



Genomic Connectivity in a Tropical Reef Fish from the Kimberley, Pilbara and Gascoyne Bioregions of Western Australia

Oliver Berry^{1,6}, Mike Travers^{2,6}, Richard Evans^{3,6}, Glenn Moore^{4,6}, Udhi Hernawan^{5,6}

¹CSIRO Oceans and Atmosphere, Crawley, Western Australia

²Fisheries Division, Department for Primary Industries and Regional Development, Hillarys, Western Australia

³Department of Biodiversity, Conservation and Attractions, Kensington, Western Australia

⁴Western Australian Museum, Perth, Western Australia

⁵Edith Cowan University, Joondalup, Western Australia

⁶Western Australian Marine Science Institution, Perth, Western Australia

WAMSI Kimberley Marine Research Program Executive Summary

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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: Mike Travers (Dept Fisheries) collects samples from the damselfish *Pomacentrus milleri* on a reef platform at Sunday Island in the Kimberley (Image: Oliver Berry)

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

Image 4: Juvenile *Pomacentrus milleri* (Image: Western Australian Museum)

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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 sub-report focuses on Miller's damselfish, *Pomacentrus milleri*, which is an obligate reef-dwelling fish endemic to the north-west coast of Australia between Perth and Arnhemland in the Northern Territory.

Pomacentrus milleri was selected as a model because it is ecologically representative of a large group of small coral reef fishes that are abundant throughout tropical Australia and the wider Indo-Pacific. It is also a demersal nester (lays eggs in nests), has a relatively short pelagic larval duration (c. 20 days), and adults permanently reside on reefs. These characteristics suggest that *P. milleri* populations should be highly responsive to local environmental and hydrodynamic conditions, implying lower connectivity between reefs and predominantly short-range recruitment relative to organisms with longer dispersal phases and larger home ranges. However, the unique complexity and power of the Kimberley hydrodynamic environment potentially enlarges the scale of connectivity and/or creates more spatially complex linkages than would be expected elsewhere (Wilson 2013). *Pomacentrus milleri* was also selected as a model because it is moderately common along sub-tropical and tropical parts of the Western Australian coast. This permitted, for the first time in Western Australia, a detailed genomic examination of broad-scale population connectivity in a marine organism.

Samples *P. milleri* individuals were collected from the Dampier Peninsula and Buccaneer Archipelago, and the Bonaparte Archipelago and north Kimberley. In addition, samples from the Pilbara and Gascoyne bioregions¹ were included to provide a regional context for the Kimberley results. We employed a genotype-by-sequencing approach to characterise genetic diversity within and between these sampling sites. Custom bioinformatics pipelines were developed to analyse this large dataset. After quality control filtering, 4,472 single nucleotide polymorphisms (SNPs) were available for analysis.

Broad-scale genetic structure between Kimberley and elsewhere

The three major bioregions sampled (Kimberley, Pilbara, Gascoyne) were all genetically differentiated from each other. The relationships between bioregions followed a strong isolation-by-distance pattern, but with the Pilbara and Gascoyne comparatively more connected to each other than the Kimberley to the Pilbara. This likely reflects the more continuous reef habitat between the Pilbara and Gascoyne. The magnitude of the genetic differentiation observed indicates that *P. milleri* populations from each bioregion exchange few recruits and are effectively demographically independent.

Fine-scale genetic structure within the Kimberley

Some sites sampled within the Dampier Peninsula-Buccaneer Archipelago (≤ 75 km apart) were genetically differentiated from each other, but the magnitude of this differentiation was low. Shenton Bluff, Bowlun (Dampier Peninsula) and Longitude Island (Buccaneer Archipelago) were consistently differentiated from other sites, but most sites were either undifferentiated or weakly differentiated without a clear geographic basis. Sites from the north Kimberley were genetically differentiated from all sites in the Dampier Peninsula-Buccaneer Archipelago region (≤ 400 km apart). Genetic differentiation between sites was largely attributable to distance between sites rather than modelled hydrodynamic connectivity. A signal of relatedness between individuals decayed to c. 350km, indicating the approximate scale of regular demographic exchange. These observations are consistent with movement and gene flow being limited on spatial scales less than hundreds of kilometres.

¹ These samples were made available through collaboration with Richard Evans at the Department of Parks and Wildlife, and historical samples from The Western Australian Department of Fisheries.

