

Project Plan SP 2014-004

Improving the understanding of West Pilbara marine habitats and associated taxa: their connectivity and recovery potential following natural and human induced disturbance

Marine Science

Project Core Team

Supervising Scientist	Richard Evans
Data Custodian	Richard Evans
Site Custodian	Richard Evans

Project status as of Dec. 11, 2019, 3:07 p.m.

Approved and active

Document endorsements and approvals as of Dec. 11, 2019, 3:07 p.m.

Project Team	granted
Program Leader	granted
Directorate	granted
Biometrician	granted
Herbarium Curator	not required
Animal Ethics Committee	not required

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Biodiversity and Conservation Science Program

Marine Science

Departmental Service

Service 6: Conserving Habitats, Species and Communities

Project Staff

Role	Person	Time allocation (FTE)
Supervising Scientist	Richard Evans	0.9
Supervising Scientist	Shaun Wilson	0.05
Supervising Scientist	Margaret Byrne	0.05
Technical Officer	Ryan Douglas	0.25
Research Scientist	Rachel Binks	0.2
Technical Officer	Bronwyn Macdonald	0.05
Technical Officer	Kathy Murray	0.01
Technical Officer	Georgina Pitt	0.01

Related Science Projects

Proposed period of the project

Jan. 7, 2014 – None

Relevance and Outcomes

Background

Disturbance is part of evolutionary history for many organisms, particularly marine organisms. The amount of connectivity between marine populations has important implications for metapopulation resilience to natural and human disturbances^{1,2}. High connectivity within marine metapopulations suggests resilience to localised impacts through the immigration of new recruits from nearby or distant populations. However, an increased frequency of disturbance cycles may disrupt the typical connectivity regimes, resulting in altered benthic and associated faunal community composition³⁻¹⁰. Extreme warming events in recent years with sea surface temperatures up to 5 °C above long-term averages on the west coast of Australia have shown that benthos and associated fauna are susceptible to thermal damage from abnormally warm sea water¹¹⁻¹³. These effects may be further exacerbated by cyclonic activity^{11,14} and human impacts, including pollution, fishing, coastal development and associated sedimentation through dredging¹⁵. While the scale of natural disturbance due to climate change is still debated, one can confidently say that anthropogenic pressures due to extraction of natural resources have increased significantly over the past decade in the relatively untouched marine environment in north-western Australia. Environmental managers require information on metapopulation resilience through connectivity in order to design and implement appropriate management regimes to maintain ecological processes in the face of increasing human pressure coupled with forecast increase in natural disturbance. Demersal marine species, organisms living on or near the seafloor, are particularly at risk from localised human or natural disturbance as they are unable to flee the pressure exerted upon them. Dispersal by most demersal species is typically achieved through a pelagic larval stage of varying duration, which has the potential to link nearby and

distant populations¹⁶. An understanding of this larval dispersal process was elusive until recent advances in trace-elemental fingerprinting (investigating the presence of geographical differentiation of natural isotopes or manually added isotopes in ear bones of fish or gastropod shells)¹⁷⁻¹⁹ and genetic studies using hypervariable markers¹⁶. These techniques have shown that 1) self-recruitment to the natal reef is common, 2) typical dispersal is within the range of tens of km, and 3) minimal dispersal events over 100's of km maintain the observed genetic homogeneity between distant marine metapopulations. These findings are supported by contemporary 3-dimensional oceanographic modelling where dispersal kernels estimate similar modal ranges with episodic long tails^{20,21}. The majority of broadscale genetic studies, using a range of neutral markers, also reflect the open nature of the marine environment where low levels of genetic structure are attributed to few migration barriers²². However, significant genetic variation has still been found in populations ranging from oceanic scale²³ to tens of km²⁴. Environmental heterogeneity also exerts selection pressure that varies in space and time and provides opportunity for local adaptation between populations^{25,26}. Population genomics is the study of genome-wide variation at the population level, which is not a new concept, but has only recently become a widely-accessible and cost-effective tool for studying evolutionary processes relevant to conservation and ecological genetics. More traditional molecular markers used in population genetics, such as microsatellites, provide valuable data but only capture putatively neutral variation from a very small proportion of the genome^{27,28}. An alternative, genome-wide marker involves single nucleotide polymorphisms (SNPs) and their greatest advantage over more traditional markers is twofold; 1) SNPs are highly abundant across the genome providing much greater resolution of evolutionary processes affecting population demography and phylogenetic history and 2) SNPs are not restricted to neutral regions, such that they can be used to detect effects of selection indicative of adaptive variation, which is of crucial importance in the face of changing climates and increased anthropogenic impacts to natural populations²⁷. Recent advances in next-generation sequencing (NGS) have facilitated the rapid discovery and genotyping of thousands of SNPs scattered throughout the entire genome in a cost-effective manner²⁸⁻³⁰. Most importantly, these techniques can be applied without preliminary knowledge of the genome under study and are widely applicable across taxa^{28,31}. The marine environment in the Pilbara region has received several extreme heating events and several cyclones in the past few years thus decreasing benthic organisms such as coral (up to 84%)¹¹. The shallow shelf reefs of the Onslow region had massive reduction from 50-5% coral cover (Chevron unpublished data). Recently, Gilmour et al⁵⁴ showed that remote atolls with deep refuges recovered within 12 years of a major coral bleaching event at Scott Reef. With few deep water refuges in the Onslow region, recovery potential of these reefs is dependent on the few remaining corals and dispersal from reefs to the west at Ningaloo and Muiron Islands and to the North at Barrow and the Montebello Islands. In addition to major coral loss due to heating, the Onslow region is currently under the influence of a four year dredging operation (Chevron Wheatstone project) which may impact on some of these coral reefs. Future natural and anthropogenic disturbance in this region may also undermine the recovery potential of these coral reefs. As such a study is required to a) determine the levels of genetic connectivity between locations in the Pilbara and investigate any genetic adaptation within the region to understand the ecological relevance of the connectivity, and b) understand the impact of recent natural stresses and conduct a demographic study of the recovery potential of reefs at a smaller scale within the Onslow region using in-situ coral settlement tiles to measure larval supply, in-situ recruit survival and growth, and growth and mortality of adults.

Aims

Expected outcome

Knowledge transfer

Tasks and Milestones

References

Study design

Methodology

Biometrician's Endorsement

granted

Data management

No. specimens

Herbarium Curator's Endorsement

not required

Animal Ethics Committee's Endorsement

not required

Data management

Budget

Consolidated Funds

Source	Year 1	Year 2	Year 3
FTE Scientist			
FTE Technical			
Equipment			
Vehicle			
Travel			
Other			
Total			

External Funds

Source	Year 1	Year 2	Year 3
Salaries, Wages, Overtime			
Overheads			
Equipment			
Vehicle			
Travel			
Other			
Total			