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Ecological Connectivity of Kimberley Marine Communities: *Synthesis Report*

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WAMSI Kimberley Marine Research Program

Synthesis Report

Project 1.1.3a

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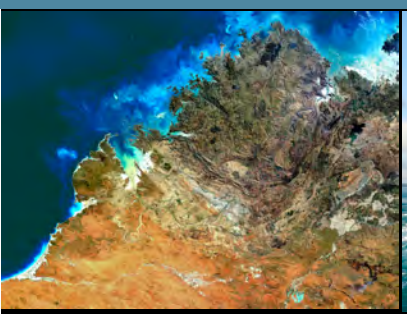
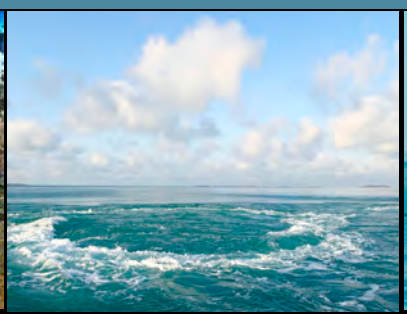
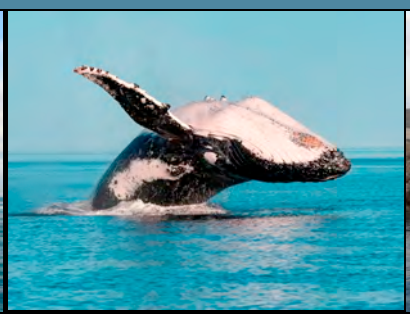


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WAMSI Kimberley Marine Research Program

Initiated with the support of the State Government as part of the Kimberley Science and Conservation Strategy, the Kimberley Marine Research Program is co-invested by the WAMSI partners to provide regional understanding and baseline knowledge about the Kimberley marine environment. The program has been created in response to the extraordinary, unspoilt wilderness value of the Kimberley and increasing pressure for development in this region. The purpose is to provide science based information to support decision making in relation to the Kimberley marine park network, other conservation activities and future development proposals.

Front cover images (L-R)

Image 1: Satellite image of the Kimberley coastline (Image: Landgate)

Image 2: Powerful currents are a feature of the Kimberley marine environment. Whirlpool in Sunday Strait (Image: Kathryn McMahon)

Image 3: Humpback whale breaching (Image: Pam Osborn)

Image 4: Coral platform exposed at low tide. Bathurst Island Buccaneer Archipelago (Image: Kathryn McMahon)

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Contents

1 Introduction

1.1 Objective of the Project

The overarching objective of KMRP Project 1.1.3 (Ecological Connectivity of Kimberley Marine Communities) was to provide the first estimates of ecological connectivity across multiple spatial scales for a suite of model/priority marine organisms in the Kimberley. More specifically, this project aimed to provide species-specific estimates of realised connectivity at a reef-scale (<1 km), inter-reef scale (1-100 km) and inter-region scale (100+ km) through genetic analyses of seven key animals and plants with contrasting dispersive life histories that are representative of common taxa.

The goals of this Synthesis Report are:

I. To synthesise the major findings and conclusions of WAMSI Project 1.1.3 – Ecological Connectivity of Kimberley Marine Communities; and

II. To place this information in local and regional contexts to benefit environmental planning and resource management.

1.2 Rationale

For most marine organisms the ocean environment provides the potential for widespread dispersal via oceanic currents, tides and wind. However, depending on the interplay between the biology of an organism and its physical environment, the *potential* for dispersal may be radically different from the *realised* dispersal. The realised connectivity between populations (i.e. the actual numbers of individuals that move between distant populations and survive to reproduce) determines the distribution and abundance of marine organisms and is especially important in the face of disturbances. For example, if the scale of an impact (e.g. over-harvesting) is larger than the routine distances of larval dispersal, then recovery is likely to be slow. Similarly, disturbances may be more significant if they impact populations that act as principal sources of larval recruitment. Therefore, to effectively manage marine resources in the Kimberley and neighbouring bioregions it is crucial to develop a realistic understanding of the extent of connectivity and to highlight the important sources of larvae that maintain healthy populations and supplement recovery after disturbance.

2 Background

The Kimberley marine bioregion (located in northwest Western Australia) is a remote, sparsely populated and poorly studied area characterised by extreme tidal ranges and strong tidal currents (Figure 1). The region is the subject of growing scientific interest because of its near-pristine state and unique biota (Wilson 2013). It is also subject to increasing interest from industry and tourism, which has motivated the establishment of strategically placed marine reserves for the management of regional biodiversity at the State and Federal levels (D.E.P. 2016; D.P.a.W. 2016).

To support these and other management strategies, there is a growing need to understand the environmental drivers that underpin the distribution and abundance of biodiversity in this bioregion. While some recent research has focused on characterising diversity of marine life in the Kimberley (e.g. Jones *et al.* 2014; Richards *et al.* 2015; Travers *et al.* 2012), spatial processes, including ecological and genetic connectivity, are important yet neglected areas of research among the biota of the inshore Kimberley (Kendrick *et al.* 2016; Underwood *et al.* 2013).

Obtaining an understanding of ecological connectivity within marine systems is fundamental to the design of effective management strategies, such as marine protected areas and regulations for the sustainable harvest of fishery resources (Magris *et al.* 2014; Ovenden *et al.* 2015). In practice however, connectivity is spatio-temporally complex, and detailed studies across multiple scales are needed to reveal the way biogeography, life-history and environment interact in individual taxa. For example, if dispersal is primarily local, recruits

produced from afar are unlikely to contribute to the local recovery of populations after a disturbance.

Nevertheless, occasional recruitment can still be important for maintaining genetic diversity over evolutionary time. Therefore, to manage marine systems effectively, it is important to develop an understanding of this multifaceted nature of connectivity.

