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No-take marine protected areas: abundance, biomass, batch fecundity and genetic connectivity of target species on the Great Barrier Reef

Thesis submitted by Richard D. Evans (BSc) Qld in February 2009

For the degree of Doctor of Philosophy in the School of Marine and Tropical Biology James Cook University

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Statement of Sources

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Declaration on Ethics

The research presented and reported in this thesis was conducted within the guidelines for
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Standard Practices and Guidelines (2001), and the James Cook University Statement and
Guidelines on Research Practice (2001). The proposed research methodology received
clearance from the James Cook University Experimentation Ethics Review Committee
(approval number A1130).

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Statement of contribution of others

I declare that this thesis is my own work, and has been supported by the following oraginsations and people. The research budget was supported by a number of organisations. They include, the ARC Centre of Excellence for Coral Reef Studies, the Australian Government's Marine and Tropical Scientific Research Facility (MTSRF), the Queensland Government's Growing the Smart State PhD Funding, Australian Coral Reef Society Terry Walker Prize 2007, JCU Merit Research Grants, JCU Graduate Research Scheme funding, the Institute of Marine Engineering Research and Technology (Imarest), the Great Barrier Reef Marine Park Authority and the CRC Reef. The research was also funded by Australian Research Council grant and a Merit Research Grant to Garry Russ.

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List of publications arising from this thesis

Chapter 2

- Evans RD, Russ GR (2004). Larger biomass of targeted reef fish in no-take marine reserves on the Great Barrier Reef, Australia. Aquatic Conservation: Mar. Freshw. Ecosyst. 14: 505-519.
- Davis KLF, Russ GR, Williamson DH, Evans RD (2004). Surveillance and poaching on inshore reefs of the Great Barrier Reef Marine Park. Coastal Management 32:373-387.
- Graham NAJ, Evans RD, Russ GR (2003). The effects of marine reserve protection on the trophic relationships of the Great Barrier Reef Marine Park, Australia.
 Environmental Conservation 30(2): 200-208.

Chapter 3

- Russ GR, Cheal AJ, Dolman AM, Emslie MJ, Evans RD, Miller I, Sweatman H,
 Williamson DH (2008). Rapid Increase in Fish Numbers Follows Creation of World's
 Largest Marine Reserve Network. Current Biology 18(12): 514-515.
- Diaz-Pulido G, McCook LJ, Dove S, Berkelmans R, Roff G, Kline DI, Weeks S, Evans RD, Williamson DH, Hoegh-Guldberg O (In review). Doom and Boom on a Resilient Reef: Climate Change, Algal Overgrowth and Coral Recovery. PLoS ONE.

Chapter 4

Evans RD, Kritzer JP, Russ GR (2008). Batch fecundity of *Lutjanus carponotatus* (Lutjanidae) and implications of no-take marine reserves on the Great Barrier Reef, Australia. Coral Reefs 27: 179-189.

Chapter 5

• Evans RD (2008). Assessment of an underwater fish biopsy probe for collecting teleost fish tissue samples. Marine Ecology Progress Series. 368: 305-308.

Chapter 6

 Evans RD, van Herwerden, L, Frisch AJ, Russ GR (In review.). Strong genetic but not spatial subdivision of two reef fish species on the Great Barrier Reef. Fisheries Research.

Publications in preparation

- Almany GR, Evans RD, Hamilton RJ, Jones GP, Matawai M, Potuku T, Rhodes KL,
 Russ GR, Sawynok B, Williamson DH (In prep.) Getting fishers involved in marine
 protected area research: two case studies from Papua New Guinea and Australia.
- Berumen ML, Evans RD, Fauvelot C, Heredia P, Hogan D, Moland E, Williamson DH
 (In prep.) Understanding Larval Connectivity in Coral Reef Systems: Questions and
 Ways to Answers.
- Evans RD, Williamson DH, Russ GR (In prep.). Temporal investigation of the nature of predator prey relationships.

