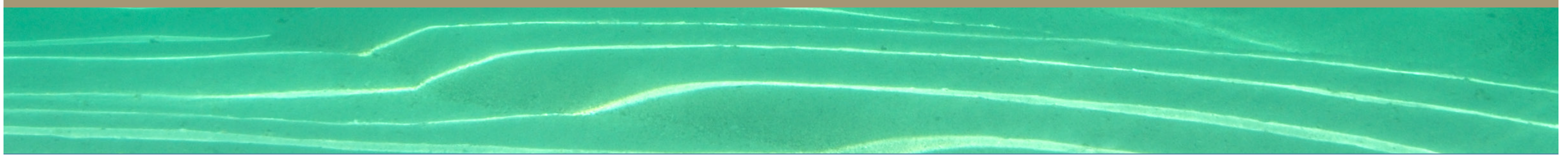
Kimberley Marine Research Program

WAMSI Project 1.1.3



Ecological Connectivity of Kimberley Marine Communities

A multidisciplinary team of researchers has been undertaking work to provide the first estimates of ecological connectivity across multiple spatial scales for a suite of marine organisms in the Kimberley. An understanding of ecological connectivity within marine systems is fundamental to the design of effective management strategies, such as marine protected areas and the identification of fishery stocks. In practice, connectivity is spatio-temporally complex and detailed studies across multiple scales are needed to begin to understand the way biogeography, life-history and environment interact in individual taxa. The Kimberley provides a new frontier for connectivity studies because of the unique tidal regime and often harsh environmental conditions. Until now, it has been unclear how such a unique hydrodynamic regime influences dispersal of marine larvae in the Kimberley.

Background

When populations of animals or plants exchange individuals their fates become linked. Linkages of this kind are often referred to by scientists as "ecological connectivity".

Depending on its magnitude, ecological connectivity has the potential to profoundly influence the resilience of communities to natural and anthropogenic disturbances.

Reproduction and recruitment underlie the maintenance of biological communities. For most marine organisms the ocean environment provides the potential for widespread dispersal via currents, tides and wind,

Within the Kimberley region, key biological communities have a range of reproductive modes. Some species operate as closed demographic units on small spatial scales (e.g. few kilometres). For these populations, variation in adult stocks has direct consequences for local recruitment and population maintenance.

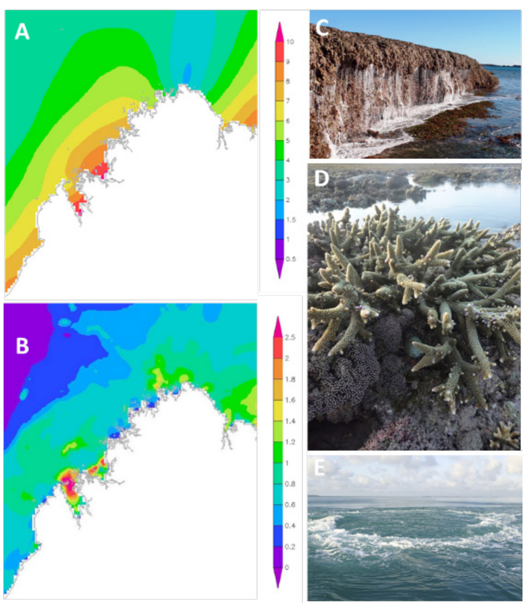


Figure 1. The dynamic Kimberley environment. A. Mean tidal range (m); B. Mean tidal current speed (m/s); C. Tallon (Jalan) Island Cascades at low tide; D. Acropora aspera exposed at low tide (Photo C & D: Zoe Richards); E. Large eddie formed by the fast flowing outgoing tide in the Buccaneer Archipelago.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

In contrast, other populations are open at these scales. For open populations, dispersal distances can range to hundreds of kilometres, and the distance and direction of dispersal is influenced by a complex combination of physical conditions and larval ecology. Understanding these patterns of larval connectivity is critical to managing the exposure of biological communities to disturbances in space and time.

This project provides the first comprehensive understanding of spatial ecology in Kimberley marine taxa.

