

**Estimating dispersal and population connectivity for
temperate reef fishes at multiple spatial scales**

Thesis submitted by

Belinda G. Curley

BSc (Hons) The University of Sydney, Australia

October 2007

For the degree of Doctor of Philosophy

in Marine Biology

within the School of Marine & Tropical Biology

James Cook University

Statement of Access

I, the undersigned, the author of this thesis, understand that James Cook University will make this thesis available for use within the University Library and, via the Australian Digital Theses network (unless granted an exemption), for use elsewhere.

I understand that, as an unpublished work, a thesis has significant protection under the Copyright Act and;

I do not wish to place any further restriction on access to this work.

October, 2007

Belinda G. Curley

Statement of Sources

Declaration

I declare that this thesis is my own work and has not been submitted in any form for another degree or diploma at any university or other institution of tertiary education. Information derived from the published or unpublished work of others has been acknowledged in the text and a list of references is given.

October, 2007

Belinda G. Curley

Statement on the Contribution of Others and Declaration on Ethics

Drafts of the thesis were revised by Mike Kingsford, Tim Glasby, Michael Gillings, Heather Patterson, and Vanessa Miller-Sims. Development of microsatellite markers and resulting publications (Curley & Gillings 2004, Curley & Gillings 2006) resulted from collaborations with Michael Gillings at Macquarie University who provided technical expertise, support with laboratory work, and assisted with final interpretation and writing up of results.

Financial support during my PhD was provided by an Australian Post-graduate Award, a scholarship from the School of Marine and Tropical Biology, and a James Cook University Doctoral Completion Award. Research was funded by an Internal Research Award (JCU), NSW Fisheries Recreational Fishing Trust Grant (B. G. Curley), James Cook University Merit Research Grant (M. Kingsford), and a Macquarie University Research Development Grant (M. Gillings).

The research presented and reported in this thesis was conducted within the guidelines for research ethics outlined in the *National statement on Ethics Conduct in Research Involving Humans* (1999), the *Joint NHMRC/AVCC Statement and Guidelines on Research Practice* (1997), the *James Cook University Policy on Experimentation Ethics (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 A827).

October, 2007

Belinda G. Curley

Acknowledgements

I would like to thank my supervisors Prof. Mike Kingsford (JCU) and Dr. Bob Creese (NSW, DPI) for guidance and intellectual input throughout my PhD. Special thanks to Mike for supporting my unorthodox approach to completing a temperate PhD in a tropical climate, and for his passion for 'panmictic' populations. A huge thank you to my undercover supervisor Dr. Tim Glasby, for lending his expertise on asymmetrical ANOVAs, experimental design, assistance in the field, and reviewing the MPA Chapter (I owe you a few hundred donuts). Thanks to Prof. Michael Gillings for his friendship, support, enthusiasm, assistance with field work, editing of multiple chapters, and patience in teaching an ecologist the dark magic of molecular biology (eggplants).

To my father, Alan Curley, who assisted in all aspects of field work, undertaking many 'pleasure dives' in the cold, dirty, raging southern seas in the name of science. For your dedication, encouragement, skill with the hack saw, intellectual input, and watching my back particularly on those bad days - thank you - there would be no data without you. Collection of Luderick for genetic analyses and tagging (which unfortunately didn't make it into this thesis) would not have been possible without the assistance of members of NSW recreational fishing clubs and staff at NSW fisheries. Special thanks to: Glen Onysko ('Esky'), Garry Bonnington ('Bonno'), Paul Cooper, Malcolm Poole, Jim from Currarong, Tony from Bass Point, Bob Thompson, Barry Wilson, Simon and co. from the Newcastle Neptunes, Graham Housefield, Simon Hartley, and James Haddy. Thank you to Marjorie Hemmings for collecting data on fishing effort for Toowoomb Bay.

Discussions with Mike Kingsford, Tim Glasby, Michael Gillings, Heather Patterson, Vanessa Miller-Sims, Yi Hu, Lyn Van Herwerden, Dean Jerry, Line Bay and Adam Stowe were valuable in establishing appropriate laboratory and statistical techniques, and/or significantly improving drafts of the thesis. Special thanks to Michael Britt for proof-reading the final product.

