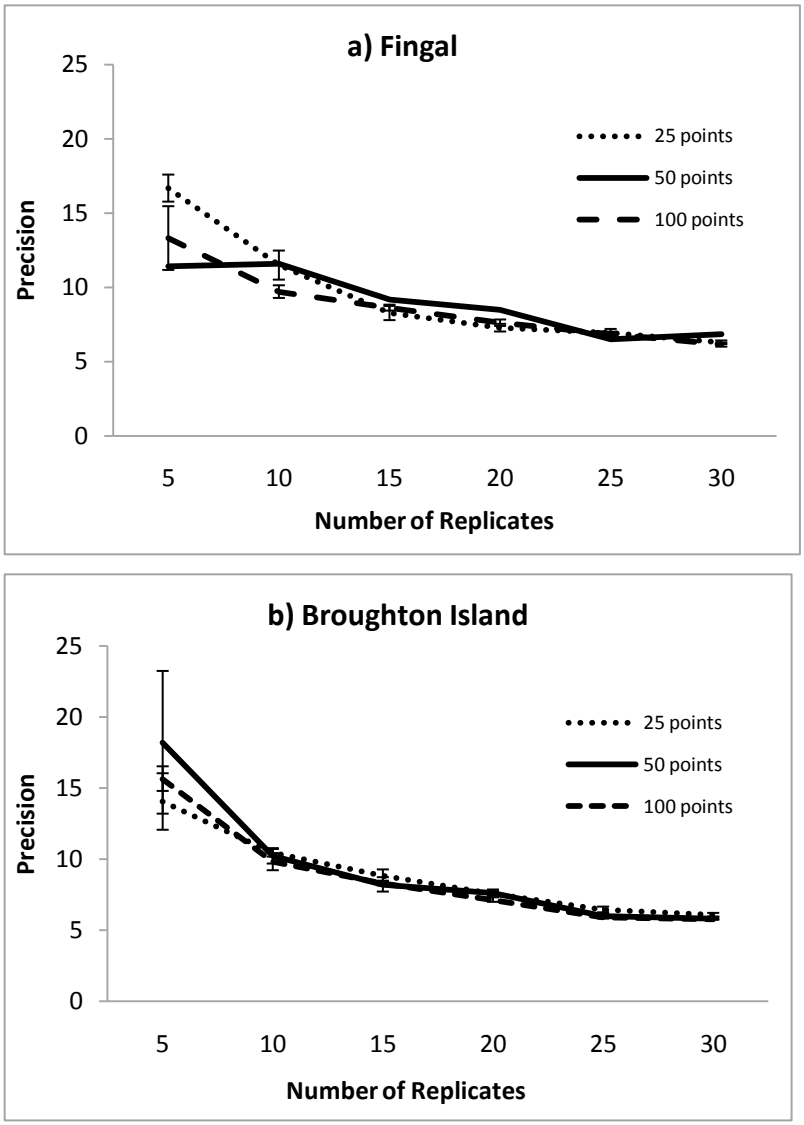

Figure 4.2: Changes in estimates of multivariate precision with increasing replication at a) Fingal and b) Broughton Island in sponge-dominated deep reef habitat in the Port Stephens-Great Lakes Marine Park. Values shown are mean precision ± standard error (n = 5) for datasets based on 5, 10, 15, 20, 25 and 30 replicate images. Symbols represent datasets calculated utilising 25, 50 and 100 grid-point matrices.

Life form Accumulation Curves

An asymptote was apparent at 25 life forms for Fingal and 26 species for Broughton Island using 25 grid points to analyse the images (Fig. 4.3 a&b) for datasets of 25 and 30 images at Fingal and 30 images at Broughton Island. Datasets based on 15 and 20 images at Fingal displayed an asymptote at 19 and 17 life forms, respectively. Datasets based on 5 and 10 images at Fingal recorded new life forms with increasing replication but an asymptote was not reached. Datasets based on 5, 10, 15, 20, 25 images at Broughton Island also displayed

an asymptote, however with less life forms recorded (10, 11, 15, 17, 20 respectively) than were recorded from datasets based on 30 images (26 life forms).

An asymptote was apparent at 27 life forms for Fingal and 30 life forms for Broughton Island using 50 grid points to analyse images (Fig. 4.3 c&d). This number of life forms was recorded from datasets based on both 25 and 30 images. Datasets based on 20 images also reached an asymptote, however there were fewer life forms recorded at both Fingal (23 life forms) and Broughton Island (24 life forms). The datasets based on 5, 10 and 15 images recorded new life forms with increasing replication but an asymptote was not detected.

An asymptote was detected at 30 life forms for Fingal and 27 life forms for Broughton Island using 100 grid points to analyse the images (Fig. 4.3 e&f). This number of life forms was recorded from datasets of 25 and 30 images at Fingal and Broughton Island, and 20 images at Broughton Island. The dataset of 20 images from Fingal also displayed an asymptote, however with less life forms recorded (27 life forms) than were recorded from datasets based on 25 and 30 images. The datasets based on 5, 10 and 15 images recorded new life forms with increasing replication but no asymptote was detected.

There was little difference between the maximum numbers of life forms recorded by varying the number of grid points when processing the images, and between the two locations. Twenty-five life forms were recorded at Fingal using a 25 grid point matrix; 27 using a 50 grid point matrix and 30 using a 100 grid point matrix. Twenty-six life forms were recorded at Broughton Island using a 25 grid point matrix; 30 using a 50 grid point matrix and 27 using a 100 grid point matrix.

In conclusion an asymptote in life form accumulation curves was apparent at n=25 images for image processing based on 50 grid points at both Fingal and Broughton Island. Increasing the number of replicates or number of grid points beyond this resulted in very little difference in the precision of datasets.

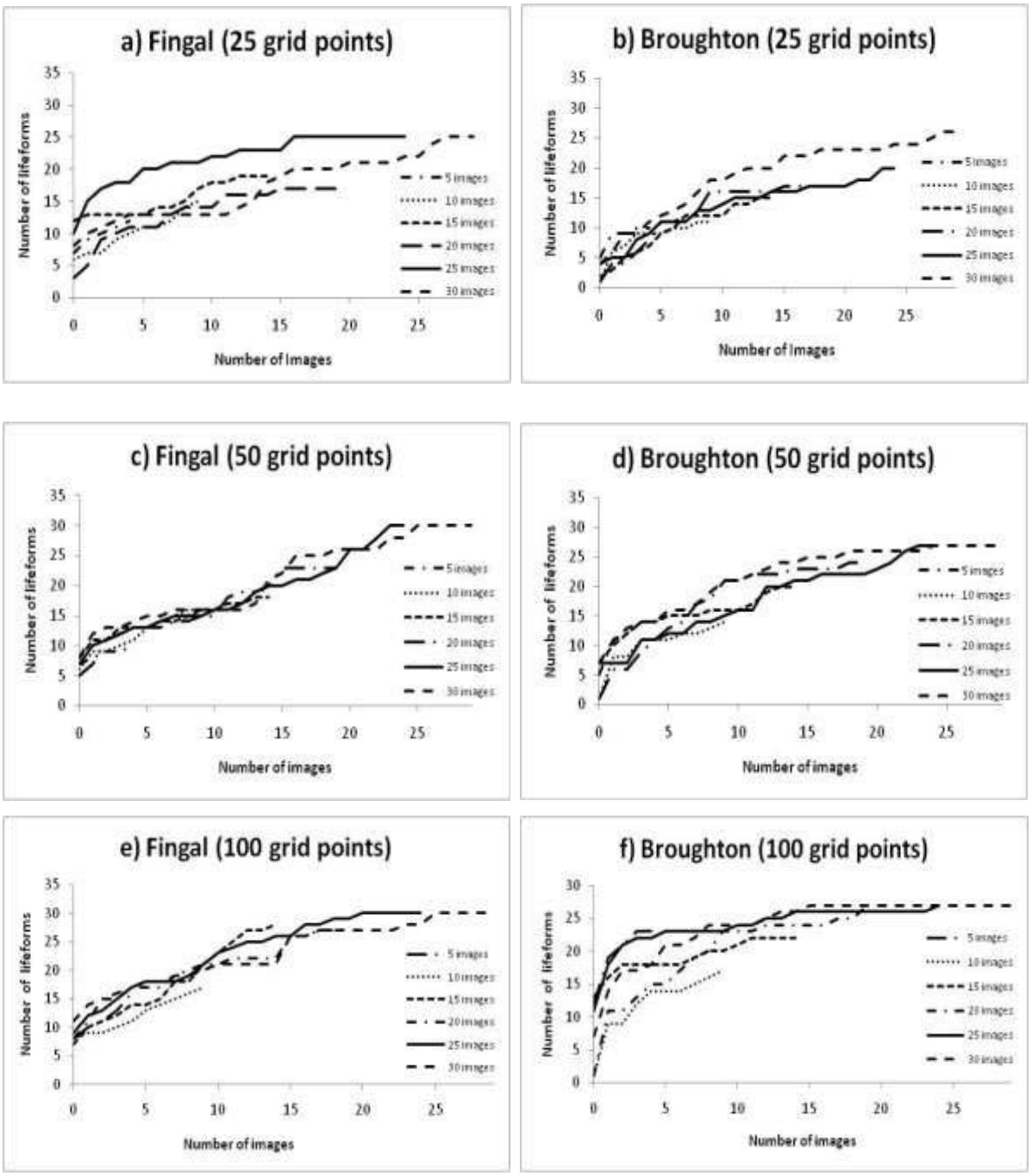

Figure 4.3: Life form accumulation curves from Fingal and Broughton Island for increasing sampling effort (number of images) and image processing (number of grid points) for sessile assemblages in intermediate reef habitat in the Port Stephens-Great Lakes Marine Park. Values shown are number of species recorded vs number of images. Symbols represent datasets calculated utilising 5, 10, 15, 20, 25 and 30 images.

Diversity of Sessile Benthic Assemblages

Forty-one life forms were recorded, representing 21 encrusting benthic organisms (3 Phaeophyta (brown algae), 7 Rhodophyta (red algae), 10 Cnidaria (corals and anemones), 6 Bryozoa (bryozoans) and 5 Ascidiacea (ascidians)) and 10 sponge morphological types. In addition, 2 substrate variables (silt matrix and sand) were recorded. Silt matrix (consisting of sediment and micro-organisms) (Roberts *et al.,* 1994) (with a mean % cover (± SE) of 27.0±2.54), filamentous red algae (15.5±0.68), sand (15.2±2.77), encrusting coralline algae (13.3±2.14), encrusting sponge (4.9±0.82) and arborescent sponge (3.9±0.66) were the dominant variables recorded (Appendix 1).

Spatial Variation in Life Forms

Life form richness varied between 4 and 16 categories per quadrat (image), and between 7 and 11 categories per location. Images captured approximately 2.1 m^2 (1.6 m x 1.3 m) of the reef. Life form richness varied among the coastal headland and among the offshore island locations, but not between environmental domains (Table 4.1, Fig. 4.4).

Cover of silt matrix varied between locations, covering 15% to 45% of the quadrat area. Cover of sand also varied between locations, covering 5% to 35% of the quadrat area. Cover of both silt matrix and sand did not differ between environmental domains, and varied significantly among the locations within each environmental domain (Table 4.1, Fig. 4.4).
A mixture of red and brown filamentous algae covered a high percentage (~15% to 20%) of the quadrat area at most locations. Cover of filamentous algae did not differ between environmental domains, and varied significantly among the locations within each environmental domain (Table 4.1, Fig. 4.4).

The most common brown algae encountered were *Distromium flabellatum* and *Ecklonia radiata*, covering between 2% and 1% of the quadrat area respectively. Brown algae occurred at all locations in cover too low for analysis (average <1% per quadrat). The most common red algae encountered belonged to the Family Corallinaceae and included geniculate taxa (*Amphiroa anceps* and *Corallina officinalis*) and encrusting coralline algae. The encrusting coralline algae were a combination of species that could not be distinguished in images. Cover of encrusting coralline algae was dominant at some locations, covering between 6% and 20% of the quadrat area. Cover of encrusting coralline algae did not differ between

environmental domains, and varied significantly among the locations within each environmental domain (Table 4.1, Fig. 4.4).

Sponges were the dominant fauna at all locations, with cover generally ranging from 10% to 15% of the quadrat area. Ten broad morphological groups (arborescent, cup, encrusting, fan, globular, lumpy, massive, papillate, repent, tubular) were recorded. Arborescent and encrusting were the most common forms recorded, with covers of 2-8% and 3-10% respectively (Fig. 4.4). Cover of arborescent sponges differed significantly between environmental domains, with a higher cover at offshore islands, and varied significantly among locations in both domains (Table 4.2). Cover of encrusting sponges did not differ between environmental domains, and varied significantly among locations in each domain (Table 4.2).

Anemones, zoanthids, scleractinians, soft corals and gorgonians were recorded at most locations in cover too low for analysis (average <1% per quadrat). The most common cnidarians recorded were the jewel anemone *Corynactis australis* and the encrusting scleractinian coral *Coscinareae mcneilli*. Bryozoans occurred at all locations in cover too low for analysis (average <1% per quadrat). The most frequently recorded bryozoans were *Triphyllozoon* sp. and *Steginoporella chartacea.* Ascidians occurred patchily across most locations in cover too low for analysis (average <1% per quadrat). The most common ascidians recorded were *Pyura spinifera*, *Cnemidocarpa pedata* and *Polycitor giganteus.*

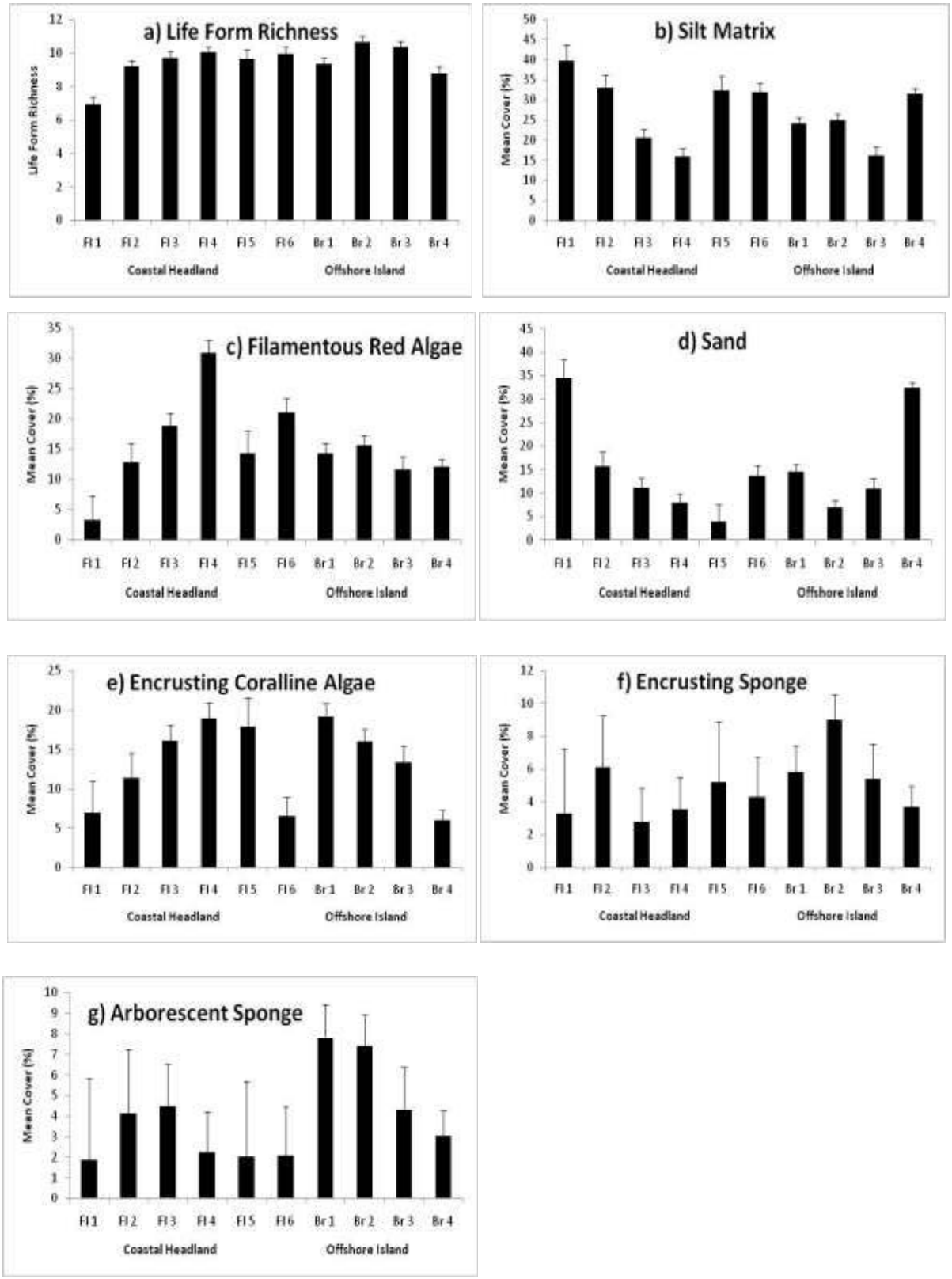

Figure 4.4: Mean lifeform richness and mean cover of variables recorded from sessile benthic assemblages in December 2010. Values shown are mean cover ± standard error (n = 25) for each location. FI: Fingal, Br: Broughton Island.

Table 4.1: Summary of results of 2-factor PERMANOVA testing for the influence of environmental domains on sessile benthic categories in sponge dominated reef in the Port Stephens-Great Lakes Marine Park.

		Life form Richness[3]			Cover Silt[3]			Cover Sand[3]		
Source of Variation	DF	MS	F	*P*	MS	F	*P*	MS	F	*P*
Environmental Domain: EnvD	1	16.85	0.59	0.54	1331.00	0.84	0.41	182.35	0.06	0.79
Location(EnvD)	8	28.79	7.20	0.001	1588.60	8.94	<0.001	2959.20	10.79	0.001
Residual	240	3.99			177.760			274.34		

		Cover Filamentous Algae[3]			Cover Encrusting Coralline Algae[2]			Cover Arborescent Sponge[1]		
Source of Variation	DF	MS	F	*P*	MS	F	*P*	MS	F	*P*
Environmental Domain: EnvD	1	721.07	0.53	0.51	172.41	0.20	0.67	481.67	6.63	0.03
Location(EnvD)	8	1370.10	15.37	<0.001	844.90	8.58	<0.001	72.67	6.34	<0.001
Residual	240	89.17			98.52			11.46		

		Cover Encrusting Sponge[2]		
Source of Variation	DF	MS	F	*P*
Environmental Domain: EnvD	1	462.71	3.53	0.09
Location(EnvD)	8	131.00	2.72	0.007
Residual	240	48.15		

1: untransformed, variances homogeneous 2: ArcSin(%) transformed, variances homogenous 3: untransformed, variances heterogeneous

Spatial Variation in Sessile Benthic Assemblages

Sessile benthic assemblages did not differ between the two environmental domains, and differed among all locations within each environmental domain (Table 4.2, Fig. 4.5). These results are reflected in the nMDS ordination (Fig. 4.5), showing overlap in the points representing the two environmental domains, and a wide dispersal of the replicate locations within each environmental domain (Fig. 4.5). Dissimilarity among benthic assemblages was unrelated to the distances between locations (Rho=-0.04, *P*=0.56).

Assemblages identified to broad taxonomic groups did not differ between environmental domains and varied significantly among locations in each domain (Table 4.2, Fig. 4.6). However, assemblages of sponge life forms differed significantly between environmental domains and among locations in each domain (Table 4.2, Table 4.3, Fig. 4.7). Separation of environmental domains on the nMDS ordination indicated high variability within both coastal headlands and offshore islands. The SIMPER analysis identified two life forms (encrusting and arborescent) as being influential in differentiating between assemblages in different environmental domains (Table 4.3). Similarity within assemblages differed between environmental domains, with 30 % similarity within coastal headlands and 42 % similarity within offshore islands.

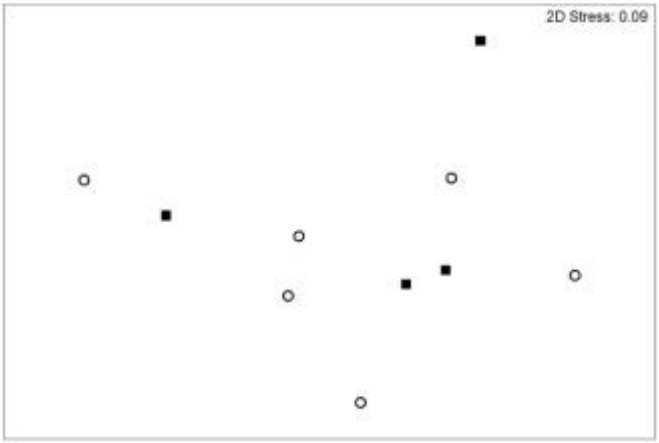

Figure 4.5: nMDS ordination plot (based on average cover of life forms at each location) depicting relative similarity of sessile assemblages of intermediate reef in the Port Stephens-Great Lakes Marine Park from offshore islands (square) and coastal headlands (circle).

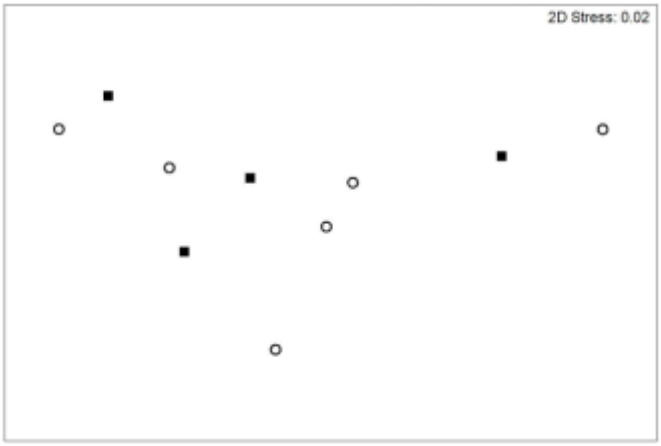

Figure 4.6: nMDS ordination plot (based on average cover of life forms at each location) depicting relative similarity of sessile assemblages identified into broad taxonomic groups in intermediate reef in the Port Stephens-Great Lakes Marine Park from offshore islands (square) and coastal headlands (circle).

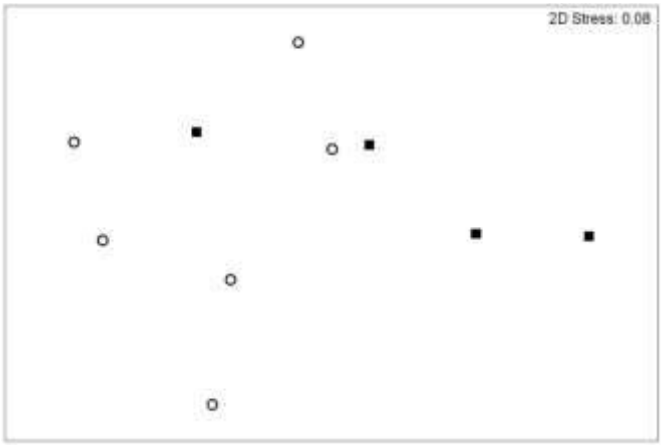

Figure 4.7: nMDS ordination plot (based on average cover of life forms at each location) depicting relative similarity of sponge life forms of intermediate reef in the Port Stephens-Great Lakes Marine Park from offshore islands (square) and coastal headlands (circle).

Table 4.2: Summary of results of 2-factor PERMANOVA testing for the influence of environmental domain on sessile benthic assemblages, assemblages identified into broad taxonomic groups and sponge life form groups in sponge dominated reef in the Port Stephens-Great Lakes Marine Park.

		Entire Sessile Benthic Assemblage			Broad Taxonomic Groups			Sponge Life Form Groups		
Source of Variation	DF	MS	F	*P*	MS	F	*P*	MS	F	*P*
Environmental Domain: EnvD	1	10826.00	1.07	0.36	2216.50	0.50	0.60	15549.00	3.00	0.03
Location(EnvD)	9	10135.00	9.22	<0.001	5677.30	8.39	0.001	6112.70	2.70	0.001
Residual: (Res)	239	1099.30			676.45			2255.40		

Table 4.3: Overall dissimilarity ($\bar{\delta}$) of sponge life forms between offshore island and coastal headland locations (SIMPER). Species regarded as being important contributors to the assemblage dissimilarity are shown in bold. Values shown in the pairwise comparisons are the average percent cover for the life form.

Life form	$\bar{\delta}_i$	% $\bar{\delta}_i$	$\bar{\delta}_i$/SD($\bar{\delta}_i$)	Mean abundance offshore island	Mean abudance coastal headland
Encrusting sponge	**18.73**	**28.05**	**1.18**	**5.97**	**4.19**
Arborescent sponge	**17.44**	**26.12**	**1.21**	**5.64**	**2.81**
Cup sponge	8.30	12.44	0.81	1.86	1.36
Massive sponge	6.99	10.47	0.59	0.54	1.93
Fan sponge	6.35	9.51	0.67	1.16	1.25
Pappilate sponge	3.09	4.64	0.44	0.27	0.69

4.4 Discussion

Precision of Multivariate Assemblage

The assemblages and single variables examined here from the sponge-dominated intermediate reef habitat class exhibited considerable spatial variability that was unrelated to environmental variation among locations. Benthic assemblages from similar habitats elsewhere also exhibit heterogeneity at a range of spatial and temporal scales (Roberts and Davis, 1996; Roberts *et al.,* 1998; Roberts, 2000; Owen, 2003; Roberts *et al.,* 2006), which makes it challenging to accurately characterise assemblages (Cao *et al.,* 2003). Furthermore, many ecological datasets are dominated by zeros but also contain large numbers (Drummond and Connell 2005). If optimal sampling effort for assemblages is not determined prior to surveys, assemblages may not be accurately described. Understanding how to best sample multivariable datasets, and to be able to describe spatial or temporal differences within and between these datasets is important for conservation planning (Underwood 1997). Most studies that undertake pilot studies prior to surveys do so to determine optimal sampling effort for single variables. This is one of the few studies that determined the optimal sampling effort for assemblages. Quantifying sampling precision of multivariate assemblages provides a basis for establishing the confidence associated with the conclusions drawn in ecological surveys (Cao *et al.,* 2003). In order to maximise the chance of adequately representing biological diversity within marine protected areas it is important that the composition and variation of assemblages is known (or represented by an effective surrogate). High resolution

surveys of sessile benthic assemblages are an important component of such planning to ensure that spatial variations in assemblages are considered, and surrogates for rocky reefs can be defined at lower hierarchical levels.

In this study the magnitude of difference between precision values was greatest between datasets based on differing numbers of images, rather than differing grid point analysis. Tests on varying the methods of assessment of univariate data sets describing subtidal turfing algae benthic assemblages also indicate that techniques that utilise the greatest replication are likely to produce the most accurate and precise estimates of taxa, and are more important than varying the intensity of grid point intercepts, random vs regular grid points, in situ vs laboratory vs photographic sampling vs computer digesting (Drummond and Connell (2005). However, increasing sampling intensity within quadrats will improve the capacity to detect rare and cryptic species (Drummond and Connell (2005), although the contribution of rare and cryptic species to the benthic assemblage in this study does not appear to be important.

In this study differences in the precision of assemblages were detected based on datasets with differing numbers of images. An asymptote was detected in precision values for assemblages based on datasets with 25 images, after which greater replication did not result in greater precision. Previous studies using photoquadrats at a similar spatial scale to this study (Roberts and Davis, 1996; Roberts *et al.,* 1998; Roberts, 2000, Owen 2003; Roberts *et al.,* 2006) sampled 10 replicate images using one metre square quadrats, without the justification from pilot studies. This study selected a sampling effort of 25 images after analysis of a range of alternative sampling regimes. Images captured approximately 2.1 m^2 (1.6 m x 1.3 m) of the reef. Previous studies that have used high resolution AUV technology have been large-scale surveys examining regional patterns in habitats utilising one kilometre long transects and analysing every 100^{th} image (Meyer *et al.,* 2011), or monitoring programs that subsampled within a 25 m x 25 m area of seabed at 20 s intervals to generate a sample set of non-overlapping images (Smale *et al.,* 2012). Remote sampling using AUV technology that result in a large amount of high-resolution data within this habitat will allow for adequate levels of replication without the substantial investment in resources required for similar surveys done via SCUBA. It is important to note that this study was undertaken on benthic assemblages that grouped sponges into broad morphological groups rather than identifying to species level, and the precision estimates for the true benthic assemblage that includes sponge species, may differ.

Sampling intensity contributed to precision and, surprisingly, the greatest sampling intensity was not the optimal choice. This study detected an asymptote in precision values for assemblages based on datasets with 25 images analysed using 50 grid points. Increasing the grid point matrix to 100 did not result in greater precision values. Previous studies have utilised 100 grid point matrices, without the justification from pilot studies, to analyse benthic assemblages within intermediate reef habitat (Roberts and Davis, 1996; Roberts *et al.,* 1998; Roberts, 2000; Owen, 2003; Roberts *et al.,* 2006). Van Rein *et al.* (2011) also concluded the use of 50 grid point intercepts was optimal to quantify the number of species and detect change in sessile benthic assemblages in temperate north-west Europe. Drummond and Connell (2005) found that increasing the sampling intensity from 50 to 100 grid point matrices when describing turfing algae benthic taxa (based on univariate data sets, the multivariate assemblage was not examined) did not have substantial effects on precision or accuracy of broad taxonomic groups.

General Diversity

The benthic fauna in sponge-dominated habitats is highly diverse in tropical (Hooper and Kennedy, 2002) and temperate Australia (Roberts and Davis, 1996). In this study the richness of sessile benthic organisms in the intermediate reef habitat of the PSGLMP varied between 4 and 16 categories per quadrat, which is within the range found by previous studies in the same habitat and depth range in nearby locations (Roberts, 1996; Roberts and Davis, 1996; Roberts *et al.,* 1998; Owen, 2003; Roberts *et al.,* 2006) (however note the intrinsic differences between these studies such as differing quadrat size and taxonomic resolution). The life form richness of sessile benthic organisms at coastal headlands and offshore islands in the PSGLMP was not different. Previous studies in sponge-dominated reef from temperate NSW have used species richness (as these studies were able to collect tissue samples to enable species identification), rather than life form richness. These previous studies have found that both depth (Roberts and Davis, 1996) and exposure (Roberts *et al.,* 2006) are important factors in sponge richness. The total richness recorded across all locations is much lower than that recorded in these previous studies, which is likely due to two reasons. First, although the AUV images have a high resolution, small and cryptic biota were difficult to detect on the images because of the height above the seafloor at which the images were taken. Second, these previous studies identified sponges to species-level rather than broad morphological groups. For example, Roberts and Davis (1996) recoded 57 sponge species off Sydney on rocky reefs of similar depth to this study. Sponge richness in this study is under-

represented as species were grouped into 10 broad morphological groups, rather than to species level. Previous diver-based and jump camera surveys (Roberts, 1996; Roberts and Davis, 1996; Roberts *et al.,* 1998; Owen, 2003; Roberts *et al.,* 2006) took sponge tissue samples to enable identification to species level, whereas by utilising AUV technology, this study was unable to take sponge tissue samples. Using the AUV has several advantages over diver-based surveys, namely that large amounts of high resolution images can be collected at greater depths at multiple locations in a day, allowing for high levels of replication at numerous spatial scales. This study used richness of sponge morphological types as a proxy for species richness, based on previous studies that have verified this assumption in Ireland (Bell and Barnes 2001) and Indonesia (Bell, 2007). A study examining the relationship between morphological richness and species richness is warranted for the sponge fauna of temperate Australia.

The Use of AUVs in Sessile Benthic Reef Assemblages

Remote videography and photography data can provide large amounts of quantitative data on biological distributions. These datasets lend themselves well to robust multivariate analyses, and assist in the ground-truthing of habitat classes derived using other remote sensing platforms (e.g. acoustics) that are at scales relevant for assessing and planning representative MPA's (Stevens, 2002; Jordan *et al.,* 2005). This is the first study to examine patterns in sessile benthic assemblages within PSGLMP utilising data collected by AUV and their relevance to the use of habitat as a biodiversity surrogate. The AUV platform that collects high resolution imagery is an effective method for sampling sessile benthic assemblages in depths below safe diving depths. To date there has been no cost-benefit analysis comparing data collected using AUVs with diver-based surveys, although this study found advantages and disadvantages of using AUVs to remotely collect data over that obtained by divers. AUVs can collect large numbers of high resolution images far quicker than divers, with multiple locations able to be sampled in a day, allowing for high levels of replication at numerous spatial scales. Additionally, AUVs collect additional information on physical parameters such as depth and temperature, and surveys can have high positional accuracy. However, a larger vessel (and hence greater cost) is required to deploy the AUV, and there is also the need for much greater ancillary equipment and expertise for survey planning, deployment and post-processing for AUV surveys. Furthermore, the AUV is not set up to take sponge samples to enable identification to species level. Individuals processing the images require familiarity with the biota typical of the benthic assemblage, as even with high

resolution images, small and cryptic biota can be difficult to detect due to the height above the seafloor that the images are taken.

Spatial Patterns in Assemblages and Categories

In this study the hypothesised difference between environmental domains (coastal headlands and offshore islands) was not a consistent source of variation for sessile benthic assemblages (the one exception being assemblages based on sponge life forms). Coastal headlands and offshore islands were considered different environmental domains due to differences in exposure and distance from shore, where offshore islands might encounter different current regimes that might also provide different larval assemblages. Previous studies in similar habitat and depth have found that a range of environmental variables, including depth (Roberts and Davis, 1996; Newton *et al.,* 2007), exposure to sewer plumes (Roberts, 1996; Roberts *et al.,* 1998), exposure to estuarine plumes (Owen, 2003), and exposure to wave action (Roberts *et al.,* 2006; Newton *et al.,* 2007) influence sessile benthic assemblages and some categories, namely cover of silt, which is more abundant at locations exposed to sewer and estuarine plumes, and cover of encrusting and phototropic taxa, which is less abundant at locations exposed to sewer or estuarine plumes. These results are in contrast to this study, where assemblages and the majority of categories did not vary between environmental domains; offshore island assemblages were as different to each other as to assemblages at coastal headlands. This is an unexpected result, given that previous studies have documented variation in taxa and assemblages in relation to environmental influences. In this study the mean depth of each location varied between 21.7 m and 32.0 m, a depth at which environmental variables that may be influencing differences in the abundance and distribution of taxa at offshore islands and coastal headlands (exposure to wave action, water turbulence, distance to shore, distance to estuarine mouth) may not be important contributors to biodiversity. The previous studies by Roberts *et al.* (1998), Owen (2003) and Roberts *et al.* (2006) were undertaken at shallower depths (20m, 20-25m, 18-20m respectively), where environmental variables appear to be more influential. Roberts *et al.* (2006) found sheltered reefs were dominated by upright sponges. In this study arborescent sponges had higher cover at offshore islands, however both offshore islands and coastal headlands are in high exposure areas. A possible explanation for this may relate to differences in small scale topography, for example the presence of large boulders or overhangs may create small areas of low water turbulence, leading to an increase in upright life forms. Another explanation, given that assemblages within the same environmental domain were as different to each other as to

those in other environmental domains, is that variation within assemblages is operating at a smaller scale than that examined in this study, and that factors such as differences in small-scale patches of different habitat types (such as vertical and horizontal rock shelves, boulders and cobbles), and small-scale differences structural complexity (for example the occurrence of complex habitat such as overhangs) may provide preferred habitat characteristics for groups of species. Small-scale habitat patchiness has been documented in sponge-dominated assemblages in Brazil, with greater abundance recorded at overhangs than vertical and horizontal walls, and higher diversity at overhangs and vertical walls than horizontal walls (Monteiro and Muricy, 2004).