Proposed publications

- Evans RD, Williamson DH, Russ GR. Effect of marine reserve protection on smaller serranid species relative to the major serranid, *Plectropomus* spp.
- Evans RD, Williamson DH, Russ GR. Effect of coral bleaching on the fish community inside and outside no-take marine protected areas.
- Harrison H, Evans RD, van Herwerden L, Jones GP, Williamson DH. Assessing the temporal genetic variation in the recruitment of target species
- Williamson DH, Evans RD, Russ GR. BACIP sampling design studying the density patterns of newly protected species, *Cheilinus undulatus* and *Cromileptes altivelis*.
- Williamson DH, Evans RD, Russ GR. Comparison of three techniques to assess populations of species targeted by hook and line fisheries.

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I dedicate this work to Tuva.

Abstract

The aim of this thesis was to understand the effects of no-take marine protected areas (MPAs) on fish and corals on the inshore reefs of the Great Barrier Reef (GBR), Australia. The study focused on the principal fishery target species, the coral trout (*Plectropomus* spp.) and a secondary target, the stripey snapper (*Lutjanus carponotatus*). The investigation of effects of no-take marine protected areas (MPAs) on the GBR was of particular significance to management during the course of this study, since the amount of no-take protection in the GBR Marine Park (GBRMP) increased from 4.5% to 33.4% in 2004. This study investigated both the effect of the original (established mid 1980's) and the new (established 2004) MPAs on the density, biomass and reproductive potential of species targeted by fisheries. It explored in detail the effect of the 2004 zoning plan on a representative sample of the reef fish community. It also investigated genetic connectivity of both *Plectropomus* spp. and *L. carponotatus* between inshore island groups separated by over 800km, including (and extending) the study area for the preceding ecological and biological studies of these species.

During the planning stages of the new (2004) zoning plan for the GBRMP, there was limited evidence that MPAs on the GBR had increased abundance of reef fish targeted by fisheries. Chapter 2 provided such evidence from the inshore reefs of the GBR. Underwater visual surveys were used to estimate the effect of MPAs on abundance of species targeted by hookand-line-fisheries around the Palm, Whitsunday and Keppel Islands, spanning 600 km of the length of the GBR. The MPAs in the original zoning plan had been protected for 14-18 years. Densities of *Plectropomus* spp. and *Lutjanus carponotatus*, both targeted by fisheries, were much higher in MPAs than fished areas in two of the three island groups. The biomass of both *Plectropomus* spp. and *L. carponotatus* were significantly greater (3.9 and 2.6 times, respectively) in the MPAs than fished areas at all three island groups. There were significantly

higher densities and biomass of legal-sized *Plectropomus* spp. >35cm Total Length (TL) (density- 3.8 times, biomass- 5.1 times) and legal-sized *L. carponotatus* >25cm TL (density-4.2 times, biomass 5.3 times) in MPAs than fished areas at all three island groups. No significant difference in abundance between MPAs and fished areas was found for two species not captured by line fisheries (*Siganus doliatus* and *Chaetodon aureofasciatus*), and there were no significant differences in benthic characteristics between MPAs and fished areas. Results suggest that no-take marine protected areas have increased biomass of targeted fish species on inshore GBR reefs.

In Chapter 3, the implementation of the new (2004) zoning plan enabled a Before-After-Control-Impact-Pair (BACIP) design to investigate the effects of the MPAs on the major fish groups and benthos on the inshore coral reefs at three island groups of the Great Barrier Reef (Palms, Whitsundays and Keppels). After three years of no-take protection, the new zoning plan had affected the density and biomass only of the major target of the hook-and-line fishery, the coral trout (*Plectropomus* spp.). The density of *Plectropomus* spp. increased from 11.1 to 15 fish 1000m⁻², and the biomass increased from 7.2 to 17.2 kg 1000m⁻² after three years of protection. No other species, fish group, family or trophic group, displayed any significant change over time attributable to the establishment of the no-take marine reserves. Regression analysis demonstrated some temporal changes in a predator-prey relationship that may, in time, indicate a secondary effect of zoning due to the increase of *Plectropomus* spp. density in the no-take areas. Benthic variables, hard coral cover, macro-algal cover and structural complexity were not affected by the rezoning. This study also demonstrated that a reduction in live coral cover due to a coral bleaching event in one region had a larger impact on the fish community structure than the implementation of no-take status.