Thanks to Vanessa Miller-Sims for reviewing the genetics components, her beautiful singing voice, being my swimming buddy, and her continuing friendship from the northern hemisphere (Hawaii here we come!). I thank Heather Patterson (M.B.) for invaluable comments on multiple drafts of the otolith chemistry chapter and for being my 'disabled' Castle Hill walking partner (BAK, J.B.). To Karin Ulstrup for her general enthusiasm, particularly on those de-stressing walks up the goat track! To Janelle Eagle for

understanding every frustration of the PhD process. Thanks to (Dr) Jillian Keating for continuous support and listening to my many 'raves' (no textas required). To Felicity Smith (Grace, 99, Foxtrot Sierra) for her persistent encouragement and excellent company at Cheyne St and at Uni. This is Bravo Charlie signing out - FINALLY!! Thanks to Kathy Danaher, Peter Said, and Michele Dunscombe for their friendship and support during my time in Townsville.

I would like to thank members of the Kingsford lab for their unique contributions to PhD life: Mark O'Callaghan, Kathy Danaher, Mike Cappo, Felicity Smith, Lisa Gershwin. Thanks to Katie Munkres and Selma Klanten (for housing the homeless). Thanks to all the staff at JCU who provided technical support and encouragement. Special mention must go to Vince and Bailey who rescued me from many computer melt-downs, and Ros Burgess who made my external years so much easier. Thank you to Jodie Wilson and the girls in the TRC for their good humour and support. To my flat mates Ann Penny, Alex Carter, Felicity Smith and the Eyre St gang for their wonderful company and encouragement. Thanks to the 'Emma lab' (Mike, Marita, Paul, Sammy and Joss) at Macquarie University for their friendship, technical assistance with genetics work, and tolerating an ecologist in the lab.

Finally I would like to thank my family. To my father who installed in me a great respect and love for the southern seas and my mother for the strength and determination to follow my heart. To my beautiful sister, Tania, who is always on the end of the line whenever I need her. To my brothers Glen and Darren, and my grandparents (Jim and Dorothy) for their encouragement over this somewhat lengthy process. Finally, to the memory of my pop (Herb), who would have been proud despite the fact that I will be 'just a fish doctor' and we 'are just going to eat them anyway'.

This thesis is dedicated to Michael Britt for his unwavering support, friendship and belief in me over so many years. Thank you Mickey.

'The relentless fury of the Sea
Knows none that it should fear,
A sullen thought is sacrifice
And in its rage will disappear'

MTB

Abstract

Knowledge of scales of dispersal and levels of population connectivity is critical for understanding population dynamics and effective management of reef fishes. These processes are important for effective design of Marine Protected Areas (MPAs) particularly if they are to generate ‘spillover’ and ‘recruitment effects’. Despite this, empirical data across appropriate spatial and temporal scales are limited. This is the first study to focus on dispersal and population connectivity for temperate reef fishes in central NSW, Australia, at scales relevant to the implementation of MPAs (100's m - 100's km). The study provides: (1) empirical data on the localised benefits of small MPAs relative to the mobility of exploited reef fishes; (2) baseline data on the utility of different methods (microsatellite markers and otolith chemistry) for determining levels of population connectivity, and potential scales of benefits of MPAs to unprotected areas. Work on microsatellite markers compared population genetic structure in species which span the post-settlement dispersal potentials of reef fishes in this region, and provides a benchmark for understanding general mechanisms which govern gene flow, and population connectivity, in central NSW.

The response of exploited reef fishes to the establishment of small MPAs ($\leq 0.2 \text{ km}^2$), was investigated relative to knowledge of post-settlement movement. Two established MPAs were surveyed: Cabbage Tree Bay (CTB) a 2.5 year old ‘no-take’ MPA, and Gordon's Bay (GB) a 12.5 year old MPA closed to spear fishing only. Abundances and sizes of four ‘sedentary’ and three ‘mobile’ fishes within each MPA were compared with three control locations at six times over two years. Temporal variation in abundances suggested that MPAs did not encompass the movement of most species, with the exception of two ‘sedentary’ species (*Cheilodactylus fuscus* and *Achoerodus viridis*). However, generalizations could not be made between estimated mobility, duration of protection and MPA response. Densities of legal-sized *C. fuscus* were 2.8-times higher and fish were larger within GB relative to controls. Legal *C. fuscus* were more abundant in shallow areas of GB indicating that spear fishing influences local depth distributions. Surprisingly, mean densities of legal-sized ‘mobile’ *Acanthopagrus australis* were 2.6-times higher in CTB relative to controls, with a similar trend for GB, and for *Girella tricuspidata* in CTB. Response of ‘mobile’ species to protection was indicative of pre-existing differences between MPAs and controls, immigration rather than recruitment of fish, and/or intraspecific variation in movement. The lack of detectable effect for all other species and differential response between MPAs were attributed to mobility relative to the scale of MPAs, inadequate protection of habitats or depths, population recovery time, and partial