In this study spatial variation was a greater source of variation than environmental domains. This variation was not based on the distance between locations; there was significant spatial variation for all variables tested, at the spatial scale of 12 km (the average distance between locations). Locations several hundred metres apart were as dissimilar to each other as locations 10s km apart. Again this high spatial variability may be due to differences in small scale topography between locations (for example large boulders or overhangs) that create large areas of substrate available for colonisation. This high degree of spatial variation is in agreement with Roberts *et al.* (2006) who documented high variability in sponge-dominated assemblages at reefs subject to high water turbulence, as would be experienced at both coastal headlands and offshore islands. Another possibility is that the lack of spatial differences at this large scale is due to a Type II error due to the lack of taxonomic resolution. This could be overcome through modifications to the AUV to make collection of sponge tissue samples (and hence species identification) possible.

This is the first study in temperate NSW to examine the effect of using broad taxonomic groups rather than species-level identification to describe patterns in sponge-dominated sessile benthic assemblages. This study found patterns between assemblages based on broad taxonomic groups and species-level identification (life form groups for sponges) to be similar. Roberts (2000) also found patterns of diversity within sessile benthic assemblages in another habitat on temperate NSW rocky reefs, kelp *Ecklonia radiata* forests, to be similar using both broad taxonomic groups and species-level identification.

Implications for Marine Protected Area Planning

Mapping of seabed habitats at a range of spatial scales is being recognised as an increasingly important component to the overall research required to identify the distribution and structure

of marine ecosystems and habitats for MPA planning (Jordan *et al.,* 2005). Habitats can act as effective surrogates for biotic assemblages in the MPA planning process, providing they are being appropriately validated (Ward *et al.,* 1999, but see Shokri and Gladstone, 2013) and all representative habitats are included (Roff *et al.,* 2003). Habitat is the most frequently chosen surrogate for designing marine reserves. The assumption is that if a certain percentage of all habitat classes are present are protected, then the specific biodiversity associated with those habitat classes will also be protected (Lindsay *et al.,* 2008). The use of habitat mapping based on the abiotic variable of depth has been widely used as a surrogate for sessile benthic assemblages in MPA planning in NSW (Breen *et al.,* 2004; New South Wales Marine Park Authority, 2006). This assumes that reef habitats within specific depth classes are homogeneous, and therefore any area of that habitat type may adequately represent the biological diversity within that habitat (Winberg *et al.,* 2007; Smith *et al.,* 2008). However, in temperate southeast Australia, high heterogeneity has been documented in marine and estuarine habitats, with Winberg *et al.* (2007) documenting high habitat heterogeneity in tidal flat macrobenthos that would influence the choice and number of MPAs required to conserve both dominant and rarer taxa. Furthermore, Smith *et al.* (2008) documented high spatial heterogeneity in shallow subtidal rocky reefs in northern NSW, and questioned the use of arbitrary measures such as percentage of a broad habitat type to allocate conservation effort in MPA zoning schemes. In examples from studies in sponge-dominated reef, sessile benthic assembles exhibit high spatial heterogeneity in response to both environmental and anthropogenic influences (Roberts, 1996; Roberts and Davis, 1996; Roberts *et al.,* 1998; Owen, 2003; Roberts *et al.,* 2006). Newton *et al.* (2007) found that depth and exposure were important sources of variation within subtidal rocky reef ascidian assemblages in PSGLMP, and that numerous locations subject to differing environmental influences would need to be protected within an MPA to adequately represent ascidian biodiversity.

The application of physical surrogates of biodiversity (e.g. habitat maps) in conservation planning requires an understanding of the spatial scales at which faunal assemblages change within a habitat, and the underlying processes responsible for this variation. Information on the latter is potentially useful for refining habitat-based surrogates. Little confidence can be placed in marine habitat classifications based solely or largely on abiotic surrogates without supplementary biological surveys. Malcolm *et al.* (2007) found that for fish assemblages on the north coast of NSW, distance-from-shore was strongly correlated with patterns of reef fish assemblages, and recommended that distance-from-shore be incorporated into habitat

classification to improve the ability of MPA to represent biological diversity. Williams *et al.* (2009) found that depth, size, complexity, configuration and anthropogenic impact all needed to be added to geomorphic features used to act as surrogates of biodiversity within Australia's deep-water reserve network.

Other than the studies by Roberts and Davis, (1996), Owen, (2003), Roberts *et al.* (2006) and Newton *et al.* (2007) there is little published information regarding the importance of environmental variables in structuring sessile benthic assemblages in sponge-dominated reefs. However, the results of these previous studies suggest that environmental influences, including depth (Roberts and Davis, 1996; Newton *et al.,* 2007), exposure (Roberts *et al.,* 2006; Newton *et al.,* 2007) and estuarine plumes (Owen, 2003) are important factors driving the structure of these assemblages. This study showed that offshore islands and coastal headlands do not support distinct assemblages (except for assemblages based on sponge life forms), and the most significant source of variation occurred among randomly selected locations. Conservation planning that aims to represent the diversity of these assemblages should therefore aim to protect multiple examples of intermediate reefs, separated by distances of 12 km (the average distance between locations in this study). One key way that small scale variability of sessile benthic assemblages in PSGLMP is dealt with is through replication of large sanctuary zones that include rocky reefs along depth gradients, latitudinal gradients and distance from estuarine influence to maximise the chance of encompassing small scale variability (NSW Marine Park Authority, 2007). This precautionary approach in part deals with the lack of data on sessile benthic assemblages through large areas of PSGLMP.

Conclusion

This study highlighted the need for pilot studies to be undertaken in order to develop justifiable sampling regimes. Without the information gained through pilot studies, either more sampling effort is expended than necessary, or else insufficient effort is applied. This study found that environmental variation in the form of coastal headlands and offshore islands did not need to be factored into the current habitat classification scheme in PSGLMP, for all variables tested except cover of arborescent sponges and assemblages of sponge life forms. However, replication would be required at this large (environmental domain) scale prior to drawing this conclusion at the environmental domain scale. In contrast, all assemblages and single variables varied substantially at relatively small spatial scales (10s

km). In terms of conserving a representative sample of biodiversity of sessile benthic assemblages within the PSGLMP framework, the results of this study suggest that multiple examples of the intermediate reef habitat at the small scale would need to be conserved to capture the biodiversity of sessile benthic assemblages, such as that currently undertaken through replication of large sanctuary zones that include rocky reefs along depth gradients, latitudinal gradients and distance from estuarine influence.

Chapter 5 Scales of spatial autocorrelation in sessile benthic assemblages of subtidal rocky reefs and implications for marine protected area planning

Abstract

Sessile benthic assemblages of temperate subtidal rocky reefs are highly variable at numerous spatial scales. The existence of spatial autocorrelation in these assemblages has implications for the spatial scales of ecological studies, monitoring designs, and decisions about the linear dimensions of areas selected to represent examples of distinct assemblages in marine protected area planning. However, information on the existence and scale of spatial autocorrelation is rarely available. This study determined scales of spatial autocorrelation in sessile benthic assemblages in subtidal rocky reefs in a marine protected area in south-east Australia in two environments (coastal headland, offshore island) and replicate locations within each environment. Assemblages were surveyed remotely using an Autonomous Underwater Vehicle (AUV). Thirty-one species of encrusting benthic organisms, ten sponge morphological groups, and two substrate variables were recorded. At a fine scale (a single 25 m transect from each location) and a larger scale (all transects over 775 m at the coastal headland environmental domain, and 2724 m at the offshore island environmental domain) there was a significant positive correlation between distance and dissimilarity of the total benthic assemblage, meaning that assemblages became more dissimilar as distance increased. Rank correlograms indicate that the spatial pattern of sessile benthic assemblages was patchy at both scales. There was no clear or consistent threshold distance at which assemblages changed from being homogeneous to heterogeneous, however at the fine scale, all locations displayed heterogeneous assemblages by the >15-25 m distance class. At the larger environmental domain scale, assemblages were homogeneous at the >350 m distance class for the offshore island environmental domain, and >325 m distance class for the coastal headland environmental domain. Biodiversity sampling is required at a fine scale for the purposes of creating habitat maps for MPA planning. Information on the existence of spatial autocorrelation and the distances over which it occurs must be considered in the design of sampling programs, as it is an extremely important consideration in monitoring. Differences between sessile benthic assemblages within differing environmental domains need to be further examined so that representative samples can be conserved within the marine park framework.

5.1 Introduction

Subtidal rocky reefs in temperate Australia support diverse and endemic assemblages and species and the habitats within these reefs support commercially important species (Ponder *et al.,* 2002; Smith *et al.,* 2010). These reefs are characterised by several distinctive habitats, the distribution of which are related to physical forces including depth and wave exposure, and biological pressures, most notably herbivory by the sea urchin *Centrostephanus rodgersii* (Underwood *et al.,* 1991). 'Fringe habitat' occurs just below low tide level to depths of approximately 3 m and is dominated by a diverse range of algae. 'Turf habitat' is characterised by a variety of turfing coralline and filamentous algae and occurs within shallow (< 10 m) water. Forests of *Ecklonia radiata* occur at 2-25 m, and are interspersed with patches of sea urchin-grazed crustose coralline algae (the 'barrens habitat'). Forests of *Phyllospora comosa* occur at nearshore reefs in southern New South Wales (NSW) at 2-25 m. *Pyura* habitat is dominated by the large solitary ascidians *Pyura gibbosa* and *P. stolinifera* and occurs at 2-25 m. Sponge-dominated 'deep reef habitat' occurs >9 m depth and is characterised by a significant density of sessile benthic animals, including sponges, corals and bryozoans unique to the habitat (Underwood *et al.,* 1991; Smith *et al.,* 2010). These rocky reef habitats have been mapped in the nearshore waters of NSW using large-scale physical and biological attributes to support conservation planning (Jordan *et al.,* 2010). Large gaps in knowledge still exist about spatial and temporal patterns within sponge-dominated reefs in temperate NSW, their associated assemblages, and the underlying ecological processes (Davis *et al.,* 2010).

In southeast Australia assemblages of sessile benthic organisms on subtidal rocky reefs are spatially and temporally dynamic, with the structure and diversity of assemblages reflecting the influences of differing environmental variables (Roberts and Davis, 1996; Roberts *et al.,* 2006; Davis *et al.,* 2010). Within the community of sessile benthic organisms, sponge assemblages are highly variable at scales of metres, 100s metres and 10s km (Roberts, 1996; Roberts and Davis, 1996; Roberts *et al.,* 1998; Owen, 2003; Roberts *et al.,* 2006). Examples from studies in rocky reef habitats elsewhere have also documented small-scale variability of benthic assemblages in the Mediterranean (Bulleri and Benedetti-Cecchi, 2006). As a result, there is a high degree of uncertainty regarding the appropriate spatial scales at which sessile benthic assemblages need to be described for effective conservation and management (Hooper and Kennedy, 2002; Worheide *et al.,* 2005).

Autocorrelation is the degree to which assemblages are similar spatially (Lloyd *et al.,* 2006). Spatial autocorrelation analyses are used to detect and describe fine-scale patterns of spatial structure in assemblages, and can greatly improve the design of sampling schemes by maximising the chance of detecting spatial patterns whilst being time- and cost-efficient (Gonzalez-Mirelis *et al.,* 2009). Spatial autocorrelation analysis is based on the fact that given a certain size of sample unit (e.g. quadrat), distance between sample units and extent of survey, variables (such as % cover of biota) measured within sample units are not independent from variables measured in nearby samples, thereby potentially biasing the results of standard statistical tests (Gonzalez-Mirelis *et al.,* 2009). When a series of geographically referenced samples are available, the relationship between spatial autocorrelation and distance can be evaluated, and the scales at which patterns of autocorrelation emerge revealed. This relationship can then be used to determine the amount of spatial detail required in sampling to effectively describe the variation in benthic assemblages (Parry *et al.,* 2003; Gonzalez-Mirelis *et al.,* 2009).

Considerations of spatial heterogeneity are important to underpin management decisions about the number, size and location of marine protected areas (MPAs) (Benedetti-Cecchi *et al.,* 2003). Understanding of the extent and scales of autocorrelation within habitats can then be used in decision-making about the size and number of MPAs required to include the range of biological diversity within the planning area. The scales of autocorrelation in marine soft sediment epibenthic assemblages have been used to recommend maximum and minimum size of habitat patches for MPA planning (Stevens, 2005). Spatial autocorrelation studies of freshwater benthic assemblages in south-eastern Australia have been used to infer patterns of spatial relationships among invertebrate assemblages within river systems (Lloyd *et al.,* 2006; MacNally *et al.,* 2006). The scales of spatial autocorrelation in sessile benthic assemblages on subtidal rocky reefs of temperate Australia are unknown.

In the context of MPA planning, the patterns of similarity across spatial scales revealed by autocorrelation studies depict the threshold at which an assemblage changes from a homogenous assemblage to a heterogeneous, patchy one (Gonzalez-Mirelis *et al.,* 2009). This information can be used to determine the linear dimensions and numbers of areas required to represent the diversity of assemblages occurring in a planning area (Stevens, 2005). For example, Gonzalez-Mirelis *et al.* (2009) found that in the Koster fjord, Sweden, areas of benthic assemblages on the seafloor approximately 38 m across are likely to be sufficiently homogenous as to consider variation within it unnecessary spatial detail in the regional

context. In Morten Bay, Australia, site spacing greater than 10 km would under represent biodiversity of soft sediment epibenthic assemblages (Stevens, 2005). Studies on spatial autocorrelation can also provide information about whether sites further apart are less similar than sites close together, and whether spatial agglomeration of sites into groups is a valid approach in deriving polygons of relative homogeneity for the purposes of creating habitat maps for MPA planning (Stevens, 2005). The planning process of MPAs has high resource (cost) and social implications, and therefore planning needs to be as efficient as possible while achieving biodiversity representation goals.

A major challenge in describing the biodiversity and spatial variability of subtidal rocky reefs involves the collection of sufficient data from the range of depths at which this habitat occurs. Data on sponge assemblages from subtidal rocky reefs in NSW have previously been collected by *in situ* diver surveys (Owen, 2003) and drop cameras (Roberts *et al.,* 1994; Roberts, 1996; Roberts and Davis, 1996; Roberts, 2006), both of which are unable to collect large amounts of field data quickly. More recently Autonomous Underwater Vehicles (AUV) have been utilised to map and describe sponge-dominated assemblages (Meyer *et al.,* 2011; Smale *et al.,* 2012). The ability of an AUV to collect large numbers of geographically referenced high quality images enables studies to be undertaken on small-scale patterns of autocorrelation in benthic habitats (Gonzalez-Mirelis *et al.,* 2009).

The aim of this study was to determine whether a relationship exists between biological dissimilarity and distance for sessile benthic organisms on sponge-dominated subtidal rocky reefs, by testing for autocorrelation within habitat patches 100s m in extent and separated by km, and between patches in coastal headland and offshore island environments. Autocorrelation analyses were done for the entire encrusting benthic assemblages and for a subset of the assemblage that consisted of sponges only (the dominant faunal group). The study tested the null hypothesis that there was no relationship between increasing distance between samples and increasing biological dissimilarity.

5.2 Methods

Study Area

Port Stephens-Great Lakes Marine Park (PSGLMP) is situated on the mid-north coast of NSW (Fig. 3.1), and includes estuaries, open coast and islands covering approximately 98,000 ha. (see detailed description in Chapter 3). Subtidal rocky reef habitat is generally

associated with rocky shore adjacent to both coastal and island headlands (Jordan *et al.,* 2010), represents approximately 3% of the PSGLMP and is classified by depth for planning purposes (New South Wales Marine Park Authority, 2006). In this study the coastal headland (Fingal) and offshore island (Broughton Island) environmental domains differed in exposure and distance from the mainland coast. Fingal is connected to the mainland via an intermittent sand spit, and the coast of Broughton Island ranges from approximately 2.5 to 6.0 km offshore.

Experimental Design and Field Sampling

Sampling occurred in sponge-dominated subtidal rocky reef within the 'intermediate' rocky reef class (25-60 m depth). Sessile benthic assemblages were remotely surveyed using the University of Sydney's Australian Centre for Field Robotics (ACFR) AUV (Rigby *et al.,* 2010; Williams *et. al.*, 2012). The AUV is equipped with high resolution stereo camera pair and strobes, multibeam sonar, depth and conductivity/temperature sensors, Doppler Velocity Log (DVL) including a compass with integrated roll and pitch sensors, Ultra Short Baseline Acoustic Positioning System (USBL) and forward looking obstacle avoidance sonar. Ten 25 m x 25 m photo sampling grids were surveyed in a range of locations grouped into two environmental domains: offshore island and coastal headland (Fig.5.1). The AUV surveyed a 25 x 25 m area (hereafter called a 'location') in which it recorded images along a 25 m line, then turned around to record images along an adjacent (<1 m distance) line until the location had been surveyed. Six locations were surveyed at the headland reef and 4 locations were surveyed at the island reef. Locations occurred within both sanctuary zones and habitat protection zones within the PSGLMP, were separated by at least 200 m, and corresponded to locations where fish assemblages were surveyed using Baited Remote Underwater Video (see detailed description in Chapter 6). The mean depth of each location varied between 21.7 m and 32.0 m.

The number of images collected by the AUV varied between 975 and 1975 per location (n=18,750 total images). There was often overlap between images (generally every 3rd to 5th image was a 'new' image without any overlap from the previous image), and when the AUV turned back to complete the next transect every ~12th image contained no overlap with adjacent transects. Prior to analysis each image was viewed in Arc GIS to detect its location and ensure it was not overlapping with the last selected image.

At each location all non-overlapping images within a randomly-selected single 25 m transect were analysed (resulting in 30 images) to test the null hypothesis that there would be no relationship between distance and biological dissimilarity at this small spatial scale. Distance between samples was calculated by counting the number of non-overlapping images and dividing by the transect distance (25 m). All transects from all locations in each environmental domain were then used for a test of the null hypothesis that there would be no relationship between distance and biological dissimilarity at this larger spatial scale. Distance between images was measured within GIS. The maximum distance between images was 775 m in the coastal headland environment and 2794 m in the offshore island environment. Therefore, to eliminate the possibility that the results of the analyses would be affected by the distances over which the tests were done, two analyses were done: all images within each environmental domain, and all images within each environmental domain over a similar geographical distance (325 m for the coastal headland environmental domain, and 375 m for the offshore island environmental domain).

Images were analysed by applying a transparent image containing 50 random points (optimal sampling intensity was determined by a pilot study (see Chapter 4) over the top of each AUV-collected image of the habitat. The organism or substrate (where no organism was present) occurring below each point was identified and recorded (Stevens, 2005; Gonzalez-Mirelis *et al.,* 2009).

A mixture of classification schemes was used to identify organisms in the selected images. Sponges were classified into broad morphological groups (arborescent, cup, encrusting, fan, globular, lumpy, massive, papillate, repent and tubular) developed by the Commonwealth Environment Research Facility (CERF) Marine Biodiversity Hub: Surrogates Program (Meyer *et al.,* 2011), as sponge species identification is not possible without tissue samples for examination. Other sessile benthic organisms were identified to species-level where possible (using Shepherd and Thomas, 1982; Edgar, 1997; Huisman, 2000; Veron, 2000; Gowlett-Holmes, 2008) and to morpho-species when identification was not possible.

Statistical Analyses

For tests done at the scales of transects and environmental domains, the distances between all possible pairs of images were calculated, and used to develop distance matrices. Bray-Curtis dissimilarity based on presence-absence data (Stevens, 2005; Gonzalez-Mirelis *et al.,* 2009) was used as the measure of assemblage dissimilarity between all possible pairs of images at each scale. Spearman's rank correlation coefficient (Rho, ρ) between Bray-Curtis dissimilarity matrices and distance matrices were calculated using the RELATE test in PRIMER 6 software (PRIMER-E Ltd, Plymouth) (Clarke and Warwick 2001). This procedure was repeated for a subset of the entire dataset that was based only on sponge morphological groups (the dominant faunal group).

Spatial patterns of the assemblage were explored by constructing multivariate rank-correlograms (Somerfield and Gage, 2000; Parry *et al.,* 2003), which allow the biotic dissimilarity of samples within a preset distance class to be compared with the biotic dissimilarity of all other samples. The following distance classes were used for the 25 m transect data set: < 3 m, >3-6 m, >6-9 m, >9- 12 m, >12-15 m, >15-25 m. The following distance classes were used for the full coastal headland environmental domain data set: < 25 m, >25-325 m, >325-550 m, >550- 600 m, >600-750 m, >750-775 m; and the full offshore island environmental domain data set: < 200 m, >200-350 m, >350-2700 m, >2700- 2724 m. Trends in the environmental domain datasets were then examined over similar spatial scales, using the following distance classes for the offshore island environmental domain data set: < 8 m, >8-16 m, >16-300 m, >300- 308 m, >308-316 m, >316-325 m; and the offshore island environmental domain data set: < 8 m, >8-16 m, >16-200 m, >200- 208 m, >208-216 m, >216-350, >350-358 m, >358-365 m, >365-375 m. These distance classes were chosen after looking at several sets of distance categories, as this combination of distance classes gave similar sample sizes in each category, so the correlation tests are powerful and the correlation coefficients can be compared (Parry *et al.,* 2003).

A separate distance matrix was constructed for each individual distance class by recoding each cell of the sample distance matrix with '1' if the sample separation fell with the distance class and '0' for all other cells (Parry *et al.,* 2003). Each distance class matrix was correlated with the Bray Curtis biological dissimilarity matrix using the RELATE test. Positive Spearman's correlation coefficients corresponded to samples that were more alike than expected by chance and vice versa (Parry *et al.,* 2003). This correlation represents a two-

tailed test because samples within each distance class may be more or less similar than all other samples (Parry *et al.,* 2003). Therefore, assuming significance of correlation at p=0.05, significant positive autocorrelation occurred when p<0.025 and significant negative autocorrelation occurred when p>0.975 (Parry *et al.,* 2003).

A multivariate rank-correlogram (Somerfield and Gage, 2000; Parry *et al.,* 2003) was constructed by plotting each correlation coefficient value against distance class. Rank-correlograms are used as a measure of the minimum radius of a patch of similar fauna and to depict the threshold at which the assemblages move from a homogenous assemblage to a heterogeneous, patchy one (Gonzalez-Mirelis *et al.,* 2009). This threshold is given by the intercept of the autocorrelation coefficient with the x-axis (Gonzalez-Mirelis *et al.,* 2009). A spatially homogenous faunal assemblage is represented by a rank-correlogram in which no Spearman's correlation coefficient values are significantly different from zero (i.e., a more or less flat line levelled around the origin axis) (Gonzalez-Mirelis *et al.,* 2009).

Figure 5.1: Location of study sites in Port Stephens-Great Lakes Marine Park. Symbols represent offshore island (square) and coastal headland (circle).

5.3 Results

General

Forty-one life forms were recorded across all locations, representing 21 categories of encrusting benthic organisms (three Phaeophyta (brown algae), seven Rhodophyta (red algae), ten Cnidaria (corals and anemones), six Bryozoa (bryozoans) and five Ascidiacea (ascidians)) and 10 sponge morphological types. In addition, two substrate variables (silt matrix, sand) were recorded. Silt matrix (consisting of sediment and micro-organisms) (Roberts *et al.,* 1994) (with a mean % cover (± SE) of 27.0±2.54%), filamentous red algae (15.5±0.68%), sand (15.2±2.77%), encrusting coralline algae (13.3±2.14%), encrusting sponge (4.9±0.82%) and arborescent sponge (3.9±0.66%) were the dominant variables recorded (Table 5.1). Sponges were the dominant fauna at both environmental domains, with 10 morphological types (arborescent, cup, encrusting, fan, globular, lumpy, massive, papillate, repent and tubular) recorded in each environmental domain (Appendix 1).

Table 5.1: Mean % cover (±SE) of the major groups of organisms and two substrate variables in sessile benthic assemblages of subtidal rocky reefs in the Port Stephens-Great Lakes Marine Park.

Location	Phaeophyta	Rhodophyta	Cnidarian	Bryozoan	Sponge	Ascidian	Silt	Sand	Depth
Coastal headland 1	0.6%±0.4	13.4%±3.9	0.7%±0.4	0.9%±0.6	9.9%±3.4	0.4%±.4	39.7%±4.0	34.5%±6.3	29.6m ±0.03
Coastal headland 2	3.3%±1.1	28.7%±6.5	0.2%±0.2	3.3%±1.5	15.5%±4.1	0.3%±0.2	33.0%±3.1	15.7%±4.1	29.1m±0.07
Coastal headland 3	5.3%±1.7	42.4%±5.2	1.4%±1.2	1.6%±0.7	14.8%±3.7	2.6%±2.4	20.7%±2.1	11.2%±2.7	23.3m±0.08
Coastal headland 4	4.5%±1.2	53.5%±8.7	1.2%±1.0	3.0%±1.0	9.8%±2.9	4.4%±1.3	15.9%±2.0	7.9%±1.2	23.1m±0.04
Coastal headland 5	1.2%±0.7	34.8%±5.7	7.3%±0.3	2.4%±1.0	11.4%±2.8	6.7%±1.6	32.3%±18.4	3.9%±1.0	21.8m±0.06
Coastal headland 6	0.1%±0.1	30.8%±3.3	0.6%±0.3	2.5%±1.0	17%±4.9	3.5%±1.1	31.9%±2.4	13.6%±1.9	24.4m±0.05
Offshore island 1	0.5%±0.3	37.2%±4.4	1.2%±0.7	1.4%±0.4	18.9%±4.2	2.2%±1.0	24.1%±1.6	14.5%±2.4	29.5m±0.03
Offshore island 2	2.0%±0.6	38.4%±6.2	1.4%±0.7	1.6%±0.8	22.5%±3.4	2.2%±0.7	24.9%±1.5	7.0%±1.2	25.5m±0.07
Offshore island 3	3.6%±0.6	52.7%±8.9	0.8%±0.6	1.2%±0.7	13.6%±3.0	1.1%±0.7	16.2%±2.1	10.9%±1.5	25.2m±0.08
Offshore island 4	0.8%±0.6	20.9%±3.4	0.4%±0.2	2.1%±0.8	11.2%±3.8	0.7%±0.5	31.6%±3.0	32.4%±5.6	32.0m±0.04

Small-scale Spatial Structure in Sessile Benthic Assemblages

At the scale of a single 25 m transect there was a significant positive correlation between distance and dissimilarity of benthic assemblages at 8 out of 10 locations (Table 5.2). Both the highest (0.58) and lowest (-0.2) correlation coefficients were recorded at locations from the offshore island environmental domain.

Further analysis of fine-scale correlation utilising a subset of the data (sponge morphological groups, the dominant fauna group) indicated no relationship between distance and dissimilarity at 8 out of 10 locations (Table 5.2). The correlation coefficient was low at all locations; the highest value (0.21) was recorded at a location within the coastal headland environmental domain.

The correlograms examining spatial patterns over small spatial scales showed that sessile benthic assemblages were patchy across all locations, as indicated by the absence of flat line relationships between distance and the correlation coefficient (Fig. 5.2). There was a significant negative result in the <3 m distance class at 9 out of 10 locations, indicating that dissimilarity did not increase as distance increased between images in this distance class. This significant negative result was also apparent at four of the locations in the >3-6 m distance class, and at two of the locations in the >6-9 m distance class. Biotic dissimilarity of samples generally increased at most locations as sample separation increased until there was a significant positive result in the >6-9 m distance class at two of the locations, a significant positive result in the >9-12 m distance class at two locations, a significant positive result at two locations in the >12-15 m distance class and a significant positive result at one location in the >15-25 m distance class (Fig. 5.2). The point at which an assemblage could no longer be regarded as being homogeneous differed among the transects. Assemblages became heterogeneous at 6-9 m (coastal headland location 6), 9-12 m (offshore island location 2, coastal headland locations 3 and 4), and 12-15 m (offshore island locations 3 and 4) (Fig. 5.2). There was no clear distance at which assemblages changed from being homogeneous to heterogeneous at offshore island location 1, and at coastal headland locations 1, 2 and 5.

Table 5.2: Spearman's rank correlation coefficients (Rho) between biological dissimilarity and distance of images from a single 25 m transect in each location, and a subset of data (sponge morphological groups) of subtidal rocky reef in the Port Stephens-Great Lakes Marine Park.

Dataset	Location	Rho	*p*
Sessile benthic assemblages	Coastal headland 1	0.23	<0.01
	Coastal headland 2	0.26	<0.01
	Coastal headland 3	0.51	<0.01
	Coastal headland 4	0.43	<0.01
	Coastal headland 5	0.17	<0.01
	Coastal headland 6	0.16	<0.01
	Offshore island 1	-0.02	0.58
	Offshore island 2	0.58	<0.01
	Offshore island 3	0.20	<0.01
	Offshore island 4	0.11	0.04
Sponge morphological groups	Coastal headland 1	0.21	<0.01
	Coastal headland 2	0.06	0.11
	Coastal headland 3	0.21	<0.01
	Coastal headland 4	0.02	0.34
	Coastal headland 5	0.06	0.15
	Coastal headland 6	0.15	0.01
	Offshore island 1	-0.08	0.92
	Offshore island 2	0.09	0.07
	Offshore island 3	0.07	0.14
	Offshore island 4	0.07	0.08

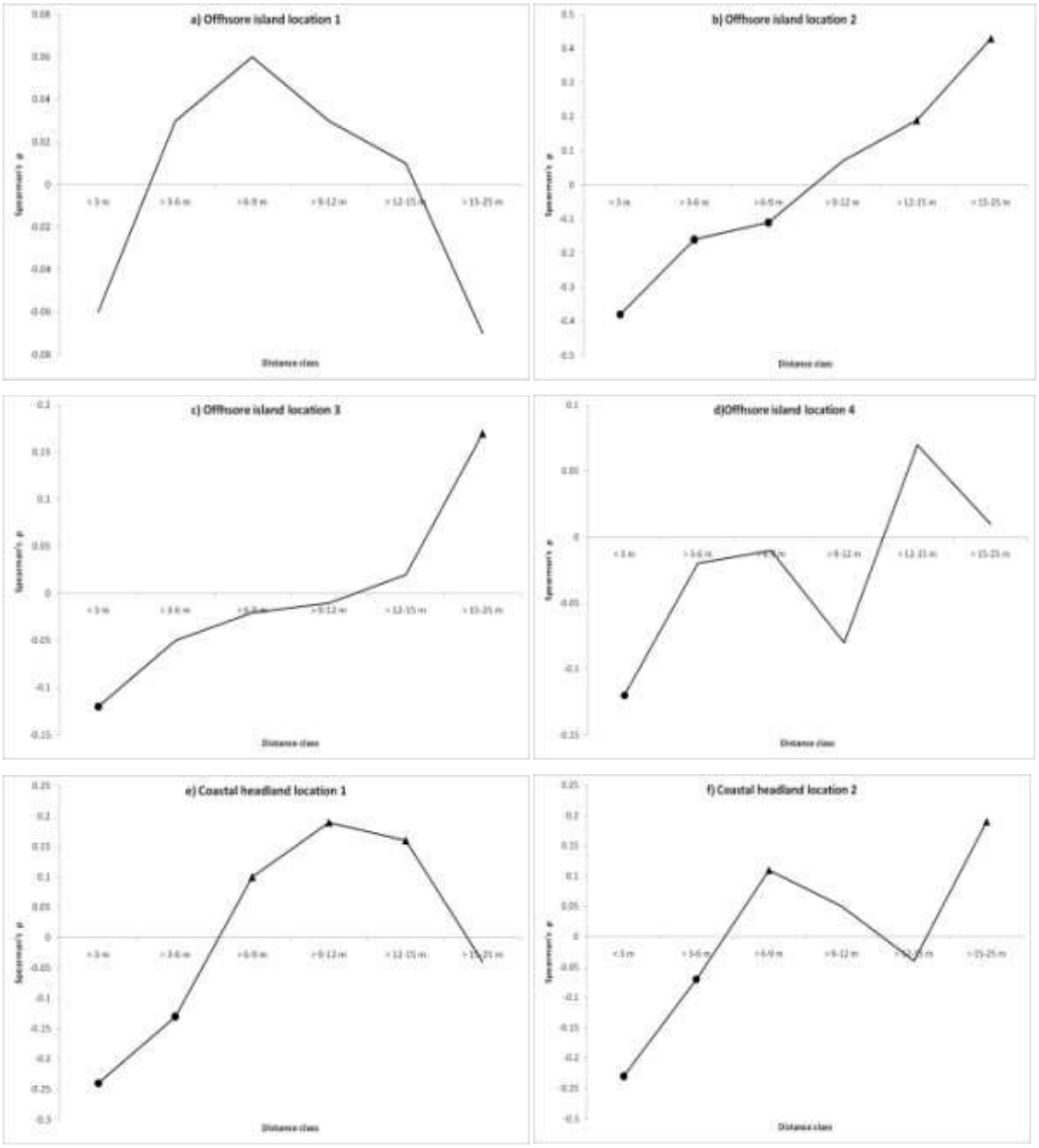

Figure 5.2: Rank-correlograms produced for each location by correlation of Bray–Curtis dissimilarity between samples separated by increasing distance class. ● indicates a significant negative result (correlation significant at $p>0.975$); ▲ indicates significant positive result (correlation significant at $p<0.025$).