Research Objectives

A team of researchers from CSIRO, the Australian Institute of Marine Science (AIMS), Department of Fisheries (DoF), Curtin University, Edith Cowan University and the WA Museum have been working in collaboration to infer the routine distances of dispersal and patterns of connectivity among key populations within the Kimberley.

***Figure 2.** The seven organisms chosen to explore connectivity in the Kimberley including details on their major functional role, life history, and null hypothesis of the expected scale of dispersal in target species. PLD = Pelagic larval duration and refers to the average period of larval competency.*

Objectives of the research project focussed on providing species- specific estimates of connectivity (reef scale; inter-reef and inter-region) through genetic analyses of key taxa with contrasting dispersive life histories but which are representative of Kimberley marine communities

The Approach

Seven organisms (two hard corals, two seagrasses, a mollusc, 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:

- important habitat forming species;
- harvested species; or
- 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 result in their larvae being differently exposed to hydrodynamic processes.

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. Genetic analyses is a widely used “indirect” method for inferring ecological connectivity. One advantage of genetic analysis is that it provides an estimate of connectivity averaged over multiple generations.

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Work was divided into two areas of investigation, fine scale and broad scale studies.

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.

The waters surrounding the northern tip of the Dampier Peninsular have been suggested to represent a barrier to the dispersal of fish, possibly due to the very high turbidity and tidal currents occurring in Sunday Strait.

Broad Scale Study

Samples for genetic analysis were collected opportunistically at an additional 67 sites through collaboration with other WAMSI projects, and /or with other research programs. Thes samples came from as far as the Northern Territory, to Shark Bay, to offshore reefs on the edge of the continental shelf.

Genetic Analyses

Samples obtained from 5009 individuals from a total of 157 sites were genotyped using either microsatellite DNA markers (seagrass) or single nucleotide polymorphism DNA markers (SNPs) (corals, mollusc, fishes). 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 populations.

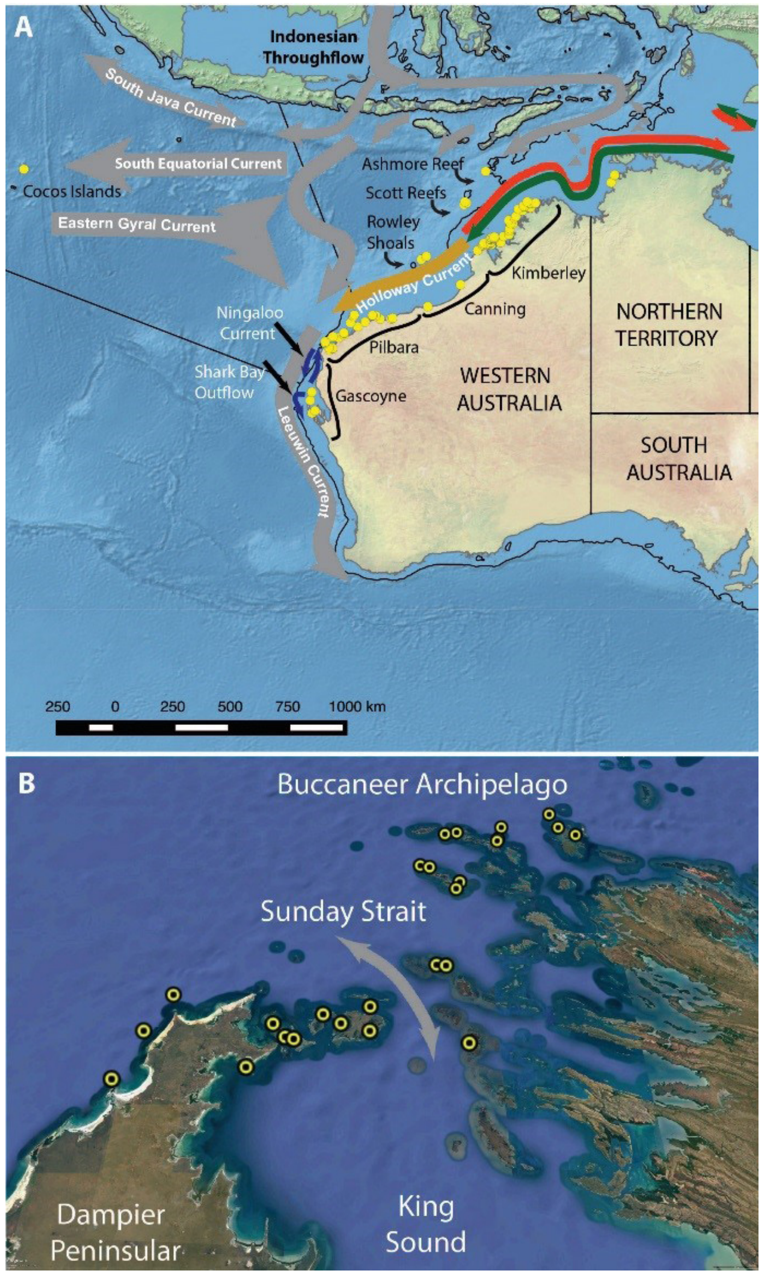
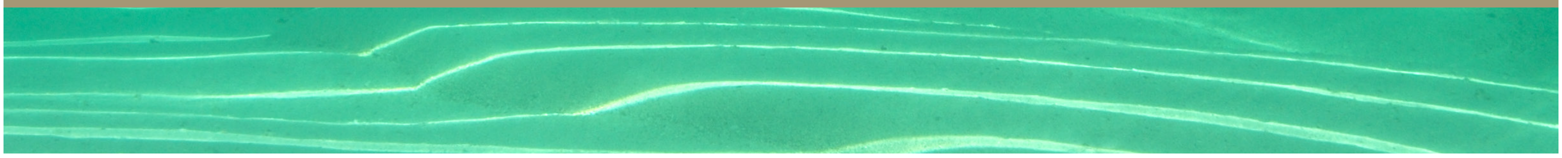