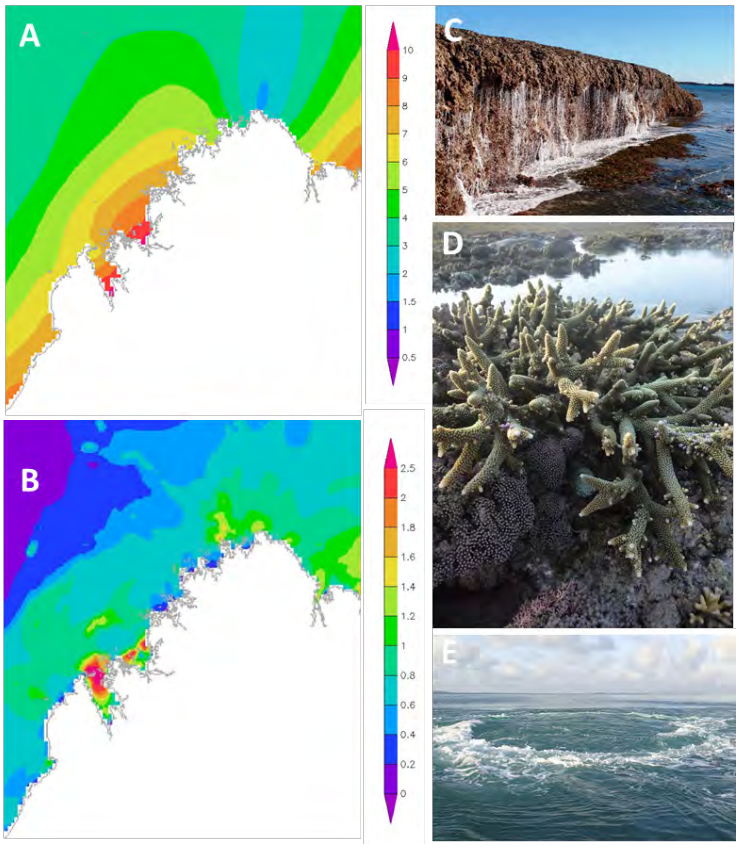

Figure 1. The dynamic Kimberley environment. A. Mean tidal range (m); B. Mean tidal current speed (m/s); C. Tallon (Jalan) Island Cascades at low tide; D. *Acropora aspera* exposed at low tide; E. Large eddy formed by the fast flowing outgoing tide in the Buccaneer Archipelago. Tidal imagery courtesy of the National Tidal Centre.

The inshore Kimberley provides a new frontier for connectivity studies because of the unique and dynamic tidal regime and often harsh environmental conditions (Figure 1). At some inshore locations tidal amplitudes reach nearly 12 metres during spring tides. This means at low tide, intertidal organisms can be exposed to direct sunlight for up to 3 hours at a time (Richards *et al.* 2015). Further, strong tidal currents interact with heterogeneous benthic topography to cause complex, unpredictable and powerful hydrodynamic conditions.

It is unclear how such a unique hydrodynamic regime influences dispersal of marine larvae in the Kimberley. Conceivably it could enhance dispersal, but equally, it could act as a disruptive barrier to dispersal. For example, under maximal tidal velocity (2.5 m/s), a passive propagule could potentially be transported more than 50 kilometres from a natal reef patch during a single (six hour) tide. Alternatively, the influence of re-circulating eddies and retention zones created by complex reef topographies or simply the returning tide may result in propagules being retained close to their natal reef (e.g. James *et al.* 2002). These local hydrodynamic effects are potentially made more complex by regional-scale currents and wind-driven effects as well as intermittent influences by cyclones (Radford *et al.* 2014). Exploring these disparate influences on connectivity with a range of model taxa that feature different life history traits will provide new information of direct relevance to conservation planning and resource management in the Kimberley.

3 Methods

3.1 Focal Taxa

Seven organisms (two hard corals, two seagrasses, a mollusc and two fishes) were chosen as models for exploring connectivity in the Kimberley at both fine and broad scales (Figure 2). These species were selected as they were either:

I. Important habitat forming species;

II. Harvested species; or

III. Representative of key trophic levels that may serve as a useful indicator for more vulnerable species.

Focal taxa were also selected according to a range of life history traits that may be influenced by different hydrodynamic processes such as:

IV. Brooded larvae with short pre-settlement durations;

V. Spawned larvae with longer pre-settlement durations;

VI. Demersal egg layer with short pelagic larval duration; and (iv) Sexual reproduction with propagules (seeds) that are dispersed in the water column (floating) or in the sediment (negatively buoyant).

Figure 2. Major functional role, life history, and expected scale of dispersal in target species. PLD = Pelagic larval duration and refers to the average period of larval competency.

3.2 Approach: Population Genetics, Genomics and Otolith Geochemistry

Connectivity is difficult to directly measure for most marine organisms because their dispersal largely occurs during a microscopic planktonic phase, and the scale of movement is potentially very large. A spatial analysis of genetic structure is a widely used "indirect" method for inferring ecological connectivity. Where genetic differences are recorded between sampling individuals or sites, it indicates that dispersal between those sites is also limited to some extent. A useful attribute of genetic analysis is its ability to infer average realised connectivity over multiple generations from a single sample in time. However, this means that inferences about demographic connectivity (i.e. the relative contribution of immigrants and emigrants to total recruitment within a generation) based on genetic analyses need to be made carefully and recognise that history and non-equilibrium population dynamics can also influence genetic structure (Lowe & Allendorf 2010).

Measurement of chemicals embedded in the constantly growing earbones (otoliths) of fishes can also provide information on their movements because unique chemical signatures reflect specific locations that the fish inhabit during their lifetime. Unlike genetic methods, otolith geochemistry is a "direct" method for inferring ecological connectivity in that it provides insight into within-generation movements for fishes at larval, juvenile and adult stages. The combination of longer-term inference from genetic techniques and short-term inference from otolith geochemistry can provide a high level of detail on the movement patterns of fishes. Regrettably, equivalent techniques are not available for other marine organisms. Approach: Sampling design

We employed a hierarchical sampling design, whereby an intensive fine scale study located in the southern Kimberley was nested within a regional study that included sites in the broader Kimberley as well as neighbouring bioregions.

3.2.1 Broad Scale Study

Samples were collected opportunistically at 67 sites in the mid-north Kimberley, Pilbara, Gascoyne, and Northern Territory through collaboration with other WAMSI projects, and /or with other research programs (e.g. AIMS offshore atoll research program; WAM Museum Woodside Collection Project; Department of Fisheries WA and NT research programs; Figure 3a). Details of the sample sites for each species can be found in taxon specific reports.