protection versus 'no-take' status of MPAs. Overall results emphasise that small MPAs can have significant ecological value, even for highly mobile species. Importantly, as MPAs become smaller their location relative to habitat and depth, local aggregations, recruitment 'hotspots', adjacent habitats, and existing fishing pressure is critical in determining responses and rates of recovery.

Microsatellite markers were developed to provide information on population connectivity at scales ≤ 400 km for reef fishes with low (*Parma microlepis*) and high post-settlement dispersal capabilities (*G. tricuspidata*). It was hypothesized that *P. microlepis* would exhibit spatial genetic structure and a significant pattern of isolation-by-distance (IBD) at these scales, whereas *G. tricuspidata* would not. Genetic differentiation at seven microsatellite loci in *P. microlepis*, and six loci in *G. tricuspidata* were examined across multiple spatial scales. *P. microlepis* was collected from; sites (separated by 1-2 km), nested within locations (separated by 10-50 km), nested within three regions (separated by 70-80 km). *G. tricuspidata* were collected from a subset of the locations sampled for *P. microlepis*. This included five locations (separated by 50-60 km) spanning three sampling regions (separated by 70-100 km). There was no evidence that post-settlement dispersal capabilities influenced genetic structure. Broad-scale genetic homogeneity and lack of IBD was well supported for both species. The proportion of the total genetic variation attributable to differences among sampling regions, locations or sites was effectively zero (e.g. $\Phi_{PT} \leq 0.003$ and $R_{ST} \leq 0.004$). The geographic distribution of genetic diversity and the high polymorphism (*P. microlepis*, H_E 0.21-0.95; *G. tricuspidata*, H_E 0.65-0.97) was indicative of high mutation rates, large effective population sizes, and high rates of gene flow. Genetic homogeneity for fishes and invertebrates in central NSW suggests that gene flow important to genetic structure is driven by factors influencing pre-settlement dispersal such as the East Australian Current (EAC) and habitat continuity. Thus, genetic homogeneity is likely in other exploited reef fishes in this region which have similar pre-settlement durations (≥ 2 weeks). Scales of genetic homogeneity may not reflect demographically relevant dispersal distances. However, it does imply that populations of *P. microlepis* and *G. tricuspidata* are well connected from an evolutionary perspective and have large effective population sizes. This reduces the genetic risks associated with natural or anthropogenic declines in local populations. Furthermore, genetic diversity across spatial scales ≤ 400 km could be conserved within small MPAs as 99-100% of the total genetic variation for both species was represented within 1-2 km of reef. Future studies using genetics to determine population connectivity of reef fishes in central NSW should focus on species with very low

dispersal capabilities, small population sizes, short life spans, and whose habitats are rare or patchily distributed along-shore.

The use of otolith chemistry as a natural tag requires the presence of differences in the aquatic environment that translate into differences in otolith chemistry. Consequently, most studies focus on populations distributed across large environmental gradients and spatial scales. This study examined spatial variation in otolith chemistry of the territorial damselfish *P. microlepis* at fine spatial scales in an exclusively marine environment. Solution-based inductively coupled plasma-mass spectrometry was used to measure the integrated otolith chemistry of individual fish, reflective of average environmental differences among regions (separated by 70-80 km), locations within regions (separated by 10-50 km), and between sites within locations (separated by 1-2 km). Mean concentrations of Sr/Ca, Ba/Ca, Mg/Ca, Mn/Ca, Cu/Ca, and Zn/Ca and multi-element signatures varied among regions, locations and sites. Fine scale differences accounted for the majority of the variability in the data and there was a trend for unique chemistries at some sites and locations. Multi-element signatures were good spatial discriminators, with 75-80% of fish correctly classified to the regions in which they were collected. It was difficult to establish simple causal relationships for variation in individual elements. However, regional multi-element signatures were highly correlated with the behaviour of the EAC which delivers water masses varying in chemistry, temperature and salinity to the different regions. Results demonstrate that the magnitude of environmental variability within open coastal regions such as central NSW facilitates the use of otolith chemistry for determining population connectivity of reef fishes at scales < 100's km.

