



Population connectivity and genetic diversity in brooding and broadcast spawning corals in the Kimberley

Jim Underwood^{1,5}, Zoe Richards^{2,3,5}, Oliver Berry^{4,5}, James Gilmour^{1,5}

¹Australian Institute of Marine Science, Townsville, Queensland

²Western Australian Museum, Perth, Western Australia

³Curtin University, Bentley, Western Australia

⁴CSIRO, Crawley, Western Australia

⁵Western Australian Marine Science Institution, Perth, Western Australia

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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.

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Front cover images (L-R)

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

Image 2: Pink *Seriatopora hystrix* nestled into *Isopora brueggemanni*; both brooding corals from the intertidal zone of Longitude Island in the Buccaneer Archipelago. (Image: Jim Underwood)

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

Image 4: *Isopora brueggemanni*, a brooding reef-builder in the intertidal zone of Irvine Island. (Image: Jim Underwood)

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Corresponding author and Institution: Oliver Berry, CSIRO Oceans and Atmosphere. oliver.berry@csiro.au

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Executive Summary

This study utilised next generation sequencing to explore patterns of ecological connectivity and genetic diversity among populations of two species of staghorn coral in the Kimberley; the brooding *Isopora brueggemanni* and broadcast spawning *Acropora aspera*. These two species display the common reproductive modes in hard corals which create the crucial three dimensional structures that provide the habitat and protection that is the foundation of coral reef ecosystems. Both species are listed as “vulnerable” on the IUCN Red List of Threatened Species based on the general estimates of reef degradation within their range as well as their inherent susceptibility to bleaching and disease.

Samples of *I. brueggemanni* (n=612) and *A. aspera* (n=563) were collected across three hierarchical spatial scales. At broad (inter-regional) scales, sites were separated by 100s of kilometres and included the offshore site of Ashmore Reef, as well as inshore reefs of the Bonaparte Archipelago in the central Kimberley, and the Buccaneer Archipelago and Dampier Peninsula in the southern Kimberley. At the intermediate (inter-reef) scale, detailed sampling was undertaken at the Buccaneer Archipelago and Dampier Peninsular, where multiple sites were separated by distances of kilometres to tens of kilometres. At the local (within-reef) scale, sampling allowed for estimates of genetic structure over distances of tens to 100s of metres. Analyses revealed considerable genetic structure within both species at all three scales.

For the brooder, *I. brueggemanni*, 2,125 SNPs revealed three discrete genetic clusters over broad scales; Ashmore Reef in the north, Kooljaman in the far west of the Dampier Peninsula, and the southern inshore Kimberley. At the intermediate scale, the observed level of genetic structure in *I. brueggemanni* indicated that connectivity over more than 20 km is generally rare. More specifically, Dampier and Buccaneer corals formed two genetic groups, but with geographically intermediate Islands of Mermaid and Tide Rip sharing genetic affinities with both groups. Therefore, these two islands appear to be important stepping stones for maintaining occasional connectivity and genetic exchange across the Sunday Strait. At fine scales, significant differentiation was detected between subsites, and colonies separated by less than 500 metres were more closely related than those further apart, indicating that most brooded larvae recruit within a few hundred metres of their natal colony. A general attenuation of gene diversity was detected with increasing latitude, indicating that effective population sizes are larger, and genetic connections to exogenous sources are stronger, in populations in the central region compared with those in the south.

For the broadcast spawner, initial genetic analysis of the entire *A. aspera* collection using a subset of SNPs revealed the presence of four lineages that were genetically distinct but morphologically cryptic. The large magnitude of genetic differentiation among these lineages indicated these lineages are reproductively isolated, even though they look the same and live side by side. The subsequent analyses of population connectivity used 2,894 SNPs to focus on the most abundant and widespread lineage, *Acropora asp-c* (n = 322). Consistent with a greater propensity for widespread dispersal in the broadcast spawned larvae compared with the brooded larvae, the overall amount of genetic subdivision in the *Acropora asp-c* lineage ($F_{ST} = 0.101$) was half that of *I. brueggemanni* ($F_{ST} = 0.230$). Nevertheless, the pattern of geographic structure evident in *Acropora asp-c* was similar to *I. brueggemanni*, with four discrete genetic clusters detected over broad scales among Ashmore Reef, central Kimberley, Buccaneer Archipelago and Dampier Peninsula. At intermediate scales, genetic patterns in *Acropora asp-c* corals also matched those found in *I. brueggemanni*; spawned larvae rarely disperse more than 35 km while corals from Tide Rip and Mermaid Islands exhibited affinities to both the Dampier and Buccaneer clusters. Lastly, at fine scales, relatedness was relatively high among corals separated by less than 500 metres, indicating that many spawned larvae recruit back to their natal reef patch. Levels of gene diversity within the *Acropora asp-c* lineage appeared to be greater in the central Buccaneer Archipelago, and attenuated to west and east from this centre, suggesting that these are the largest and most well connected populations of this species in the region.

The oceanographic model supported the broad scale genetic patterns, with no evidence of any inter-regional connectivity via ocean currents between the offshore and inshore reefs. However, a more biologically realistic oceanographic model is required to properly capture the complex fine-scale hydrodynamics in this region.

Implications for management

The key finding from this study is that ecological connectivity among populations of both the brooding coral and broadcast spawning coral is restricted to the scale of reef or reef patch, with few larvae dispersing more than 35 kilometres from their natal reef patch. This finding has important ramifications for the managers, policy makers and custodians of coral reefs of the Kimberley. Specifically, it implies that locally produced recruits are crucial to the persistence of coral populations, and recovery after disturbance will rarely be supplemented through the input of larvae from locations that are more than a few tens of kilometres away. Therefore, if the intention of Marine Protected Areas (MPA's) and Indigenous Protected Areas (IPA's) is to protect hard corals, they must consider the importance of local recruitment for population maintenance, recovery and adaptation to environmental change by ensuring the maintenance of connectivity networks among reef patches by positioning multiple sanctuaries over scales of less than a few tens of kilometres.

Further specific management considerations include:

- Exchange of genes between the inshore Kimberley and the offshore coral reefs is negligible meaning that inshore populations will rely on maintenance of standing genetic variation to recover from and adapt to natural and anthropogenic impacts.
- The Dampier Peninsula and Buccaneer Archipelago need to be managed as demographically independent systems, with the important consideration that Tide Rip and Mermaid Islands provide stepping stones of genetic exchange that likely augments population resilience and adaptation over multiple generations.
- For the brooding coral, the west coast of Dampier Peninsula appears to support a small, isolated, and genetically unique population that is demographically independent from populations east of the Dampier Peninsula.
- The high genetic diversity at the central Kimberley site of West Montalivet in the Bonaparte Archipelago indicates that these reefs are important reservoirs of genetic variation and have strong connections with other populations, making them priorities for conservation.
- The discovery of four genetically divergent lineages within *Acropora aspera* means that morphological assessments of biodiversity of hard corals in the Kimberley are likely substantial underestimates. Additionally, the effective population size of each lineage will be much smaller, and consequently more vulnerable to disturbance, than expected if assessments are based on distribution of the single morphospecies.

The details of this report are currently subject to a journal publication process. For more information contact the author: Dr Jim Underwood, Australian Institute of Marine Science J.Underwood@aims.gov.au.