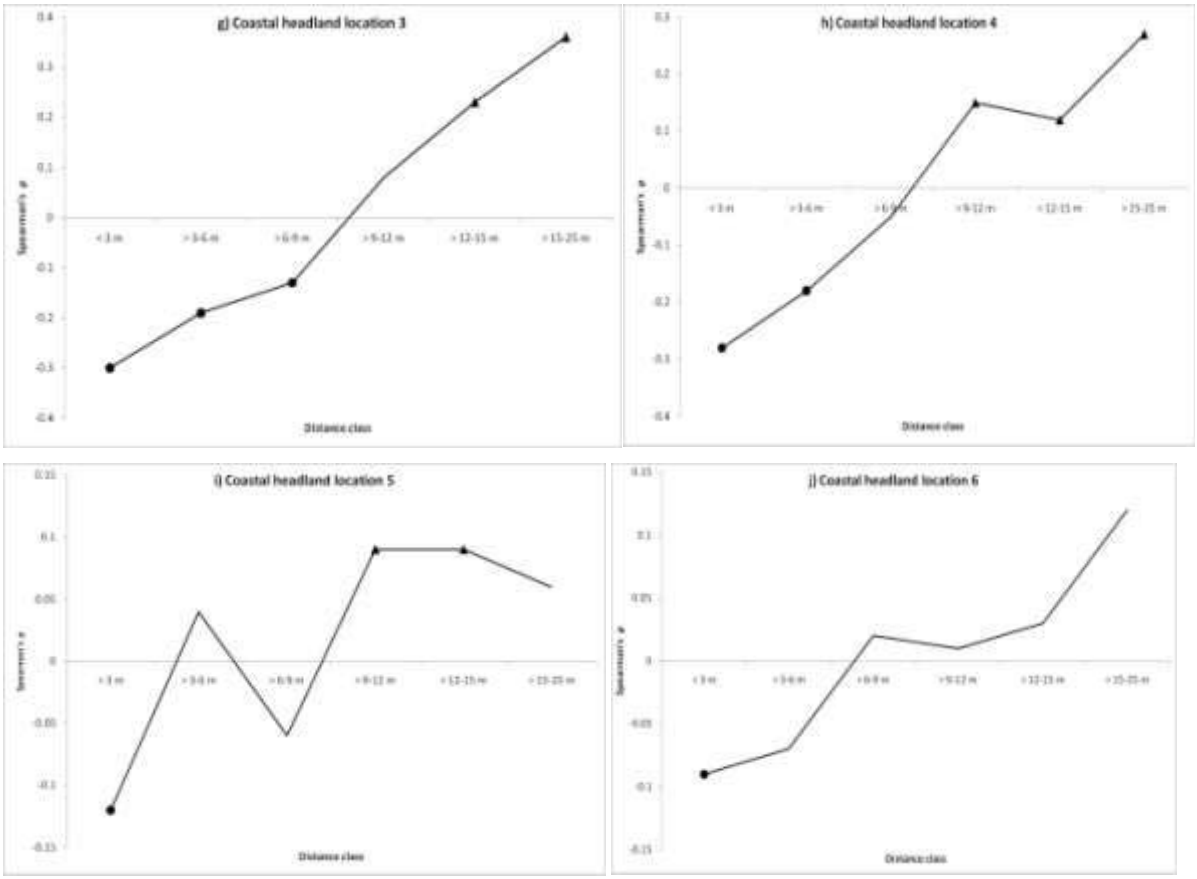

Figure 5.3 (continued): Rank-correlograms produced for each location by correlation of Bray–Curtis dissimilarity between samples separated by increasing distance class. ● indicates a significant negative result (correlation significant at $p>0.975$); ▲ indicates significant positive result (correlation significant at $p<0.025$).

Large-scale Spatial Structure in Sessile Benthic Assemblages

Analysis of correlation at a larger scale (all transects within the offshore island and coastal headland environmental domains) indicated a significant positive correlation between distance and dissimilarity of benthic assemblages, with the correlation coefficient greater at the offshore island environmental domain (0.28) than at the coastal headland environmental domain (0.13) (Table 5.3). This significant positive correlation was also apparent when the dataset included transects over similar spatial scales at both environmental domains, with the correlation coefficient greater at the offshore island environmental domain (0.30) than at the coastal headland environmental domain (0.10) (Table 5.3).

Further analysis of larger scale correlation utilising a subset of the data (sponge morphological groups, the dominant fauna group) again indicated a significant positive correlation between distance and dissimilarity of benthic assemblages, with the correlation

coefficient greater at the coastal headland environmental domain (0.15) than at the offshore island environmental domain (0.10) (Table 5.3). This significant positive correlation was also apparent when the sponge assemblage dataset included transects over similar spatial scales at both environmental domains, with the correlation coefficient greater at the offshore island environmental domain (0.13) than at the coastal headland environmental domain (0.06) (Table 5.3).

Table 5.3: Spearman's correlation coefficients (Rho) between biological dissimilarity and distance between all transects in offshore island and coastal headland environmental domains, and a subset of data (sponge morphological groups) for subtidal rocky reef in the Port Stephens-Great Lakes Marine Park.

Data set	Group	Rho	*p*
Sessile benthic assemblages	Coastal headland	0.13	<0.01
	Offshore island	0.28	<0.01
Sponge morphological groups	Coastal headland	0.15	<0.01
	Offshore island	0.10	<0.01
Sessile benthic assemblages over similar spatial scale	Coastal headland	0.10	<0.01
	Offshore island	0.30	<0.01
Sponge morphological groups over similar spatial scale	Coastal headland	0.06	0.04
	Offshore island	0.13	<0.01

The correlograms examining spatial patterns over the larger spatial scale showed there was a significant negative result at the offshore island environmental domain for distance classes less than 200 m for the full benthic assemblage data set, and for distance classes less than 350 m for the sponge assemblage data set. There was a significant positive result for both the full benthic assemblage data set and the sponge assemblage data set for distance classes greater than 350 m (Fig. 5.3).

There was a significant negative result at the coastal headland environmental domain for distance classes less than 25 m for the full benthic assemblage data set, and for distance classes less than 325 m for the sponge assemblage data set. There was a significant positive result for both the full benthic assemblage data set and the sponge assemblage data set for distance classes greater than 325 m (Fig. 5.4).

Homogenous assemblages were first detected in the >200- 350 m distance class at the offshore island environmental domain for the full benthic data set, and in the >350-2700 m distance class for the sponge assemblage data set. Homogenous assemblages were first detected in the >25- 325 m distance class at the coastal headland environmental domain for both the full benthic data set and the sponge assemblage data set. Assemblages at both environmental domains fluctuated back to heterogeneous at the largest distance class (>2700-2742 m at the offshore island, and >750-775 m at the coastal headland environmental domain), indicating the inherent patchiness of assemblages at this scale (Fig. 5.3 and 5.4).

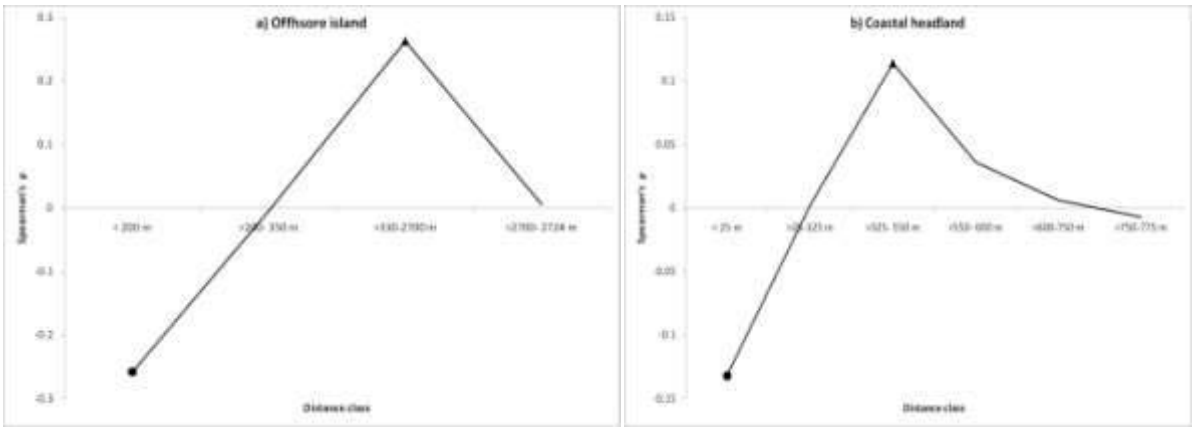

Figure 5.4: Rank-correlograms for benthic assemblages produced for coastal headland and offshore island environmental domain by correlation of Bray–Curtis dissimilarity between samples separated by distance class in PSGLMP. ● indicates a significant negative result ($p > 0.975$); ▲ indicates significant positive result ($p < 0.025$).

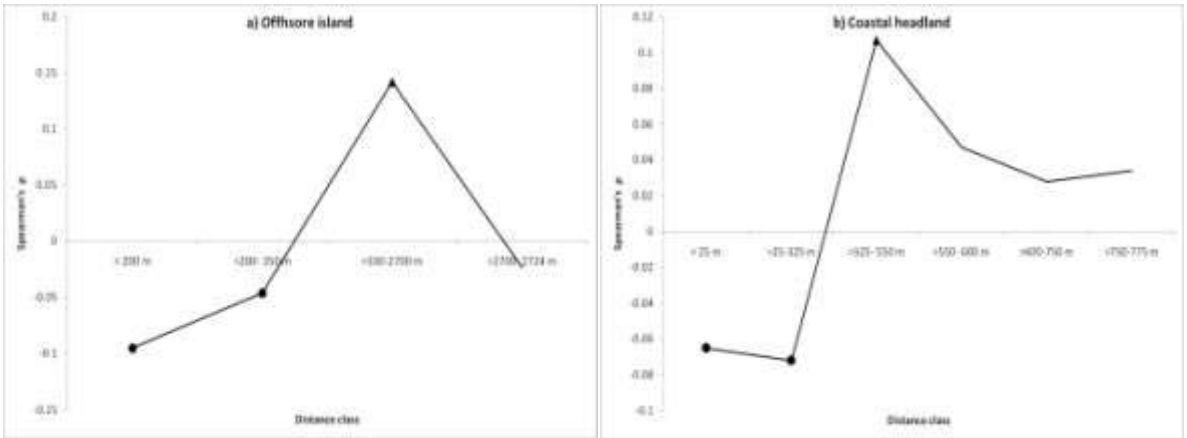

Figure 5.5: Rank-correlograms for sponge assemblage data produced for coastal headland and offshore island environmental domain by correlation of Bray–Curtis dissimilarity between samples separated by distance class in PSGLMP. ● indicates a significant negative result ($p > 0.975$); ▲ indicates significant positive result ($p < 0.025$).

When these trends were examined over similar spatial scales, there was a significant negative result at the offshore island environmental domain for distance classes less than 200 m for the full benthic assemblage data set, and for distance classes less than 16 m for the sponge assemblage data set. There was a significant positive result for the full benthic assemblage data set for distance classes greater than 200 m and for sponge assemblage data set for distance classes greater than 16 m (Fig. 5.5).

There was a significant negative result at the coastal headland environmental domain for distance classes less than 8 m for both the full benthic assemblage data set and for the sponge assemblage data set. There was a significant positive result for both the full benthic assemblage data set and the sponge assemblage data set for distance classes greater than 8 m (Fig. 5.6).

Homogenous assemblages were first detected in the >16- 200 m distance class at the offshore island environmental domain for both the full benthic data set and the sponge assemblage data set. Homogenous assemblages were first detected in the >8- 16 m distance class at the coastal headland environmental domain for both the full benthic data set and the sponge assemblage data set. Assemblages at both environmental domains fluctuated back to heterogeneous as the distance classes increased for the offshore island sponge assemblage (at the 200-208 m distance class) and for both the full benthic data set and the sponge assemblage data set at the coastal headland environmental domain (distance class >300-308 m), again indicating the inherent patchiness of assemblages at this scale (Fig. 5.5 and 5.6).

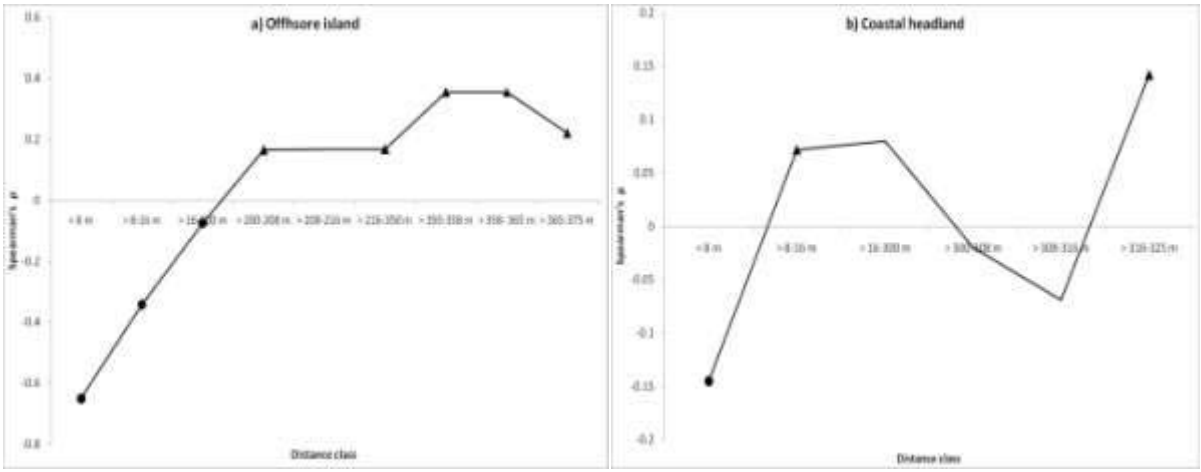

Figure 5.6: Rank-correlograms for benthic assemblage data over similar spatial scales, produced for coastal headland and offshore island environmental domain by correlation of Bray–Curtis dissimilarity between samples separated by distance class in PSGLMP. ● indicates a significant negative result ($p > 0.975$); ▲ indicates significant positive result ($p < 0.025$).

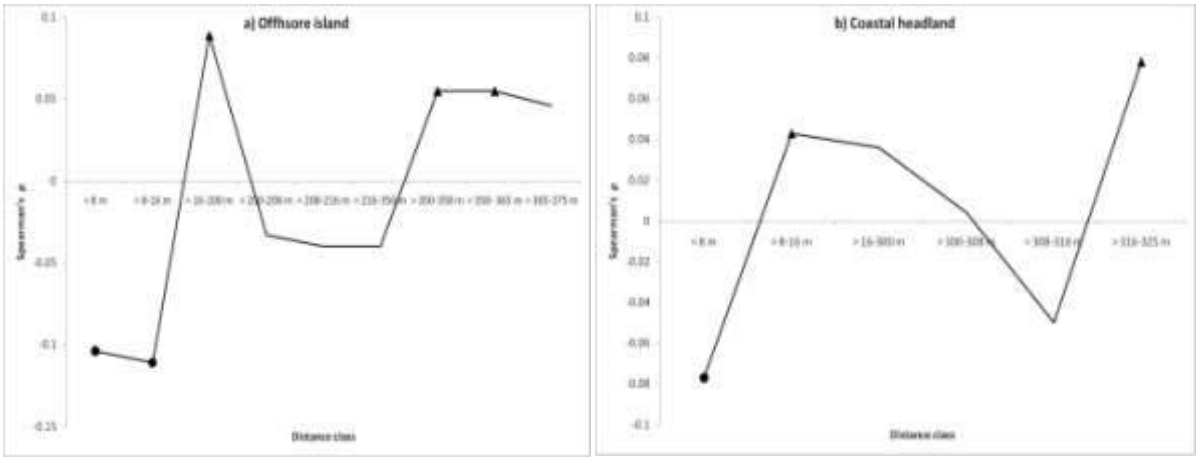

Figure 5.7: Rank-correlograms for sponge assemblages over similar spatial scales, produced for coastal headland and offshore island environmental domain by correlation of Bray–Curtis dissimilarity between samples separated by distance class in PSGLMP. ● indicates a significant negative result ($p > 0.975$); ▲ indicates significant positive result ($p < 0.025$).

5.4 Discussion

Spatial Patterns in Assemblages

The suite of species recorded in this study is similar to the suite of species recorded in other studies conducted in the same habitat and depths in other locations in temperate NSW (Roberts, 1996; Roberts and Davis 1996; Roberts *et al.,* 1998; Owen, 2003; Roberts *et al.,*

2006). Scales of autocorrelation have not been reported from these previous studies, and the key point from this study is that in this examination of autocorrelation, the existence of small-scale spatial variation is confirmed and is not only important but warrants consideration in conservation planning. This study found a significant positive relationship between distance and dissimilarity for the total benthic assemblage at fine (25 m) and large (environmental domain) spatial scales, indicating that assemblages were becoming more dissimilar as distance increased to 775 m in the coastal headland environment and 2794 m in the offshore island environment. The magnitude of the correlations differed among locations and between environmental domains, and also differed for the full set of species and for the subset of the sponge assemblage. The results of this study are in agreement with previous sessile benthic assemblage studies in deep reef habitat which showed dissimilarity tends to increase as distance increases between samples (Roberts and Davis, 1996; Roberts *et al.,* 2006).

High spatial variability in sessile benthic assemblages in temperate NSW has been documented at numerous scales with the structure and patterns of sessile benthic assemblages changing among replicates within a site (one metre scale), between sites (100's metres) and between locations (10's kilometres) (Roberts, 1996; Roberts and Davis, 1996; Owen, 2003; Roberts, 2006). This is in agreement to the results of this study, which found that sessile benthic assemblages were patchy, moving between homogenous and heterogeneous assemblages over a small linear distance.

A number of factors could be driving this pattern, such as the inherent patchiness of a habitat (e.g. due to the occurrence of small-scale patchiness in physical structure including vertical and horizontal rock shelves, boulders and cobbles) and small-scale differences in structural complexity (for example the occurrence of complex habitat such as overhangs) that provide preferred habitat characteristics for groups of species. Small-scale habitat patchiness has been documented in sponge-dominated assemblages in Brazil, with greater abundance recorded at overhangs than vertical and horizontal walls, and higher diversity at overhangs and vertical walls than horizontal walls (Monteiro and Muricy, 2004).

In this study there was a difference between coastal headland and offshore island environmental domains for both patterns of autocorrelation of assemblages, and the threshold distance at which assemblages changed from being homogenous to heterogeneous. This indicates that the environmental influences that differ between the headland and island, such

as distance to shore, distance from the entrance to the Port Stephens estuary, exposure, and local oceanography, may be influencing the composition of sessile benthic assemblages, the relative abundance of taxa within these assemblages, and the ecological processes underlying the composition and structure of these assemblages. Previous studies of sessile benthic assemblages of subtidal rocky reefs in temperate NSW indicate assemblages are influenced by environmental variables, including depth (Roberts and Davis, 1996; Newton *et al.,* 2007), exposure to sewer plumes (Roberts, 1996; Roberts *et al.,* 1998), exposure to estuarine plumes (Owen, 2003), and exposure to wave action (Roberts *et al.,* 2006; Newton *et al.,* 2007). Examples from overseas also indicate that exposure to wave action reduces the number of sponge species and morphological diversity (Bell and Barnes, 2000a; Bell and Barnes, 2000b; Monteiro and Muricy, 2004). Other than these studies outlined above, there is little published information regarding the importance of environmental variables in structuring sessile benthic assemblages in sponge-dominated reefs in temperate NSW. Differences between sessile benthic assemblages in PSGLMP within differing environmental domains need to be further examined so that representative samples can be conserved within the marine park framework.

Implications for Marine Protected Area Planning

This is the first study to examine scales of autocorrelation in sessile benthic assemblages in sponge-dominated reef in temperate NSW. In the context of MPA planning, patterns of similarity from autocorrelation studies across differing spatial scales depict the patch sizes of assemblages and the distances between neighbouring patches (Legendre and Fortin, 1989). This information can be used to determine the minimum linear dimensions of areas needed to include significant spatial variability in assemblage structure (Stevens, 2005). In this study assemblages were generally patchy and there was no clear threshold consistent across all locations and both environmental domains where assemblages were homogenous, indicating that spatial patterns of sessile benthic assemblages are inherently patchy at the scales examined in this study. However, at the fine (25 m) scale, by the >15 m class assemblages at 8 out of 10 transects had changed from homogenous to heterogeneous. Undertaking biodiversity sampling and monitoring programs at this fine scale (25 m) is therefore a valid approach in order to derive polygons of relative homogeneity for the purposes of creating habitat maps for MPA planning (Stevens, 2005).

At the larger environmental domain scale, assemblages were homogeneous at the >350 m distance class for the offshore island environmental domain, and >325 m distance class for the coastal headland environmental domain. At both the offshore island and coastal headland environmental domain assemblages generally then fluctuated between heterogeneous and homogenous. Spatial agglomeration of sites in deriving polygons of relative homogeneity for the purposes of creating habitat maps for MPA planning is therefore required at a fine scale.

The shape of line of the correlograms indicates a mosaic of patches can be detected. At both the transect and environmental domain scales, various autocorrelation profiles show peaks and valleys, which indicates the entry into a different patch of habitat (Gonzalez-Mirelis *et al.,* 2009). Some autocorrelation profiles continue to present a similar structure with no peaks or valleys, which indicate that the samples are within the same patch of habitat, and some contain secondary peaks and valleys, possibly suggesting a nested pattern of patches (Gonzalez-Mirelis *et al.,* 2009).

This study found patterns within sessile benthic assemblages are operating at a small spatial scale. This is in agreement with Roberts, (1996); Roberts and Davis, (1996); Roberts *et al.* (1998); Owen, (2003) and Roberts *et al.* (2006) who documented high levels of small-scale variability within sponge-dominated assemblages. Banks *et al.* (2005) found that a representative system of MPAs should include the complete range of environmental gradients or habitat types, at any given scale, to maximise the protection of marine biodiversity. In terms of conserving a representative sample of biodiversity of sessile benthic assemblages within the MPA framework, the results of this study suggest that small scale survey units (such as 25 m transects) are needed to capture the biodiversity of sessile benthic assemblages.

Mapping of seabed habitats is used to identify the distribution and structure of marine ecosystems and habitats for MPA planning (Jordan *et al.,* 2005). Habitats can act as effective surrogates for species diversity in the MPA planning process, providing they are being appropriately validated (Ward *et al.,* 1999, but see Shokri and Gladstone, 2013) and all representative habitats are included (Roff *et al.,* 2003), however there is a need for these surveys to be undertaken using appropriate spatial scales so that representative areas of habitat can be captured in conservation planning. Habitat is the most frequently chosen surrogate for designing marine reserves. The assumption is that if a certain percentage of all habitat classes are present are protected, then the specific biodiversity associated with those habitat classes will also be protected (Lindsay *et al.,* 2008). This assumes that habitats are homogeneous, and

therefore any area of that habitat type will represent the full spectrum of ecological diversity within that habitat (Winberg *et al.,* 2007; Smith *et al.,* 2008). However, in temperate southeast Australia, sessile benthic assembles from sponge-dominated reefs exhibit high spatial heterogeneity in response to environmental influences over small spatial scales (Roberts, 1996; Roberts and Davis, 1996; Owen, 2003; Roberts *et al.,* 2006). The use of habitat mapping as a surrogate for biodiversity within sponge-dominated reef needs to account for the differences between assemblages in different environmental domains over small spatial scales. In conclusion, using autocorrelation for the first time this study confirms the results of other studies in similar habitats, that small-scale spatial variation is not only important but therefore warrants consideration in conservation planning.

Chapter 6 Sources of variation in the biodiversity of rocky reef fishes and the implications for surrogacy schemes for conservation planning

Abstract

Marine protected areas aim to conserve representative samples of the range of biological diversity. Habitat classification schemes are often used as biodiversity surrogates in the absence of spatial inventories of biodiversity. However, the validity of these schemes as representations of biodiversity variation is often unknown. A potential confounding factor is spatial variation in biodiversity arising from environmental variables unaccounted for in the habitat classification scheme. This study quantified spatial and temporal variability in rocky reef fish biodiversity within a single habitat (sponge-dominated subtidal rocky reef) used for marine park spatial planning in New South Wales, Australia. Locations represented three putatively different environments: estuary, coastal headland and offshore island. Seventy species (36 families) were observed over two sampling periods. The majority of species recorded were of economic importance. Fish assemblages differed between offshore island, coastal headland and estuarine environmental domains in both 2009 and 2010. Fish assemblages at coastal headlands, but not offshore island and estuary, changed significantly through time. Depth exerted a significant influence on fish assemblages in all environmental domains. There was a significant difference in the abundance of five species, *Ophthalmolepis lineolatus, Heterodontus portusjacksoni, Trachurus novaezelandiae*, *Prionurus microlepidotus* and *Scorpis lineolata,* between environmental domains. Depth significantly influenced the abundance of three species, and the abundance of four species differed between times. The results of this study have important consequences for future marine park planning, indicating that representative samples of fish assemblages from offshore islands, coastal headlands and/or estuarine environmental domains within a single habitat type are required to adequately conserve representative samples of fish biodiversity within the marine park.

6.1 Introduction

In the absence of detailed spatial information on marine biodiversity, the development of habitat-based biodiversity surrogates is central to many schemes that identify sites to contribute to a representative system of marine protected areas (MPAs) (Banks and Skilleter, 2002). This approach assumes that biodiversity differs among habitats, an assumption that has been tested in many different habitats (e.g. O'Hara, 2001; Curley *et al.,* 2002; Bloomfield and Gillanders, 2005; Jelbart *et al.,* 2007). Therefore, mapping of seabed habitats for use as

surrogates for fauna diversity may be a cost effective method of biodiversity assessment for MPA planning (Jordan *et al.,* 2005). In temperate Australia, there is some evidence that habitats may act as effective surrogates in the design of MPAs (Ward *et al.,* 1999 but see Shokri and Gladstone, 2013).

A major goal of marine conservation planning is to conserve representative examples of the variability of marine biodiversity, with biodiversity typically defined to include species, assemblages, habitats, and ecosystems. Although the bio-physical dimensions of habitats are captured in habitat classification schemes and the associated maps, there is frequently considerable variation in the structure of assemblages within habitats that may not be represented by habitat classification schemes (Gladstone, 2007, Winberg *et al.,* 2007). Sources of within-habitat variation in fish assemblages in temperate Australia include depth (Connoll and Lincoln-Smith, 1999; Williams and Bax, 2001; Travers *et al.,* 2006; Chatfield *et al.,* 2010; Malcolm *et al.,* 2011), exposure (Valesini *et al.,* 2004), temperature, turbidity and salinity (Loneragan *et al.,* 1987; Hydnes *et al.,* 1999; West and Walford, 2000; Kanandjembo *et al.,* 2001; Smith and Sinerchia, 2004) The strong influence that environmental influences have in structuring both habitats and fish assemblages in temperate New South Wales (NSW) suggests that fish assemblages within the same habitat type may differ at locations in differing environmental domains. This has implications for the principals of comprehensive, adequate, and representativeness within MPA design (NSW Marine Parks Authority, 2001). For example, Malcolm *et al.* (2010) found that for subtropical fish assemblages in NSW, distance-from-shore was strongly correlated with patterns of variation of reef fish assemblages and species richness, and recommended that distance-from-shore be incorporated into habitat classification to improve the ability of MPA to represent biological diversity. Furthermore, Winberg *et al.* (2007) reported that macrobenthic assemblages in tidal flat habitats in temperate NSW were spatially heterogeneous in terms of taxonomic turnover, abundance, richness and diversity, and that conservation of whole tidal mudflat habitat, rather than sections of the habitat, is essential for this habitat type to be used to represent taxonomic diversity.

Subtidal rocky reefs in temperate Australia support diverse, highly endemic and commercially important habitats, assemblages and species (Ponder *et al.,* 2002). These reefs are characterised by several distinctive habitats, the distribution of which are related to physical forces including depth and wave exposure, and biological pressures, most notably herbivory by the sea urchin *Centrostephanus rodgersii* (Underwood *et al.,* 1991). Sponge-

dominated 'deep reef habitat' occurs >9 m depth and is characterised by a significant density of sessile benthic animals, including a number of sponges, corals and bryozoans unique to the habitat (Underwood *et al.,* 1991). Subtidal rocky reef habitat represents approximately 3% of Port Stephens-Great Lakes Marine Park (PSGLMP) (NSW Marine Parks Authority, 2006), and is classified by depth for planning purposes into three categories: shallow 0-25 m, intermediate 25-60 m and deep 60-200 m (Jordan *et al.,* 2010). These reef classes are not structured further despite occurring within estuaries, around offshore islands and coastal headlands (NSW Marine Park Authority, 2006). Given the strong influence that environmental factors have on the structure of fish assemblages, it is possible that fish assemblages within the same sponge-dominated rocky reef habitat type may differ at locations in differing environmental domains.

Different environmental domains support different sets of species, and may be used to represent environmental heterogeneity and therefore act as biodiversity surrogates (Margules *et al.,* 2002). Exposure (Valesini *et al.,* 2004), distance from shore (Malcolm *et al.,* 2010), temperature, turbidity and salinity (Loneragan *et al.,* 1987; Hydnes *et al.,* 1999; West and Walford, 2000; Kanandjembo *et al.,* 2001; Smith and Sinerchia, 2004) are all important environmental factors that influence reef fish in temperate Australia. The aim of this study was to test for an effect of environmental domain (estuary, headland, island) on the biodiversity of fishes within a single habitat (sponge-dominated rocky reef). The approach taken by this study was to survey rocky reef fishes in multiple examples of each putative environment at multiple times, in PSGLMP, Australia. The study tested the hypothesis that fish biodiversity differed within differing environmental domains in the same sponge-dominated rocky reef habitat, and this difference was consistent through time.

6.2 Methods

Study Area

PSGLMP is situated on the mid-north coast of NSW (Fig. 3.1), and includes estuaries, coastline and offshore waters (to ~6 km) over approximately 80 km of coastline and an area of 98,000 ha (see detailed description in Chapter 3). In this study environmental domains were considered to be locations influenced by a set of environmental conditions unique to that domain. The estuary environmental domain is located within Port Stephens estuary, is tidally influenced, and subject to different salinity, temperature, exposure and turbidity than the coastal headland and offshore island environmental domains. The coastal headland

(Fingal) and offshore island (Broughton Island) environmental domain differed in exposure and distance from shore. Fingal is connected to the mainland via a sand spit, and Broughton Island is approximately 2 km offshore. There is approximately 20 km of subtidal unvegetated sand separating these two environmental domains.

Figure 6.1: Location of study sites in Port Stephens-Great Lakes Marine Park. Symbols represent offshore island (triangle), coastal headland (square), and within Port Stephens estuary (circle).

Experimental Design and Field Sampling

Sampling occurred in sponge-dominated rocky reef habitat. Thirty-six replicates were surveyed in a range of locations grouped into three putative environmental domains: offshore islands (15 replicates), coastal headlands (18 replicates), and estuary (three replicates) (Fig.6.1). Variation in the areas of available habitat within each environmental domain led to an uneven number of replicates being sampled within environmental domains (ie there was very little sponge-dominated rocky reef within the estuary and at Cabbage Tree and Boondelbah Island); therefore replicates within an environment were not grouped by a

location factor. Temporal consistency was tested by sampling at two times (September 2009 and September 2010). Locations occurred within both sanctuary zones and habitat protection zones within the PSGLMP. Sanctuary zones prohibit all forms of fishing whilst habitat protection zones have some restrictions on commercial fishing (i.e. no trawling). The subtidal rocky reef habitat at the locations surveyed consisted of a mix of large boulders and crevices, with a biogenic covering of sponges, coral, ascidians, bryozoans, algae, sediment and sand, over a depth range of 11.0 m to 34.8 m.

Fishes were sampled with baited remote underwater video stations (BRUVS) with replicates separated by at least 200 m (Malcolm *et al.,* 2007) and deployed to achieve 30 min of recording per replicate (Malcolm *et al.,* 2007). BRUVS were constructed as in Malcolm *et al.* (2007), and consisted of a video camera in an underwater housing, an attachment frame, a bait-pole with bait, and a rope and float system linking the BRUV to the surface. The BRUVS were baited with approximately 1kg of chopped pilchards (*Sardinops neopilchardus*), which were mashed into a plastic mesh bait bag and attached to the end of a bait-pole at a distance of 1.5 m from each camera (Malcolm *et al.,* 2007). The cameras were all similar digital Canon HG21's handycams with wide-angle lenses. The field of view was standardised to a distance of approximately 2 m behind the bait, to minimise the effects of water visibility on the measure of relative abundance and species richness (Malcolm *et al.,* 2007).

Fish were identified to species-level (using Hutchings and Swainston, 1986; Edgar, 1997; Kuiter, 2000) and an index of relative abundance of each species (MaxN), species richness and time each species was first sighted were recorded. MaxN is the maximum number of individual fish of each species in the frame at any one time during the video (Malcolm *et al.,* 2007). Species were additionally classified depending on their economic importance as recreational and/or commercially targeted fish species (Scandol *et al.,* 2008).

Statistical Analyses

Multivariate analyses were undertaken using PRIMER 6 and PERMANOVA+ software (PRIMER-E Ltd, Plymouth) (Clarke and Warwick, 2001). Two-factor permutational multivariate analysis of variance (PERMANOVA) (Anderson, 2001) was used to test the hypothesis that fish assemblages differed between environmental domains and these differences were consistent between sampling times. Time was analysed as an orthogonal factor with two levels (2009, 2010) and was analysed as fixed because the two years were

likely to be an insufficient representation of the possible extent of temporal variation (Anderson and Millar, 2004). Environmental domain was analysed as a fixed orthogonal factor with three levels (coastal headland, offshore island, estuary). Depth data from each replicate was included as a covariate in the PERMANOVA to test if the influence of environmental domains was still apparent when depth was considered. Depth was included as a covariate as the mean depth differed between coastal headland (26.6 m ±0.9 SE in 2009; 26.0 m ±0.8 SE in 2010), offshore island (26.0 m ±1.1 SE; 26.8 m ±1.4 SE) and estuary (14.0 m ±1.4 SE; 13.3 m ±0.7 SE) environmental domains. This PERMANOVA design was also utilised to undertake univariate analyses for total MaxN, and MaxN of the most abundant species and species richness of fishes.

Relative differences in fish assemblages among environmental domains were visualised by non-metric multidimensional scaling ordination plots. PERMANOVA and the nMDS ordinations were done on a Bray-Curtis similarity matrix of square-root transformed data. Univariate PERMANOVA tests were based on a Euclidean distance similarity matrix. Homogeneity of variances was first tested by Cochran's C test using GMAV software (Institute of Marine Science, University of Sydney), and data were transformed using ln (X + 1) where necessary to eliminate heterogeneous variances. When heterogeneous variances could not be eliminated by transformation the raw data were used and a modified significance level of p=0.01 was used (Underwood, 1981).

The PERMANOVA test on fish assemblages showed a significant time x environmental domain effect, and the pairwise tests show this occurred as assemblages in one environmental domain did not change over time whereas the others did. The pairwise tests also showed that differences among environmental domains were consistent through time; therefore the SIMPER analysis was undertaken to identify species responsible for differences in assemblages between environmental domains but not through time. Large values (i.e.> 1) of the ratio of $\overline{\delta}_i$/SD($\overline{\delta}_i$) for a species (where $\overline{\delta}_i$ is the average contribution of the ith species to the overall dissimilarity ($\overline{\delta}$) between two groups, and SD is standard deviation), and values of $\overline{\delta}_i$ > 3% (Terlizzi *et al.,* 2005) were used to indicate a species was an important contributor to dissimilarity between environments (Clarke, 1993).