Figure 3. Map of the study sites where genetic samples were collected in A) The broad scale study, and B) The fine scale study. Depicted on panel A are the major surface currents in the Indo-Australian region. Red, green and amber coloured lines indicate flow direction in summer, winter and autumn, respectively.



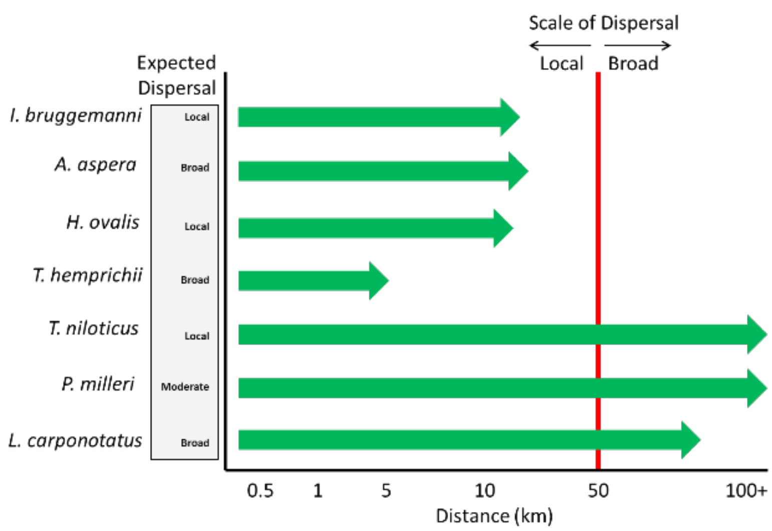


Figure 4. Expected and realised scale of connectivity of focal species in the Dampier Peninsula and Buccaneer Archipelago. The maximum detectable scale of genetic structure (green arrow) is based on spatial autocorrelation analyses and the genetic correlation coefficient (r) between individuals.

Coupled with the finding of a highly divergent population of *I. bruggemanni* on the western side of Dampier Peninsula, these results reinforce that the tip of Dampier Peninsula constitutes an important faunal break for some marine taxa

Broad scale: Little connectivity exists between the inshore and offshore Kimberley

At a broad scale, the inshore Kimberley reef biotas are demographically independent from the offshore 'oceanic' coral reef biotas such as those on Rowley Shoals, Scott Reef and Ashmore Reef (Figure 5.). This likely reflects the limited hydrodynamic connectivity between these reefs.

This is the first time that realised connectivity between coastal Kimberley and offshore reefs has been examined.