3.2.2 Fine Scale Study

The geographic focus for the fine scale study was the complex archipelago of rocky islands and semi-submerged reefs that form the Dampier Peninsula and Buccaneer Archipelago in the southern Kimberley (Figure 3b). The region falls within the southern portion of the Kimberley bioregion, but it also adjoins the King Sound and Canning bioregions. Wherever possible a common sampling design was used which involved collecting samples from 20-50 individuals of each species from up to 26 sites. Sites were generally 200-300 m^2 and were separated by 1-15 km. Details of the sample sites for each species can be found in taxon specific reports.

3.3 Genetic and Geochemistry Analyses

Samples obtained from a total of 5009 individuals and 157 sites were genotyped using either single nucleotide polymorphism DNA markers (SNPs; corals, mollusc, fishes) or microsatellite DNA markers (seagrass) (Table 1). Wherever possible, taxa were sampled at the same geographic location. SNP genotyping is a state of the art method for population genomic analysis. Its application in the majority of the taxa studied here represents a significant advance over previous connectivity studies on coral reefs due to its increased power to characterise relationships among sites. Fish otolith geochemical analyses were undertaken to provide individual life-histories of fishes by recording the chemical signatures of the environment at larval, juvenile and adult stages as proxies for changes in habitat (environment). Trace elements can provide evidence of movements between different marine habitats while changes in strontium and oxygen isotopes provide evidence of movement between marine and estuarine environments. The combinations of these measurements can be used to construct a detailed understanding of the population structure and movements of individual fish over the course of their lives

Table 1. Total number of sites sampled and individuals genotyped for each focal taxa.

Species	Sites	Individuals	Markers
A. aspera_C	14	388	2894
I. brueggemanni	17	1093	2125
T. hemprichii	17	749	16
H. ovalis	11	407	9
T. niloticus	17	514	5428
P. milleri	28	842	4472
L. carponotatus	53	1016	4468
Total	**157**	**5009**	**19412**

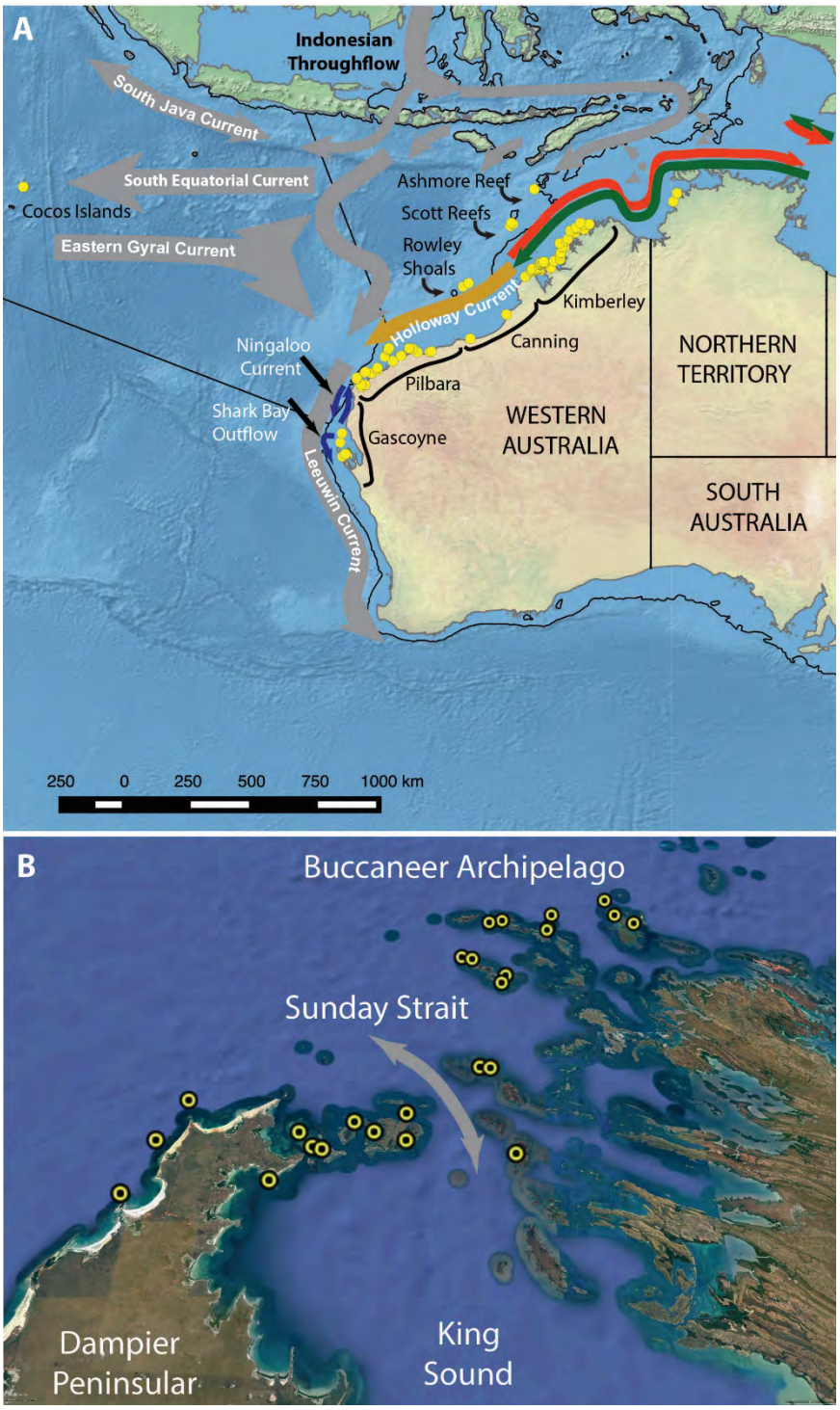

Figure 3. Map of the study sites where genetic samples were collected. A) The broad-scale study; B) The fine scale study. Depicted on panel A are the major surface currents in the Indo- Australian region (adapted from D'Adamo *et al.* 2009; Domingues *et al.* 2007; Schiller 2011; Sprintall *et al.* 2002). Red, green and amber coloured lines indicate flow direction in summer, winter and autumn, respectively.