6.3 Results

General

Seventy species (36 families) were observed over the two sampling periods, representing 11 species (eight families) from the class Chondrichthyes and 60 species (28 families) from the class Actinopterygii. Fifty eight species (31 families) were recorded in 2009, comprising 11 species (8 families) from the class Chondrichthyes and 47 species (23 families) from the class Actinopterygii. Sixty one species (32 families) were recorded in 2010, comprising 9 species (8 families) from the class Chondrichthyes and 52 species (24 families) from the class Actinopterygii. Labridae was the most speciose family recorded, with 10 species. Thirteen species were recorded as single individuals. Of the species recorded 67% were of economic importance (Appendix 2).

A total of 9160 individuals were observed by combining MaxN data from all replicates. The most abundant species recorded during both sample periods were yellowtail scad (*Trachurus novaezelandiae*) (Carangidae) (representing 30% combined MaxN), mado (*Atypichthys strigatus*) (Kyphosidae) (28%), snapper (*Pagrus auratus*) (Sparidae) (6%), silver sweep (*Scorpis lineolata*) (Kyphosidae) (5%), Maori wrasse (*Ophthalmolepis lineolatus*) (Labridae) (5%), one spot puller (*Chromis hypsilepis*) (Pomacentridae) (2%) and tarwhine (*Rhabdosargus sarba)* (Sparidae) (2%).

Atypichthys strigatus was the species most commonly first sighted in 2009 and *Ophthalmolepis lineolatus* in 2010. The first individuals recorded did not differ between environmental domains. The first individual was sighted at all environmental domains in both sample periods within five seconds of the BRUV reaching the reef.

Spatial and Temporal Variation in Fish Assemblages

Fish assemblages differed between offshore island, coastal headland and estuarine environmental domains in both 2009 and 2010 (Table 6.1, Fig. 6.2, Fig. 6.3). The pairwise test undertaken to explore the significant Time x Environmental Domains interaction indicated that fish assemblages of coastal headlands, but not offshore island and estuary, changed significantly through time. Depth exerted a significant influence on fish assemblages in all environmental domains (however noting that the shallowest locations were all in the estuary environmental domain which may represent a confounding factor). Separation of environmental domains on the nMDS ordination indicated the most variability was within estuarine locations within 2009, however in 2010 all locations displayed high variability. Analysis using the PERMADISP routine to test the homogeneity of assemblages indicated a

significant difference between the variability of assemblages in the different environmental domains in 2009 ($F_{6.3}$, p=0.009) and 2010 ($F_{5.6}$, p=0.021).

Table 6.1: Summary of results of 2-factor PERMANOVA testing for the influence of time and environmental domains (with depth as covariate) on fish assemblages of subtidal reef habitat in the Port Stephens-Great Lakes Marine Park.

Source of Variation	DF	MS	F	*P*
Depth: De	1	7934.60	7.54	0.001
Time: Ti	1	3787.10	3.60	0.001
Environmental Domain: EnvD	2	3512.20	3.34	0.001
Ti x EnvD	2	2289.50	2.18	0.002
Residual	65	1052.30		

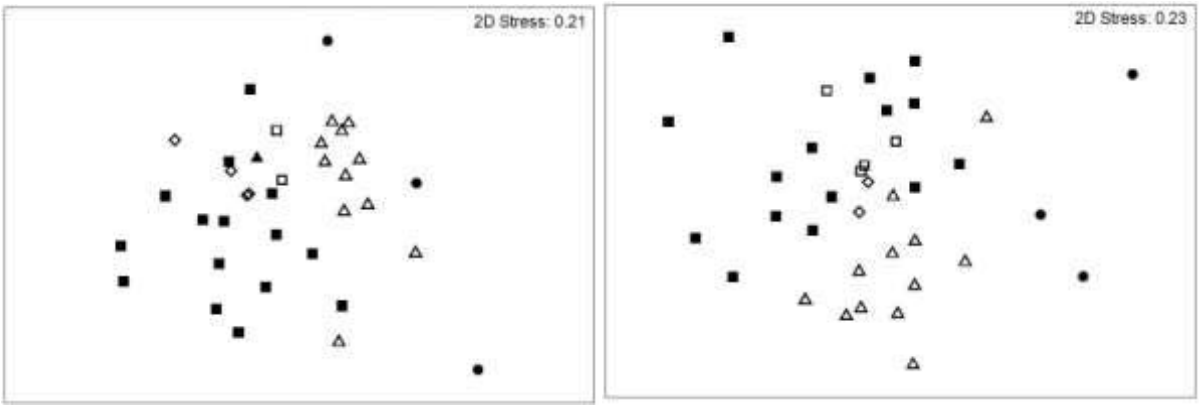

Figure 6.2: nMDS ordination plots (based on MaxN of each species) depicting similarity in fish assemblages of sponge-dominated reef habitat in the Port Stephens-Great Lakes Marine Park in September 2009 (left) and 2010 (right). Symbols represent offshore islands (open symbols- Broughton Island = triangle, Cabbage Tree Island = square, Boondalbah Island = diamond), coastal headlands (Fingal = square) and within the Port Stephens estuary (little beach, halifax park and fly point = circle).

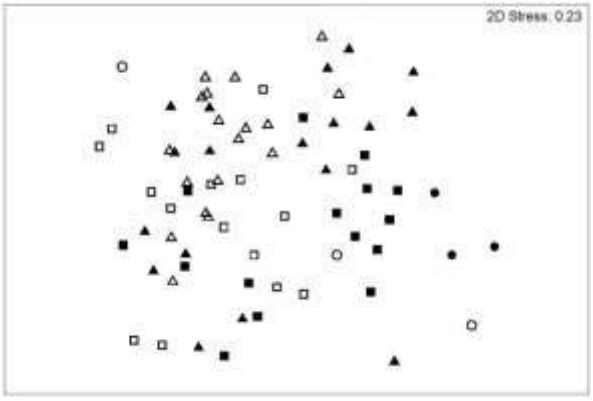

Figure 6.3: nMDS ordination plots (based on MaxN of each species) depicting similarity in fish assemblages of sponge-dominated reef habitat in 2009 (open symbols) and 2010 (filled symbols) in the Port Stephens-Great Lakes Marine Park. Symbols represent offshore islands (triangle), coastal headlands (square) and within the Port Stephens estuary (circle).

The SIMPER analysis identified eight species as being influential in differentiating between fish assemblages in different environmental domains (Table 6.2). Of these species, variation in the abundance of *Trachurus novaezelandiae, Atypichthys strigatus*, *Scorpis lineolata, Pagrus auratus* and *Rhabdosargus sarba* were the important species distinguishing between offshore island and coastal headland domains (higher MaxN of *A. strigatus*, *S. lineolata* and *R. sarba* at offshore island domain; higher MaxN of *T. novaezelandiae* and *P. auratus* at coastal headland domain). Variation in the abundance of *A. strigatus*, *S. lineolata, P. auratus*, *R. sarba,* Australian sawtail *(Prionurus microlepidotus)* (Acanthuridae) and red morwong (*Cheilodactylus fuscus*) (Cheilodactylidae) were the important species distinguishing between offshore island and estuary domains (higher MaxN of *A. strigatus* at offshore island domain; higher Max N of *S. lineolata, P. auratus*, *R. sarba, P. microlepidotus* and *C. fuscus* at estuary domain). Variation in the abundance of *T. novaezelandiae A. strigatus*, *P. auratus*, *R. sarba, P. microlepidotus* and *Heterodontus portusjacksoni* (Heterodontidae) were the important species distinguishing between coastal headland and estuary domains (higher MaxN of *T. novaezelandiae* and *H. portusjacksoni* at coastal headland domain; higher MaxN of *A. strigatus*, *P. auratus*, *R. sarba* and *P. microlepidotus* at estuary domain). A SIMPER analysis was also undertaken within the coastal headland domain, to determine what species caused the significant change in coastal headland fish assemblages through time. Variation in the abundance of *T. novaezelandiae, A. strigatus* and *P. auratus* were the important species distinguishing the coastal headland assemblages through time, with all three species increasing in MaxN between 2009 and 2010 (Table 6.2).

Table 6.2: Summary of results of SIMPER analysis showing the contributions of individual fish species to dissimilarity of assemblages of each environmental domain, and each time within the coastal headland domain. Species regarded as being important contributors to the assemblage dissimilarity are shown in bold (see Methods). Values shown in the pairwise comparisons are the average MaxN for the species, $\bar{\delta}$ i is the average contribution of the ith species to the overall dissimilarity ($\bar{\delta}$) between two groups, and SD is standard deviation.

Taxon	Island vs Headland			Island vs Estuary			Headland vs Estuary			Coastal Headlands 2009 vs 2010		
	$\bar{\delta}_i$	$_{\%}\bar{\delta}_i$	$\bar{\delta}_i/SD(\bar{\delta}_i)$	$\bar{\delta}_i$	$_{\%}\bar{\delta}_i$	$\bar{\delta}_i/SD(\bar{\delta}_i)$	$\bar{\delta}_i$	$_{\%}\bar{\delta}_i$	$\bar{\delta}_i/SD(\bar{\delta}_i)$	$\bar{\delta}_i$	$_{\%}\bar{\delta}_i$	$\bar{\delta}_i/SD(\bar{\delta}_i)$
Trachurus novaezelandiae	**8.19**	**15.28**	**1.24**	4.42	7.09	0.66	**7.29**	**11.6**	**1.14**	**9.07**	**16.6**	**1.54**
Atypichthys strigatus	**7.68**	**14.32**	**1.43**	**7.53**	**12.08**	**1.37**	**6.30**	**10.02**	**1.05**	**6.28**	**11.5**	**1.18**
Scorpis lineolata	**3.06**	**5.70**	**1.28**	**3.88**	**6.23**	**1.24**	3.17	5.03	0.79	2.63	4.81	1.01
Pagrus auratus	**2.29**	**4.28**	**1.20**	**4.14**	**6.64**	**2.37**	**4.17**	**6.63**	**1.73**	**3.91**	**7.16**	**1.71**
Rhabdosargus sarba	**1.85**	**3.44**	**1.14**	**2.46**	**3.95**	**1.19**	**2.41**	**3.83**	**1.10**	1.80	3.30	1.19
Prionurus microlepidotus	NA	NA	NA	**3.56**	**5.71**	**1.22**	**3.83**	**6.08**	**1.21**	NA	NA	NA
Cheilodactylus fuscus	0.76	1.42	0.82	**2.45**	**3.93**	**1.05**	2.59	4.12	0.98	0.72	1.32	0.72
Heterodontus portusjacksoni	1.31	2.44	1.03	1.45	2.33	1.30	**1.92**	**3.06**	**1.34**	1.35	2.48	0.90

Spatial and Temporal Variation in Fish Species

The PERMANOVA test indicated there was no difference in the total MaxN of all fishes, MaxN of economic species, MaxN of *Cheilodactylus fuscus***,** *Rhabdosargus sarba, Chromis hypsilepis* and species richness between environmental domains. Five species, *Ophthalmolepis lineolatus, Heterodontus portusjacksoni, Trachurus novaezelandiae*, *Prionurus microlepidotus* and *Scorpis lineolata,* showed a significant difference between environmental domains (although with *S. lineolata* the influence was not consistent through time) (Fig. 6.4, Table 6.3). There was a greater abundance of *O. lineolatus* and *P. microlepidotus* in the estuary environmental domain than the coastal headland and offshore island environmental domain, and greater abundance of *H. portusjacksoni* and *T. novaezelandiae* in the coastal headland and offshore island environmental domain than the estuary environmental domain. There was greater abundance of *S. lineolata* in the estuary environmental domain than the coastal headland and offshore island environmental domain in 2009, however in 2010 the trend was reversed. The total MaxN of crimson banded wrasse *(Notolabrus gymnogenis)* (Labridae), *Atypichthys strigatus*, *Pagrus auratus*, and *S. lineolata* differed significantly through time (Fig. 6.4, Table 6.3). The total MaxN of *N. gymnogenis* and *P. auratus* increased between 2009 and 2010, and the total MaxN of *A. strigatus* and *S. lineolata* decreased between 2009 and 2010. Depth had a significant infuence on the abundance of *P. microlepidotus, P. auratus* and *T. novaezelandiae* (Table 6.3).

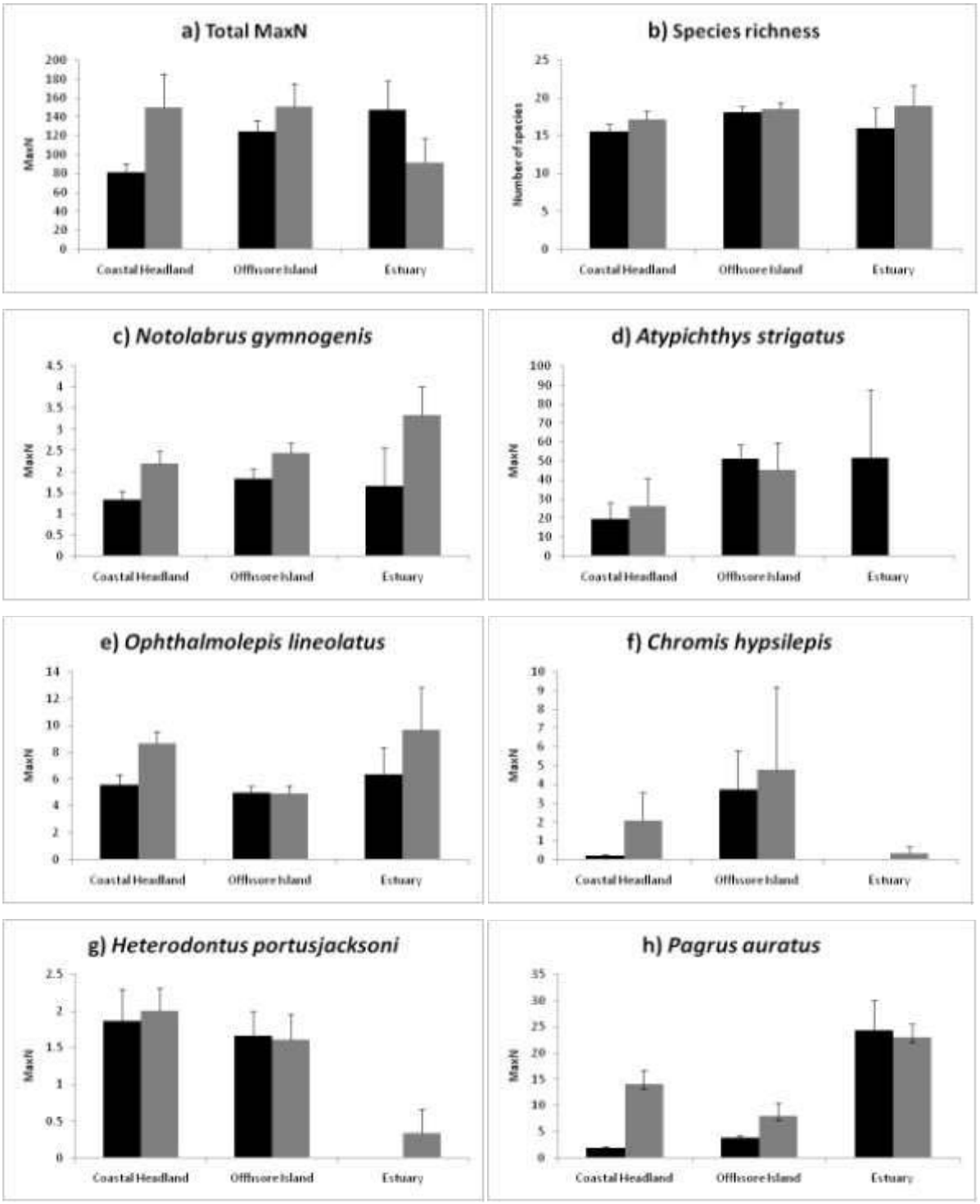

Figure 6.4: MaxN of fishes in sponge-dominated subtidal rocky reef habitat in 2009 (dark) and 2010 (light). Values shown are mean MaxN (+SE) at each domain.

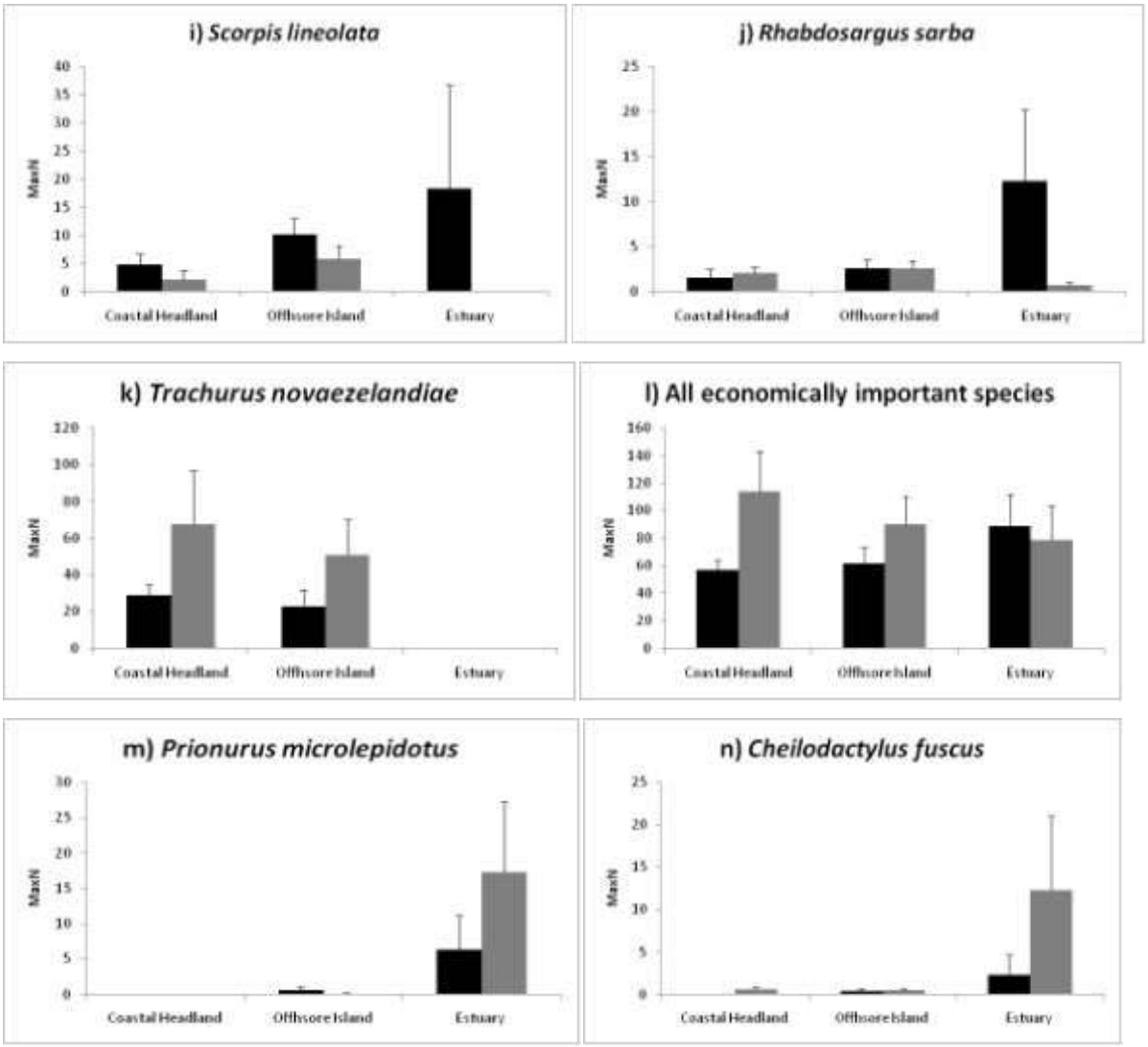

Figure 6.4 continued: MaxN of fishes in sponge-dominated subtidal rocky reef habitat in 2009 (dark) and 2010 (light). Values shown are mean MaxN (+SE) at each domain.

Table 6.3: Summary of results of 2-factor PERMANOVA testing for the influence of time and environmental domains on total MaxN, MaxN of abundant species and species richness of fishes in sponge dominated reef habitat in the Port Stephens-Great Lakes Marine Park.

		Total MaxN[3]			Species Richness[1]			*Notolabrus gymnogenis*[1]			*Atypichthys strigatus*[2]		
Source of Variation	DF	MS	F	*P*	MS	F	*P*	MS	F	*P*	MS	F	*P*
Depth	1	1618.70	1.97	0.14	7.08	0.06	0.89	404.17	0.37	0.89	4016.50	1.51	0.13
Time: Ti	1	1915.4	2.33	0.11	172.62	1.52	0.22	3639.20	3.32	0.01	12782.00	4.80	<0.01
Environmental Domain: EnvD	2	1457.4	1.77	0.14	275.79	2.24	0.10	1683.40	1.53	0.16	5940.20	2.23	0.11
Ti x EnvD	2	882.61	1.07	0.37	67.92	0.60	0.55	829.76	0.76	0.60	3171.90	1.12	0.24
Residual	65	882.06			113.64			1096.40			2663.5		

		Ophthalmolepis lineolatus[1]			*Chromis hypsilepis*[2]			*Heterodontus portusjacksoni*[1]			*Pagrus auratus*[1]		
Source of Variation	DF	MS	F	*P*	MS	F	*P*	MS	F	*P*	MS	F	*P*
Depth	1	593.98	1.21	0.27	3896.40	0.81	0.85	4122.40	1.67	0.09	5252.80	3.95	0.01
Time: Ti	1	1374.40	2.80	0.09	3900.10	0.81	0.90	1991.80	0.80	0.55	13985.00	10.52	<0.01
Environmental Domain: EnvD	2	1862.80	3.80	0.02	4791.40	1.00	0.45	6545.70	2.64	0.01	7378.10	5.55	<0.01
Ti x EnvD	2	1096.10	2.23	0.09	5010.10	1.04	0.31	3045.90	1.22	0.21	4398.30	3.31	0.01
Residual	65	490.38			4802.50			2482.00			1329.90		

Table 6.3 (continued): Summary of results of 2-factor PERMANOVA testing for the influence of time and environmental domains on total MaxN, MaxN of abundant species and species richness of fishes in sponge dominated reef habitat in the Port Stephens-Great Lakes Marine Park.

		Scorpis lineolata[2]			*Rhabdosargus sarba*[2]			*Trachurus novaezelandiae*[2]		
Source of Variation	DF	MS	F	*P*	MS	F	*P*	MS	F	*P*
Depth	1	3646.6	1.15	0.27	6480.00	1.79	0.08	7693.20	2.20	0.02
Time: Ti	1	7287.00	2.30	0.02	2242.40	0.62	0.95	4518.20	1.29	0.14
Environmental Domain: EnvD	2	8449.30	2.67	<0.01	2939.90	0.81	0.65	11436.00	3.28	<0.01
Ti x EnvD	2	3147.60	1.00	0.42	3838.70	1.06	0.33	4398.20	1.26	0.15
Residual	65	3160.80			3622.30			3490.00		

		Prionurus microlepidotus[3]			*Cheilodactylus fuscus*[2]			Economic species[2]		
Source of Variation	DF	MS	F	*P*	MS	F	*P*	MS	F	*P*
Depth	1	6053.70	1.22	0.01	3926.20	0.85	0.71	23.00	0.33	0.57
Time: Ti	1	4649.20	0.94	0.82	5976.30	1.29	0.12	163.06	2.37	0.12
Environmental Domain: EnvD	2	7189.90	1.46	<0.01	6156.40	1.33	0.06	76.22	1.11	0.34
Ti x EnvD	2	4077.90	0.83	1.00	3858.00	0.83	0.85	29.99	0.44	0.67
Residual	65	4929.10			4646.00			68.76		

1: untransformed, variances homogeneous
2: ln(x+1) transformed, variances homogenous
3: untransformed, variances heterogeneous

6.4 Discussion

Spatial Patterns in Assemblages and Species Influential in Differentiating Among Domains

Many of the species found to be abundant and/or influential in differentiation of fish assemblages in this study were also found to be important in differentiating the assemblages of three other MPAs in NSW, including PSGLMP (Malcolm *et al.,* 2007). The use of these species within state-wide assessments to examine habitat as surrogates for biodiversity over may be possible. Fish assemblage structure differed between coastal headlands, offshore islands and estuarine environmental domains within sponge-dominated subtidal rocky reef habitat. Differences in salinity, temperature, exposure, proximity to seagrass beds and turbidity are likely to be key environmental factors influencing differences between estuarine fish assemblages and the offshore island and coastal headland fish assemblages (Loneragan *et al.,* 1987; Edgar *et al.,* 1999; Edgar *et al.,* 2000; Kanandjembo *et al.,* 2001). Fluctuations in temperate and salinity have been documented within Port Stephens estuary (Mason and Bell, 1995), which differ from oceanic temperature and salinity conditions, and are likely to be important environmental factors contributing to differences between estuarine and oceanic fish assemblages. The role of estuaries as habitat for juvenile fish is also likely to be key environmental factor influencing differences between estuarine fish assemblages and the offshore island and coastal headland fish assemblages. For example, the abundance of *Cheilodactylus fuscus, Prionurus microlepidotus, Rhabdosargus sarba* and *Pagrus auratus*, identified as being influential species in differentiating between the estuary environmental domain and the oceanic (coastal headland and offshore island) environmental domains, are known to occur as juveniles within protected rocky coastal estuaries, sometimes within large schools (Kuiter, 2000; Curley *et al.,* 2013).

Distance from shore, differences in exposure, wave energy or proximity to the estuary are likely to be key environmental factors influencing differences between offshore island and coastal headland fish assemblages. Malcolm *et al.* (2010) found that distance from shore significantly influenced reef fish assemblages in similar depths to this study, and attributed the differences between coastal headland and offshore island fish assemblages to differences in recruitment due to the influence of the East Australian Current at offshore islands. Fulton *et al.* (2013) found that wave energy is a powerful force in shaping patterns of coral reef fish biodiversity on the Great Barrier Reef. The proximity to the estuary may also be influencing fish assemblages at the coastal headland environmental domain. The abundance of *Pagrus*

auratus, identified as being an influential species differentiating between the coastal headland and offshore island environmental domain, are known to occur as juveniles within estuaries and migrate to coastal rocky reefs when mature (Kuiter, 2000; Curley *et al.,* 2013). Specific habitats within Port Stephens estuary are highly important for juvenile *P.auratus* (Poulos *et al.,* 2013). Small scale differences in habitat structure, prey availability or biodiversity of the sponge-dominated habitat may also be driving differences between fish assemblages.

In this study, depth exerted a significant influence on fish assemblages in all environmental domains, and the abundance of several species, highlighting the importance of this variable to fishes in sponge-dominated rocky reef habitat. This result is supported by several studies of fish assemblages in rocky reef habitats in south-eastern Australia where depth is also shown to be an important factor driving the structure of these assemblages (Connoll and Lincoln-Smith, 1999; Williams and Bax, 2001; Travers *et al.,* 2006; Malcolm *et al.,* 2011). Depth may be acting as a proxy for a range of influencing factors, such as food availability, habitat biogenic diversity or stability.

Temporal Patterns in Assemblages

Fish assemblages at the coastal headland environmental domain changed significantly through time. At least some of the species driving these patterns are schooling taxa and schools are highly mobile, meaning that large differences can occur even in a single transect over very short time periods. Additionally four of the most abundant species recorded in this study, *Notolabrus gymnogenis, Atypichthys strigatus*, *Pagrus auratus* and *Scorpis lineolata* varied significantly through time. This study was undertaken in September 2009 and September 2010, so temporal changes in abundance due to annual recruitment (for example late summer and early autumn for *N. gymnogenis* (Morton and Gladstone, 2011) and *P. auratus* (Fowler and Jennings, 2003) would not have been a reason for this significant temporal variation. The temporal variation in this study is in contrast to previous studies on rocky reef fish assemblages in temperate NSW, where temporal variation has been shown to be relatively minor compared to spatial variation (Gladstone, 2007; Malcolm *et al.,* 2007). However, both these studies were undertaken over large spatial scales, where great spatial variation was documented, and temporal variation, although minor in comparison, was still documented. The use of abiotic surrogates for diversity in MPA planning relies on stability of assemblage patterns through time (Malcolm *et al.,* 2010). This study found significant temporal variation of fish assemblages, highlighting the need for further studies examining

long-term temporal variation in sponge-dominated reef habitat in NSW temperate rocky reefs in order to assess the usefulness of habitat mapping as a surrogate for long-term patterns of diversity in rocky reef fish assemblages.

General Diversity

BRUVs are an effective method for sampling rocky reef fish assemblages and have been used previously in PSGLMP. Previous studies along the NSW central coast, including PSGLMP, have recorded a similar species assemblage as to that recorded in this study. This study recorded 70 species (36 families) using BRUVs, Malcolm *et al.* (2007) recorded 60 species (36 species) using BRUVs, Lindfield (2007) recorded 84 species (45 families) using BRUVs and Gladstone (2007) recorded 104 species (41 families) using UVC. Malcolm *et al.* (2007) concluded that Port Stephens-Great Lakes MPA was an important area for Chondrichthyes, with 10 species recorded in rocky reef habitat. This study supports this conclusion, with 11 species recorded (8 families) over the two sample periods (10 species common to both studies).

BRUVs are a powerful technique for detecting large cryptic scavengers, including eels, sharks and rays in rocky reefs (Malcolm *et al.,* 2007) although small, cryptic reef-associated species are better detected using underwater visual census (UVC) (Lowry *et al.,* 2012). This study recorded a high number of large cryptic species not recorded using UVC in PSGLMP (Gladstone, 2007), that could otherwise not be sampled in a non-destructive manner, important for studies undertaken within MPAs. Cryptic species contribute to defining patterns of biodiversity for conservation planning in freshwater systems in Australia (Cook *et al.,* 2008), and cryptic seahorses (*Hippocampus* sp.) have been used as flagship species in Philippines to engender support for the creation of MPAs (Yasue *et al.,* 2012), however the importance of cryptic species in MPA planning has not been explored in temperate NSW rocky reefs.

Some potential factors that may bias estimates of abundance include inter-specific behavioural interactions between species at the bait (Malcolm *et al.,* 2007). In particular, when sharks were aggressively feeding on the bait, this often attracted more species to the bait bag and appeared to encourage more species to feed on scraps of bait dislodged from the bag. BRUVs are biased towards species attracted to baits, however this bias may be advantageous for conservation and fisheries management purposes, as it provides information on species that are targeted or caught as by-catch with baits (Malcolm *et al.,* 2007). Although

fish bait are used with BRUVs to attract predators and scavengers, a cross-section of the overall reef fish is generally recorded, representing a range of trophic guilds including large predatory fish, herbivores and planktivores (Malcolm *et al.,* 2007; Watson *et al.,* 2005). Current also has an effect on bait plume size, which can present difficulties when aiming to separate treatment effects (Heagney *et al.,* 2007; Taylor *et al.,* 2013).

The time of first arrival of fish can be an indicator of high population density of fish, where the higher the population, the sooner fish approach the bait (Cappo *et al.,* 2004). In this study the first individual was sighted at all environmental domains in both sample periods within five seconds of the BRUV reaching the reef, indicating population density may be similar between environmental domains.

Although beyond the scope of this assessment, size of fish can be measured with stereo BRUVS, which could be incorporated into future studies to consider size-related habitat use of many fish species.

Implications for Marine Protected Area Planning

The use of habitat mapping is widely used as a surrogate for fauna assemblages for MPA planning in Australia (Ward *et al.,* 1999; Banks *et al.,* 2005; Winberg *et al.,* 2007; Lindsay *et al.,* 2008; Last *et al.,* 2010; Malcolm *et al.,* 2010, Malcolm *et al.,* 2011) and New Zealand (New Zealand Department of Conservation and Ministry of Fisheries (2011). It has also been applied in the design of the Representative Areas Program of the Great Barrier Reef (GBR) (GBR Marine Park Authority). However the precision of these surrogates is rarely tested. The use of habitat mapping when choosing MPA candidate sites assumes that habitats are homogeneous, and therefore any area of that habitat type will represent the full spectrum of ecological diversity within that habitat (Winberg *et al.,* 2007; Smith *et al.,* 2008). However, in temperate southeast Australia, high heterogeneity has been documented for marine and estuarine habitats. Critics of the use of surrogates of biodiversity for MPA design state that this approach lacks systematically surveyed biological data (Ward *et al.,* 1999; Banks and Skilleter, 2002; Ponder *et al.,* 2002), and in particular there is limited information on the spatial scales at which faunal assemblages change in taxonomic composition within a habitat type (Winberg *et al.,* 2007). Smith *et al.* (2008) documented high spatial heterogeneity in shallow subtidal rocky reefs in northern NSW, and questioned the use of arbitrary measures such as percentage of a broad habitat type to allocate conservation effort in MPA zoning schemes. Malcolm *et al.* (2010) found that for subtropical fish assemblages in NSW, distance-

from-shore was strongly correlated with patterns of reef fish assemblages, and recommended that distance-from-shore be incorporated into habitat classification to improve the ability of MPA to represent biological diversity. Williams *et al.* (2009) found that depth, size, complexity, configuration and anthropogenic impact all needed to be added to geomorphic features used to act as surrogates of biodiversity within Australia's deep-water reserve network. However there are examples of studies that have found remotely measured environmental variables effective surrogates for fish biodiversity, such as Berger and Possingham (2008) who found that depth, exposure and distance from estuary were influential in determining the distribution of coral reef fishes at a regional scale. There is further need for more studies examining diversity in different habitats and regions within NSW to ascertain the potential use of habitat surrogates for MPA planning, and through time to examine temporal stability of these trends, particularly as it is the method currently used to design MPAs for NSW and Australia.

Although there are many environmental and biological variables that influence fish assemblages in temperate Australia, such as habitat type (Curley *et al.,* 2002; Smith *et al.,* 2008; Chatfield *et al.,* 2010) and depth (Connoll and Lincoln-Smith, 1999; Williams and Bax, 2001; Chatfield *et al.,* 2010), there is still value in defining broad assemblage patterns for representative planning (Malcolm *et al.,* 2010). The results of this study show that the influence of environmental domains needs to be considered and incorporated into the habitat classification to improve the ability of MPA to represent biological diversity. The MaxN of economic species was highest within the estuary environmental domain, emphasizing the importance of conservation of these habitats for economical important fish. The conservation and management of economically important species is of particular interest for MPA planners given the new focus on managing threats in the NSW marine estate. MPAs selected without the benefit of intra-habitat variation in species assemblages will be unrepresentative; the upper range of currently promoted targets for MPA establishment (ie 30%) should be regarded as a minimum for biodiversity conservation (Gladstone, 2007). Banks *et al.* (2005) found that a representative system of MPAs should include the complete range of environmental gradients or habitat types, at any given scale, to maximise the protection of marine biodiversity. The results of this study indicate that a representative sample of fish assemblages from offshore islands, coastal headlands and/or estuarine environmental domains are required to adequately conserve representative samples of fish

biodiversity within sponge-dominated rocky reef habitat, such as that currently contained within the habitat classification scheme of PSGLMP.