Key Findings

Fine scale: spatial scales of connectivity differ between taxa

Habitat forming organisms (coral, seagrass) typically exhibited the most localised population structure, with evidence for limitations to dispersal evident on scales of 10s of kilometres or less. In the remaining organisms (fishes, trochus), population structure was weaker or not detectable, and limits to dispersal were evident on scales of 100+ kilometres (Figure 4). Some of these results were unexpected.

Fine scale patterns: population boundaries are shared between several taxa

Major population divisions were identified in several taxa, notably the habitat-forming corals, and seagrasses, and the pelagic spawning fish, but not the mollusc, nor the damselfish.

Broadly, the divisions in seagrasses, corals and fish were between the Dampier Peninsula and Buccaneer Archipelago sites, but the positions and breadths of the boundaries differed for individual taxa.

Fine scale: Important stepping-stone locations and transition zones exist

Tide Rip, Mermaid and Bedford Islands provide important stepping-stone links of exchange between the Dampier and Buccaneer Archipelago systems for corals and seagrasses.

Fine scale process: King Sound, Sunday Strait and barriers to dispersal

Another significant 'transition zone' was evident in *L. carponotatus* across a distance of <40km at the tip of the Dampier Peninsula in the vicinity of the Sunday Strait.

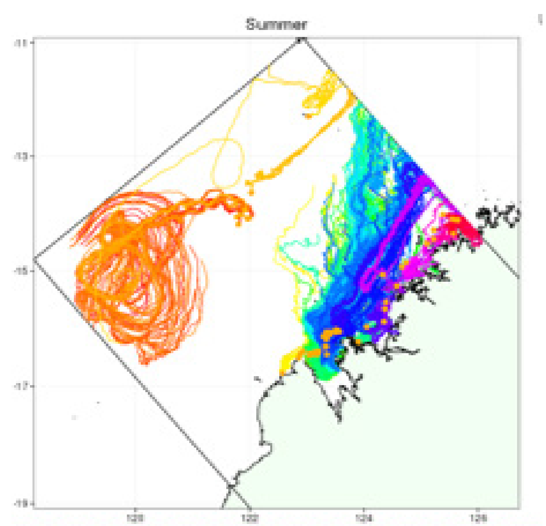


Figure 5. Seasonal particle tracking plots. Indicated are the modelled particle trajectories based on 40 days pelagic larval duration. Colours represent sites. Data courtesy of Ming Feng (CSIRO; WAMSI Kimberley Project 2.2.7), and plots courtesy Dirk Slawinski (CSIRO).

Broad scale: Taxon specific connectivity between the Kimberley and neighbouring bioregions

The species that were sampled across the broader northwest coast of Australia were inconsistent in their broad-scale patterns of connectivity. The seagrass *T. hemprichii* and the damselfish *P. milleri* exhibited a sharp discontinuity between the Kimberley and Pilbara (Figure 6.), indicating negligible exchange.

In contrast, Pilbara and Kimberley populations of *L. carponotatus*, exhibited weak genetic distinctiveness

Broad and fine scale: The distribution of genetic diversity is taxon specific

Within the Dampier Peninsular – Buccaneer Archipelago region, some organisms (corals, seagrasses) exhibited large variation between sites in levels of genetic diversity observed, whereas others (fishes, trochus) typically exhibited similar levels of diversity at each site.

While no specific sites were identified as genetic diversity hotspots (i.e. areas with high genetic diversity and unique variants that represent evolutionary potential and evolutionary novelty within the Kimberley) for either fish species or for *T. niloticus*, multiple sites were identified as genetic diversity hotspots for coral and seagrass.

Cryptic genetic lineages in the broad cast spawning coral

Four genetically distinct, but morphologically cryptic, genetic lineages living side by side were detected in the coral *A. aspera*, strongly suggesting that they represent new species.