4 Key Findings

The key findings of this study are summarized in Figure 4:

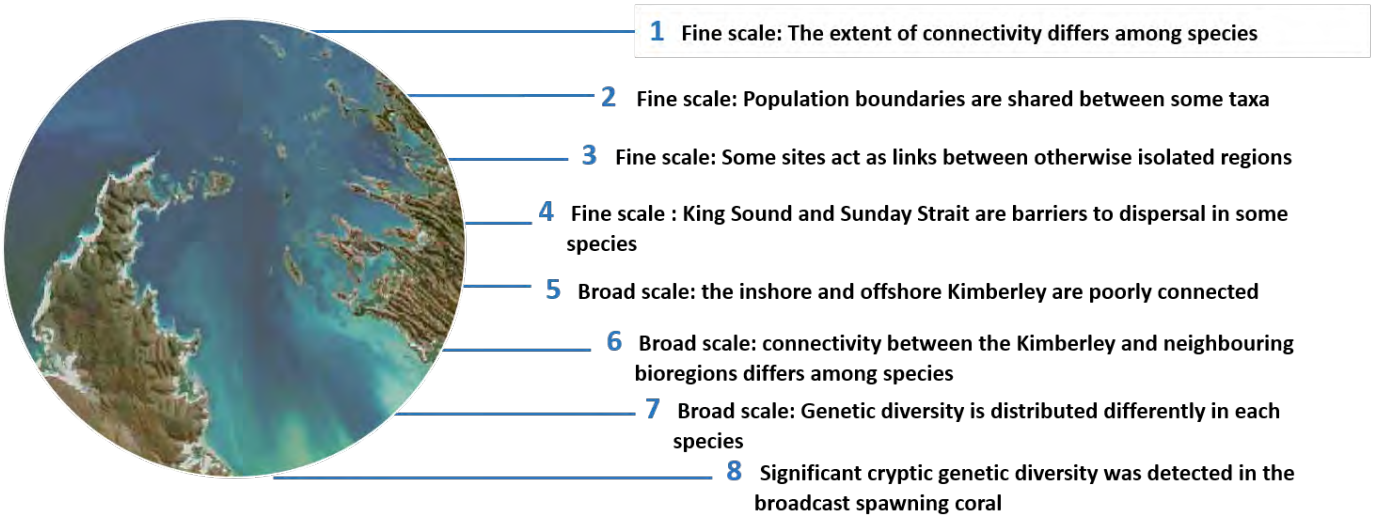

Figure 4. Key findings of KMRP Ecological Connectivity Project 1.1.3.

4.1 Fine scale: The extent of connectivity differs among species

A key finding of this study is that despite experiencing a common set of environmental conditions, the extent of ecological connectivity differed among the focal organisms, and not always in predictable ways. Habitat forming organisms (coral, Report 1.1.3.1; seagrass, Report 1.1.3.2) typically exhibited the most localised population structure, with evidence for limitations to routine dispersal evident on scales of 10s of kilometres or less. In the remaining organisms (fishes, Reports 1.1.3.4a and b; trochus, Report 1.1.3.3), population structure was weaker or not detectable, and limits to dispersal were evident on scales of 80 to several 100s kilometres (Figure 5). Some of these results were unexpected. For example, the seagrass with floating seeds had finer scale genetic structure compared with the seagrass with sinking seeds, and similarly, the pelagic spawning fish also had finer scale genetic structure compared to the benthic spawning fish. Further, the mollusc with a short larval duration exhibited the lowest level of genetic structure of all taxa (Figure 5). **Clearly, expectations of realised connectivity based on simple life history characteristics are unreliable, and patterns therefore need to be assessed on a species by species basis**.

4.2 Fine scale: Population boundaries are shared between some taxa

Major population boundaries were identified in several taxa, notably the habitat-forming corals (Report 1.1.3.1), and seagrasses (Report 1.1.3.2), and the pelagic spawning fish (Report 1.1.3.4b), but not the mollusc (Report 1.1.3.3), nor the damselfish (Report 1.1.3.4a). Broadly, the divisions in seagrasses, corals and fish were between the Dampier Peninsula and Buccaneer Archipelago sites, but the specific positions and breadths of the boundaries differed for individual taxa (Figure 6). For example, in *T. hemprichii,* the seagrass with buoyant seeds, the northern Buccaneer Archipelago sites were differentiated from those in the southern Buccaneer Archipelago and Dampier Peninsula (Figure 6A), whereas both the broadcast spawning and brooding corals exhibited a strong division between the Dampier Peninsula and the Buccaneer Archipelago (Figure 6B). A division also exists in the fish, *L. carponotatus*, but it occurred as a broad transition zone in which the genetic composition changes across a distance of *c*. 40km at the tip of the Dampier Peninsula from the Kimberley bioregion signature to the Pilbara/Canning bioregion signature (see also Major Finding 6). In contrast, *T.*

niloticus forms a single highly-mixed genetic unit within the Dampier Peninsula and Buccaneer Archipelago, suggesting considerable exchange of larvae occurs throughout this region. Section 4.4 below further evaluates the reasons why a barrier may exist between Buccaneer Archipelago and Dampier Peninsula.