The thesis provides clear implications for management of reef fishes in central NSW, testable hypotheses, and priorities for future research. Overall results demonstrate the ecological value of small MPAs for protecting reef fishes of varying mobility, as well as population genetic diversity representative of broader-spatial scales. The determination of scales of 'spillover' of eggs, larvae and adults remains the greatest challenge. This study suggests that levels of gene flow will limit the utility of microsatellite markers for providing information on population connectivity for most reef fishes in central NSW. Given this, a combination of otolith chemistry, artificial tags, and modelling are the most promising techniques for future studies. Such studies should focus on species which demonstrated localised responses to MPA (e.g. *C. fuscus*, *G. tricuspidata*, and *A. australis*).

Table of Contents

Acknowledgements.....	i
Abstract.....	iii
Table of Contents.....	vi
List of Tables.....	viii
List of Figures.....	x
Chapter 1: General Introduction	1
1.1. Introduction.....	1
1.2. Management of reef fishes using Marine Protected Areas.....	1
1.3. Dispersal and population connectivity of reef fishes.....	2
1.4. Methods for measuring dispersal and population connectivity.....	4
1.4.1. Artificial Tags.....	5
1.4.2. Spatial and temporal variation in abundance.....	6
1.4.3. Otolith chemistry	7
1.4.4. Genetic Markers.....	8
1.5. Outline of thesis.....	10
Chapter 2: Movement of exploited temperate reef fishes and their response to small Marine Protected Areas	16
2.1. Introduction.....	16
2.2. Methods	18
2.2.1. Study areas and experimental design.....	18
2.2.2. Data analysis	21
2.3. Results.....	23
2.3.1. Temporal variation in legal and large fishes.....	23
2.3.2. Cabbage Tree Bay (MPA1)	23
2.3.3. Gordon's Bay (MPA2)	24
2.3.4. Spatial and temporal variation in sub-legal and small fishes.....	25
2.3.5. Variation in abundance of fishes among control locations, sites (with locations) and depths	26
2.3.6. Spatial variation of habitats	27
2.4. Discussion.....	45
2.4.1. Conclusion	50
Chapter 3: Along-shore variation in otolith chemistry of the temperate damselfish <i>Parma microlepis</i>	52
3.1. Introduction.....	52
3.2. Methods	54
3.2.1. Sample collection and age determination	54
3.2.2. Sample preparation and analysis.....	55
3.2.3. Statistical analyses	56
3.3. Results.....	58
3.4. Discussion.....	68
3.4.1. Conclusion	73
Chapter 4: Population connectivity in the temperate damselfish <i>Parma microlepis</i> : analyses of genetic structure across multiple spatial scales.....	74
4.1 Introduction.....	74
4.2. Methods	77
4.2.1. Sampling design and genetic analyses.....	77
4.2.2. Statistical analyses	78

4.3. Results.....	80
4.4. Discussion.....	91
4.4.1. Conclusions.....	96
Chapter 5: Population connectivity in the highly dispersive temperate fish <i>Girella tricuspidata</i> : analyses of population genetic structure	97
5.1. Introduction.....	97
5.2. Methods	99
5.2.1. Sampling design and genetic analyses.....	99
5.2.2. Statistical analyses	100
5.3. Results.....	102
5.4. Discussion.....	111
5.4.1. Conclusion	116
Chapter 6: Key findings, implications and future research	118
6.1. Marine Protected Areas	118
6.1.1. Is there a correlation between mobility and response to protection?.....	118
6.1.2. Other important factors for determining responses to protection.....	119
6.1.3. Conclusions on the benefits of small MPAs for protecting reef fishes	123
6.2. Population Genetics	124
6.2.1. Population genetic structure for fishes with varying dispersal potential at scales ≤ 400 km.....	124
6.2.2. Major factors contributing to genetic homogeneity in central NSW.....	126
6.2.3. What can genetics tell us about population connectivity for <i>P. microlepis</i> and <i>G. tricuspidata</i> ?	127
6.2.4. Implications of genetic homogeneity for management and MPAs.....	128
6.3. Otolith chemistry	129
6.3.1. Is there enough environmental variability at spatial scales < 100 's km to facilitate use of otolith chemistry in central NSW?.....	129
6.3.2. Applications of otolith chemistry to determine levels of dispersal and population connectivity.....	130
6.4. Concluding remarks.....	132
References.....	133
Appendix A: Marine Protected Areas.....	149
Appendix B: GPS Co-ordinates.....	173
Appendix C: Population Genetics <i>P. microlepis</i>	174
Appendix D: Population Genetics <i>G. tricuspidata</i>	181