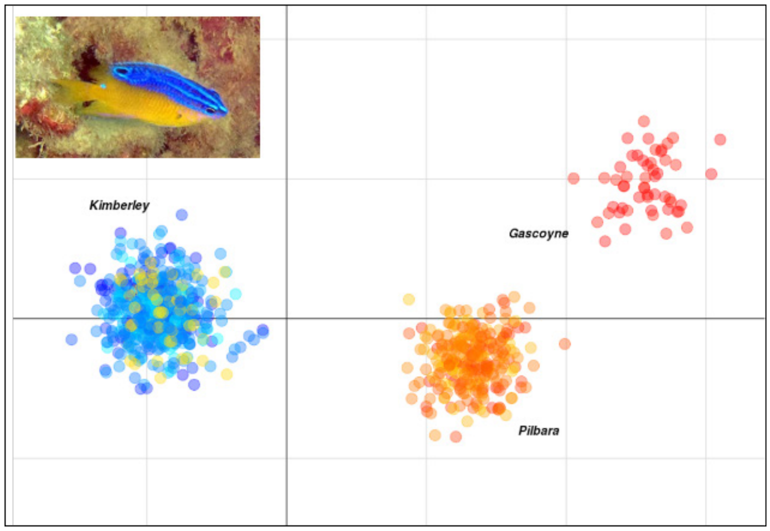


Figure 6. Discriminant analysis of principle components for the damselfish Pomacentrus milleri illustrating the genetic distinction, and hence demographic independence of bioregions.

Management Implications

1. To protect hard corals and seagrasses marine protected areas and Indigenous protected areas need to incorporate networks of sanctuaries that are separated by less 20 to 30 kilometres.
2. Corals and seagrasses of Buccaneer Archipelago and Dampier Peninsula need to be managed as demographically independent populations that exchange evolutionary important genes.
3. Current estimates of species diversity in corals in the Kimberley are likely to be substantial underestimates.
4. Management of trochus on the Dampier Peninsular and Buccaneer Archipelago should treat the region as being effectively a single stock on the ecological timeframes relevant to harvest management.
5. Management of trochus at offshore oceanic reefs should treat each group of oceanic reefs as being effectively isolated on the ecological timeframes relevant to harvest management.
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 bioregions in the harvested stripey snapper, *L. carponotatus*, occurs in a broad transition zone located near the Sunday Strait. *L. carponotatus* from Gascoyne bioregion represents an independent stock.
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.

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Future Work

Considering this study was conducted primarily on samples collected from the macro-tidal western Kimberley, additional data from the less tidal central and northern Kimberley would reveal whether the scales of connectivity identified here apply to other parts of the region.

The high level of cryptic diversity revealed in *A. aspera* indicates that current estimates of species diversity in hard corals may be substantial underestimates. Further taxonomic work is required to substantiate this.

Who will use this information?

Assessing the significance of environmental impacts of varying scales and severity requires an understanding of the patterns of larval connectivity for key taxa.

The results of this study provide information of direct relevance to management. Connectivity within and between marine reserves is a significant consideration in managing the resilience of coral reef communities and the Commonwealth Government's approach to the design of marine reserves.

Considering that no spatial studies have previously been undertaken in the Kimberley, and that understanding connectivity is critical to the efficient management of marine assets, this project will provide quality data with applied benefits.

Information generated as part of this research will also be of relevance to the Kimberley Science and Conservation Strategy, and the proposed Great Kimberley Marine Park network which includes Lalang-garram/Camden Sound Marine park and the proposed Lalang-garram / Horizontal Falls Marine Park.

Figure 7. Azden Howard (Bardi-Jawi Rangers) and Jim Underwood during fieldwork on Sunday Island.

Type of data collected

Data generated as part of this research includes tissue samples collected by hand during reef walking, snorkeling and fish trapping; microsatellites genotyped by fragment length analysis; SNPs genotyped via DartSeq genotype-by-sequencing. Genotypes have been generated from seven marine organisms:

1. *Tectus niloticus* - gastropod
2. *Pomacentrus milleri* - fish
3. *Lutjanus carponotatus* - fish
4. *Halophila ovalis* - seagrass
5. *Thalassia hemprichii* - seagrass
6. *Isopora brueggmanni* - coral
7. *Acropora aspera* - coral

Data available in:

All metadata is publically available via the CSIRO, AIMS and Pawsey data access portals.

Project Team

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Figure 8. Oliver Berry and Trevor Sampi (Bardi Jawi Rangers) undertaking field work from One Arm Point.

western australian
marine science institution

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