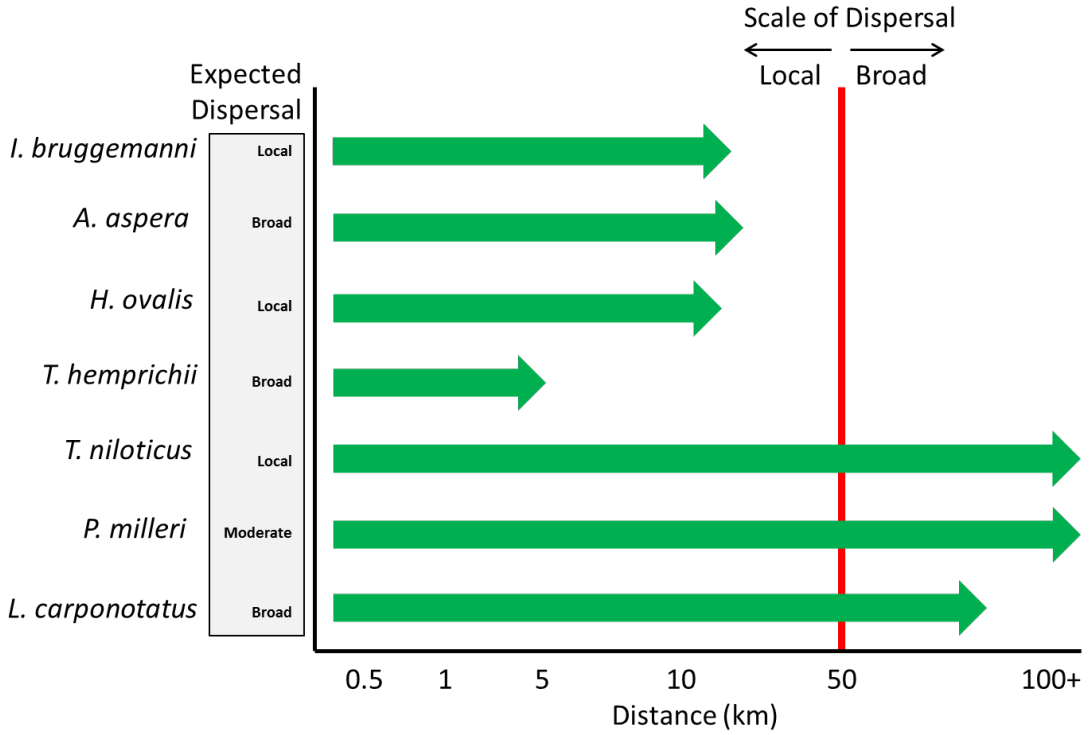

Figure 5. Expected and realised scale of connectivity of focal species in the Dampier Peninsula and Buccaneer Archipelago. The maximum detectable scale of genetic structure (green arrow) is based on spatial autocorrelation analyses and the genetic correlation coefficient (r) between individuals.

4.3 Fine scale: Some sites act as links between otherwise isolated regions

Although restricted connectivity was detected in the region of Sunday Strait and the Dampier Peninsula for corals (Report 1.1.3.1), seagrasses (Report 1.1.3.2), and *L. carponotatus* (Report 1.1.3.4b), exchange of genes across this barrier over multiple generations occurs through the important stepping-stones at Tide Rip, Mermaid and Bedford Islands for corals and seagrass. For *L. carponotatus* a similar transition zone was detectable between Tallon Island and Emeriau Point (Dampier Peninsula).

4.4 Fine scale: King Sound, Sunday Strait are barriers to dispersal in some species

The region at the mouth of King Sound is characterised by the largest tropical tidal range and the fastest tidal currents in the world including the input of massive volumes of freshwater in a highly turbid plume from the Fitzroy catchment in the wet season; a time when propagules from many of these species are in the plankton. These extreme environmental conditions appear to restrict connectivity. Coupled with the finding of a highly divergent population of *I. bruggemanni* on the western side of Dampier Peninsula, these results demonstrate that the tip of Dampier Peninsula is an important intra-specific genetic barrier for various marine taxa with range of life histories.

4.5 Broad scale: The inshore and offshore Kimberley are poorly connected

The species of corals (Report 1.1.3.1) and trochus (Report 1.1.3.3) that were sampled over broader scales at the offshore reefs of Rowley Shoals, Scott Reefs, and Ashmore Reef showed that these inshore Kimberley reef populations are highly divergent from the offshore 'oceanic' reef populations, strongly indicating that these regions are ecologically and evolutionary independent. This likely reflects the limited hydrodynamic

connectivity between these reefs (Figure 7), but in addition, genetic patterns suggest strong environmental differences between these regions has driven local adaptation in these species.

4.6 Broad scale: connectivity between the Kimberley and neighbouring bioregions differs among species

The species that were sampled across the broader northwest coast of Australia exhibited some consistencies in their broad-scale patterns of connectivity. The seagrass *T. hemprichii* (Report 1.1.3.2) and the damselfish *P. milleri* (Report 1.1.3.4a) exhibited a sharp discontinuity between the Kimberley and Pilbara, indicating negligible exchange, and probably reflecting discontinuous habitat between these regions. In contrast, Pilbara and Kimberley populations of *L. carponotatus* (Report 1.1.3.4b), exhibited only weak genetic distinctiveness. Furthermore in *L. carponotatus*, the transition zone between Kimberley and Pilbara genetic groups occurred at Sunday Strait rather than corresponding to the Pilbara and Kimberley Bioregions like *T. hemprichii* and *P. milleri*. *Lutjanus carponotatus* samples from the Northern Territory were weakly genetically distinct from those in the Kimberley, but it is unclear whether this represents limited demographic exchange, or incomplete sampling in the intervening region.

The otolith geochemistry results (Chapters 1.1.3.4c) generally concur with the findings of the genetic companion studies of the two fish species (Chapters 1.1.3.4a, b), and add support to their conclusions that the movements of both species are restricted between the Kimberley, Pilbara and Gascoyne management bioregions. This preliminary result should be considered cautiously as the margin otolith microchemistry only reveals movements in the adult phase and additional core samples will need to be analysed to allow interpretation of population connectivity during larval and post-larval phases. Furthermore, while the marginal elemental composition of *P. milleri* otoliths from Shark Bay differed significantly from all bioregions further north, thereby paralleling genetic results, there was no such difference for *L. carponotatus*. This may be a genuine environmental effect, reflecting the more offshore oceanic marine environment where *L. carponotatus* samples were collected (Bernier and Dorre Islands) compared to the more enclosed and inshore marine environment where *P. milleri* samples were collected within the western Gulf of Shark Bay.

4.7 Broad scale: Genetic diversity is distributed differently in each species

Within the Dampier Peninsula – Buccaneer Archipelago region, some organisms (coral (Report 1.1.3.1), seagrass (Report 1.1.3.2)) exhibited large variation between sites in amount of genetic diversity observed, whereas others (fishes (Report 1.1.3.4a and b), trochus (Report 1.1.3.3)) exhibited similar amounts of diversity at each site. Across the broader northwest coast of Australia, species varied significantly in their distributions of genetic diversity. Populations of the seagrass *T. hemprichii* from the Kimberley exhibited significantly lower genetic diversity than those in the Pilbara. In contrast, in the damselfish *P. milleri*, genetic diversity was highest in the Kimberley and declined progressively with latitude towards the Gascoyne bioregion. In the stripey snapper, *L. carponotatus,* levels of genetic diversity were consistent across the entire northwest coast. These contrasting results likely reflect: 1) differences in population size; 2) differences in connectivity between regions (physical and environmental); and 3) differences in colonisation history of the different regions. Further, multiple hotspots (i.e. areas with high genetic diversity or unique variants) were identified at particular sites for coral and seagrass (e.g. West Montalivet for *I. brueggemanni* and Bedford Island south for *H. ovalis*), and these are discussed further in the specific taxon reports.

