The population genetic structure of coral reef fishes on the Great Barrier Reef.

PhD thesis submitted by
Line Kolind Bay
(B. Sc. Hons.)
November 2005

For the degree of Doctor of Philosophy
School of Marine Biology and Aquaculture
School of Tropical Biology
James Cook University
Townsville, Queensland
Australia

Statement of access

I, the undersigned, author of this work, understand that James Cook University will make this thesis available for use within the University Library, via the Australian Theses Network, or by other means allow access to users in other approved libraries. I understand that as an unpublished work, a thesis has significant protection under the Copyright Act and;

All users consulting this thesis will have to sign the following statement:

“In consulting this thesis, I agree not to copy or closely paraphrase it partly or in whole without the written consent of the author; and to make proper public written acknowledgement for any assistance, which I have obtained from it”.

Beyond this, I do not wish to place any restriction on access to this thesis.

(Signature) (Date)

Statement of sources

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 Information derived from the published or unpublished work of others has been duly acknowledged in the text and a list of references is given.

(Signature)　　　　(Date)

Statement of contribution of others

All data chapters of this thesis include collaborative work with my supervisors Prof. Ross H. Crozier and Dr. M. Julian Caley. Chapter 3 is a collaboration with Monica Gagliano and Karin Buechler. While undertaking these collaborations I was responsible for the project concept and design, the collection of the majority of samples, the laboratory work, analysis, synthesis and preparation of manuscripts for submission to peer reviewed journals. Karin Buechler provided the samples used in Chapter 3 and Karin Buechler, Monica Gagliano, Shilo Ludke and undertook the laboratory work for this chapter.

I obtained financial support from James Cook University, Australian Museum, Australian Coral Reef Society, CRC Reef, PADI Aware and GBRMPA. My supervisors also assisted with funds obtained from ARC (RHC, MJC), James Cook University (RHC), Hermon Slade Foundation (MJC) and the estate of W. V. Scott (MJC).

Acknowledgements

I thank the many people who helped me conduct and complete the research in this thesis. In particular, I express my gratitude to:

- My supervisors and mentors, Julian Caley and Ross Crozier for their ongoing support, encouragement and advice. Thank you for sharing your vast scientific knowledge and experience with me. The quality and quantity of your supervision has been beyond expectation and I am grateful for everything.
- The organisations that provided financial assistance: James Cook University, Australian Museum, Australian Coral Reef Society, CRC Reef, PADI Aware, GBRMPA and grants awarded to my supervisors.
- The numerous volunteers and research station staff who helped me conduct the fieldwork for this thesis. Thanks to Lyle, Anne, Marianne, Lance, Bob, Tania, Matt, Ali and the crew of the MV Escape for your logistic and technical help in the field. Many thanks to volunteers for your time, enthusiasm and endurance during field collections: Lewis Anderson, Charlotte Berkstrom, Julian Caley, Martial Depczynski, Ashley Frisch, Monica Gagliano, Jeremy Goldberg, JP Hobbs, Karin Kassahn, Ailsa Kerswell, Nicolai Konow, Rhona, Ewen, Kalle and Tasman McPhee, Bryan Murphy, Laura Nagel, Maria Rodrigues and Graham Teakle.
- Michael Kingsford and Karin Buechler for samples and Lynne van Herwerden for sequences.
- Ainsley Calladine, Howard Choat, Lynne van Herwerden, Dean Jerry, Geoff Jones, Madeleine van Oppen, Michelle Waycott and Lynn Woodward, everyone in the Crozier lab and especially Ching Crozier, fellow postgraduate students at JCU, in particular Karin Buechler, Dani Ceccarelli, Martial Depczynski, Janelle Eagle, Chris Fulton, Monica Gagliano, Bridget Green, Selma Klanten, Nicolai Konow, Cathie Page and Renae Tobin for general discussion, advice and support.
- Finally I thank my three lovely boys Ewen, Kalle and Tasman for their love and support. I am grateful for your patience and encouragement while sailing in rough seas, the doldrums and smooth waters. This thesis is as much your achievement, as it is mine.