List of Tables

Table 1.1. Summary of dispersal capabilities of common temperate reef fishes in NSW based on empirical data and anecdotal information.....	13
Table 2.1. Description of scales of movement and methods used to harvest reef fishes used in this study.....	28
Table 2.2. Description of subtidal habitat categories and the depth ranges over which they were recorded.....	30
Table 2.3. Example of complete asymmetrical ANOVA comparing the abundance of <i>C. fuscus</i> at two MPAs and three control locations	31
Table 2.4. Significance of <i>F</i> -ratios for most relevant levels of ANOVA for all species.	32
Table 2.5. Semi-parametric permutational ANOVA comparing habitat assemblages among locations and depths for sampling times 2-6.....	33
Table 2.6. Habitat types contributing to greater than 15% of the average dissimilarity between depths at each sampling time 2-6	33
Table 3.1. ANOVA comparing elemental ratios in the otoliths of <i>P. microlepis</i>	60
Table 3.2. Percentage of variation attributed to each factor in ANOVA performed on untransformed data (a) Comparison among two regions and (b) Comparison among three regions.....	61
Table 3.3. PERMANOVA for comparison of multi-element signatures (Sr, Ba, Mg, Mn, Cu, Zn ratioed to Ca) among regions, locations and sites.....	61
Table 3.4. Number of <i>P. microlepis</i> correctly classified to the region in which they were collected using jackknife cross-validation procedure based on quadratic DFA of multi-element signatures.....	62
Table 4.1. Summary statistics for seven microsatellite loci in <i>P. microlepis</i> collected at 11 locations in central NSW, Australia. Shown are sample sizes (<i>n</i>), the number of alleles (<i>A</i>), allele size range (bp) and the observed and expected heterozygosities (<i>H_O</i> and <i>H_E</i>) for individual locations and all samples combined.....	82
Table 4.2. Allelic and genotypic differentiation at seven microsatellite loci in <i>P. microlepis</i> collected from 11 locations.	84
Table 4.3. Pairwise comparisons of allelic and genotypic differentiation for locus PM1E12 in <i>P. microlepis</i> collected from 11 locations.	84
Table 4.4. AMOVA showing partitioning of genotypic (Φ -statistics) and size-based (<i>R</i> -statistics) variation across regions (separated by 70-80 km), locations (separated by 10-50 km) and sites (separated by 1-2 km). (a) Without regional partitioning of data, <i>n</i> =16; (b) data partitioned into three regions (Port Stephens, Sydney and Jervis Bay), sites pooled <i>n</i> =32.....	85
Table 5.1. Summary statistics for six microsatellite loci in <i>G. tricuspidata</i> collected at five locations in central NSW, Australia. Shown are sample sizes (<i>n</i>), the number of alleles (<i>A</i>), allele size range (bp) and the observed and expected heterozygosities (<i>H_O</i> and <i>H_E</i>) for individual locations and all samples combined.....	105
Table 5.2. Allelic and genotypic differentiation at six microsatellite loci in <i>G. tricuspidata</i> collected from five locations.	106
Table 5.3. Pairwise comparisons of genotypic differentiation for locus GT2A10 in <i>G. tricuspidata</i> collected from five locations.	106
Table 5.4. AMOVA showing partitioning of genotypic (Φ -statistics) and size-based (<i>R</i> -statistics) variation across different spatial scales: (a) among locations (separated by 50-60 km); (b) among regions (separated by 70-100 km, locations pooled).	