With evidence that no-take protection increased biomass of *Lutjanus carponotatus* (Chapter 2), Chapter 4 investigated body size to fecundity relationships and examined the potential benefits of increased batch fecundity in MPAs compared to fished areas around the Palm, Whitsunday and Keppel Island Groups, Great Barrier Reef, Australia. *Lutjanus carponotatus* batch fecundity increased with fork length in a non-linear relationship that was best described by a power function. Batch fecundity differed by more than one hundredfold among individuals, with a range from 7,074 to 748,957 eggs in fish ranging from 184 to 305mm fork length. Furthermore, egg diameter increased with fish size. Based on underwater visual census, the potential batch fecundity per unit area in all three island groups ranged from 1.0 to 4.2 times greater in the MPAs than in the fished areas from 2001 - 2004. In 2002, a mean 2.3 fold difference in biomass between MPAs and fished areas converted to a mean 2.5 fold difference in batch fecundity per unit area. Greater batch fecundity, longer spawning seasons and potentially greater larval survival due to larger egg size from bigger individuals may enhance the potential benefits of MPAs on the Great Barrier Reef significantly.

Increased density, biomass and egg production per unit area of the focal species within no-take marine protected areas on inshore reefs of the Great Barrier Reef (GBR) lead to the question: are no-take MPAs connected via larval transport to each other and/or to fished areas? The phylogenetic and population genetic study in this thesis (Chapter 6) is a broad scale analysis of the genetic connectivity of *Plectropomus maculatus* and *Lutjanus carponotatus* within and between inshore islands of the GBR. DNA sequences from the mitochondrial (mt) control region were analysed to determine whether there was any genetic partitioning between populations from four island groups (Palms, Whitsundays, Keppels and Capricorn Bunkers) spanning a latitudinal gradient of approximately 800 km. Tissue samples for part of this study were collected by a new *in situ* biopsy probe (Chapter 5). Analysis of molecular variance (AMOVA) indicated high levels of gene exchange between locations within and between the

island groups. Phylogenetic analysis showed no geographic partitioning but identified two distinct lineages for both species that were distributed throughout the sampled range, suggesting that both *L. carponotatus* and *P. maculatus* were admixtures of differentiated lineages, rather than stable populations. Coalescence analysis showed that *P. maculatus* may be up to four times younger than *L. carponotatus* on the GBR and lineages may be either: i) refugial expansions between glacial maximums during the Holocene and Pleistocene periods; and/or ii) one lineage in each species may represent migrants from outside the GBR. Sampling from further afield will help to answer this question. The study showed that populations of both species within the sampling range were panmictic. Under current conditions they may be managed as a single stock across the sampled range of the GBR. It also showed that the coexistence of two genetically distinct lineages throughout the sampled area increases genetic diversity up to fourfold for both species.

Overall, no-take MPAs on the inshore reefs of the GBR have been effective at increasing density and biomass of two species targeted by fishers, *Plectropomus* spp. and *Lutjanus* carponotatus, and egg production per unit area (*L. carponotatus* only). With current knowledge of larval dispersal and such high levels of gene flow over large expanses from north to south along the GBR, one would expect that there would be some larval export from no-take marine protected areas to fished areas. More detailed larval marking or parentage analysis will be required to demonstrate unequivocal larval links.

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and at two resurveys in 2006 and 2007. Note the different y-axis

in the top	for Pomacentridae in 2004 compare
<0.05; **:	three plots. NS: not significant; (
62	p<0.01; ***: p<001
e) and no-	Figure 3.9: Benthic variables measured in fish
unday and	take protected areas (solid line) o
IP in 2004	Keppel Islands from before the re-z
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