The Kimberley is less connected than the Pilbara

The pattern of isolation-by-distance observed in the Kimberley was not replicated within the Pilbara. Only 22% of pairwise comparisons between Pilbara sites were genetically differentiated, whereas in the Kimberley 78% of pairwise comparisons between sites were genetically differentiated. These observations are consistent with more extensive movement occurring between reefs in the Pilbara than the Kimberley.

Evidence for local adaptation

Pomacentrus milleri is subject to directional selection across its sampled range. Adaptation under the influence of directional selection was detected among sites within the Kimberley, but not within the Pilbara. This likely reflects the greater habitat and hydrodynamic variation and complexity in the Kimberley than the Pilbara.

Genetic diversity is highest in the Kimberley

We observed a marked decline in genetic diversity from north to south (Kimberley to Gascoyne). This likely reflects higher densities of *P. milleri* in the north, and potentially a prevailing southwards current leading to asymmetric gene flow southwards.

Implications for Management

- The Kimberley and Pilbara bioregions exchange few recruits and should be considered as largely independent on the ecological timeframes relevant to management.
- With a greater level of genetic diversity, Kimberley populations of *P. milleri*, are likely to be more resilient to environmental and anthropogenic stresses than those in the Pilbara. However, once impacted, the recovery potential of populations in the Kimberley is reduced as a consequence of more restricted movements between reefs. By implication, sanctuary zones in the Kimberley should be more closely spaced than elsewhere in the Pilbara to provide for optimal protection and management of *P. milleri* and similar species.
- Pilbara populations of *P. milleri* are likely to recover from small scale localised impacts through recruitment from other reefs in the Pilbara with which they are highly connected. However, lower genetic diversity in this region means that resilience to impacts may be lower, relative to Kimberley populations.
- Gascoyne populations of *P. milleri* are potentially the most vulnerable among those sampled due to reduced genetic diversity and greater isolation.

Residual knowledge gaps

- *Pomacentrus milleri* is a useful model for small reef-dependent species. However, this study has only examined a fraction of the species' range. *Pomacentrus milleri*'s range extends into the Northern Territory and New Guinea. The extent of connectivity between *P. milleri* in Western Australia and other regions is unknown.
- Although the results presented here have revealed evidence for geographically structured adaptive diversification in *P. milleri*, the specific environmental drivers have not been identified.
- *Pomacentrus milleri* shares a life history with many small reef-dependent fish species. It is anticipated that this would be reflected in comparable population genetic structure in similar species, but this hypothesis requires empirical testing.

Scientific Abstract

Complex ocean currents promote adaptive diversification and lower dispersal in a tropical reef fish from north-western Australia.

Two important goals of biological conservation are to identify regions of high evolutionary novelty, and to manage them at appropriate spatial scales. Characterising these attributes is a technical challenge, particularly in the marine environment where sampling and observation may be difficult. In poorly studied regions, population genomic approaches potentially offer opportunities to simultaneously examine spatial processes as well as contemporary evolutionary diversification. Here we show that a common damselfish from north-western Australia exhibits more spatial genetic structure and greater putative adaptive genetic diversity in a macro-tidal region than a meso-tidal region. Using genome scans consisting of 4,472 SNP loci applied to 847 samples of the damselfish *Pomacentrus milleri*, we detected marked genetic sub-division between the macro-tidal Kimberley bioregion (up to 12 metre tides) and the meso-tidal Pilbara and Gascoyne bioregions (range of spring tides 1-5 metre). Individually, these bioregions also differed in the extent of population sub-division; spatial autocorrelation was detectable over several hundred kilometres in the Kimberley, but undetectable in the Pilbara. This implies, paradoxically, that the substantially stronger currents in the Kimberley promote shorter range dispersal than in the Pilbara, possibly because larval retention zones are created by the region's complex bathymetry, and currents are predominantly tidal rather than along-shore. The Kimberley also exhibited significantly more neutral genetic diversity than the other bioregions, as well as 108 putatively adaptive outlier loci, whereas no outlier loci were detected elsewhere. We conclude that the Kimberley bioregion likely represents an important source of evolutionary novelty in *P. milleri*, and that optimal management of this and similar species would occur on smaller spatial scales than elsewhere in north-western Australia.

Please Note:

The details of this report are currently subject to a journal publication process. For more information contact the author: Dr Oliver Berry, CSIRO Oceans and Atmosphere. oliver.berry@csiro.au