Φ_{PT}/R_{ST} = the fraction of all the variation that distinguishes locations or regions..	107
Table A.1. Asymmetrical ANOVA comparing the abundance of <i>A. viridis</i> at two MPAs (CTB, Cabbage Tree Bay; GB, Gordon's Bay) and three control locations.	149
Table A.2. Asymmetrical ANOVA comparing the abundance of Monacanthidae at two MPAs (CTB, Cabbage Tree Bay; GB, Gordon's Bay) and three control locations.	150
Table A.3. Asymmetrical ANOVA comparing the abundance of <i>G. elevata</i> at two MPAs (CTB, Cabbage Tree Bay; GB, Gordon's Bay) and three control locations.	151
Table A.4. Asymmetrical ANOVA comparing the abundance of <i>G. tricuspidata</i> and <i>A. australis</i> at two MPAs (CTB, Cabbage Tree Bay; GB, Gordon's Bay) and three control locations.	152
Table A.5. Asymmetrical ANOVA comparing the abundance of <i>K. sydneyanus</i> at two MPAs (CTB, Cabbage Tree Bay; GB, Gordon's Bay) and three control locations.	153
Table B. 1. GPS co-ordinates for collection sites given in Fig. 3.1 and Fig. 4.1.	173

List of Figures

Fig. 1.1. Temperate reef fishes used to test hypotheses in thesis. 'Sedentary' species: a) <i>Parma microlepis</i> , b) <i>Achoerodus viridis</i> , c) <i>Cheilodactylus fuscus</i> , d) Monacanthidae (e.g. <i>Meuschenia trachylepis</i>), e) <i>Girella elevata</i> . 'Mobile' species: f) <i>Kyphosus sydneyanus</i> , g) Sparidae (e.g. <i>Acanthopagrus australis</i>), h) <i>Girella tricuspidata</i> .	12
Fig. 2.1. (a) Sydney region of NSW, Australia showing position of two Marine Protected Areas (MPAs) (Gordon's Bay and Cabbage Tree Bay) and three control locations (Toowoan Bay, Terrigal and Long Bay). (b) Sampling design used to estimate abundance of fishes at MPA and control locations.	34
Fig. 2.2. Mean abundance (+ SE) of legal <i>C. fuscus</i> (≥ 200 mm standard length) in shallow and deep areas of reef in MPA and control locations at six sampling times.	35
Fig. 2.3. Mean abundance (+ SE) of large <i>A. viridis</i> (≥ 200 mm standard length) in shallow and deep areas of reef in MPA and control locations at six sampling times.	36
Fig. 2.4. Mean abundance (+ SE) of large Monacanthidae (≥ 200 mm standard length) in shallow and deep areas of reef in MPA and control locations at six sampling times.	37
Fig. 2.5. Mean abundance (+ SE) of legal <i>G. elevata</i> (≥ 250 mm standard length) in shallow and deep areas of reef in MPA and control locations at six sampling times.	38
Fig. 2.6. Mean abundance (+ SE) of legal <i>G. tricuspidata</i> (≥ 200 mm standard length) in shallow and deep areas of reef in MPA and control locations at six sampling times.	39
Fig. 2.7. Mean abundance (+ SE) of legal <i>A. australis</i> (≥ 200 mm standard length) in shallow and deep areas of reef in MPA and control locations at six sampling times.	40
Fig. 2.8. Mean abundance (+ SE) of large <i>K. sydneyanus</i> (≥ 200 mm standard length) in shallow and deep areas of reef in MPA and control locations at six sampling times.	41
Fig. 2.9. Size frequency for exploited reef fishes at MPA and control locations for six sampling times pooled. <i>F</i> -ratios from ANOVA comparing mean size of fish among locations are given below each species name.	42
Fig. 2.10. Non-metric MDS ordinations comparing the composition and relative percentage of habitat types in (a) MPA (Cabbage Tree Bay (CTB), Gordon's Bay (GB)) and control locations (Toowoan Bay (TB), Terrigal (TER), Long Bay (LB)), and (b) shallow and deep areas of reef.	44
Fig. 2.11. Mean percentage occurrence (+ SE) of six habitat types in shallow (0 - 3.5 m) and deep (4 - 12 m) areas of reef.	44
Fig. 3.1. The central coast of NSW, Australia, showing three sampling regions: Port Stephens, Sydney and Jervis Bay. Within each region, the locations (1-4) and sites (within locations) at which <i>P. microlepis</i> were collected are shown.	63
Fig. 3.2. Mean standard length and age (\pm SE) of <i>P. microlepis</i> at each of two sites within locations, across three sampling regions: Port Stephens, Sydney and Jervis Bay	64
Fig. 3.3. Sr/Ca concentrations versus otolith weight for (a) raw and (b) de-trended data. An example of how the effect of otolith weight (used as a proxy for age and fish	