4.8 Cryptic genetic diversity exists in the broadcast spawning coral

Four genetically distinct, but morphologically cryptic, genetic lineages were detected in the *A. aspera* collection (Report 1.1.3.1), strongly suggesting that these lineages are reproductively isolated, even though they look the same and live side by side, and thus likely represent unique evolutionary significant units and/or unrecognised species.

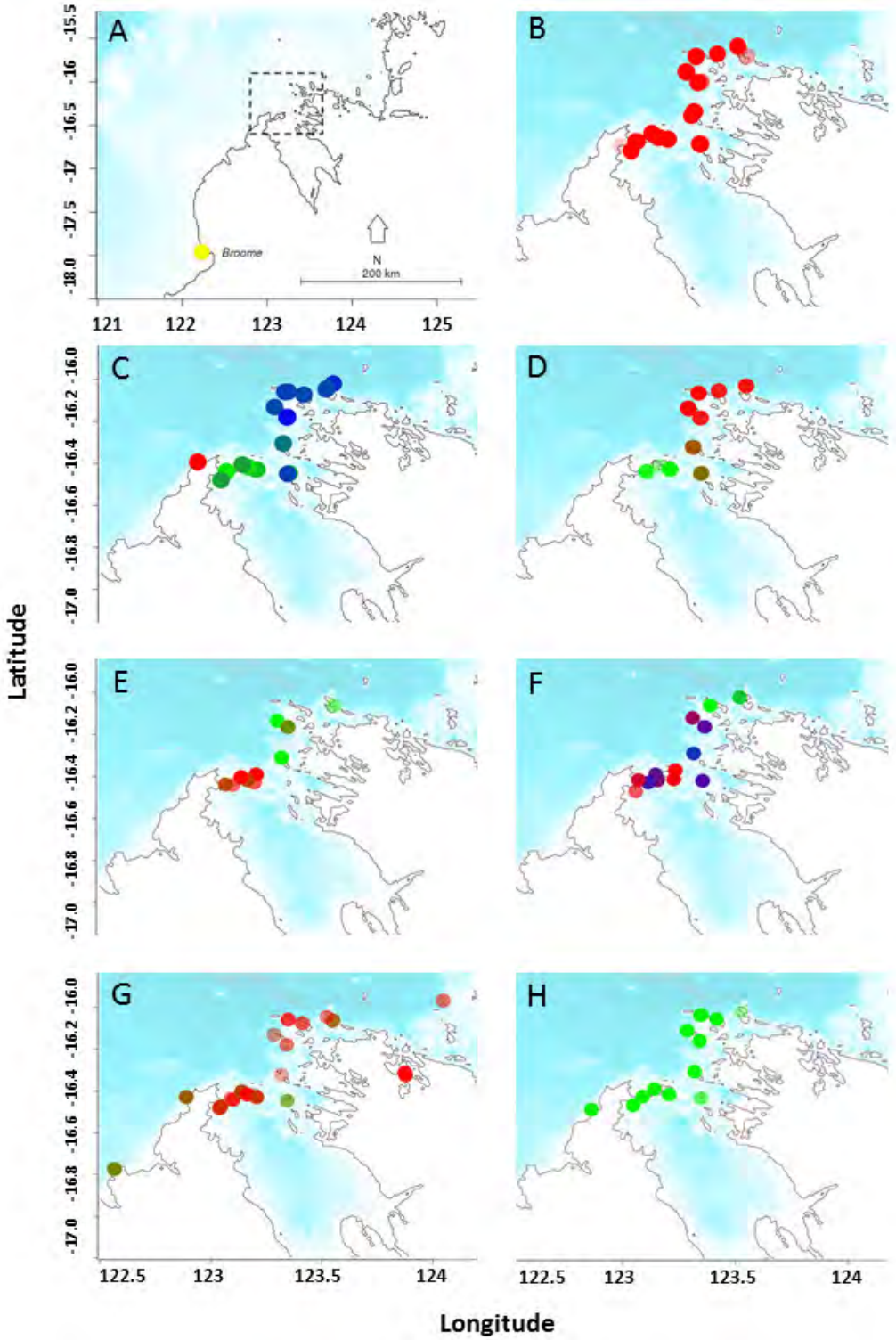

Figure 6. Population structuring within the southern Kimberley. A) The region where fine-scale analysis was conducted; B) A single interconnected population exists for the harvested mollusc *T. niloticus*; C) Three population clusters were evident in the brooding coral *Isopora brueggemanni*; D) Two population clusters were evident in the broadcast spawning coral *Acropora aspera* but zones of admixture occurred in Sunday Strait; E) Two population clusters were evident in the seagrass *Halophila ovalis*; F) Three population clusters were detected for *Thalassia hemprichii*; G) Two population clusters were evident in the pelagic spawning fish *L. carponotatus* but one transitioned to the other across the study region; H) A single population was detected for the demersal nesting reef fish *P. milleri*.