Chapter 7 Sources of variation in the biodiversity of rocky reef fishes and the implications for surrogacy schemes for conservation planning: the influence of biogenic attributes of habitats

Abstract

Biogenic attributes of habitat influence the distribution and abundance of coral and rocky reef fishes, with high correlation reported between habitat biological diversity and fish species richness from a range of habitats. Habitat classification schemes are often used as surrogates for fauna biodiversity to identify sites to contribute to a representative system of marine protected areas (MPAs). However, the validity of these schemes as representations of biodiversity variation is often unknown. This study examined variability in the biodiversity of fish and sessile benthic assemblages in sponge-dominated subtidal rocky reef habitat within the Port Stephens-Great Lakes Marine Park. Specifically, variation within sponge-dominated habitat due to influences of environmental domains was examined. Baited remote underwater videos were deployed at numerous locations in differing environmental domains. Sessile benthic assemblages were surveyed remotely using an autonomous underwater vehicle. The influence of variation in sessile benthic assemblages on the associated assemblage of fishes was examined to determine the usefulness of sessile benthic assemblages as a surrogate for variation in fish biodiversity in relation to MPA planning. Forty-one species (23 families) of fishes, twenty-one species of encrusting benthic organisms, 10 sponge morphological types, and 2 substrate variables were recorded. Habitat biological diversity was unrelated to spatial variation in fish assemblages. There was no significant correlation in assemblage variation or species richness between fish and sessile benthic assemblages. Two variables (% cover ascidians, % cover sponge) together explained a significant amount of variation for the total MaxN of fishes. Habitat variation was not a good surrogate of biodiversity for fish assemblages, one variable only (ascidian cover) explained a significant amount of variation in fish assemblages, and it was only a relatively small per cent. In the context of MPA planning, biodiversity of sessile benthic assemblages is not a suitable surrogate for biodiversity of fish assemblages.

7.1 Introduction

Temperate marine habitats in Australia are diverse (Butler *et al.,* 2010), and support valuable commercial and recreational fisheries. Threats to marine biodiversity, in the form of climate change, coastal development, pollution, invasive species, fisheries overexploitation and

catchment discharges, are accelerating, fully encompass species ranges, and are of sufficient magnitude to cause species extinction in temperate Australia (Edgar *et al.,* 2005). Marine Protected Areas (MPAs) have been established in many countries principally as a tool to protect a selection of biodiversity by removing or reducing impacts from a range of threats.

Marine conservation planning frequently uses habitats as surrogates for spatial variation in biodiversity when selecting and designing MPAs, in situations where there is insufficient data on the distribution and abundance of species-level biodiversity (Stevens and Connolly, 2004; Banks *et al.,* 2005; Winberg *et al.,* 2007; Banks and Skilleter, 2010; Malcolm *et al.,* 2012). The logic behind this is the demonstrated association that has been shown between some habitat types and biodiversity (Ward *et al.,* 1999) (but see Shokri and Gladstone, 2013). However, the correlation between habitats and faunal assemblages has not been tested in many habitats, and the application of habitats as surrogates in MPA planning has been tested infrequently. The effectiveness of habitat in predicting reef fish assemblage structure on subtropical coral reefs in NSW found variations in fish assemblages were moderately correlated with habitat variations, and a combination of habitat and geographical distance resulted in greater surrogate precision than habitat alone (Lindsay *et al.,* 2008).

Reef fish are important contributors to the ecology of temperate rocky reefs (Jones and Andrew, 1990; Babcock *et al.,* 1999; Shears and Babcock, 2002) through their roles in herbivory, predation, feeding, excretion and as prey (Kingsford, 1998). Rocky reef fish assemblages in temperate and subtropical waters of NSW are highly diverse and include numerous economic species (Curley *et al.,* 2002; Gladstone, 2007; Malcolm *et al.,* 2007; Curley *et al.,* 2013). Fish assemblages can be used as surrogates of biodiversity for other faunal groups in the selection and design of MPAs (Ward *et al.,* 1999; Lindsay *et al.,* 2008). Quantifying features important in structuring fish assemblages is an important pre-requisite to implementation of measures to conserve regionally representative ecosystems (Ley, 2005).

Characteristics of the seabed habitat is a key factor influencing the structure of rocky reef fish assemblages (Curley *et al.,* 2002; Lindsay *et al.,* 2008; Chatfield *et al.,* 2010; Poulos *et al.,* 2013). For example, Curley *et al.* (2002) reported that fish assemblages differ among *Ecklonia radiata* kelp forests, urchin-grazed barrens, and sponge dominated reef habitats in temperate NSW. In addition to the significant variation in fish assemblages that occurs among different habitats, there is frequently substantial variation within a single habitat (Gladstone, 2007; Malcolm *et al.,* 2007). Spatial variability in fish assemblages in temperate

Australia has also been related to depth (Connoll and Lincoln-Smith, 1999; Malcolm *et al.,* 2011), exposure (Valesini *et al.,* 2004) and distance from shore (Malcolm *et al.,* 2011).

The biogenic attributes of temperate subtidal reefs in Australia include a large coverage of sessile benthic organisms. Assemblages of sessile benthic organisms on temperate subtidal reefs in southern Australia are diverse, structurally complex, highly endemic and are a commercially important part of Australia's marine diversity (Keough, 1999; O'Hara, 2002; Ponder *et al.,* 2002; Fromont *et al.,* 2006). On reefs below around 20 m depth, sponges are the dominant fauna, with ascidians, cnidarians, bryozoans and algae also occurring (Roberts *et al.,* 1994; Roberts, 1996; Roberts and Davis, 1996; Roberts *et al.,* 1998). Assemblages of sessile benthic organisms are spatially and temporally variable, with the structure and diversity of assemblages reflecting the influences of differing environmental variables (Roberts and Davis, 1996; Owen, 2003; Roberts *et al.,* 2006) operating at scales of metres, 100s metres and 10s kilometres (Roberts, 1996; Roberts and Davis, 1996; Owen, 2003; Roberts *et al.,* 2006).

The biogenic attributes of habitat (such as cover of sponges, ascidians and corals) influence the distribution and abundance of coral and rocky reef fishes (Holbrook *et al.,* 1990; Friedlander and Parish, 1998; Ferreira *et al.,* 2001; Syms and Jones, 2001; Friedlander *et al.,* 2003). Previous studies have documented high correlation between habitat biological diversity (i.e. the diversity of the benthic assemblage such as sponges, ascidians and corals) and fish species richness on coral reefs (Roberts and Ormond, 1987; Messmer *et al.,* 2011), rocky reefs (Moore *et al.,* 2010) and artificial reefs (Clynick *et al.,* 2007; Rooker *et al.,* 1997). Studies on rocky reef fish in temperate Australia have found that habitat topographic complexity is an important factor structuring assemblages (Tuya *et al.,* 2009; Rees *et al.,* 2013). However it's not known whether the habitat biological diversity of sponge-dominated sessile benthic assemblages in temperate south east Australia influences fish assemblages, or if any correlation of biodiversity between fish and sessile benthic assemblages exists. If correlation between fish and sessile benthic assemblages occurs, then one group could act as a biodiversity surrogate for the other.

Surveys of fish and sessile benthic assemblages on subtidal temperate reefs have traditionally been undertaken using diver-based methods (Smith *et al.,* 1999; Curley *et al.,* 2002; Gladstone, 2007) however these methods are restricted to relatively shallow depths, and short periods of time. Baited remote underwater video stations (BRUVs) have several advantages

over diver-based underwater visual census (UVC) techniques for surveys of fish biodiversity: BRUVS can be operated in low-visibility conditions, at greater depths than SCUBA, require fewer personnel, remove biases associated with diver-related fish behaviour, are more effective at detecting larger predatory fish and shy cryptic species (Willis and Babcock, 2000; Willis *et al.,* 2000; Cappo *et al.,* 2004; Watson *et al.,* 2005; Colton and Swearer, 2010). Surveys of sessile benthic assemblages in subtidal reefs have previously included *in situ* diver surveys (Owen, 2003) and drop cameras (Roberts *et al.,* 1994; Roberts, 1996; Roberts and Davis, 1996; Roberts, 2006), both of which are unable to collect large amounts of field data quickly and have a limited spatial coverage. The use of Autonomous Underwater Vehicles (AUVs) to survey sessile benthic assemblages can overcome the limitations of diver-based surveys and drop cameras, as AUVs can collect large numbers of high quality images suitable for biodiversity assessment, collect additional information on physical parameters such as depth and temperature, and survey pathways can be directed and linked with GPS (Rigby *et al.,* 2010; Williams *et. al.*, 2012).

The aim of this study was to examine the influence of biogenic variation (measured as variation in sessile benthic assemblages) in one habitat on the associated assemblages of rocky reef fishes. The approaches taken were to test whether there was a relationship in the spatial variation of biodiversity in both groups, and to determine the most important features of benthic assemblages that influenced fish assemblages. This was done by quantifying spatial variation in both fish and sessile benthic assemblages within a single habitat (sponge-dominated rocky reef) within Port Stephens-Great Lakes Marine Park (PSGLMP). Field data were gathered by BRUVS for fishes and AUV for sessile benthic assemblages.

7.2 Methods

Study Area

PSGLMP is situated on the mid-north coast of NSW (Fig. 7.1), and includes estuaries, coastline and offshore waters (to ~6 km) over approximately 80 km of coastline and an area of 98,000 ha (see detailed description in Chapter 3). Subtidal rocky reef habitat represents approximately 3% of the PSGLMP (NSW Marine Parks Authority, 2006) and is classified by depth for planning purposes into three categories: (shallow 0-25 m, intermediate 25-60 m and deep 60-200 m) (Jordan *et al.,* 2010). This study occurred within sponge-dominated subtidal rocky reef habitat in the intermediate (25-60 m) habitat class.

Figure 7.1: Location of study sites in Port Stephens-Great Lakes Marine Park. Symbols represent offshore island (square) and coastal headland (circle).

Experimental Design and Field Sampling

Fishes were surveyed in September 2010 with 10 replicate BRUVS drops on sponge-dominated rocky reefs in the intermediate habitat class adjacent to an offshore island (n=4) and a coastal headland (n=6) (Fig.7.1). The subtidal rocky reef habitat at the locations surveyed consisted of a mix of large boulders and crevices, with a biogenic covering of sponges, coral, ascidians, bryozoans, algae, sediment and sand, over a depth range of 21.7 m and 32.0 m. The reefs surveyed were zoned as either sanctuary zones or habitat protection zones within the PSGLMP. Sanctuary zones prohibit all forms of fishing whilst habitat protection zones in this marine park restrict certain commercial trawling, netting and line fishing.

BRUVS were constructed as in Malcolm *et al.* (2007), and consisted of a video camera in an underwater housing, an attachment frame, a bait-pole with bait, and a rope and float system linking the BRUV to the surface. The BRUVS were baited with approximately 1 kg of chopped pilchards (*Sardinops neopilchardus*), which were mashed into a plastic mesh bait

bag and attached to the end of a bait-pole at a distance of 1.5 m from each camera (Malcolm *et al.,* 2007). The cameras were all similar digital Canon HG21's with wide-angle lenses. The field of view was standardised to a distance of approximately 2 m behind the bait, to minimise the effects of water visibility on the measure of relative abundance (Malcolm *et al.,* 2007). BRUVS were deployed for 30 min per replicate with replicates separated by at least 200 m (Malcolm *et al.,* 2007).

Fish were identified to species-level (using Hutchings and Swainston, 1986; Edgar, 1997; Kuiter, 2000) and an index of relative abundance of each species (MaxN) and species richness recorded. MaxN is the maximum number of individual fish of each species in the frame at any one time during the video (Malcolm *et al.,* 2007). Species were additionally classified as 'economic' if they were a target or secondary species in either the commercial or recreational fishing sectors of NSW (Scandol *et al.,* 2008).

Sessile benthic assemblages were remotely surveyed in September 2010 using the University of Sydney's Australian Centre for Field Robotics (ACFR) AUV (Rigby *et al.,* 2010; Williams *et al.,* 2012). The AUV was equipped with a pair of high resolution cameras and strobes, multibeam sonar, depth and conductivity/temperature sensors, Doppler Velocity Log (DVL) including a compass with integrated roll and pitch sensors, Ultra Short Baseline Acoustic Positioning System (USBL) and forward looking obstacle avoidance sonar. One 25 m x 25 m photo grid was surveyed at each of the six coastal headland and four offshore island locations, and overlapped the position where BRUVS had been deployed (Fig.7.1).

The number of images collected by the AUV varied between 975 and 1975 per location (n=18750 total images). There was often overlap between images (generally every 3rd to 5th image was a 'new' image without any overlap from the previous image), and when the AUV turned back to complete a loop every 12th image contained no overlap. Prior to analysis each image was opened in Arc GIS to detect its location and ensure it was not overlapping with the last selected image. A subset of AUV images was randomly selected to identify and quantify the biodiversity of sessile benthic organisms in each location. A pilot study determined the optimal number of AUV images (n=25) and grid points (n=50) to be overlaid on each image (see detailed description in Chapter 4). The cover of biota was determined by applying a transparent image over the top of each image 50 regular points, where the categories under each point were recorded. The cover and species richness of sessile benthic organisms were determined using Coral Point Count with Excel extensions (CPCe) (Kohler and Gill, 2006), a

program developed for the determination of benthic substrate coverage using regular point count methodology. A mixture of classification schemes was used to record organisms in the selected images. Sponges were classified into broad morphological groups (arborescent, cup, encrusting, fan, globular, lumpy, massive, papillate, repent and tubular) developed by the Commonwealth Environment Research Facility (CERF) Marine Biodiversity Hub: Surrogates Program (Meyer *et al.,* 2010), as sponge species identification is not possible without tissue samples for examination. Other sessile benthic organisms were identified to species-level where possible (using Shepherd and Thomas, 1982; Edgar, 1997; Huisman, 2000; Veron, 2000; Gowlett-Holmes, 2008) and to morphospecies when identification was not possible.

Statistical Analyses

The hypothesis that species richness of fishes and sessile benthic organisms were correlated was tested by determining the strength and significance of the Spearman's rank correlation coefficient. The hypothesis that spatial variation in the assemblages of fishes and sessile benthic assemblages were correlated was tested using the RELATE test in PRIMER (PRIMER-E Ltd, Plymouth) (Anderson *et al.,* 2008) for both the entire fish assemblage and the subset of reef-associated fishes. This test was based on the Bray Curtis similarity matrix of each group, using the untransformed data (for benthic assemblages), square-root transformed data (for fish assemblages), and presence-absence transformed data (for both fish and benthic assemblages). Transformation of multivariate data sets is done to reduce the overriding influence of a few very abundant and/or rare species (Clarke, 1993), and different transformations were compared because patterns of multivariate similarity are known to be sensitive to the type of data transformation (Olsgard *et al.,* 1997, Olsgard *et al.,* 1998).

Spatial structuring of the fish assemblages was visualised by principal coordinates analysis (PCO) (Anderson *et al.,* 2008). PCO is an ordination technique that projects the samples onto a 2-dimensional space that retains the scales of the resemblance matrix, and therefore provides a meaningful visual depiction of the value of inter-sample similarities. The MaxN of each species in each location was determined; species that occurred as single individuals or occurred at only one location were considered unlikely to be structuring spatial variation in assemblages and so were excluded from the analyses (this resulted in the exclusion of nine species and retention of 33 species). The data were square-root transformed to reduce the influence of a few highly abundant species. A Bray-Curtis similarity matrix was used for the PCO. Analyses were undertaken with PRIMER 6 & PERMANOVA+ software (Primer-E).

Distance-based redundancy analysis (dbRDA), a form of multivariate multiple regression (Legendre and Anderson, 1999; McArdle and Anderson, 2001), was used to determine the set of habitat attributes that explained variation in the fish assemblages. The procedure was done with the DISTLM routine in the PERMANOVA+ add-in to PRIMER 6 software, using the Bray-Curtis similarity matrix of the fish assemblages as the response variable, and the suite of habitat attributes as the predictor variables. These habitat attributes included 41 categories and life forms of biogenic habitat attributes, three physical attributes (% cover sand, silt, depth), and one environmental attribute (whether the location was adjacent to a coastal headland or island). To reduce the total number of predictor variables for testing, biogenic habitat attributes were aggregated into five groups: brown algae, red algae, sponge, bryozoan and ascidian. For each photo-quadrat the % cover value for each category and life form within a group was summed, and the location-average % cover value for each group was determined from the total set of photo-quadrats analysed in each location. Draftsman plots of untransformed benthic habitat variables (Clarke and Ainsworth, 1993) showed no evidence of skewness or curvilinear relationships and so the untransformed data were used. The pair-wise correlation matrix for the five groups of biogenic habitat attributes and three physical attributes showed % covers of red algae and silt were highly correlated (i.e. r $\geq$0.95), and so silt was excluded from subsequent analyses (retention of silt and exclusion of red algae had no effect on the outcomes of analyses). The attribute 'environment' was included as a categorical variable, indicating whether the location was adjacent to a coastal headland or island.

The smallest set of habitat variables that together explained a significant amount of variation in the fish assemblages was determined by a step-wise selection procedure in DISTLM, with adjusted R^2 used as the selection criterion. The dbRDA routine in PERMANOVA+ was used to visualise the relationship (based on Pearson linear correlation) between the selected habitat attributes and the fish assemblages. The dbRDA routine is an ordination technique that overlays vectors for the selected habitat variables on the spatial arrangement of locations, with the length and direction of a vector indicative of the magnitude of the correlation between the variable and the depicted arrangement of locations (Anderson *et al.,* 2008).

The influence of the set of biogenic and physical habitat attributes on species richness, and total MaxN of fish, was assessed. Analyses were done on the Euclidean distance matrix of each variable, using a step-wise selection procedure in DISTLM, with adjusted R^2 used as the selection criterion. As a measure of the habitat biological diversity, the Shannon-Wiener

diversity index H' was calculated from the % cover data of sessile benthic taxa and lifeforms (Roberts and Ormond, 1987). The relationship between H' and the fish assemblage, fish species richness, and total MaxN of fish was tested in DISTLM, using the 'All specified' selection procedure and R^2. The correlation between H' fish assemblages was also tested using the RELATE test in PRIMER (PRIMER-E Ltd, Plymouth) (Anderson *et al.,* 2008) for both the entire fish assemblage and the subset of reef-associated fishes (see Appendix 3 for species lists within each assemblage). This test was based on the Bray Curtis similarity matrix of each group, on square-root transformed abundance data (for fish assemblages) and untransformed habitat biological diversity data (for sessile benthic assemblages).

7.3 Results

Fish Assemblages

Forty-one species (23 families) were observed, comprising 8 species (8 families) of Chondrichthyes and 33 species (15 families) from the class Actinopterygii. Monacanthidae (leatherjackets) was the most speciose family recorded, with six different species. Eight species were recorded as single individuals. Of the species recorded 31 (75%) were of economic importance and 33 (80%) were classified as reef-associated fish (Appendix 3).

A total of 1150 individuals were observed by combining MaxN data from all replicates. The most abundant species were yellowtail scad (*Trachurus novaezelandiae*) (Carangidae) (representing 28% of the MaxN), mado (*Atypichthys strigatus*) (Scorpididae) (23%), snapper (*Pagrus auratus*) (Sparidae) (11%), Maori wrasse (*Ophthalmolepis lineolatus*) (Labridae) (6%), old wife (*Enoplosus armatus*) (Enoplsidae) (6%), silver sweep (*Scorpis lineolata*) (Scorpididae) (3%) and silver trevally (*Pseudocarnax dentex*) (Carangidae) (2%).

Sessile Benthic Assemblages

Forty-one life forms were recorded, representing 21 encrusting benthic organisms (three Phaeophyta (brown algae), seven Rhodophyta (red algae), ten Cnidaria (corals and anemones), six Bryozoa (bryozoans) and five Ascidiacea (ascidians) and ten sponge morphological types. In addition, two substrate variables (silt matrix and sand) were recorded. Silt matrix (consisting of sediment and micro-organisms) (Roberts *et al.,* 1994) (with a mean % cover (± SE) of 27.0±2.54), filamentous red algae (15.5±0.68), sand (15.2±2.77), encrusting coralline algae (13.3±2.14), encrusting sponge (4.9±0.82) and arborescent sponge (3.9±0.66) were the dominant variables recorded (Table 7.1).

Table 7.1: Mean % cover (±SE) of the major groups of organisms and two substrate variables recorded in sponge-dominated rocky reef habitat in the Port Stephens-Great Lakes Marine Park.

Location	Phaeophyta	Rhodophyta	Cnidarian	Bryozoan	Sponge	Ascidian	Silt	Sand	Depth
Coastal headland 1	0.6%±0.4	13.4%±3.9	0.7%±0.4	0.9%±0.6	9.9%±3.4	0.4%±.4	39.7%±4.0	34.5%±6.3	29.6m ±0.03
Coastal headland 2	3.3%±1.1	28.7%±6.5	0.2%±0.2	3.3%±1.5	15.5%±4.1	0.3%±0.2	33.0%±3.1	15.7%±4.1	29.1m±0.07
Coastal headland 3	5.3%±1.7	42.4%±5.2	1.4%±1.2	1.6%±0.7	14.8%±3.7	2.6%±2.4	20.7%±2.1	11.2%±2.7	23.3m±0.08
Coastal headland 4	4.5%±1.2	53.5%±8.7	1.2%±1.0	3.0%±1.0	9.8%±2.9	4.4%±1.3	15.9%±2.0	7.9%±1.2	23.1m±0.04
Coastal headland 5	1.2%±0.7	34.8%±5.7	7.3%±0.3	2.4%±1.0	11.4%±2.8	6.7%±1.6	32.3%±18.4	3.9%±1.0	21.8m±0.06
Coastal headland 6	0.1%±0.1	30.8%±3.3	0.6%±0.3	2.5%±1.0	17%±4.9	3.5%±1.1	31.9%±2.4	13.6%±1.9	24.4m±0.05
Offshore island 1	0.5%±0.3	37.2%±4.4	1.2%±0.7	1.4%±0.4	18.9%±4.2	2.2%±1.0	24.1%±1.6	14.5%±2.4	29.5m±0.03
Offshore island 2	2.0%±0.6	38.4%±6.2	1.4%±0.7	1.6%±0.8	22.5%±3.4	2.2%±0.7	24.9%±1.5	7.0%±1.2	25.5m±0.07
Offshore island 3	3.6%±0.6	52.7%±8.9	0.8%±0.6	1.2%±0.7	13.6%±3.0	1.1%±0.7	16.2%±2.1	10.9%±1.5	25.2m±0.08
Offshore island 4	0.8%±0.6	20.9%±3.4	0.4%±0.2	2.1%±0.8	11.2%±3.8	0.7%±0.5	31.6%±3.0	32.4%±5.6	32.0m±0.04

Linkages Between Fish and Sessile Benthic Assemblages

The RELATE analysis based on square-root transformed fish data and untransformed benthic data indicated no significant correlation in assemblage variation between all fish and sessile benthic assemblages, and between reef-associated fish and sessile benthic assemblages (Table 7.2). There was also no significant correlation in species richness between all fish and sessile benthic assemblages, and between reef-associated fish and sessile benthic assemblages (Table 7.2). Similar trends were reported from data sets based on presence-absence transformed fish and benthic assemblages (Table 7.2).

Table 7.2: Correlation between fish and sessile benthic assemblages, and fish assemblages and habitat biological diversity (RELATE).Values shown are Spearman rank correlation coefficients (ρ) and their P-values for the entire fish assemblage and reef-associated fish assemblage.

Transformation	Square-root transformed (fish data), untransformed (benthic data)		Presence-absence transformed (fish and benthic data)	
Group	ρ	*P*	ρ	*P*
Species richness: fish and benthic assemblages	-0.25	0.95	NA	
Species richness: reef-associated fish and benthic assemblages	-0.24	0.97	NA	
Assemblage variation: fish and benthic assemblages	0.28	0.07	-0.24	0.89
Assemblage variation: reef- associated fish and benthic assemblages	0.08	0.33	0.02	0.48
Assemblage variation: fish and habitat biological diversity	-0.21	0.85	-0.15	0.74
Assemblage variation: reef- associated fish and habitat biological diversity	-0.15	0.75	-0.26	0.89

There is an absence of a clear pattern on the unconstrained PCO plot, except all island samples have high values on PCO 1 axis (Fig. 7.2). The species vectors that are overlaid on the PCO plot indicate the species that have a linear relationship with the PCO axes, and may be responsible for the structuring of assemblage variation. The species shown on the PCO have a positive correlation with PCO 1 axis (white ear (*Parma microlepis*) (Pomacentridae)), a negative correlation with PCO 1 axis (*Trachurus novaezelandiae*, *Atypichthys strigatus*, girdled parma (*Parma unifasciata*) (Pomacentridae), a positive correlation with PCO 2 axis

(*Pseudocaranx dentex*, truncate coral fish (*Chelmonops truncatus*) (Chaetodontidae), ocean leatherjacket (*Nelusetta ayraudi)* (Monacanthidae), *Pagrus auratus*, tarwhine (*Rhabdosargus sarba*) (Sparidae), and a negative correlation with PCO 2 axis (sergeant baker (*Latropiscis purpurissatus)* (Aulopidae), black reef leatherjacket (*Eubalichthys bucephalus)* (Monacanthidae), and eastern wirrah (*Acanthistius ocellatus*) (Serranidae)).

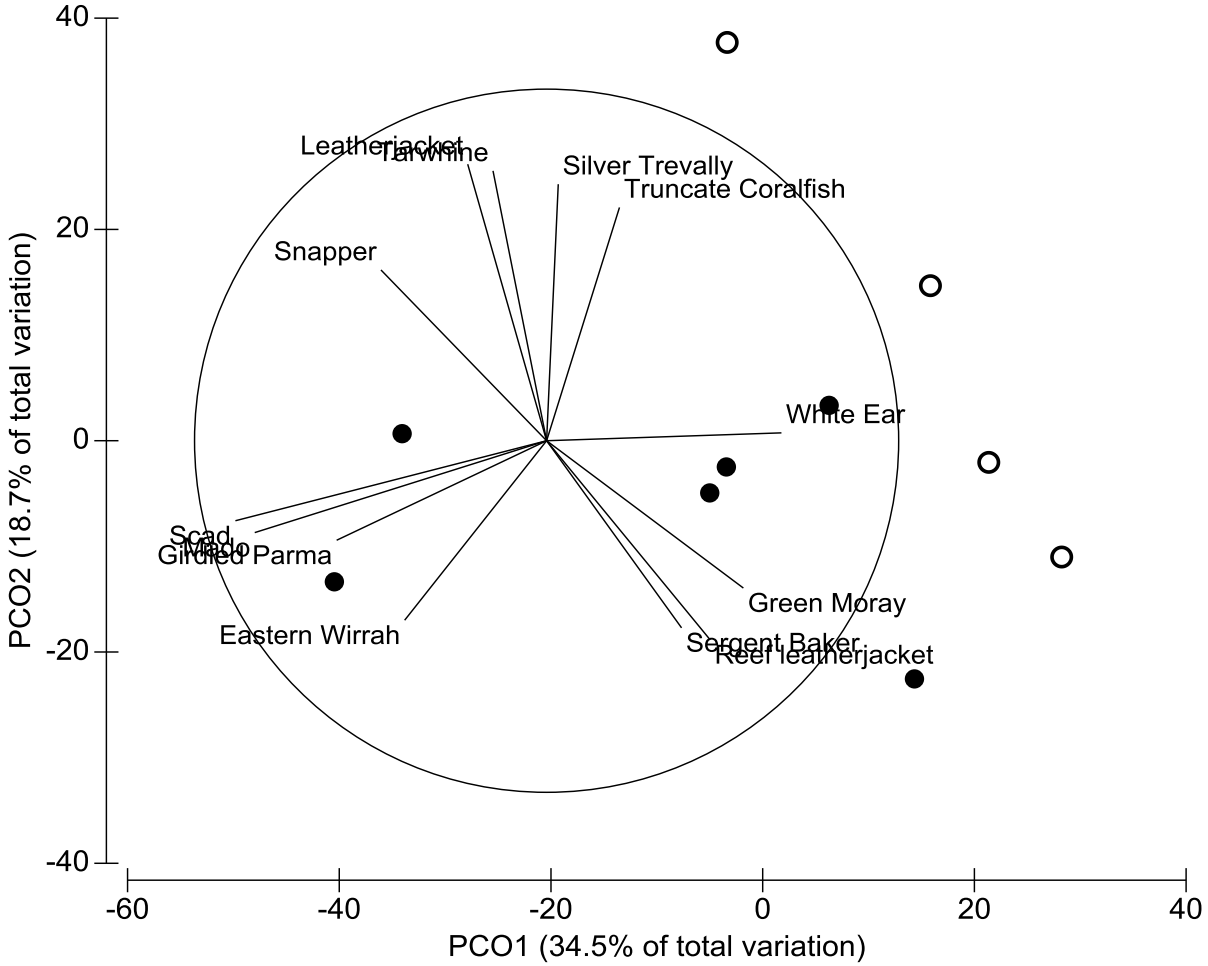

Figure 7.2: Unconstrained PCO plot of the spatial structure of fish assemblages sampled on subtidal reefs in the Port Stephens-Great Lakes Marine Park (solid symbols represent headlands, hollow symbols represent islands). The vector overlays represent species with a Pearson correlation of at least 0.65 with the PCO axes.

Two variables explained a significant proportion of variation in the fish assemblages: % cover ascidians, and depth (Table 7.3). However, the DISTLM stepwise procedure, using adjusted R^2 as the selection criterion, selected only % cover ascidians (adjusted R^2=12.2%, P=0.02, n=9999 permutations). Addition of further variables did not lead to a significant

increase in explained variation. Other approaches to variable selection in DISTLM that were explored (BEST procedure using AIC as selection criterion, substitution of % cover red algae with % cover silt) also selected % cover ascidians as the single significant explanatory variable.

Table 7.3: Results of marginal tests in a DISTLM analysis showing the proportion of variation in spatial variation of fish assemblages explained by each of the habitat attributes. Environment is a categorical variable (headland, island).

Habitat Attribute	Pseudo-*F*	*P*	Proportion explained variation
Brown algae	1.23	0.27	0.13
Red algae	1.22	0.27	0.13
Sponge	1.34	0.21	0.14
Bryozoan	1.11	0.35	0.12
Ascidian	2.25	0.02	0.22
Sand	1.14	0.34	0.12
Depth	2.15	0.03	0.21
Environment	2.04	0.06	0.20

The influence of % cover of ascidians on the structuring of the assemblages in the PCO ordination was visualized by overlaying vectors in dbRDA (Fig. 7.3). dbRDA axis 1 was negatively correlated with % cover ascidians (r=-0.75), showing that ascidian cover decreased from left to right. The 2 dbRDA axes depicted 56% of the variation in the fitted model and 49.1% of the total variation.

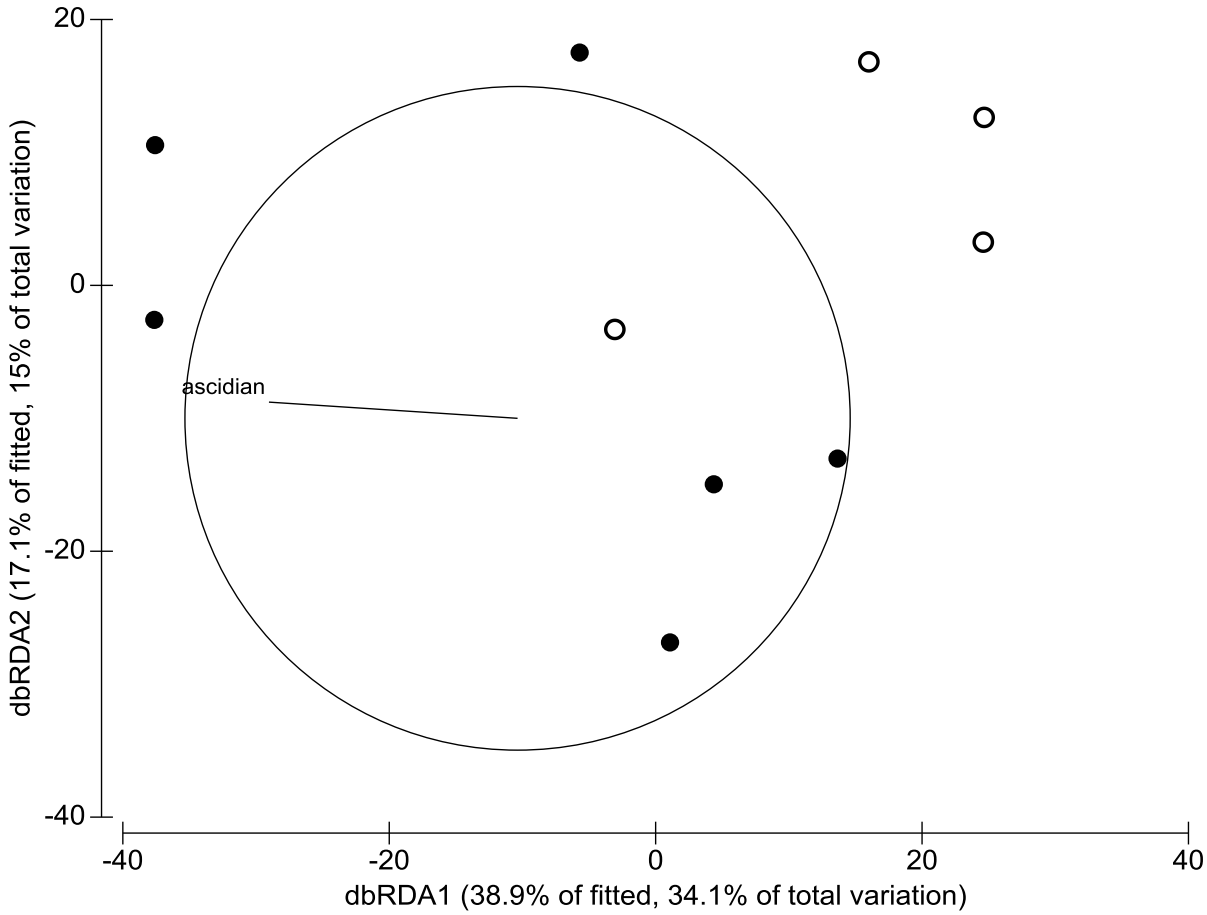

Figure 7.3: dbRDA ordination plot showing the spatial structure of fish assemblages sampled on subtidal reefs in the Port Stephens-Great Lakes Marine Park (solid symbols represent headlands, hollow symbols represent islands) overlaid with the vectors of the environmental variable that explained a significant amount of variation in the assemblages. The vector represents the direction and magnitude of the Pearson correlation of the variable with the dbRDA axes.

None of the measured habitat variables explained a significant amount of variation in fish species richness (Table 7.4). Two variables (% cover ascidians, % cover sponge) together explained 78.7% (adjusted R^2) of the spatial variation in total MaxN (Table 7.5).

Table 7.4: Results of marginal tests in a DISTLM analysis showing the proportion of variation in spatial variation of species richness and total MaxN independently explained by each of the habitat attributes. Environment is a categorical variable (headland, island).