length) was removed by subtracting the slope of the regression relationship multiplied by otolith weight from the elemental data.....	65
Fig. 3.4. Mean elemental concentrations (\pm SE) in <i>P. microlepis</i> collected from each of two sites (separated by 1-2 km) within locations (separated by 10-50 km) across three regions: Port Stephens, Sydney and Jervis Bay (separated by 70-80 m).....	66
Fig. 3.5. Canonical variate plot summarising variation in otolith multi-element signatures for <i>P. microlepis</i> among three regions Port Stephens, Sydney, Jervis Bay and locations within regions. Standardized discriminant function coefficients are shown on secondary axes.....	67
Fig. 4.1. Geographic distribution of <i>P. microlepis</i> in Australia including three sampling regions in central NSW: Port Stephens, Sydney and Jervis Bay. Within each region, the locations (1-4) and sites (within locations) at which fish were collected are shown.	86
Fig. 4.2. The relationship between locus polymorphism and the magnitude of genetic differentiation detected in <i>P. microlepis</i>	87
Fig. 4.3. The relationship between geographic distance (km) and genetic distance (Pairwise R_{ST} / Φ_{ST}) for <i>P. microlepis</i> collected from 11 locations.....	88
Fig. 4.4. Spatial autocorrelation analyses (a) within each region: Port Stephens (PS), Sydney (Syd) and Jervis Bay (JB), and (b) across all regions.....	89
Fig. 4.5. Principal coordinates analyses of multi-locus genotypes of <i>P. microlepis</i> collected from three regions in NSW. Port Stephens, Sydney, Jervis Bay.....	90
Fig. 5.1. Geographic distribution of <i>G. tricuspidata</i> in Australia, and three sampling regions in central NSW (Port Stephens, Sydney and Jervis Bay). Sampling locations within each region are shown.....	108
Fig. 5.2. The relationship between geographic distance (km) and genetic distance (pairwise Φ_{ST} or R_{ST}) for <i>G. tricuspidata</i> collected from five locations.....	109
Fig. 5.3. Spatial autocorrelation analyses of genotypic distances in <i>G. tricuspidata</i> across a range of geographical distance classes.....	109
Fig. 5.4. Principal coordinates analyses of multi-locus genotypes of <i>G. tricuspidata</i> collected from five locations within three regions in central NSW. Port Stephens, Sydney, Jervis Bay.....	110
Fig. A.1. Size frequency of <i>C. fuscus</i> at MPA and control locations for six sampling times.....	154
Fig. A.2. Size frequency of <i>A. viridis</i> at MPA and control locations for six sampling times.....	156
Fig. A.3. Size frequency of Monacanthidae at MPA and control locations for six sampling times.	158
Fig. A.4. Size frequency of <i>G. elevata</i> at MPA and control locations for six sampling times.....	160
Fig. A.5. Size frequency of <i>G. tricuspidata</i> at MPA and control locations for six sampling times.	162
Fig. A.6. Size frequency of <i>A. australis</i> at MPA and control locations for six sampling times.....	164
Fig. A.7. Size frequency of <i>K. sydneyanus</i> at MPA and control locations for six sampling times.	166
Fig. A.8. Mean abundance (+ SE) of sub-legal <i>C. fuscus</i> (100-150 mm standard length) in shallow and deep areas of reef in MPA and control locations at six sampling time.	168

Fig. A.9. Mean abundance (+ SE) of small <i>A. viridis</i> (≤ 150 mm standard length) in shallow and deep areas of reef in MPA and control locations at six sampling times.	169
Fig. A.10. Mean abundance (+ SE) of small Monacanthidae (≤ 150 mm standard length) in shallow and deep areas of reef in MPA and control locations at six sampling times.	170
Fig. A.11. Mean abundance (+ SE) of sub-legal <i>G. elevata</i> (≤ 200 mm standard length) in shallow and deep areas of reef in MPA and control locations at six sampling times.	171
Fig. A.12. Mean abundance (+ SE) of small <i>K. sydneyanus</i> (≤ 150 mm standard length) in shallow and deep areas of reef in MPA and control locations at six sampling times.	172
Fig. C.1. Allele frequency distributions for seven microsatellite loci in <i>P. microlepis</i> collected from 21 sites in central NSW Australia.	177
Fig. C.2. Allele frequency distributions for locus PM1E12 in <i>P. microlepis</i> at each of 11 locations in central NSW Australia.	179
Fig. D.1. Allele frequency distributions for six microsatellite loci in <i>G. tricuspidata</i> collected from five locations in central NSW Australia.	184