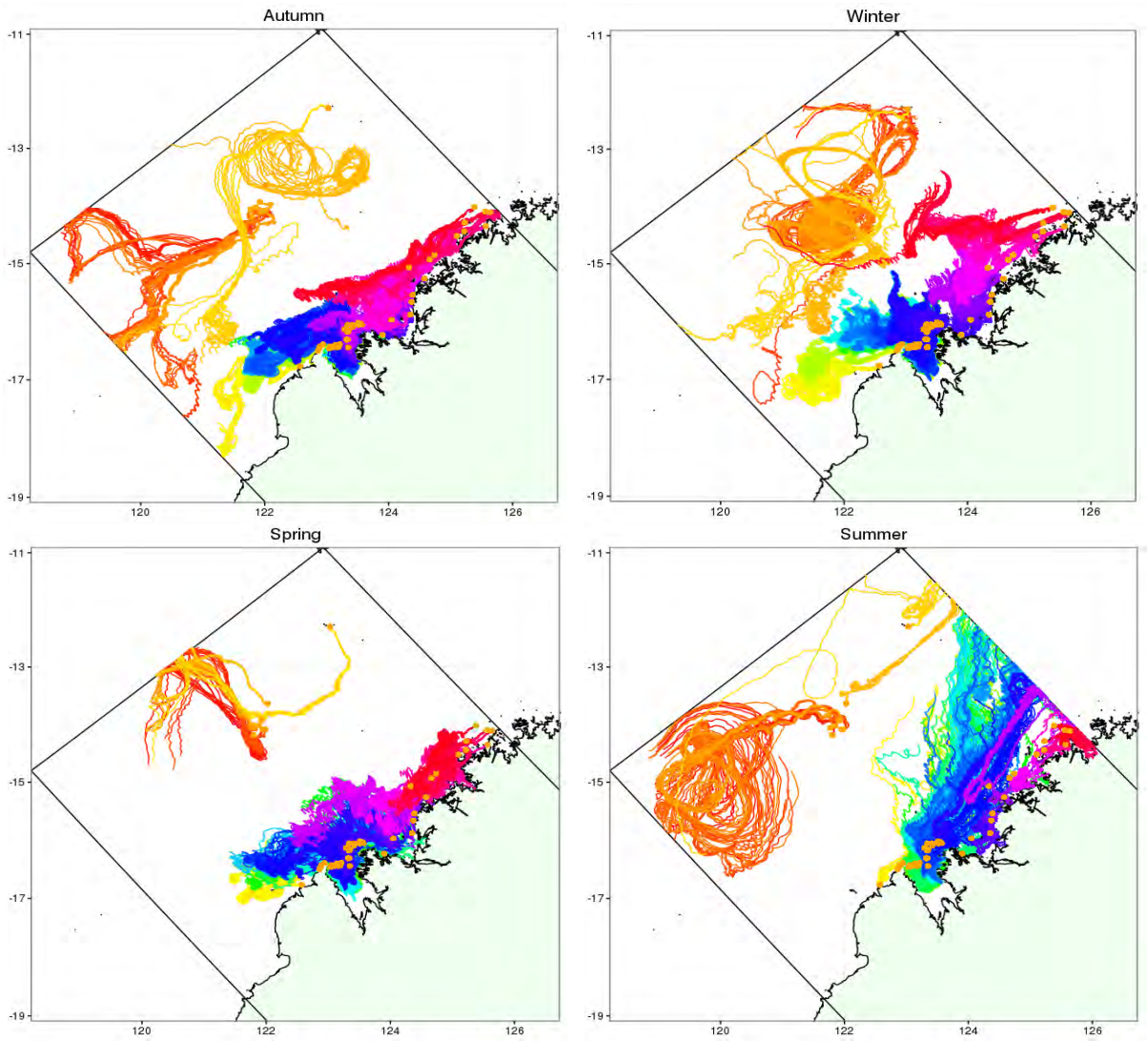

Figure 7. Seasonal particle tracking plots. Indicated are the modelled particle trajectories for passive particles based on 40 days pelagic larval duration. Orange circles represent sampling sites, with particles from each site designated by a unique colour. Data courtesy of Ming Feng (CSIRO; WAMSI Kimberley Project 2.2.7), and plots courtesy Dirk Slawinski (CSIRO).

5 Overarching Implications for Management

This research has highlighted commonalities and disparities in patterns of connectivity among taxa representing a range of trophic levels and life histories. Many of these findings have important implications for management of Kimberley marine ecosystems. Threats to these ecosystems include local anthropogenic impacts such as overfishing, tourism, industrial development and oil spills, as well as the impacts of climate change, which operates over broader spatial scales and longer time-frames. The resilience of marine ecosystems to these threats depends critically on how they affect ecological processes such as connectivity, which promote population persistence and regeneration. Management strategies that protect healthy sources of recruits and maintain the exchange of adaptive genes will nurture resilience in marine ecosystems. To this end, below we summarise how the patterns of connectivity identified in this project would best inform management of Kimberley marine ecosystems. Following this, we provide answers to the original questions posed in the KMRP Agreement for the Ecological Connectivity 1.1.3 project (Appendix 1):

1. **To protect hard corals, the crucial habitat forming organisms of coral reef ecosystems and also seagrass, an important food source for dugongs and turtle, and a nursery habitat for fishes, marine protected areas and indigenous protected areas need to incorporate strategies that account for the spatial dispersal of these organisms.** Protected areas that are large enough to encompass routine dispersal distances of corals (10–20 km), and are spaced at similar distances, will not only maintain self-replenishment, but also aid recovery after disturbance through connectivity between protected areas.

2. **Corals and seagrasses of Buccaneer Archipelago and Dampier Peninsula need to be managed as demographically independent populations**. Furthermore, negligible exchange between the inshore Kimberley and the offshore coral reefs and neighbouring bioregions means that populations of the inshore Kimberley are reliant on standing genetic variation as the basis of adaptation to climate change or other disturbances.

3. **Current estimates of species diversity in corals are likely to be substantial underestimates**. The cryptic *Acropora* coral lineages detected here reveal that current assessments of the diversity of hard coral species in the Kimberley are likely substantial underestimates and further integrated taxonomic research is needed to clarify species diversity patterns in all taxon groups.

4. **Management of *T. niloticus* on the Dampier Peninsula and Buccaneer Archipelago should treat the region as being effectively a single stock on the ecological timeframes relevant to harvest management.** Over-harvested sites within this region will be replenished with recruits from neighbouring sites within years, assuming they exist, and allowing for the slow growth of the species.

5. **Management of *T. niloticus* at offshore oceanic reefs should treat each oceanic shoal as being effectively isolated on the ecological timeframes relevant to harvest management.** Recruitment from outside will not replenish over-harvested stocks at these locations. Occasional recruits may be drawn from other offshore shoals, but will contribute to genetic diversity not offset over-harvest. Supplementation of populations should recognise that coastal *T. niloticus* populations may be mal-adapted to oceanic conditions.