	Species richness			Total MaxN		
Habitat attribute	Pseudo-*F*	*P*	Proportion explained variation	Pseudo-*F*	*P*	Proportion explained variation
Brown algae	0	0.95	0	0.79	0.41	0.09
Red algae	0.01	0.91	0	1.58	0.25	0.16
Sponge	2.42	0.16	0.23	4.60	0.06	0.37
Bryozoan	0.39	0.53	0.05	2.09	0.20	0.21
Ascidian	0.83	0.40	0.09	10.07	0.02	0.56
Sand	2.31	0.18	0.22	1.54	0.22	0.16
Depth	0.71	0.42	0.08	4.19	0.08	0.34
Environment	0.22	0.71	0.03	1.73	0.27	0.18

Table 7.5: Results of DISTLM analysis (based on step-wise selection and adjusted R^2, n=9999 permutations) showing the proportion of spatial variation in total MaxN of fishes that is significantly explained by the selected habitat attributes. Addition of further habitat attributes did not add a significant amount to the proportion of explained variation.

Habitat Attribute	Adjusted R^2	Pseudo-*F*	*P*	Proportion explained variation	Cumulative proportion explained variation
Ascidian	0.50	10.07	0.02	0.56	0.56
Sponge	0.79	11.67	0.01	0.28	0.83

Values of habitat biological diversity varied from 1.41 to 2.05 (Table 7.6). The highest value was at an offshore island replicate and the lowest at a coastal headland replicate, although all

values were relatively similar. The RELATE analysis indicated no significant correlation between habitat biological diversity and the entire fish assemblage, and between habitat biological diversity and the reef-associated fish assemblage (Table 7.2). Values of habitat biological diversity explained a very small percent of the variation in each of the attributes (total assemblage, species richness and total MaxN) of the fish and reef-associated fish assemblages, as evidenced by the low R^2 values, and none explain a significant percent of variation (Table 7.7).

Table 7.6: Habitat biological diversity values (Shannon-Wiener diversity index H').

Location	FI 1	FI 2	FI 3	FI 4	FI 5	FI 6	Br 1	Br 2	Br 3	Br 4
H'	1.41	1.68	1.85	1.96	1.91	1.94	1.89	2.05	2.01	1.66

Table 7.7: Summary of results of DISTLM test for the relationship between the Shannon-Weiner biological diversity of the habitat, and attributes of the fish assemblage. MaxN data for the total fish assemblage and the reef-associated fish assemblage were square-root transformed prior to analysis.

Fish Assemblage Attribute	R^2	Pseduo-F	P
Total fish assemblage	7.9%	0.60	0.77
Species richness of fishes	5.1%	0.43	0.54
Total MaxN of fishes	5.2%	0.44	0.55
Reef-associated fish assemblage	5.7%	0.49	0.89
Species richness of reef-associated fishes	2.3%	0.19	0.68
Total MaxN of reef-associated fishes	0.7%	0.05	0.82

7.4 Discussion

Linkages Between Fish and Sessile Benthic Assemblages

This study found no significant correlation in spatial variation in assemblages of all fish and sessile benthic assemblages, or between reef-associated fish and sessile benthic assemblages. Differing data transformation techniques (e.g. to reduce the influence of dominant species) did not alter this outcome. The effects of data transformation on spatial patterns of assemblage similarity have been reported in other studies (Olsgard *et al.,* 1997; Olsgard *et al.,* 1997; Bertasi *et al.,* 2009). There was no correlation in species richness of fishes (all fish, reef-associated) and sessile benthic assemblages, with values of habitat biological diversity explaining a very small percent of the variation in both all fish assemblages and reef-associated fish assemblages. Two variables (% cover ascidians, % cover sponge) together explained a significant amount of variation for the total MaxN of fishes. However, habitat variation was not a good surrogate of biodiversity for fish assemblages, as one variable only (ascidian cover) explained a significant amount of variation in fish assemblages, and it was only a relatively small percent. This is a similar resulted to that reported by Gladstone and Owen (2005), where spatial patterns in algae, invertebrate and rocky reef fish assemblages in temperate NSW were unrelated. Studies from coral reef systems have also reported low correlation in the biodiversity of fish and coral assemblages (Beger *et al.,* 2007; Beger *et al.,* 2003).

Previous studies have reported mixed results for effects of changes in biogenic habitat attributes on fish assemblages. While epibiota are major biogenic components of hard substrata in marine habitats, Coleman and Connell (2001) found the amount of epibiota associated with pier pilings had little effect on fish assemblages. Similarly, Roberts (2007) found epibiota did not have an important influence on the fish assemblages within an estuarine channel on the NSW central coast. A study on coral reef fish reported that fishes were distributed without regard to differences in habitat structure among reefs (Sale *et al.,* 1994). In contrast to this, changes in fish assemblages on the NSW central coast have been documented when biogenic habitat features are impacted by sewage outfalls (Smith and Suthers, 1999; Roberts *et al.,* 1998). Changes in fish assemblages have also been documented as the biogenic features of artificial reefs develop (Clynick *et al.,* 2007; Rooker *et al.,* 1997), and changes in fish assemblages following habitat damage caused by trawling (Pitcher *et al.,* 2004).

It is surprising that this study did not find a relationship between biogenic habitat attributes and fish assemblages, given that the biogenic habitat attributes (such as sponges, bryozoans, ascidians and cnidarians) provide resources for fish assemblages such as food, camouflage, refuge sites, breeding sites, increased structural diversity, and increased number of microhabitats/niches available (Holbrook *et al.* 1990; Coleman and Connell 2001). Provision of camouflage and refuge sites may be particularly influential to small cryptic species, such as blennies, which are known to rely heavily on refuges being present in their habitat (Coleman and Connell 2001). This study utilised BRUVs to survey fish assemblages, which makes detection of small cryptic species difficult unless they are visible within the field of view. Small, cryptic reef-associated species are more effectively surveyed using UVC than BRUVs (Lowry *et al.,* 2012). It is possible that if the fish surveys in this study were adapted to include the detection of small, cryptic species, (for example including UVC surveys with emphasis on searching for small, cryptic reef-associated species) then a stronger relationship between biogenic habitat attributes and fish assemblages may have been evident.

There are many environmental and biological variables that influence fish assemblages in temperate Australia, such as habitat type (Curley *et al.,* 2002; Smith *et al.,* 2008; Chatfield *et al.,* 2010), depth (Connoll and Lincoln-Smith, 1999; Williams and Bax, 2001; Moore *et al;* 2010; Malcolm *et al.,* 2011), exposure (Valesini *et al.,* 2004), distance from shore (Malcolm *et al.,* 2010) and water column characteristics such as temperature, turbidity and salinity (Loneragan *et al.,* 1987; Hydnes *et al.,* 1999; West and Walford, 2000; Kanandjembo *et al.,* 2001; Smith and Sinerchia, 2004).This study found that variation in fish assemblages was largely unrelated to variation in the biogenic attributes of the habitat, with one variable only (ascidian cover) explaining a significant but minor amount of variation in fish assemblages. Ascidian larvae provide a food source for rocky reef fish in temperate Australia (Russ, 1980) and coral reef fish in Australia (Olson and McPherson, 1987), and mature ascidians provide habitat for the invertebrate prey items of fishes, such as echinoderms and molluscs (Edgar, 2001). Additionally, ascidians like *Pyura spinifera,* a stalked colonial ascidian commonly recorded in this study, also provide structural diversity to rocky reefs, which is important for protection of reef fish from predators (Edgar, 2001). Given that the dominant sessile benthic groups recorded in this study (sponge, ascidians, bryozoans and cnidarians), can provide food and shelter for reef-associated fish, it is surprising that other variables did not explain a significant amount of the variation in fish assemblages. Presumably as cover of sponges, ascidians, bryozoans and cnidarians increased, so too would food availability and structural

diversity, both of which are important to reef-associated fish and may have resulted in increased MaxN of fishes. However this wasn't the case, both assemblage variation and richness of sessile benthic assemblages was independent of assemblage variation and richness fish assemblages.

In this study, variation in habitat biological diversity was unrelated to spatial variation in fish assemblages. This is an unexpected result, as increases in habitat biological diversity is often predicted to increase the diversity in fish assemblages because a greater variety of habitats increases the opportunities for species to specialise on different resources and coexist (Messmer *et al.,* 2011). Previous studies have documented high correlation between habitat biological diversity and fish species richness on coral reefs (Roberts and Ormond, 1987; Messmer *et al.,* 2011). Habitat structure also influences rocky reef fishes in temperate Australia, with fish species richness highly correlated with reefs characterised by a mosaic of habitats (Moore *et al.,* 2010). However there are no previous studies that examine the correlation between sponge-dominated reef habitat biological diversity and rocky reef fish diversity; as previous studies in rocky reef habitat have focused on linkages between fish biodiversity and habitat topographic complexity, rather than habitat biological diversity. This is likely due to the difficulty of documenting the biodiversity of sessile benthic assemblages, particularly in sponge-dominated habitat where identification of sponges (the dominant fauna) is only possible by collecting tissue samples that need to be identified by experts.

There is also little information regarding the importance of habitat topographic complexity for rocky reef fishes in temperate Australia, apart from two studies. Firstly, Tuya *et al.* (2009) documented the importance of habitat topographic complexity to the spatial patterns of abundance of adult and sub-adult labrid fishes inhabiting rocky reefs in south-western Australia. An increase in labrid fishes was documented with increase in small topographical structural elements < 1 m (such as cracks, caves and holes) (Tuya *et al.,* 2009). Secondly, Rees *et al;* (2013) used estimates of several spatial metrics from swath acoustic bathymetry to examine the relationship between habitat complexity and temperate rocky reef and sessile invertebrate assemblages in central NSW. Reefs with vertical relief exhibited a strong positive relationship with sessile invertebrate abundance and species richness (Rees *et al.,* 2013). Reef slope showed a significant negative relationship with fish abundance, whilst reef cover showed a significant positive relationship with fish abundance and diversity (Rees *et al.,* 2013). In the Mediterranean, habitat topographic complexity drives a large part of spatial variability in the distribution, species richness, biomass and abundance of rocky reef fishes,

with higher habitat topographic complexity correlated to higher number of fish species and greater abundances (Garcia-Charton and Perez-Ruzafa, 2001; Garcia-Charton *et al.,* 2004; Ribeiro *et al.,* 2005). Such patterns suggest that similar processes may be influencing reef fish communities in temperate Australian waters, and further examination of this is warranted.

Implications for Marine Protected Area Planning

Where strong and predictable correlations between fish assemblages and habitat types exist, habitat maps can be used as effective surrogates for biodiversity for the purpose of MPA planning. There are examples of studies that report strong correlations between fish and habitat, and this can increase the likelihood of an effective framework for designing MPAs (Curley *et al.,* 2002). In temperate Australia, fish assemblages differ between habitat types (Curley *et al.,* 2002; Lindsay *et al.,* 2008; Poulos *et al.,* 2013), reef type (Smith *et al.,* 2008) and substrate type (Chatfield *et al.,* 2010). However, habitats are spatially heterogeneous at many scales, providing a diverse range of resources for species, and to date there has been no studies explaining the influence of intra-habitat variation of fish assemblages and correlation with intra-habitat variation of habitat (but see Chapter 6 where intra-habitat variation of fish assemblages was documented between coastal headland, offshore island and estuarine environments within sponge-dominated rocky reef in PSGLMP). If habitat maps are used as surrogates for diversity of fish assemblages, then it is necessary for the scale and strength of the relationship of fishes to habitats be reconciled with the level of map resolution (Anderson *et al.,* 2009).

Maps of seabed habitats based on physical and depth characteristics are used as a surrogate of diversity for fish assemblages in MPA planning in NSW (Malcolm *et al.,* 2011; 2012). Results of this study indicate that in the context of MPA planning, surveys of variation in habitat attributes within sponge-dominated rocky reef cannot be used as an alternative to biodiversity assessments of fishes, as the biodiversity of sessile benthic assemblages does not act as a surrogate for biodiversity of fish assemblages. If detailed biological data are not available when planning the location of MPAs, and maps of rocky reef habitat based solely on depth are used as surrogates of biodiversity for fish assemblages, then detailed fish surveys should be undertaken before the configuration of no-take zones are defined to increase the likelihood that there is an adequate representation of fish assemblages (Newton *et al.,* 2007). More research is required into the use of variation in habitat attributes as

surrogates of diversity for fish assemblages within other habitats to test the effectiveness of using habitat classification schemes in the development of a representative system of MPAs.

Chapter 8 The effectiveness of a habitat classification scheme as a surrogate for offshore fish biodiversity in a marine protected area[1]

Abstract

Marine protected area planning aims to conserve representative samples of the range of biological diversity. In the absence of spatial inventories of biodiversity, habitat classification schemes are used as biodiversity surrogates. The validity of these schemes as biodiversity surrogates is, however, often unknown prior to their implementation. This study tested the habitat classification scheme used in New South Wales' marine parks that includes a category of unvegetated unconsolidated habitats that is further classified by depth. The validity of the unconsolidated group of habitats as a surrogate for variation in fish biodiversity was tested in the Port Stephens-Great Lakes Marine Park by sampling two habitats (shallow depth 10 m, intermediate depth 40 m) at multiple spatial scales and replicate times. Twenty-four species (17 families) were recorded in the shallow habitat, and 20 species (16 families) recorded in the intermediate depth habitat. Assemblage structure and the abundance of two common species, blue-spotted flathead (*Platycephalus caerulepunctus)* and fiddler ray (*Trygonorrhina fasciata)* differed between shallow and intermediate habitats, indicating the habitat classes are effectively representing variation in biodiversity. A modification to the habitat scheme to include an additional habitat of estuarine shallow habitat would improve the scheme's surrogacy value. Representative samples of these habitats in a range of locations are required to adequately conserve representative samples of fish biodiversity within the marine park.

8.1 Introduction

Identifying the ranges and sources of natural variability in marine biodiversity is an essential pre-requisite for implementing measures to conserve biodiversity within marine protected areas (MPAs) (Garcia-Charton *et al.,* 2000; Ley, 2005). These types of data are not available for most marine species, particularly at the spatial scales relevant to planning and designing MPAs (Curley *et al.,* 2002; Gladstone 2007). Habitat-based biodiversity surrogates have a potentially important role in the identification of sites that will contribute to a representative system of MPAs (Banks and Skilleter, 2002). This approach assumes that biodiversity differs among habitats (e.g. O'Hara, 2001), and that faunal assemblages have strong associations

[1] This chapter has been formatted for submission to the journal *Aquatic Conservation: Marine and Freshwater Ecosystems* (submitted by Vanessa Owen and William Gladstone, 5th September 2014).

with environmental variables (Chatfield *et al.,* 2010). In temperate Australia, there is some evidence that habitats may act as effective surrogates for faunal diversity in the design of MPAs (Ward *et al.,* 1999). Therefore, mapping of habitats for use as surrogates for fauna diversity may be a cost effective method of biodiversity assessment for MPA planning (Jordan *et al.,* 2005).

The habitat classification scheme used in marine parks in New South Wales (NSW), Australia, categorises habitats according to bottom type (unconsolidated, consolidated), depth (shallow 0-25 m, intermediate 25-60 m, deep 60-200 m), sediment type (mud, muddy sand, sand), and vegetation type if applicable (seagrass, mangroves, saltmarsh, macrophytes) (Malcolm *et al.,* 2010). Although the design of MPAs in NSW uses habitat as a surrogate for diversity, the precision of the surrogate has not been tested, apart from Malcolm *et al.* (2010) and Schultz *et al.,* (2014), who tested the applicability of the habitat classification system for fishes in the Solitary Islands Marine Park. In both of these cases the pre-existing abiotic habitat classification scheme only partially represented the range of fish assemblages of unconsolidated habitats in the region. The precision of habitat in predicting reef fish assemblage structure on a subtropical coral reef in NSW has also been tested by Lindsay *et al.* (2008), who found that variations in fish assemblage were moderately correlated with habitat variations, and a combination of habitat and geographical distance resulted in greater surrogate precision than habitat alone.

MPA effectiveness in representing variation in biodiversity is contingent on understanding key ecological patterns and processes at appropriate spatial scales (Grober-Dunsmore *et al.,* 2007; Pittman and Brown, 2011). Often the combined influence of environmental gradients must be considered in order to understand how the environment structures fish assemblages (Chatfield *et al.,* 2010). The strong influence that physical environmental variables have in structuring faunal assemblages within a habitat suggests that habitat classes may need to be more finely partitioned to represent fully the likely influences on biodiversity. For example, within-habitat variation in the biodiversity of reef fishes has been related to variations in depth (Curley *et al.* 2002), wave exposure (DeMartini *et al.,* 2009), and distance-from-shore (Malcolm *et al.,* 2010). In the latter study, the authors found that for subtropical fish assemblages in NSW, distance-from-shore was strongly correlated with patterns of reef fish assemblages, and recommended that distance-from-shore be incorporated into habitat classification to improve the ability of MPA to represent biological diversity.

Subtidal unvegetated unconsolidated habitats dominate (in terms of area) the world's coastlines; however studies in these habitats lag behind those of other coastal ecosystems (Brown and McLachlan, 2006). The NSW coast has 775 ocean beaches that make up 62 percent of the shoreline (NSW Marine Estate Management Authority, 2013). Relative to studies of reef fishes, there is very little published information relating to spatial and temporal variation in unvegetated unconsolidated habitats and the underlying ecological factors and processes structuring fish assemblages in this habitat (Cappo *et al.,* 2007; Travers *et al.,* 2010; Schultz *et al.,* 2012). A review of the published information relating to fish assemblages in unvegetated unconsolidated habitat indicates this habitat represents important habitat for fish assemblages including true residents such as flatfishes and elasmobranchs, and non-residents that occur in large numbers, including juveniles of many species (Brown and McLachlan, 2006). Large-scale environmental variables have a major role in structuring fish assemblages in offshore unvegetated unconsolidated habitat (Inoue *et al.,* 2008), with species richness correlated with temperature (Clark *et al.,* 1996a; Suda *et al.,* 2002; Wilbur *et al.,* 2003; White and Potter, 2004), salinity (Pessanha and Araujo, 2003), turbidity (Clark *et al.,* 1996a), depth (Ruiz *et al.,* 1993; Gibson *et al.,* 1996; Chatfield *et al.,* 2010), and wave exposure (Clark *et al.,* 1996b; Clark, 1997).

Habitat mapping in NSW marine parks indicate that unvegetated unconsolidated habitat is the dominant habitat within Port Stephens-Great Lakes Marine Park (PSGLMP) (representing approximately 87% of the subtidal area of the Park), and this value is likely to be indicative of the dominance of unvegetated unconsolidated habitats in offshore waters elsewhere in NSW. In southeast Australia there appears to be only three studies examining fish assemblages in unvegetated unconsolidated habitat. In one study depth was found to be an important factor structuring offshore demersal fish assemblages on the inner continental shelf (Gray and Otway, 1994). In the other studies, small scale differences in fish assemblages were documented at increasing distances from rocky reefs (Schultz *et al.,* 2012), and significant differences in fish assemblages across depths, distance from shore and medium spatial scales were documented in Solitary Islands Marine Park (Schultz *et al.,* 2014). The aim of the current study was to examine the usefulness of habitat classification schemes as biodiversity surrogates, by testing the value of an existing habitat classification scheme for representing the diversity of fish in unvegetated unconsolidated habitat within PSGLMP.

8.2 Methods

Study Area

PSGLMP is situated on the mid-north coast of NSW (Fig. 3.1), and includes estuaries, coastline and islands over approximately 80 km of coastline (see detailed description in Chapter 3). The predominant habitat within the PSGLMP is the unvegetated unconsolidated group of habitats (representing 87% of the seabed area) that are further classified according to sediment characteristics and depth. This study occurred in two habitat classes dominated by sand: subtidal sand 0-25 m, and subtidal sand 25-60 m, hereafter called the 'shallow' and 'intermediate' habitats. Locations were chosen to occur within different environmental domains, to examine if locations in differing environments (such as within an estuary) are required within the MPA framework to conserve representative samples of biodiversity.

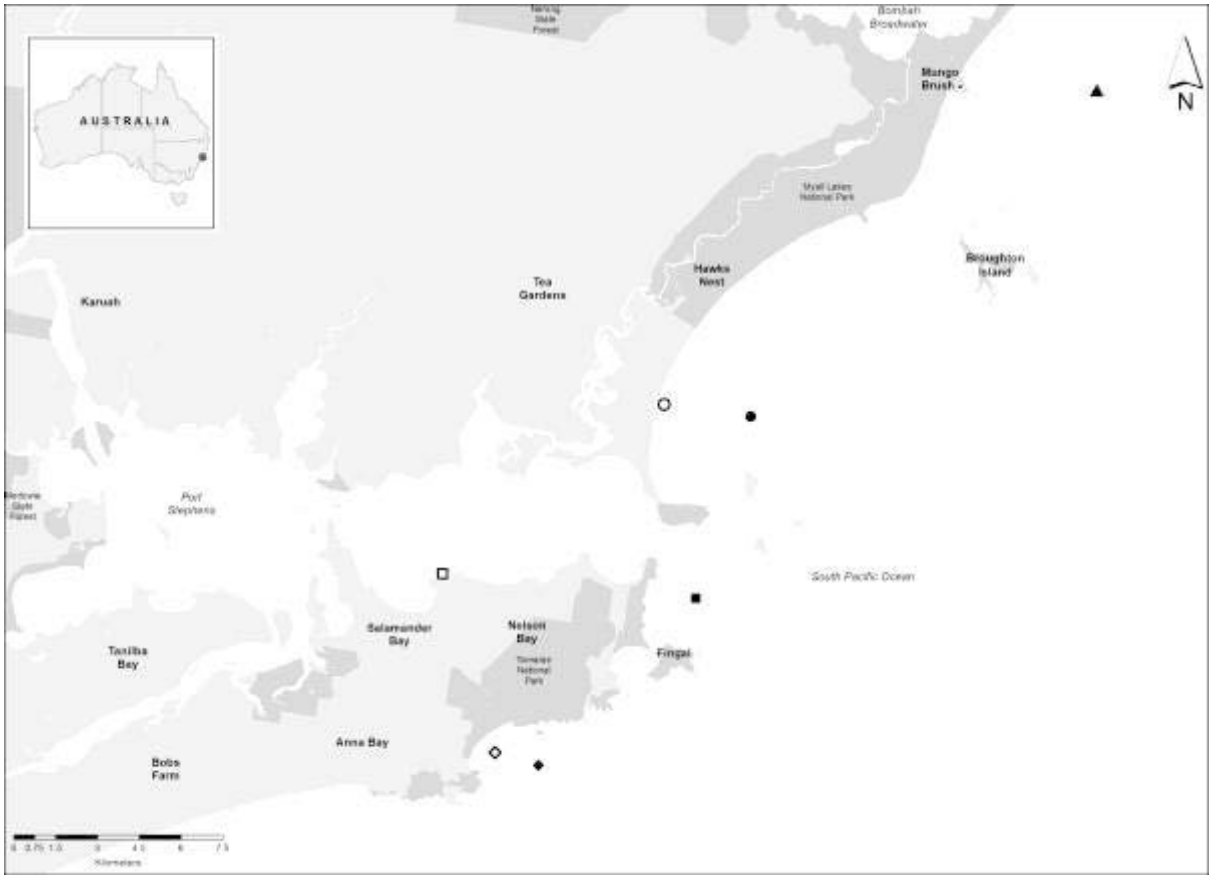

Figure 8.1: Location of study sites in Port Stephens-Great Lakes Marine Park. Pairs of symbols represent locations and different depths (empty symbol: shallow; filled symbol: intermediate depth).

Experimental Design and Field Sampling

The hypothesis that fish biodiversity differed between the shallow (0-25 m) and intermediate (25-60 m) habitats, and this difference was consistent through time and over spatial scales of 100s of m to 10s of km was tested by sampling at four different locations (separated by 10s of km) within each of the shallow and intermediate habitats, and at two sites (separated by ~ 1 km) within each location (Fig.8.1). All sites were > 200 m from reef to avoid the influence of reef species (Schultz *et al.,* 2012). Temporal consistency was tested by sampling at two times (March and September 2009). All sites were located within habitat protection zones within the PSGLMP. Fishes were sampled with baited remote underwater video stations (BRUVS) with n=4 replicates per site separated by 200 m (Malcolm *et al.,* 2007). BRUVS were constructed as in Malcolm *et al.* (2007), and consisted of a video camera in an underwater housing, an attachment frame, a bait-pole with bait, and a rope and float system linking the BRUV to the surface. The BRUVS were baited with approximately 1kg of chopped pilchards (*Sardinops neopilchardus*), which were mashed into a plastic mesh bait bag and attached to the end of a bait-pole at a distance of 1.5 m from each camera (Malcolm *et al.,* 2007). The cameras were all similar digital handycams with wide-angle lenses. The field of view was standardised to a distance of approximately 2 m estimated behind the bait, to maximise the effects of water visibility on the measure of relative abundance (Malcolm *et al.,* 2007). BRUVS were deployed to achieve 45 min of recording per replicate based on the results of an earlier pilot study that found this time recorded maximal species richness (Yona and Gladstone, unpublished data).

Fish were identified to species-level (using Hutchings and Swainston, 1986; Edgar, 1997; Kuiter, 2000) and an index of relative abundance of each species (MaxN), species richness, time each species was fist sighted, and the activity (feeding, swimming or stationary) of each species were recorded. MaxN is the maximum number of individual fish of each species in the frame at any one time during the video (Malcolm *et al.,* 2007). Species were additionally classified as 'economic' if they were a target species in either the commercial or recreational fishing sectors of NSW (Scandol *et al.,* 2008).

Statistical Analyses

Four-factor permutational multivariate analysis of variance (PERMANOVA, Anderson 2001) was used to test the hypothesis that fish biodiversity differed between the shallow (0-25 m) and intermediate (25-60 m) habitats, and this difference was consistent through time and over

spatial scales of 100s of m to 10s of km. Time was analysed as a fixed, orthogonal factor with two levels (March, September). Time was analysed as a fixed factor because, with two levels, it is not possible to draw general conclusions about temporal variation. Habitat class was analysed as a fixed, orthogonal factor with two levels (shallow, intermediate). Location was analysed as a random factor nested in Habitat, with four levels. Site was analysed as a random factor with two levels nested in location. PERMANOVA was done on a Bray-Curtis similarity matrix of square-root transformed data, and permutation of residuals under a reduced model (n=9999 permutations). Relative differences in fish assemblages were visualised by non-metric multidimensional scaling ordination plots, using the average abundance of each species in each site at each sampling time. The PERMDISP routine was used to test if the variability within assemblages differed between habitats. The similarity percentages (SIMPER) procedure was used to identify taxa responsible for differences in assemblages between habitats. Large values (i.e.> 1) of the ratio of $\overline{\delta}_i$/SD($\overline{\delta}_i$) for a species (Clarke, 1993) and species with $\%\overline{\delta}_i$> 3% (Terlizzi *et al.,* 2005) were used to identify species that were important contributors to dissimilarity. Multivariate analyses were undertaken using PRIMER 6 & PERMANOVA+ software (PRIMER-E) (Anderson *et al.,* 2008).

Four-factor analysis of variance (ANOVA) was used to test the hypothesis for single variables, using the same design as the multivariate analyses. Homogeneity of variances was tested by Cochran's C test and data were transformed where necessary to eliminate heterogeneous variances. Where it was not possible to eliminate heterogeneous variances through transformation the analysis was undertaken on untransformed data because ANOVA is robust to departures from this assumption (Underwood, 1997). The variables tested were: species richness, total MaxN, MaxN of nine most abundant species, MaxN sharks, MaxN rays, and MaxN economic species. The SNK test was used to explore significant main effects and interactions. Analyses were done with GMAV software (Institute of Marine Science, University of Sydney).

8.3 Results

General

Thirty species (22 families) were observed over the two sampling periods, representing 10 species (8 families) from the class Chondrichthyes and 20 species (14 families) from the class

Actinopterygii (Appendix 4). Twenty-four species (17 families) were recorded in the shallow habitat, comprising 8 species (6 families) from the class Chondrichthyes and 16 species (11 families) from the class Actinopterygii. Twenty species (16 families) were recorded in the intermediate habitat, comprising 8 species (7 families) from the class Chondrichthyes and 12 species (9 families) from the class Actinopterygii. Fourteen species occurred in both shallow and intermediate habitats, with 10 species (9 families) unique to the shallow habitat, and 6 species (6 families) unique to the intermediate habitat. Of the species recorded 63% were of economic importance.

A total of 4738 individuals were observed by combining MaxN data from all replicates. The most abundant species recorded in both habitats consistently through time were all of economic importance. The most abundant species in shallow habitat were yellowtail scad (*Trachurus novaezelandiae* Carangidae representing 35% total MaxN), sandy sprat (*Hyperlophus vittatus* Clupeidae 23%), sand flathead (*Platycephalus bassensis* Platycephalidae 7%), yellowfin bream (*Acanthopagrus australis* Sparidae 6%) and fiddler ray (*Trygonorrhina fasciata* Rhinobatidae 6%). The most abundant species in intermediate habitat were *P. bassensis* (25%), *T. novaezelandiae* (24%), blue-spotted flathead (*P. caerulepunctus* Platycephalidae 12%), trumpeter whiting (*Sillago maculata* Sillaginidae 12%), and ocean leatherjacket (*Nelusetta ayraudi* Monacanthidae 9%).

Platycephalus bassensis was the species most commonly first sighted in both shallow and intermediate habitats, over both sample periods. The first *P. bassensis* was sighted earlier in intermediate habitat (mean±SE=1.5±0.2 mins in March (n=32), 2.3±0.4 mins in September (n=32)) than shallow habitat (3.2±0.6 mins in March (n=32), 6.3±0.8 mins in September (n=32)). The majority of individuals of all species in shallow and intermediate habitats in March, and intermediate habitat in September, were attracted to the bait without actively feeding. An equal number of individuals in shallow habitat in September were observed attracted to, and feeding on, the bait.

Spatial and Temporal Variation in Fish Assemblages

Fish assemblages of shallow and intermediate habitats were consistently separated in the nMDS ordination plots (Fig. 8.2). Additionally, within the shallow habitat, fish assemblages within the estuary consistently separated from fish assemblages outside the estuary (Fig.8.2). PERMANOVA showed that fish assemblages differed significantly between the shallow and intermediate habitats, and this difference was consistent through time, as shown by the

absence of a significant Time x Habitat interaction (Table 8.1). The PERMDISP routine showed that assemblages in the shallow habitat were significantly more variable (43.1±1.32) than the intermediate habitat (31.4±0.95, $F_{1,126}$=51.58, P=0.001). The significant TimexSite(Location(Habitat)) interaction in both shallow and intermediate habitats occurred because the patterns of variation between the sites within each location differed between the two sampling periods. The significant TimexLocation(Habitat) interaction occurred because most pairwise comparisons of locations in the shallow habitat were significant in March and none were significant in the intermediate habitat, and some (but not all) pairwise comparisons of locations were significant in both habitats in September.

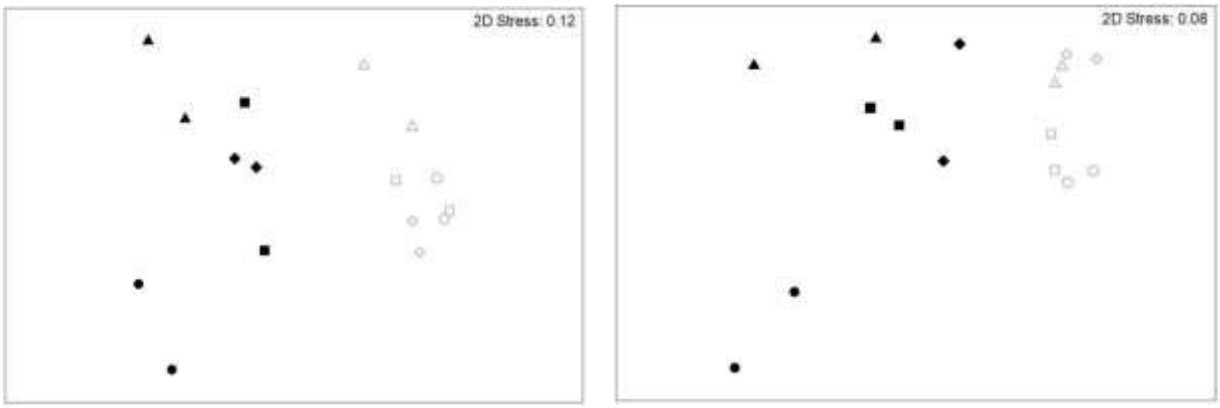

Figure 8.2: nMDS ordination plots (based on site-average MaxN of each species) depicting similarity in fish assemblages of offshore unvegetated unconsolidated habitats from shallow (filled symbols; estuary is a circle) and intermediate (unfilled symbols) depths in the Port Stephens-Great Lakes Marine Park in March (left) and September (right) 2009. Symbols represent 4 locations within each depth, and 2 sites within each location.

Table 8.1: Summary of results of 4-factor PERMANOVA testing for the influence of time, habitat (shallow, intermediate depth), locations (habitat) and sites (locations(habitat)) on fish assemblages of the Port Stephens-Great Lakes Marine Park.

Source of Variation	DF	MS	Pseudo-F	*P*(perm)
Time: Ti	1	11469.00	3.84	0.03
Habitat: Ha	1	65955.00	6.78	0.03
Location: Lo(Ha)	6	9723.00	5.25	<0.01
Ti x Ha	1	2850.60	0.95	0.44
Site: Si((Lo)Ha)	8	1853.40	2.34	<0.01
Ti x Lo(Ha)	6	2985.00	2.21	0.03
Ti x Si(Lo(Ha))	8	1348.10	1.70	<0.01
Residual	96	793.50		

The SIMPER analysis identified 11 species as being influential in differentiating between fish assemblages of the two habitats. Of these species, variation in the abundance of *Trachurus novaezelandiae*, *Hyperlophus vittatus*, *Platycephalus bassensis*, *P. caerulepunctus*, *Sillago maculata* and *Nelusetta ayraudi* were consistently influential (Table 8.2). Differences between assemblages were consistent through time, with 42% and 39% similarity within shallow habitat in March and September respectively, and 58% and 60% similarity within intermediate habitat in March and September respectively. There was 68% dissimilarity between shallow and intermediate habitats in both March and September.

Table 8.2: Overall dissimilarity ($\overline{\delta}$ i) in fish assemblages between habitats (SIMPER). Species regarded as being important contributors to the assemblage dissimilarity are shown in bold. Values shown in the pairwise comparisons are the average MaxN for the species.