6. **The Kimberley and Pilbara bioregions exchange few recruits in seagrasses and reef-obligate damselfishes, and therefore operate largely independently on the ecological timeframes relevant to management.**

7. **Demographic exchange between the Kimberley and Pilbara/Canning bioregions in the harvested stripey snapper, *L. carponotatus*, occurs in a broad transition zone located near the Sunday Strait. *The distinctiveness of the Shark Bay L. carponotatus samples from all other bioregions indicates that the Gascoyne management boundary is not supported because sites north of Shark Bay have greater affinities to sites in the Pilbara Bioregion.* This information should be considered within management arrangements.**

8. **Genetic differentiation between samples of *L. carponotatus* from the Kimberley and Northern Territory may represent limited demographic exchange between these separately-managed stocks, but to be confirmed this requires further samples from the intermediate region.**

6 Outcomes and Benefits

This project provides the first estimates of ecological connectivity for a range of animals and plants in the Kimberley marine bioregion. This data set indicates the region is largely demographically and genetically independent from neighbouring bioregions, but further research is needed to examine the relationships with the central and northern Kimberley and the broader biogeographic relationships with Indonesia. New empirical data generated in this project can be considered in the design of marine protected areas especially in the size required to protect self-sustaining populations. The new information also informs management of fishery stocks and will benefit future risk assessments for numerous species of high interest to state management agencies (Department of Parks and Wildlife, Department of Fisheries [WA]) because of their habitat-forming nature and/or commercial and indigenous harvest.

This project has also improved links and collaboration in marine science between State and Commonwealth agencies, universities, industry and indigenous rangers and communities (Bardi Jawi and Mayala) in Western Australia. The approach used in this project can serve as a template for investigating ecological connectivity in other bioregions throughout Western Australia (e.g. Pilbara), while the results can form the basis for developing hypotheses about levels of connectivity in other bioregions.

7 Conclusion

Population "connectivity" depends on the magnitude of immigration and migration within and between populations and has the potential to profoundly influence the resilience of communities to natural and anthropogenic disturbances. When coupled with the distribution of biological communities, patterns of connectivity provide meaningful justification for marine protected area design and other resource management decisions.

Results of this study suggest for all taxa examined (with the exception of *T. niloticus*) movement and gene flow in the southern Kimberley is limited to scales of less than ~ 20km. There are important hotspots of genetic diversity along with transition zones which act as conduits of gene flow and dispersal between otherwise isolated reefs. The macro-tidal conditions experienced in the Dampier Peninsula – Buccaneer Archipelago are largely a barrier to the immigration of larvae from outside the Kimberley bioregion and in the case of *A. aspera* may have led to a high level of cryptic speciation. Moreover the Kimberley bioregion and some areas within it is largely a demographically independent system, requiring targeted management to safeguard its unique marine resources.

By delivering the first region-specific and multi-species assessment of connectivity we have provided an empirical basis for planning and managing the regional network of Kimberley marine parks and reserves, and significantly improved the knowledge base for environmental planning and impact and risk assessments by other groups.

8 References

D'Adamo ND, Fandry C, Buchan S, Domingues C (2009) Northern sources of the Leeuwin Current and the 'Holloway Current' on the North West Shelf. Journal of the Royal Society of Western Australia 92, 53-66.

D.E.P. (2016) Marine. http://www.environment.gov.au/topics/marine

D.P.a.W. (2016) Marine Environment. https://www.dpaw.wa.gov.au/management/marine/

Domingues CM, Maltrud ME, Wijffels SE, Church JA, Tomczak M (2007) Simulated Lagrangian pathways between the Leeuwin Current System and the upper-ocean circulation of the southeast Indian Ocean. Deep-Sea Research Part II -Topical Studies in Oceanography 54, 797-817.

James MK, Armsworth PR, Mason LB, Bode L (2002) The structure of reef fish metapopulations: modelling larval dispersal and retention patterns. Proceedings of the Royal Society B-Biological Sciences 269, 2079-2086.

Jones D, Bryce C, J F, G M (2014) Marine Biodiversity of the Kimberley 1880s-2009. In: Records of the Western Australian Museum.

Kendrick GA, Wilkinson SP, Friedman K, et al. (2016) Strategic marine ecological research priorities for CALM Act marine parks and reserves 2016–2021. Conservation Science of Western Australia 10.

Lowe WH, Allendorf FW (2010) What can genetics tell us about population connectivity? Molecular Ecology 19, 3038-3051.

Magris RA, Pressey RL, Weeks R, Ban NC (2014) Integrating connectivity and climate change into marine conservation planning. Biological Conservation 170, 207-221.

Ovenden JR, Berry O, Welch DJ, Buckworth RC, Dichmont CM (2015) Ocean's eleven: a critical evaluation of the role of population, evolutionary and molecular genetics in the management of wild fisheries. Fish and Fisheries 16, 125-159.

Radford B, Babcock R, Van Niel K, Done T (2014) Are cyclones agents for connectivity between reefs? Journal of Biogeography 41, 1367-1378.

Richards ZT, Garcia RA, Wallace CC, Rosser NL, Muir PR (2015) A Diverse Assemblage of Reef Corals Thriving in a Dynamic Intertidal Reef Setting (Bonaparte Archipelago, Kimberley, Australia). Plos One 10(2): e0117791.

Schiller A (2011) Ocean circulation on the North Australian Shelf. Continental Shelf Research 31, 1087-1095.

Sprintall J, Wijffels S, Chereskin T, Bray N (2002) The JADE and WOCE I10/IR6 Throughflow sections in the southeast Indian Ocean. Part 2: velocity and transports. Deep-Sea Research Part Ii-Topical Studies In Oceanography 49, 1363-1389.

Travers MJ, Potter IC, Clarke KR, Newman SJ (2012) Relationships between latitude and environmental conditions and the species richness, abundance and composition of tropical fish assemblages over soft substrata. Marine Ecology Progress Series 446, 221-241.

Underwood JN, Wilson SK, Ludgerus L, Evans RD (2013) Integrating connectivity science and spatial conservation management of coral reefs in northwest Australia. Journal for Nature Conservation 21, 163-172.

Wilson B (2013) Biogeography of the Australian North West Shelf: Environmental Change and Life's Response Elsevier.