Taxon	Shallow vs. Intermediate Habitat					
	Mar-09			Sep-09		
	$\overline{\delta}_i$	$\%\overline{\delta}_i$	$\overline{\delta}_i$/SD($\overline{\delta}_i$)	$\overline{\delta}_i$	$\%\overline{\delta}_i$	$\overline{\delta}_i$/SD($\overline{\delta}_i$)
Hyperlophus vittatus	**6.59**	**10.92**	**1.01**	**6.93**	**11.8**	**1.05**
Trachurus novaezelandiae	**6.57**	**10.89**	**1.39**	**7.94**	**13.52**	**1.43**
Platycephalus bassensis	**6.51**	**10.78**	**1.72**	**5.81**	**9.9**	**2.41**
Sillago maculata	**6.2**	**10.28**	**1.94**	**5.36**	**9.12**	**1.07**
Nelusetta ayraudi	**5.16**	**8.54**	**1.16**	**4.29**	**7.3**	**1.22**
Platycephalus caerulepunctus	**4.5**	**7.46**	**2.01**	**7.69**	**13.1**	**4.38**
Sillago ciliata	**3.81**	**6.32**	**1.35**	**2.13**	**3.63**	**1.12**
Aptychotrema rostrata	**2.84**	**4.71**	**1.89**	1.65	2.82	1.26
Urolophus sufflavus	1.25	2.07	1.2	**2.63**	**4.48**	**2.47**
Heterodontus portusjacksoni	0.98	1.62	0.71	**2.14**	**3.64**	**1.13**

Spatial and Temporal Variation in Species

There was no difference in the MaxN of most species between habitats. Two species, *Platycephalus caerulepunctus* and *Trygonorrhina fasciata,* showed a significant habitat interaction (Fig. 8.3, Table 8.3). There was a greater abundance of *P. caerulepunctus* in intermediate habitat than in shallow habitat, and greater abundance of *T. fasciata* in shallow habitat than in intermediate habitat. All other species exhibited a range of responses, including significant Time, Location and Site interactions (Table 8.3). The MaxN of *Sillago ciliata* (Sillaginidae) differed through time, with most individuals recorded in March 2009. Species richness, MaxN sharks, and the MaxN of *Sillago maculata* and *Hyperlophus vittatus*

differed between locations. Most sharks were recorded at two locations. *H. vittatus* were only recorded at three locations in shallow habitat. The MaxN of *P. bassensis* differed between sites. When pooled together all rays differed through time at the habitat level. Shovelnose ray (*Aptychotrema rostrata)* (Rhinobatidae) and *Trachurus novaezelandiae* differed through time at the location level. The MaxN of all species combined, all economic species combined, and of *Nelusetta ayraudi* differed between sample times at the site level.

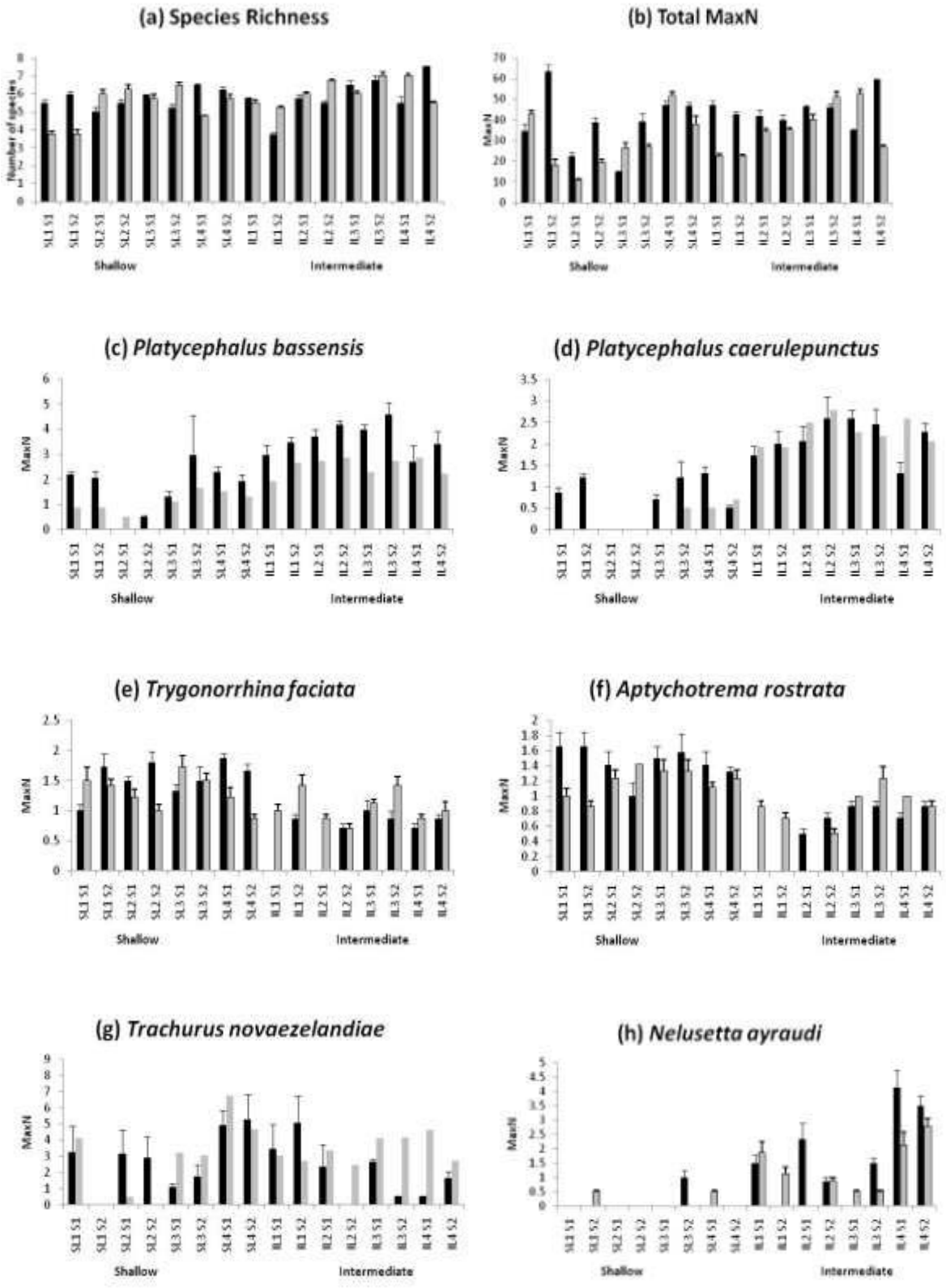

Figure 8.3: MaxN and species richness of fishes in shallow and intermediate habitat in March and September 2009. Values shown are mean MaxN ± standard error (n=4) for each replicate site at each location. SL: Shallow Location, IL: Intermediate Location, S1: Site 1, S2: Site 2. Colours represent two sample periods within each habitat.

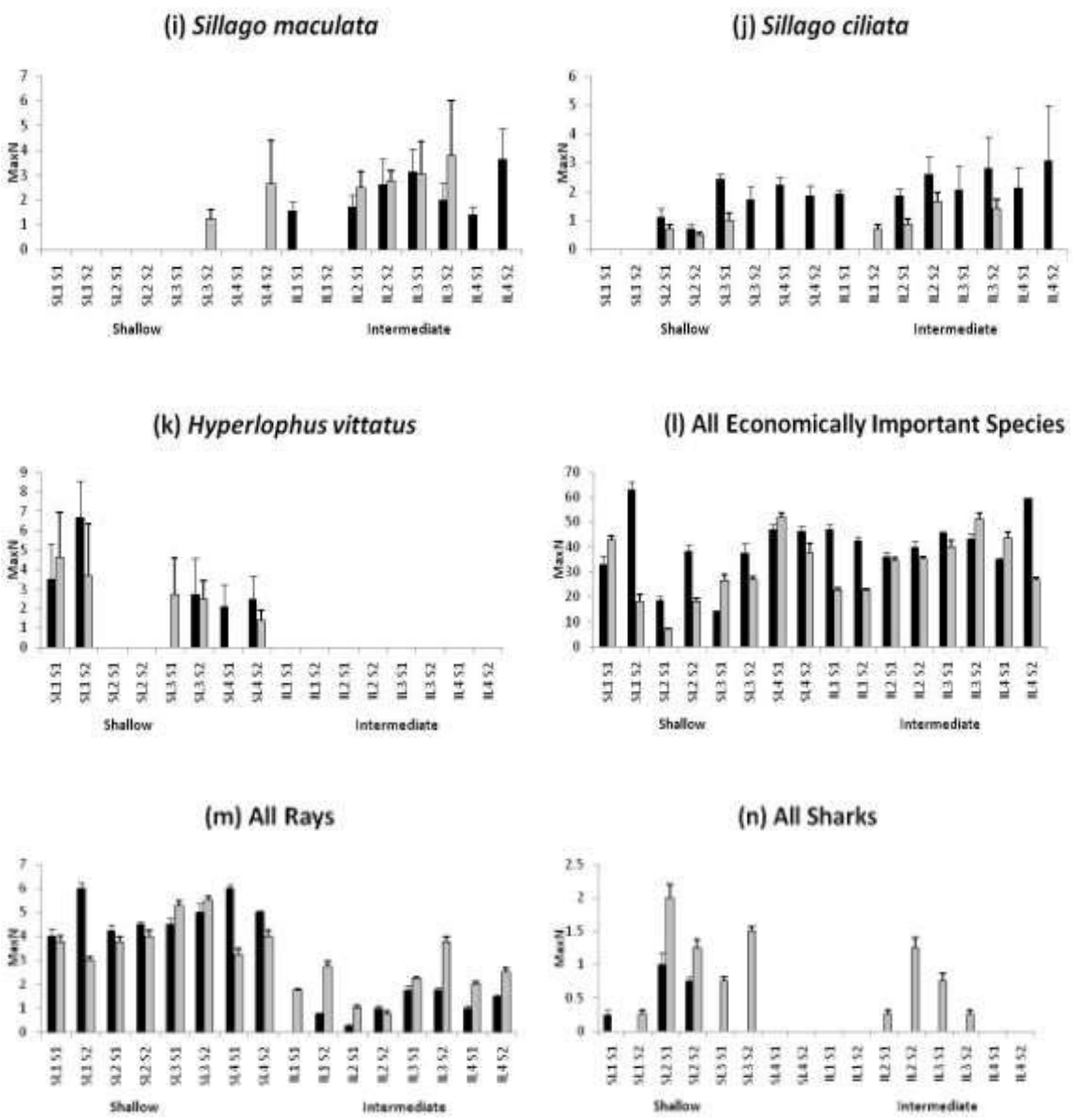

Figure 8.3 continued**:** MaxN and species richness of fishes in shallow and intermediate habitat in March and September 2009. Values shown are mean MaxN ± standard error (n=4) for each replicate site at each location. SL: Shallow Location, IL: Intermediate Location, S1: Site 1, S2: Site 2. Colours represent two sample periods within each habitat.

Table 8.3: Summary of results of four factor ANOVA testing for the influence of time, habitat (shallow, intermediate depth), locations (habitat) and sites (locations(habitat)) on fish assemblages of the Port Stephens-Great Lakes Marine Park.

		Total MaxN[1]			Species Richness[1]			*Aptychotrema rostrata*[1]			*Trygonorrhina fasciata*[1]			*Platycephalus bassensis*[4]		
Source of Variation	DF	MS	F	*P*	MS	F	*P*	MS	F	*P*	MS	F	*P*	MS	F	*P*
Time: Ti	1	2655.38	7.66	0.03	0.28	0.07	0.8	1.32	0.71	0.43	0.03	0.01	0.93	722	20.48	<0.01
Habitat: Ha	1	1319.7	1.12	0.33	7.03	1.22	0.31	46.32	33.75	0.01	52.53	48.96	<0.01	1906.53	31.45	<0.01
Location(Ha): Lo(Ha)	6	1173.41	5.86	0.01	5.78	5.44	0.02	1.37	11.71	0.01	1.07	0.93	0.52	60.61	2.78	0.09
Site(Lo(Ha)): Si(Lo(Ha))	8	200.15	0.71	0.68	1.06	0.52	0.83	0.12	0.14	0.14	1.16	1.15	0.34	21.78	2.23	0.03
Ti x Ha	1	0.07	0	0.99	3.78	0.9	0.38	7.51	4.05	0.1	13.78	3.95	0.09	180.5	5.12	0.06
Ti x Lo(Ha)	6	346.46	0.43	0.84	4.2	1.6	0.26	1.85	4.65	0.03	3.49	2.66	0.1	35.25	2.56	0.1
Ti x Si(Lo(Ha))	8	798.71	2.83	0.01	2.62	1.3	0.26	0.4	0.48	0.87	1.31	1.31	0.25	13.75	1.41	0.2
Residual: (Res)	96	281.93			2.03			0.84			1.01			9.78		

		Platycephalus caerulepunctus[3]			*Sillago ciliata*[4]			*Sillago maculata*[4]			*Trachurus novaezelandiae*[3]			*Nelusetta ayraudi*[3]		
Source of Variation	DF	MS	F	*P*	MS	F	*P*	MS	F	*P*	MS	F	*P*	MS	F	*P*
Time: Ti	1	0.03	0.11	0.76	347.82	18.9	0.01	2	0.03	0.87	8.02	0.78	0.41	2.1	2.04	0.2
Habitat: Ha	1	48.9	90.24	<0.01	86.13	4.11	0.09	639.03	5.62	0.06	0.36	0.01	0.91	23.43	3.4	0.11
Location(Ha): Lo(Ha)	6	0.54	3.43	0.06	20.97	1.36	0.33	113.68	4.1	0.04	24.45	6.06	0.01	6.9	17.21	<0.01
Site(Lo(Ha)): Si(Lo(Ha))	8	0.16	0.99	0.45	15.37	1.06	0.4	27.73	0.95	0.48	4.03	1.88	0.07	0.4	3.12	<0.01
Ti x Ha	1	1.18	4.16	0.09	39.38	2.06	0.2	21.13	0.33	0.59	3.57	0.35	0.58	1.9	1.84	0.22
Ti x Lo(Ha)	6	0.28	0.87	0.55	19.12	2.4	0.13	64.5	1.59	0.26	10.32	4.53	0.03	1.03	1.81	0.21
Ti x Si(Lo(Ha))	8	0.33	2.05	0.06	7.97	0.55	0.82	40.48	1.38	0.21	2.28	1.06	0.4	0.57	4.45	<0.01
Residual: (Res)	96	0.16			14.5			29.29			2.14			0.13		

Table 8.3(continued): Summary of results of four factor ANOVA testing for the influence of time, habitat (shallow, intermediate depth), locations (habitat) and sites (locations(habitat)) on fish assemblages of the Port Stephens-Great Lakes Marine Park.

		All Sharks[4]			All Rays[1]			All Economic Species[1]			*Hyperlophus vittatus*[2]		
Source of Variation	DF	MS	F	*P*	MS	F	*P*	MS	F	*P*	MS	F	*P*
Time: Ti	1	4.88	5.34	0.06	0.5	0.14	0.72	2646.28	6.59	0.04	0.29	0.36	0.57
Habitat: Ha	1	3.45	1.22	0.31	276.13	52.44	<0.01	1212.78	0.94	0.37	27.8	3.43	0.11
Location(Ha): Lo(Ha)	6	2.83	8.05	0.01	5.27	4.68	0.03	1285.39	5.42	0.02	8.11	15.65	<0.01
Site(Lo(Ha)): Si(Lo(Ha))	8	0.35	1.13	0.35	1.13	0.52	0.84	237.34	0.86	0.56	0.52	0.7	0.69
Ti x Ha	1	0.2	0.21	0.67	0.03	8.49	0.03	1.13	0	0.96	0.29	0.36	0.57
Ti x Lo(Ha)	6	0.91	3.16	0.07	3.56	2.02	0.18	401.64	0.56	0.75	0.81	0.67	0.68
Ti x Si(Lo(Ha))	8	0.29	0.93	0.5	1.75	0.8	0.6	715.72	2.6	0.01	1.21	1.63	0.13
Residual: (Res)	96	0.31			2.18			275.19			0.74		

1: untransformed, variances homogeneous

2: ln(x+1) transformed, variances homogenous

3: sqrt(x+1) transformed, variances homogeneous

4: untransformed, variances heterogeneous

8.4 Discussion

Spatial Patterns in Assemblages and Species

This study showed that there were differences between fish assemblages, and differences in the abundance of two species between shallow (0-25 m), and intermediate (25-60 m) habitats. Gray and Otway (1994) also reported differences in fish assemblages within unvegetated unconsolidated habitat among differing depths (30 m, 50 m, 100 m) in southeast Australia. Although these depths are different to the depths of the habitats examined in this study, the results of Gray and Otway (1994) at least demonstrate that depth is an important abiotic factor structuring fish assemblages in unvegetated unconsolidated habitats. Other than the study by Gray and Otway (1994), there is little published information regarding the importance of depth for structuring fish assemblages within unvegetated unconsolidated habitat, apart from Schultz *et al.,* (2014), who documented significant differences in fish assemblages across depths, distance from shore, and over the medium spatial scales in the Solitary Island Marine Park. However, the results of studies for fish assemblages in rocky reef habitat in south-eastern Australia (Connoll and Lincoln-Smith, 1999; Williams and Bax, 2001; Travers *et al.,* 2006; Lindfield, 2007; Malcolm *et al.,* 2011) and the Mediterranean (Tuneai *et al.,* 2006) suggest that depth is an important factor driving the structure of these assemblages. Depth may be acting as a proxy for a range of influencing factors, such as abiotic influences such as temperature and salinity, predation pressures and prey availability (Williams and Bax, 2001).

Proximity to estuary influenced fish assemblages in both shallow and intermediate habitat, although the influence was not consistent through time. In this study the significant TimexLocation(Depth) interaction occurred in shallow habitat because there was significant variation among locations in March, and significant variation between the estuary location and offshore locations in September. The significant TimexLocation(Depth) interaction occurred in intermediate habitat because there was no significant variation among locations in March, and significant variation between the estuary location and offshore locations in September. A number of environmental influences may also be driving this difference, including exposure, salinity, sediment type (marine sand vs offshore sand) or proximity to seagrass beds. Salinity, temperature and turbidity have been shown to be key environmental factors structuring temperate Australian estuarine fish assemblages (Loneragan *et al.,* 1987; Edgar *et al.,* 1999; Edgar *et al.,* 2000; West and Walford, 2000; Kanandjembo *et al.,* 2001;

Kanou *et al.,* 2007). Sediment type has a strong role in structuring marine benthic assemblages (Mair *et al.,* 2009), and has been shown to act as an effective surrogate for macroinvertebrate assemblages (Neely and Zajac, 2008; Dixon-Bridges *et al.,* 2014), although the relevance to Australian fish assemblages has not been tested.

In both shallow and intermediate habitat species were highly variable at the site (separated by ~ 1 km) and location (separated by ~ 30 km) scale, a result consistent with those of studies in rocky reef habitat within PSGLMP (Gladstone, 2007; Malcolm *et al.,* 2007). This result is also consistent with Gray and Otway (1994), who documented small scale spatial variation within 30 m, 60 m and 100 m depth classes in south eastern Australia. Some potential reasons for this spatial variation may be related to availability of resources or small-scale variation in habitat, such as sediment type or size. This study found assemblages in shallow habitat were more variable than those in intermediate habitat, which may be a reflection of environmental influences such as storm and high sea events, which would be more influential in the higher energy shallower habitat (Brown and McLachlan, 2006).

Temporal Patterns in Species and Assemblages

The use of abiotic surrogates for biodiversity in MPA planning relies on stability of assemblage patterns through time (Malcolm *et al.,* 2010). The results of this study indicate differences between the shallow and intermediate habitat classes in assemblage structure were consistent through time, although the abundance of many species differed through time. Gray and Otway (1994) also documented high temporal variability in fish species from offshore unvegetated unconsolidated habitat in south eastern Australia, and stable patterns of assemblage structure through time. Temporal variation of fish assemblages on rocky reefs in temperate NSW has been shown to be relatively minor compared to spatial variation (Gladstone, 2007; Malcolm *et al.,* 2007), a result consistent with this study. This study found complex spatial and temporal patterns in variation of some species, with patterns of variation between sites differing among locations, depths and times. Some possible factors underlying the temporal variation in species, where it occurs, may include seasonal recruitment patterns, mobility of fishes (especially schooling species) and environmental influences such as storm and high sea events. Variation in bait plume area due to differences in current velocity within estuary BRUV replicates can also result in significant temporal variability in fish assemblages (Taylor *et al.,* 2013), although all estuary replicates in this study were undertaken at high slack tide, minimising the influence of tides.

General Diversity

BRUVs are an effective method for sampling fish assemblages in unvegetated unconsolidated habitats. In this study 63% of species recorded were of economic importance, highlighting the importance of unvegetated habitat for economically important fishes. This result supports that reported by Gladstone *et al.* (2012) who found the majority of species recorded in surveys of unvegetated unconsolidated estuarine habitat in temperate NSW were also of economic importance. This study recorded a similar species assemblage to that recorded by Yona (2008) using BRUVs in shallow offshore unvegetated habitat on the NSW Central Coast. In this study the BRUVs recorded lower species richness as to that previously recorded in intermediate and deep offshore unvegetated habitat using trawls in south eastern Australia (Gray and Otway 1994), however BRUVs and trawls are known to record significantly different components of fish assemblages (Cappo *et al.,* 1997). It should also be noted that the study by Gray and Otway was undertaken in deeper depths than the current study, and therefore differences in species richness would likely occur no matter what survey method was utilised. The study by Gray and Otway (1994) was undertaken over a longer time period (18 months), with replicate samples collected in all seasons, which would result in the ability to record higher species richness due to seasonal differences in fish assemblages. There were 12 species recorded in this study by BRUVs that were not recorded in trawls by Gray and Otway (1994), which included sharks (*Mustelus antarticus* and spotted catshark (*Asymbolis analis* (Scyloirhinidae)), rays (smooth stingray (*Dasyatis brevicaudata*) and blue-spotted stingray (*D. kuhlii* (Dasyatidae)), and coastal inshore species such as sand whiting (*Sillago ciliata*) (Sillaginidae).

The results of this study, when compared to studies undertaken in rocky reef habitat within PSGLMP, show a substantial difference between fish assemblages on rocky reefs and nearby unvegetated unconsolidated habitats at similar depths. Sixty species were recorded by Malcolm *et al.* (2007) on rocky reefs in PSGLMP using BRUVs, and 15 species were recorded in this study from intermediate habitat in March and 16 in September. The following 15 species were common to both studies: fiddler ray (*Trygonorrhina fasciata)*, shovelnose ray (*Aptychotrema rostrata)*, eagle ray (*Myliobatis australis*) (Myliobatidae), smooth stingray (*Dasyatis brevicaudata)*, mado (*Atypichthys strigatus*) (Scorpididae), sweep (*Scorpis lineolata*) (Scorpididae), blue-spotted flathead (*Platycephalus caeruleopunctatus*), yellowtail scad (*Trachurus novaezelandiae*), yellowfin bream (*Acanthopagrus australis*), old wife (*Enoplosus armatus*) (Enoplsidae), six-spine leatherjacket (*Meuschenia freycineti)*

(Monacanthidae), *Nelusetta ayraudi*, eastern smooth boxfish (*Anoplocapros inermis)* (Ostraciidae), Port Jackson shark (*Heterodontus portusjacksoni*) (Heterodontidae), and gummy shark (*Mustelus antarcticus*) (Triakidae). In this study BRUVs were located at least 1 km from rocky reefs, and the above species were sighted throughout the 45 minute tape (not just towards the end of the tape). A pilot study was undertaken prior to this work, examining the rate of spread of the bait plume by tracking the distance travelled by rhodamine dye along rocky reef at differing exposures and tides. The rhodamine dye travelled between 180 m and 230 m in 30 minutes. It's therefore unlikely that the fish were drawn off rocky reefs to the BRUVs via the bait plume. No species were recorded as single individuals, indicating that these fish commonly perceived as reef fish may not just be confined to reefs (however see Schulz *et al.* (2012), who found no influence of reef fish in unvegetated unconsolidated habitats > 200 m from reef). This study recorded ten species (eight families) in unvegetated habitat that were not recorded in rocky reef habitat by Malcolm *et al.* (2007): pilchard (*Sardinops neopilchardis*) (Clupeidae), sandy sprat (*Hyperlophus vittatus*), sand flathead (*Platycephalus bassensis),* sand whiting (*Sillago ciliata*), trumpeter whiting (*Sillago maculata*), flounder (*Pseudorhombus* sp.), (Paralichthyidae), weeping toado (*Torquigener pleurogramma*) (Terradonidae), eastern striped trumpeter (*Pelates sexlineatus*) (Terapontidae), bar-tail goatfish (*Upeneus tragula*) (Mullidae) and two-spot lizardfish (*Synodus dermatogenys*) (Synodontidae).

The time of first arrival of fish can be an indicator of high population density of fish, where the higher the population, the sooner fish approach the bait (Cappo *et al.,* 2004). In this study *Platycephalus bassensis* was the species most commonly sighted first in both shallow and intermediate habitat, and was one of the species with the largest total MaxN. The first individual *P. bassensis* was sighted earlier in intermediate habitat than in shallow habitat, and the species was recorded in greater abundance in intermediate habitat than in shallow habitat.

Malcolm *et al.* (2007) concluded that PSGLMP was an important area for Chondrichthyes, with 11 species (seven sharks, four rays) recorded in rocky reef habitat. This study supports this conclusion, with 10 Chondrichthyes (three sharks, seven rays) recorded in unvegetated habitat (seven species common to both studies). The seven Chondrichthyes common to both studies were *Asymbolis analis*, *Dasyatis brevicaudata*, *Heterodontus portusjacksoni, Trygonorrhina fasciata*, *Myliobatis australis, Aptychotrema rostrata* and *Mustelus antarcticus.* Surprisingly, although the migratory *H. portusjacksoni* is known to aggregate on rocky reefs in NSW to breed (Powter and Gladstone, 2008), this study demonstrates that

adjacent habitats (i.e. sand) are also utilised. Unvegetated habitat is vitally important for these other species, which inhabit estuaries, and coastal inshore waters (Kuiter, 2000).

BRUVs are a powerful technique for detecting large cryptic scavengers, including eels, sharks and rays in rocky reefs (Malcolm *et al.,* 2007). Note however the recent survey by Lowry *et al.* (2012), who reported that small, cryptic reef-associated species are better detected using underwater visual census (UVC). This study recorded a high number of large cryptic species that camouflage and hide in the substrate such as *Platycephalus bassensis*, *P. caerulepunctus* and *Trygonorrhina fasciata* that would otherwise be difficult to sample in a non-destructive manner, important for studies undertaken within MPAs. Cryptic species contribute to defining patterns of biodiversity for conservation planning in freshwater systems in Australia (Cook *et al.,* 2008), and may also be important in marine systems.

Some potential factors that may bias estimates of MaxN include inter-specific behavioural interactions at the bait (Malcolm *et al.,* 2007). In particular, when large (> 2 m) *Dasyatis brevicaudata* and *Myliobatis australis* were feeding all fish species often avoided or were excluded from the bait bag, due to the sheer size of individuals feeding. Conversely, when *Mustelus antarcticus* and *Heterodontus portusjacksoni* individuals were aggressively feeding on the bait, this often attracted *Sillago maculata* individuals to the bait bag and appeared to encourage the species to feed on scraps of bait dislodged from the bag.

Implications for Marine Protected Area Planning

The use of habitat mapping based on the abiotic variables of depth and sediment or reef type is used as a surrogate for fauna assemblages in MPA planning in NSW. However the precision of these surrogates is rarely tested. The use of habitat mapping when choosing MPA candidate sites in NSW assumes that habitats are homogeneous, and therefore any area of that habitat type will represent the full spectrum of ecological diversity within that habitat (Winberg *et al.,* 2007; Smith *et al.,* 2008). However, in temperate southeast Australia, high heterogeneity has been documented for marine and estuarine habitats, with Winberg *et al.* (2007) documenting high habitat heterogeneity in tidal flat macrobenthos that would influence the choice and number of MPAs required to conserve both dominant and rarer taxa. Furthermore, Smith *et al.* (2008) documented high spatial heterogeneity in shallow subtidal rocky reefs in northern NSW, and questioned the use of arbitrary measures such as percentage of a broad habitat type to allocate conservation effort in MPA zoning schemes. Critics of the use of surrogates of biodiversity for MPA design state that this approach lacks

systematically surveyed biological data (Ward *et al.,* 1999; Banks and Skilleter 2002; Ponder *et al.,* 2002), and in particular there is limited information on the spatial scales at which faunal assemblages change in taxonomic composition within a habitat type (Winberg *et al.,* 2007). Smith *et al.* (2008) highlighted the need of biotic data at appropriate scales for conservation planning for rocky reefs in northern NSW. Malcolm *et al.* (2007) found that for subtropical fish assemblages in NSW, distance-from-shore was strongly correlated with patterns of reef fish assemblages, and recommended that distance-from-shore be incorporated into habitat classification to improve the ability of MPA to represent biological diversity. Williams *et al.* (2009) found that depth, size, complexity, configuration and anthropogenic impact all needed to be added to geomorphic features used to act as surrogates of biodiversity within Australia's deep-water reserve network. In this study the assemblage structure and abundance of two common species differed between shallow and intermediate habitats, and that depth was an effective surrogate for the diversity of fish assemblages in unvegetated habitat in PSGLMP. There is further need for more studies examining diversity in different habitats and regions within NSW to ascertain the potential use of habitat surrogates for MPA planning, and through time to examine temporal stability of these trends, particularly as it is the method currently used to design MPAs for NSW and Australia.

In this study sandy sprat (*Hyperlophus vittatus*) occurred exclusively in shallow habitat, and Trumpeter whiting (*Sillago maculata*) occurred almost exclusively in intermediate habitat. The potential role of these species as indicator species for these habitat classes should be explored further in the context of potentially simplifying future fish surveys within these habitats in NSW MPA.

Although there are many environmental and biological variables that influence fish assemblages in temperate Australia, such as habitat type (Curley *et al.,* 2002; Smith *et al.,* 2008; Chatfield *et al.,* 2010) and depth (Connoll and Lincoln-Smith, 1999; Williams and Bax, 2001; Chatfield *et al.,* 2010), there is still value in defining broad assemblage patterns for representative planning (Malcolm *et al.,* 2010). This study showed depth (shallow vs intermediate) in subtidal unvegetated unconsolidated habitat is an effective surrogate for the diversity of fish assemblages in PSGLMP. The current habitat mapping for PSGLMP categorises subtidal unvegetated unconsolidated habitats by depth and sediment characteristics, therefore the current habitat mapping accurately represents the diversity of fishes in unvegetated unconsolidated habitat. The current utilisation of habitat mapping in MPA planning is an appropriate method of capturing biodiversity of fish fauna.

Analysis of the PSGLMP zoning map indicates that only 15% of the mapped unvegetated unconsolidated group of habitats are protected within sanctuary zones. Within this group of unvegetated, unconsolidated habitats 14% of the mapped shallow, 12% of the mapped intermediate, and 20% of the mapped deep unconsolidated habitats are conserved within sanctuary areas. The results of this study indicated that shallow and intermediate habitat supported different fish assemblages, as did shallow marine habitat and shallow estuarine habitat. The variation in location-level assemblages means that sanctuary areas in both shallow (estuarine and marine) and intermediate habitat are therefore required to conserve a representative sample of fish biodiversity in this habitat. These criteria have been met, but given that 63% of species recorded in this study were of economic importance, perhaps a greater emphasis should be placed on more complete protection of fishes within these habitats by increasing the area of sanctuary zones.

Banks *et al.* (2005) found that a representative system of MPAs should include the complete range of environmental gradients or habitat types, at any given scale, to maximise the protection of marine biodiversity. The results of this study indicate that in shallow habitat a representative sample of unvegetated unconsolidated fish assemblages in both offshore and estuarine locations are required to adequately conserve representative samples of fish biodiversity. However, in intermediate habitat the inclusion of locations in differing environmental domains was not required to capture the biodiversity of fish fauna. Locations in differing environmental domains within intermediate habitat supported similar fish assemblages.

Chapter 9 General Discussion and Conclusion

The effectiveness of marine protected areas (MPAs) in conserving biodiversity depends not only on them being no-take, well enforced, old (>10 years), large (>100 km^2), and isolated by deep water or sand (Edgar *et al.,* 2014), but also on whether the MPAs were selected via conservation planning principles (Margules and Pressey, 2000) rather than via ad hoc or opportunistic decision-making. Advances in acoustic technology have enabled the production of high resolution maps of seabed habitats that can be used to create habitat maps, which is quicker and cheaper than sampling species abundances over similar spatial extents. These habitat maps are often used as biodiversity surrogates for fish and sessile benthic assemblages within MPAs. The efficacy of habitat classification schemes as biodiversity surrogates in conservation planning is poorly understood (Ward *et al.,* 1999; Mumby *et al.,* 2008; Shokri and Gladstone, 2013). The intra-habitat variability and precision of these biodiversity surrogates is largely unknown. The aim of this thesis was to assess the effectiveness of habitat classification schemes as surrogates for biodiversity conservation in Port Stephens-Great Lakes Marine Park (PSGLMP).

To achieve this aim, the fourth chapter looked at intra-habitat variability in the biodiversity of sessile benthic assemblages within sponge-dominated subtidal rocky reef. It firstly determined optimal sampling effort required for a representative description of sessile benthic assemblages in sponge-dominated reef, and secondly tested whether these assemblages varied in different environments (coastal headlands, offshore islands) where the habitat occurred. The results of this chapter indicated that habitat mapping based on depth only categories is not a suitable surrogate for the biodiversity of rocky reef sessile benthic assemblages in sponge-dominated reef habitat in PSGLMP. Multiple samples of sessile benthic assemblages from a range of locations subject to differing environmental influences are required to adequately conserve representative samples of biodiversity within PSGLMP. The results of this study would influence the current zoning scheme in PSGLMP by increasing the amount of sponge-dominated rocky reef within sanctuary areas, to capture representative areas of biodiversity within this habitat. Although the majority of survey sites occurred within sanctuary areas, this study showed that biodiversity in this habitat varied at very fine scales, so that even nearby habitat outside sanctuary zones within similar depths and environmental domains to that occurring within sanctuary zones could support different assemblages. Essentially all sponge-dominated rocky reef requires some form of protection (either within sanctuary or habitat protection zones) to meet the principles of comprehensive, adequate and

representativeness. This study has advanced the knowledge of rocky reef sessile benthic assemblages in sponge-dominated reef habitat in PSGLMP by documenting the great small-scale spatial variability in both offshore island and coastal headland environmental domains. It would enable a more representative habitat classification scheme to be developed, that includes locations subject to a range of differing environmental variation as well as depth, to conserve biodiversity. More studies are required on the sources of variation in biodiversity of this habitat to improve the suitability of habitat classification schemes so they can act as a surrogate for biodiversity for the range of assemblages conserved within PSGLMP. The most urgent of these (I believe) is a study which examines links between sponge species diversity and sponge morphological diversity. Currently there is so much uncertainty surrounding sponge taxonomy, biology and ecology, even though they are the dominant fauna group within deep reef habitat. This study utilised an autonomous underwater vehicle (AUV) to survey this habitat, and relied on the assumption that sponge morphological diversity correlated to sponge species diversity (as has been demonstrated Ireland (Bell and Barnes, 2001) and in Indonesia (Bell, 2007a)). Sponge taxonomy in temperate NSW is so poorly known and so few species are distinctive that ecologists are left with few options other than to assume linkages between sponge morphological diversity and species diversity, particularly with the movement away from *in situ* surveys to using AUVs. The most pressing factor to further advance the knowledge and conservation within this habitat is the need to develop a user-friendly sponge identification guide for temperate sponge-dominated rocky reef species, and to test assumptions such as linkages between sponge morphological diversity and species diversity. This would need to be done by taking *in situ* photos of sponges as well as tissue samples over a variety of spatial scales, identifying these samples, and producing a user-friendly identification guide similar to those currently available for fish, algae and other invertebrates.

The fifth chapter built on the results of the fourth chapter and reported on scales of autocorrelation in sessile benthic assemblages within sponge-dominated subtidal rocky reef. A significant positive correlation between distance and dissimilarity was found, meaning that assemblages became more dissimilar as distance increased. There was no clear threshold distance consistent across all locations and environmental domains where assemblages changed from being homogeneous to heterogeneous. Biodiversity sampling in this habitat is required at a fine scale (25 m) for the purposes of creating habitat maps for MPA planning. Information on the existence of spatial autocorrelation and the distances over which it occurs

must be considered in the design of sampling programs, as it is an extremely important consideration in monitoring. The results of this chapter provide the first understanding of spatial autocorrelation in these sponge-dominated rocky reef assemblages in temperate NSW. This information is critical for designing surveys of sessile benthic assemblages that result in representative areas of habitat being conserved within the MPA framework. The further use of AUV technology to survey this habitat would be of beneficial use as it collects a high volume of data over large geographical areas at depths not accessible through SCUBA. The results of this chapter would again influence the current zoning scheme in PSGLMP by increasing the amount of sponge-dominated rocky reef within sanctuary areas, to capture the small-scale variation of biodiversity within this habitat.

The sixth chapter quantified spatial and temporal variability in the biodiversity of rocky reef fishes among locations in different environmental domains within the sponge-dominated subtidal rocky reef habitat class. Habitat mapping based on depth categories is not a suitable surrogate for biodiversity of fish assemblages in sponge-dominated reef habitat in PSGLMP. A representative sample of fish assemblages from offshore islands, coastal headlands and/or estuarine environmental domains are required to adequately conserve representative samples of fish biodiversity, such as that currently contained within the habitat classification scheme of PSGLMP. The results of this chapter would not influence the current zoning scheme in PSGLMP greatly, other than reinforcing the need for sponge-dominated rocky reef within different environmental domains to occur within the mapped sanctuary areas. This study has advanced the knowledge of rocky reef fish assemblages in sponge-dominated reef habitat in PSGLMP by documenting spatial variability in offshore island, coastal headland and estuary environmental domains, highlighted the importance of large-scale environmental factors in structuring these assemblages, and would enable a more representative habitat classification scheme to be developed, that includes environmental variation as well as depth. The conservation of fish biodiversity in PSGLMP would benefit from additional studies examining other sources of variation that need to be incorporated into the current habitat classification schemes so that it can act as an effective surrogate for fish biodiversity. The stability of habitats over the long-term should also be assessed to determine if habitats can continue to act as surrogates for fish biodiversity in the long term (decades), particularly in the presence of climate change and potential changes which may occur within fish assemblages (such as an increase in tropical taxa) as a result in changes to abiotic influences such as sea temperature.

The seventh chapter examined the influence of biogenic attributes of habitats on sources of variation in the biodiversity of rocky reef fishes. The relationship between fish and sessile benthic assemblages within sponge-dominated subtidal rocky reef was examined to determine the usefulness of these groups as surrogates of biodiversity in relation to MPA planning in PSGLMP. Biodiversity of sessile benthic assemblages in sponge-dominated reef habitat in PSGLMP does not act as a surrogate for biodiversity of fish assemblages. In the context of marine protected area planning, surveys of variation in habitat attributes within sponge-dominated rocky reef cannot be used as an alternative to biodiversity assessments of fishes, as variation in the structure of sessile benthic assemblages is not associated with variation in the structure of fish assemblages. This is the first study to examine the influence of attributes of sponge-dominated reef habitat on rocky reef fish biodiversity. More research is required into the use of variation in habitat attributes as surrogates of diversity for fish assemblages within other habitats to test the effectiveness of using habitat classification schemes in the development of a representative system of MPAs. Improvements in the data collected by AUVs, including being able to measure the height of benthic taxa, the height and rugosity of small-scale topographic complexity, would improve this assessment.

The eighth chapter reported on the effectiveness of a depth-based habitat classification scheme as a surrogate for offshore fish biodiversity within subtidal unvegetated habitat. Habitat mapping based on depth is a suitable surrogate for biodiversity of fish assemblages in unvegetated habitats in PSGLMP. A representative sample of fish assemblages in both offshore and estuarine locations are required to adequately conserve representative samples of fish biodiversity in shallow habitat, whereas locations in differing environmental domains within intermediate habitat supported similar fish assemblages. The results of this chapter would not influence the current zoning scheme in PSGLMP to any great extent. The variation in location-level assemblages means that sanctuary areas in both shallow (estuarine and marine) and intermediate habitat are required to conserve a representative sample of fish biodiversity in this habitat. These criteria have been met within the current PTGLMP zoning, but given that 63% of species recorded in this study were of economic importance, perhaps a greater emphasis should be placed on more complete protection of fishes within these habitats by increasing the area of sanctuary zones. This study provided the first information on the biodiversity of fish assemblages within subtidal unvegetated habitat in PSGLMP, spatial and temporal variation of these assemblages, and the influence of environmental domains within this habitat. The stability of these trends over the long-term should also be

assessed to determine if habitats continue to act as surrogates for fish biodiversity in the long term (decades), particularly in the presence of threats such as climate change and associated changes to abiotic influences such as sea temperate, salinity and sea level. This study examined two depth categories: shallow subtidal sand 0-25 m, and intermediate sand 25-60 m. A more complete assessment of the effectiveness of the depth-based habitat classification scheme as a surrogate for offshore fish biodiversity would be gained by also assessing the deep sand 60- 200 m category. However, modifications to the field survey would need to be undertaken so that a mechanical winch could haul the Baited Remote Underwater Cameras (BRUVs) in and out of the water at this greater depth, and the possibly of installing a light source onto the BRUV explored in order to increase visibility.

This thesis assessed the effectiveness of habitat classification schemes as surrogates for biodiversity conservation in PSGLMP, and found that that habitat mapping based on depth is a suitable surrogate for biodiversity of fish assemblages in unvegetated habitats. Habitat mapping based on depth only categories is not a suitable surrogate for biodiversity of rocky reef sessile benthic assemblages, nor fish assemblages in sponge-dominated reef habitat. In the context of MPA planning, sessile benthic assemblages are not a suitable surrogate for biodiversity of fish assemblages. More studies are required to effectively understand what additional information needs to be incorporated into habitat classification schemes so that it can act as a surrogate for biodiversity for the range of assemblages conserved within the MPA.

Appendices

Appendix 1: Species (or sponge lifeforms) recorded by AUVs in sponge-dominated rocky reef habitat in Port Stephens-Great Lakes Marine Park. Numeric values are mean % cover at each location.

Lifeform	Coastal headland 1	Coastal headland 2	Coastal headland 3	Coastal headland 4	Coastal headland 5	Coastal headland 6	Offshore island 1	Offshore island 2	Offshore island 3	Offshore island 4
Ecklonia radiata	0.08	0.32	0.96	0.12	0.44	0	0	0	0	0.64
Zonaria sp.	0.12	0	0	0	0	0	0	0	0	0
Distromium flabellatum	0.36	3	4.32	4.36	0.72	0.04	0.52	1.96	3.56	0.12
Filamentous Red Algae	3.32	12.84	18.92	31	14.32	21.04	14.28	15.72	11.68	12.08
Amphiroa anceps	0	0	0	0	0	0	0	0.48	1.32	0.32
Martensia australis	1.24	0.68	0.52	0	0.8	0.16	0.04	0	0.12	0.08
Peyssonnelia novae-hollandiae	1.76	3.28	6.64	3.56	1.72	3.04	2.72	2.2	2.92	2.08
Gelidium australe	0.12	0.16	0.2	0	0	0	0.96	0	0	0.2
Plocamium cartilagineum	0	0.28	0	0	0	0	0	3.92	23.28	0
Encrusting coralline	7	11.44	16.08	18.92	17.96	6.56	19.2	16.04	13.4	6.08
Arborescent sponge	1.88	4.16	4.48	2.24	2.04	2.04	7.8	7.4	4.32	3.04
Cup sponge	1.2	2.16	2.28	0.52	0.76	1.24	1.52	2.36	2.12	1.44
Encrusting sponge	3.28	6.12	2.76	3.52	5.2	4.28	5.8	9	5.4	3.68
Fan sponge	0.6	0.72	1.36	0.92	0.76	3.16	1.88	1.52	0.8	0.44
Globular sponge	0	0	0	0.2	0.16	0.4	0.12	0.2	0.12	0.12
Lumpy sponge	0.16	0	0	0.32	0.76	1.56	0.52	1.64	0	0.04
Massive sponge	1.04	1.12	3	1.44	1.68	3.28	0.36	0.24	0.32	1.24
Papillate sponge	1.44	1.2	0.52	0.28	0	0.72	0.08	0	0	1
Repent sponge	0.28	0	0.12	0.28	0	0.24	0.6	0	0	0.12
Tubular sponge	0	0.04	0.28	0.04	0.08	0.12	0.2	0.16	0.48	0.12
Parazoanthus sp.	0.32	0	0	0.04	0.08	0	0	0	0	0.16
Balanophyllia bairdiana	0.24	0.16	0.16	0.08	0.04	0.2	0.04	0.16	0	0.24
Corynactis australis	0.16	0	0	0.28	5.68	0.04	0	0	0	0
Coral sp.	0	0.08	0.24	0.28	0.28	0.12	0.04	0.08	0.12	0
Erythropdium hicksoni	0	0	0.68	0	0	0	0	0	0	0
Coscinaraea mcneilli	0	0	0.36	0.24	0	0	1	0.92	0.72	0

Appendix 1: Species (or sponge lifeforms) recorded by AUVs in sponge-dominated rocky reef habitat in Port Stephens-Great Lakes Marine Park. Numeric values are mean % cover at each location.

Lifeform	Coastal headland 1	Coastal headland 2	Coastal headland 3	Coastal headland 4	Coastal headland 5	Coastal headland 6	Offshore island 1	Offshore island 2	Offshore island 3	Offshore island 4
Tubastrea sp.	0	0	0	0.12	0.04	0.16	0.04	0	0	0
Mopsella zimmeri	0	0	0	0.12	0.08	0.08	0	0.24	0	0
Dendronepthya sp.	0	0	0	0	0.4	0	0	0	0	0
Anthothoe albocincta	0	0	0	0	0.68	0	0.08	0	0	0
Bugula dentata	0.08	0.08	0.08	0	0.08	0	0	0.08	0	0.04
Bugula dissimilis	0	0.84	0.68	0.96	0.52	0.92	0.2	0.12	0.32	1.56
Steginoporella chartacea/truncata	0.28	1.12	0.04	0.28	1.08	0.92	0	0.28	0.36	0
Triphyllozoon moniliferum	0.52	1.04	0.8	1.72	0.72	0.68	1.2	1.16	0.52	0.48
Iodictyum phoeniceum	0	0.24	0	0	0	0	0	0	0	0
Botrylloides magnicoecum	0.2	0	0	0	0	0	0	0	0	0
Hermanis momus	0	0	0.04	0.28	0.2	0.04	0.76	0.12	0.28	0.28
Pyura spinifera	0	0	0.04	1.16	4.32	2.08	0.56	0.68	0.32	0.04
Cnemidocarpa pedata	0.08	0.28	0.32	2.84	2.04	1.36	0.84	1.28	0.32	0.24
Clavelina meridonalis	0.08	0	0.08	0	0.08	0.04	0	0	0.16	0
Polycitor giganteus	0	0	2.12	0.08	0.08	0	0.04	0.08	0	0.12
Silt Matrix	39.64	32.96	20.68	15.92	32.28	31.92	24.08	24.92	16.16	31.6
Sand	34.52	15.68	11.24	7.88	3.92	13.56	14.52	7.04	10.88	32.4

Appendix 2: Species recorded by BRUVs in sponge-dominated rocky reef habitat in Port Stephens-Great Lakes Marine Park. Numeric values are mean MaxN at each environmental domain (estuary, offshore island, coastal headland) in 2009 and 2010 (E: economically important species).

Taxon		2009			2010		
		Estuary	Offshore island	Coastal headland	Estuary	Offshore island	Coastal headland
Chondrichthyes							
Echeneidae	*Echeneis naucrates*	0.00	0.00	0.00	0.00	0.00	0.07
Dasyatidae	*Dasyatis brevicaudata E*	0.00	0.22	0.07	0.00	0.22	0.00
Heterodontidae	*Heterodontus galeatus E*	0.33	0.00	0.00	0.00	0.00	0.00
Heterodontidae	*Heterodontus portusjacksoni E*	0.00	1.67	1.87	0.33	1.61	2.67
Muraenidae	*Gymnothorax prasinus*	1.33	1.67	1.33	2.33	1.11	1.67
Muraenidae	*Enchelycore ramosa*	0.33	0.00	0.00	0.00	0.00	0.00
Myliobatidae	*Myliobatis australis E*	0.33	0.00	0.07	0.33	0.06	0.20
Odontaspididae	*Carcharias taurus*	0.00	0.06	0.00	0.00	0.00	0.20
Orectolobidae	*Orectolobus maculatus E*	0.33	0.00	0.07	0.00	0.00	0.07
Rhinobatidae	*Trygonorrhina fasciata E*	0.67	0.00	0.00	0.67	0.06	0.00
Rhinobatidae	*Aptychotrema rostrata E*	0.33	0.00	0.00	0.00	0.00	0.07
Scyliorhinidae	*Asymbolus analis E*	0.33	0.33	0.73	1.67	0.22	0.20
Urolophidae	*Urolophus sufflavus E*	0.00	0.00	0.00	0.33	0.06	0.00
Actinopterygii							
Acanthuridae	*Prionurus microlepidotus E*	6.33	0.56	0.00	17.33	0.11	0.00
Aulopodidae	*Aulopus purpurissatus E*	0.33	0.33	0.27	0.00	0.17	0.47
Aulostomidae	*Aulostomus maculatus E*	0.00	0.00	0.00	0.00	0.06	0.00
Carangidae	*Pseudocaranx dentex E*	0.00	0.28	0.53	0.00	1.67	2.40
Carangidae	*Seriola lalandi E*	0.00	1.94	0.00	0.00	0.06	0.00
Carangidae	*Trachurus novaezelandiae E*	0.00	22.67	28.73	0.00	50.61	67.87
Chaetodontidae	*Chelmonops truncatus*	0.33	0.11	0.20	0.00	0.22	0.07
Cheilodactylidae	*Nemadactylus douglasii E*	0.00	0.89	1.27	0.00	1.11	0.93
Cheilodactylidae	*Cheilodactylus vestitus E*	0.33	0.00	0.00	0.33	0.11	0.13
Cheilodactylidae	*Cheilodactylus ephippium E*	0.00	0.00	0.00	0.00	0.00	0.07
Cheilodactylidae	*Cheilodactylus fuscus E*	2.33	0.44	0.07	12.33	0.56	0.60
Chironemidae	*Chironemus marmoratus E*	0.00	0.06	0.00	0.00	0.00	0.00
Dinolestidae	*Dinolestes lewini E*	0.00	0.17	0.07	0.00	0.28	0.00
Diodontidae	*Dicotylichthys punctulatus*	0.00	0.00	0.07	0.00	0.00	0.00
Enoplosidae	*Enoplosus armatus*	0.00	1.06	0.13	0.00	4.67	0.53
Girellidae	*Atypichthys strigatus*	51.67	51.44	19.60	0.00	45.50	26.33
Kyphosidae	*Girella tricuspidata E*	0.00	0.06	0.00	0.00	0.17	0.00
Kyphosus	*Kyphosus sydneyanus E*	0.00	0.06	1.20	0.00	0.33	0.00
Labridae	*Austrolabrus maculatus*	0.00	0.00	0.00	0.00	0.06	0.00
Labridae	*Halichoeres nebulosus*	0.00	0.00	0.00	1.33	0.00	0.00
Labridae	*Coris picta*	1.00	1.89	0.60	1.33	0.94	1.67
Labridae	*Notolabrus gymnogenis E*	1.67	1.83	1.33	3.33	2.44	2.20
Labridae	*Achoerodus viridis E*	0.33	0.61	0.20	0.67	1.06	0.60

Appendix 2 (continued): Species recorded by BRUVs in sponge-dominated rocky reef habitat in Port Stephens-Great Lakes Marine Park. Numeric values are mean MaxN at each environmental domain (estuary, offshore island, coastal headland) in 2009 and 2010 (E: economically important species).

Taxon		2009			2010		
		Estuary	Offshore island	Coastal headland	Estuary	Offshore island	Coastal headland
Labridae	*Coris sandeyeri E*	0.00	0.00	0.00	0.00	0.06	0.00
Labridae	*Pseudolabrus psittaculus*	0.00	0.00	0.00	0.33	0.00	0.00
Labridae	*Eupetrichthys angustipes*	24.33	3.78	1.87	23.00	8.06	14.13
Labridae	*Ophthalmolepis lineolatus E*	6.33	5.00	5.60	9.67	4.94	8.67
Monacanthidae	*Eubalichthys bucephalus E*	0.00	1.39	0.40	0.00	0.72	0.33
Monacanthidae	*Nelusetta ayraudi E*	0.00	0.72	0.00	0.00	0.67	0.13
Monacanthidae	*Eubalichthys mosaicus E*	0.00	0.06	0.00	0.00	0.33	0.07
Monacanthidae	*Meuschenia freycineti E*	0.67	1.33	1.07	1.33	1.22	2.20
Monacanthidae	*Acanthaluteres vittiger E*	0.00	0.00	0.00	0.00	0.00	0.33
Monacanthidae	*Meuschenia scaber E*	0.00	1.33	0.87	0.00	1.61	0.67
Monacanthidae	*Meuschenia trachylepis E*	0.00	0.06	0.33	1.00	1.11	0.73
Monacanthidae	*Meuschenia flavolineata E*	0.00	0.11	0.00	0.00	0.00	0.00
Moridae	*Lotella rhacina E*	0.00	0.11	0.13	0.00	0.11	0.00
Mullidae	*Upeneichthys lineatus E*	0.00	0.17	2.13	0.00	1.06	0.20
Mullidae	*Parupeneus spilurus E*	0.33	2.39	0.13	2.33	0.56	3.20
Odacidae	*Odax cyanomelas E*	0.00	0.00	0.00	0.33	0.00	0.00
Pempheridídae	*Pempheris multiradiata*	0.00	0.06	0.00	0.00	0.00	0.07
Pomacentridae	*Parma unifasciata*	0.00	0.00	0.13	1.00	0.00	0.53
Pomacentridae	*Mecaenichthys immaculatus*	0.00	0.00	0.00	1.67	0.00	0.13
Pomacentridae	*Chromis hypsilepis*	0.00	3.72	0.20	0.33	4.78	2.07
Pomacentridae	*Parma microlepis*	0.33	1.06	0.60	1.33	1.33	0.80
Scorpaenidae	*Scorpaena cardinalis*	2.00	1.17	0.93	2.00	1.06	1.73
Scorpididae	*Scorpis lineolata E*	18.33	10.11	4.80	0.00	5.83	2.20
Serranidae	*Acanthistius ocellatus E*	0.33	0.78	0.47	0.33	0.44	0.87
Serranidae	*Epinephelus coioides E*	0.67	0.00	0.00	1.33	0.11	0.00
Serranidae	*Hypoplectrodes maccullochi*	1.00	0.44	0.67	1.33	0.56	0.80
Sparidae	*Pagrus auratus E*	1.00	0.00	0.00	0.00	0.00	0.00
Sparidae	*Rhabdosargus sarba E*	12.33	2.56	1.60	0.67	2.56	2.07
Sparidae	*Acanthopagrus australis E*	0.00	0.00	0.93	0.00	0.00	0.00
Terapontidae	*Terapon jabua E*	0.00	0.00	0.00	0.00	0.06	0.00
Terapontidae	*Pelates sexlineatus E*	11.67	0.00	0.00	1.00	0.06	0.00
Tetraodontidae	*Canthigaster callisterna*	0.00	0.06	0.00	0.00	0.06	0.00
Trachichthyidae	*Trachichthys australis*	0.00	0.00	0.07	0.00	0.00	0.00

Appendix 3: Species recorded by BRUVs in sponge-dominated intermediate rocky reef habitat in Port Stephens-Great Lakes Marine Park. Numeric values are MaxN at each location (E: economically important species; R: reef fish).

Taxon		Coastal headland 1	Coastal headland 2	Coastal headland 3	Coastal headland 4	Coastal headland 5	Coastal headland 6	Offshore island 1	Offshore island 2	Offshore island 3	Offshore island 4
Chondrichthyes											
Dasyatidae	*Dasyatis brevicaudata E R*	0	0	0	0	0	0	0	0	0	1
Heterodontidae	*Heterodontus portusjacksoni E*	2	3	3	0	2	1	5	2	0	4
Myliobatidae	*Myliobatis australis E R*	0	1	0	0	1	1	0	0	0	0
Odontaspididae	*Carcharias taurus E*	0	0	0	0	1	2	0	0	0	0
Scyliorhinidae	*Asymbolus analis E R*	0	1	0	0	1	0	1	0	0	0
Actinopterygii											
Aulopodidae	*Aulopus purpurissatus E R*	1	0	1	0	0	0	0	1	0	0
Carangidae	*Pseudocaranx dentex E*	0	10	0	0	1	0	0	2	15	0
Carangidae	*Seriola lalandi E*	0	0	0	0	0	0	0	1	0	0
Carangidae	*Trachurus novaezelandiae E*	3	1	60	120	140	0	0	0	0	0
Chaetodontidae	*Chelmonops truncatus E R*	0	0	0	0	0	0	0	0	1	2
Cheilodactylidae	*Nemadactylus douglasii E R*	1	1	1	0	2	0	2	2	1	0
Cheilodactylidae	*Cheilodactylus vestitus E R*	0	0	1	0	0	0	0	0	0	0
Cheilodactylidae	*Cheilodactylus fuscus E R*	0	0	1	0	0	1	0	1	0	0
Dinolestidae	*Dinolestes lewini E*	0	0	0	0	0	0	0	0	3	0
Echeneidae	*Echeneis naucrates*	0	0	0	0	0	1	0	0	0	0
Enoplosidae	*Enoplosus armatus R*	0	0	2	0	0	0	1	0	5	60
Labridae	*Coris picta E R*	0	0	0	0	0	1	0	1	0	0
Labridae	*Notolabrus gymnogenis E R*	2	2	1	2	1	3	2	2	1	3
Labridae	*Achoerodus viridis E R*	0	1	1	1	1	0	1	2	1	1
Labridae	*Coris sandeyeri E R*	0	0	0	0	0	0	0	0	1	0
Labridae	*Ophthalmolepis lineolatus E R*	4	10	3	11	11	11	4	4	5	11
Monacanthidae	*Eubalichthys bucephalus E R*	2	0	1	0	0	0	0	2	0	0

Appendix 3 (continued): Species recorded by BRUVs in sponge-dominated intermediate rocky reef habitat in Port Stephens-Great Lakes Marine Park. Numeric values are MaxN at each location (E: economically important species; R: reef fish).

Taxon		Coastal headland 1	Coastal headland 2	Coastal headland 3	Coastal headland 4	Coastal headland 5	Coastal headland 6	Offshore island 1	Offshore island 2	Offshore island 3	Offshore island 4
Monacanthidae	*Eubalichthys mosaicus E R*	0	0	0	0	1	0	1	0	0	0
Monacanthidae	*Meuschenia freycineti E R*	3	4	6	0	2	1	3	0	1	1
Monacanthidae	*Meuschenia scaber E R*	1	1	1	2	1	1	5	4	1	2
Monacanthidae	*Meuschenia trachylepis E R*	0	0	0	2	4	0	1	1	1	1
Mullidae	*Upeneichthys lineatus E R*	0	1	1	0	0	0	0	1	1	0
Mullidae	*Parupeneus spilurus E R*	0	1	0	0	4	2	0	1	0	1
Muraenidae	*Gymnothorax prasinus R*	2	3	1	1	0	0	2	2	0	1
Pomacentridae	*Parma unifasciata R*	0	0	0	5	0	3	0	0	0	0
Pomacentridae	*Mecaenichthys immaculatus R*	0	0	1	0	0	0	0	0	0	0
Pomacentridae	*Chromis hypsilepis R*	0	0	0	0	0	0	1	0	0	0
Pomacentridae	*Parma microlepis R*	0	0	0	0	0	0	1	1	0	1
Rhinobatidae	*Trygonorrhina fasciata E R*	0	0	0	0	0	0	0	0	1	0
Scorpaenidae	*Scorpaena cardinalis R*	1	1	1	1	1	3	1	1	0	2
Scorpididae	*Atypichthys strigatus*	0	0	1	180	80	3	0	0	1	0
Scorpididae	*Scorpis lineolata*	25	1	0	0	0	1	2	5	0	0
Serranidae	*Acanthistius ocellatus E R*	2	1	0	3	0	2	0	0	0	0
Serranidae	*Hypoplectrodes maccullochi R*	0	0	1	0	0	2	1	0	0	1
Sparidae	*Pagrus auratus E R*	12	12	2	7	30	22	4	0	32	2
Sparidae	*Rhabdosargus sarba E R*	0	2	4	1	1	0	0	0	13	0

Appendix 4: Species recorded by BRUVs in unvegetated habitat from shallow and intermediate habitat in March and September 2009 in Port Stephens-Great Lakes Marine Park. Numeric values are mean MaxN at each site (E: economically important species).

Taxon		Mar-09															
		Shallow Habitat								Deep Habitat							
		SL1 S1	SL1 S2	SL2 S1	SL2 S2	SL3 S1	SL3 S2	SL4 S1	SL4 S2	DL1 S1	DL1 S2	DL2 S1	DL2 S2	DL3 S1	DL3 S2	DL4 S1	DL4 S2
Chondrichthyes																	
Dasyatididae	*Dasyatis brevicaudata E*	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Dasyatididae	*Dasyatis kuhlii E*	0.00	0.00	0.00	0.00	0.00	0.50	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Heterodonitidae	*Heterodontus portusjacksoni E*	0.50	0.00	1.00	0.87	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Myliobatididae	*Myliobatis australis E*	0.00	0.00	0.00	0.50	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Rhinobatidae	*Aptychotrema rostrata E*	1.66	1.66	1.41	1.00	1.50	1.58	1.41	1.32	0.00	0.00	0.50	0.71	0.87	0.87	0.71	0.87
Rhinobatidae	*Trygonorrhina fasciata E*	1.00	1.73	1.50	1.80	1.32	1.50	1.87	1.66	0.00	0.87	0.00	0.71	1.00	0.87	0.71	0.87
Scyloirhinidae	*Asymbolis analis E*	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Torpedinidae	*Hypnos monopterygium E*	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.50	0.00	0.00
Triakidae	*Mustelus antarcticus E*	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Urolophidae	*Urolophus sufflavus E*	0.50	0.50	0.00	0.00	0.71	0.00	0.71	0.71	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Actinopterygii																	
Carangidae	*Pseudocaranx dentex E*	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Carangidae	*Trachurus novaezelandiae E*	3.28	0.00	3.16	2.92	1.12	1.73	4.95	5.27	3.46	5.07	2.35	0.00	2.65	0.50	0.50	1.66
Clupeidae	*Sardinops neopilchardus E*	0.00	2.50	0.00	0.00	0.00	2.74	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Clupeidae	*Hyperlophus vittatus E*	3.54	6.71	0.00	0.00	0.00	2.74	2.12	2.50	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Enoplosidae	*Enoplosus armatus*	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2.12	0.00	0.00	0.00	0.00	0.00
Microcanthidae	*Atypichthys strigatus*	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.00	0.00	0.71	1.00	0.00	0.00
Monacanthidae	*Meuschenia freycineti E*	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.50	0.00	0.87	0.00
Monacanthidae	*Nelusetta ayraudi E*	0.00	0.00	0.00	0.00	0.00	1.00	0.00	0.00	1.50	0.00	2.35	0.87	0.00	1.50	4.15	3.50
Mullidae	*Upeneus tragula*	0.00	0.00	0.00	0.50	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Ostraciidae	*Anoplocapros inermis*	0.00	0.00	0.00	0.00	0.71	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.32	0.00	0.00
Paralichthyidae	*Pseudorhombus* sp. *E*	0.00	0.00	0.00	0.50	0.00	0.50	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Platycephalidae	*Platycephalus caerulepunctus E*	0.87	1.22	0.00	0.00	0.71	1.22	1.32	0.50	1.73	2.00	2.06	2.60	2.60	2.45	1.32	2.29
Platycephalidae	*Platycephalus bassensis E*	2.18	2.06	0.00	0.50	1.32	2.96	2.29	1.94	2.96	3.46	3.71	4.18	3.97	4.58	2.69	3.39
Scorpididae	*Scorpis aequipinnis E*	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Sillaginidae	*Sillago ciliata E*	0.00	0.00	1.12	0.71	2.45	1.73	2.24	1.87	1.94	0.00	1.87	2.60	2.06	2.83	2.12	3.08
Sillaginidae	*Sillago maculata E*	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.58	0.00	1.73	2.65	3.16	2.00	1.41	3.67
Sparidae	*Acanthopagrus australis E*	0.00	0.50	1.41	4.39	0.50	0.00	0.50	0.00	0.00	0.00	0.71	0.50	0.00	0.00	0.50	1.73
Synodontidae	*Synodus dermatogenys*	0.00	0.00	0.50	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Terapontidae	*Pelates sexlineatus E*	0.00	0.00	0.00	2.12	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Terraodonidae	*Torquigener pleurogramma*	1.22	0.50	1.94	0.00	0.00	1.22	0.00	0.50	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00

Appendix 4 (continued): Species recorded by BRUVs in unvegetated habitat from shallow and intermediate habitat in March and September 2009 in Port Stephens-Great Lakes Marine Park. Numeric values are mean MaxN at each site (E: economically important species).

Taxon		Sep-09															
		Shallow Habitat								Deep Habitat							
		SL1 S1	SL1 S2	SL2 S1	SL2 S2	SL3 S1	SL3 S2	SL4 S1	SL4 S2	DL1 S1	DL1 S2	DL2 S1	DL2 S2	DL3 S1	DL3 S2	DL4 S1	DL4 S2
Chondrichthyes																	
Dasyatididae	*Dasyatis brevicaudata E*	0.00	0.00	0.00	0.50	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.50	0.00	0.87
Dasyatididae	*Dasyatis kuhlii E*	0.00	0.00	0.50	0.50	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Heterodonitidae	*Heterodontus portusjacksoni E*	0.00	0.50	1.41	0.87	0.71	1.12	0.00	0.00	0.00	0.00	0.50	1.12	0.00	0.00	0.00	0.00
Myliobatididae	*Myliobatis australis E*	0.50	0.00	0.00	0.00	0.00	0.00	0.00	0.50	0.00	0.50	0.00	0.00	0.00	0.00	0.50	0.00
Rhinobatidae	*Aptychotrema rostrata E*	1.00	0.87	1.22	1.41	1.32	1.32	1.12	1.22	0.87	0.71	0.00	0.50	1.00	1.22	1.00	0.87
Rhinobatidae	*Trygonorrhina fasciata E*	1.50	1.41	1.22	1.00	1.73	1.50	1.22	0.87	1.00	1.41	0.87	0.71	1.12	1.41	0.87	1.00
Scyloirhinidae	*Asymbolis analis E*	0.00	0.00	0.00	0.71	0.50	0.50	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Torpedinidae	*Hypnos monopterygium E*	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Triakidae	*Mustelus antarcticus E*	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.87	0.50	0.00	0.00
Urolophidae	*Urolophus sufflavus E*	0.50	0.50	0.71	0.71	0.71	1.22	0.71	1.22	0.00	0.00	0.50	0.00	0.00	0.00	0.00	0.00
Actinopterygii																	
Carangidae	*Pseudocaranx dentex E*	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Carangidae	*Trachurus novaezelandiae E*	4.12	0.00	0.50	0.00	3.24	3.04	6.76	4.69	3.04	2.69	3.39	2.45	4.12	4.15	4.64	2.69
Clupeidae	*Sardinops neopilchardus E*	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Clupeidae	*Hyperlophus vittatus E*	4.61	3.71	0.00	0.00	2.74	2.45	0.00	1.41	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Enoplosidae	*Enoplosus armatus*	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Microcanthidae	*Atypichthys strigatus*	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	3.04	0.00
Monacanthidae	*Meuschenia freycineti E*	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.71	0.00	0.71	0.00	0.00	0.50	0.71	0.00
Monacanthidae	*Nelusetta ayraudi E*	0.00	0.50	0.00	0.00	0.00	0.00	0.50	0.00	1.87	1.12	0.00	0.87	0.50	0.50	2.12	2.78
Mullidae	*Upeneus tragula*	0.00	0.00	0.00	0.50	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Ostraciidae	*Anoplocapros inermis*	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Paralichthyidae	*Pseudorhombus* sp. *E*	0.00	0.00	0.00	0.00	0.50	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Platycephalidae	*Platycephalus caerulepunctus E*	0.00	0.00	0.00	0.00	0.00	0.50	0.50	0.71	1.94	1.94	2.50	2.78	2.29	2.18	2.60	2.06
Platycephalidae	*Platycephalus bassensis E*	0.87	0.87	0.50	0.00	1.12	1.66	1.50	1.32	1.94	2.65	2.74	2.87	2.29	2.74	2.87	2.24
Scorpididae	*Scorpis aequipinnis E*	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Sillaginidae	*Sillago ciliata E*	0.00	0.00	0.71	0.50	1.00	0.00	0.00	0.00	0.00	0.71	0.87	1.66	0.00	1.41	0.00	0.00
Sillaginidae	*Sillago maculata E*	0.00	0.00	0.00	0.00	0.00	1.22	0.00	2.65	0.00	0.00	2.50	2.78	3.04	3.81	0.00	0.00
Sparidae	*Acanthopagrus australis E*	0.00	0.00	0.50	3.54	0.00	0.00	0.00	0.50	0.00	0.00	0.71	0.00	0.00	0.87	0.00	0.00
Synodontidae	*Synodus dermatogenys*	0.00	0.00	0.71	0.71	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Terapontidae	*Pelates sexlineatus E*	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Terraodonidae	*Torquigener pleurogramma*	0.00	0.00	1.80	0.87	0.00	0.00	0.00	0.50	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00

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