General Abstract

The population genetic structure of species may be determined by complex interactions among many ecological, evolutionary and genetic processes. I investigated the population genetic structure of coral reef fishes on the Great Barrier Reef (GBR), Australia to better understand how these various processes may interact in a natural system. I firstly examined the spatial genetic structure of a low dispersal species to determine if its genetic structure varied among spatial scales and among regions located in the centre and on the periphery of its distributional range. I then examined the population genetic structure of species with different dispersal potentials and among species sampled at central and peripheral locations in their species range.

Using mtDNA control region sequences and three microsatellite loci, I examined the spatial genetic structure of a direct developing coral reef fish, *Acanthochromis polyacanthus,* with comparatively low dispersal rates. The spatial genetic structure of this species was scale-dependent with evidence of isolation-by-distance among regions, but not within regions. Very strong genetic structure was detected among reefs within regions consistent with a metapopulation model. Pairwise genetic distances increased from offshore and older populations, to inshore and younger ones, supporting a metapopulation propagule-pool model of colonisation. Genetic diversities, mismatch, and coalescence analyses all identified large variation in the demographic history of this species among populations and regions. Evidence of genetic bottlenecks was detected by mismatch analysis in the majority of populations sampled, but in most populations these bottlenecks appeared to be older since genetic diversities and coalescence based population growth estimates did not indicate recent genetic bottlenecks. In contrast, three populations displayed low genetic diversities and large population growth rates indicating a more recent genetic bottleneck. Reductions in genetic diversities of local populations resulted in overall lower genetic diversity and a higher regional expansion rate in the southern region located towards the distributional margin of this species. In all, these results suggest that *A. polyacanthus* exists as a metapopulation within regions on the GBR and that metapopulation dynamics may differ among regions located in the centre and on the periphery of this species.

The pelagic larval duration (PLD) can both affect and record the ecology and evolution of coral reef fishes and emerging evidence suggests that this trait displays

considerable intraspecific variation. Here I present new estimates of PLD for ten species of Pomacentridae and two species of Gobiidae, and coupled with previously published estimates, examine spatial and temporal variation of PLDs within and among these species. In eight of the twelve species examined here, within-population mean PLDs differed between sampling times, locations within regions, and among regions. In contrast, the range of these same PLD estimates overlapped at all spatial and temporal scales examined in eleven of the twelve species, but not between regions in one species (*Amphiprion melanopus*). Therefore, despite tight error estimates typically associated with estimates of PLD taken from a particular population at a particular time in some taxa, the overlapping ranges in PLD reported here indicate that the length of the pelagic larval phase is a much more plastic trait than previously appreciated.

Pelagic larval duration (PLD) is a commonly used proxy for dispersal potential in coral reef fishes. Here I examine the relationship between PLD, genetic structure and genetic variability in coral reef fishes from one family (Pomacentridae) that differ in mean larval duration by more than a month. Genetic structure was estimated in eight species using a mitochondrial molecular marker (control region) and in a sub-set of five species using nuclear molecular markers (ISSRs). Estimates of genetic differentiation were similar among species with pelagic larvae, but differed between molecular markers. The mtDNA indicated no structure while the ISSR indicated some structure between the sampling locations. I detected a relationship between PLD and genetic structure using both markers. These relationships, however, were caused by a single species, *Acanthochromis polyacanthus*, which differs from all the other species examined here in lacking a larval phase. With this species excluded, there was no relationship between PLD and genetic structure using either marker. Genetic diversities were generally high in all species and did not differ significantly among species and locations. Nucleotide diversity and total heterozygosity were negatively related to maximum PLD, but again, these relationships were caused by *A. polyacanthus* and disappeared when this species was excluded from these analyses. These genetic patterns are consistent with moderate gene flow among well-connected locations and indicate that at this phylogenetic level (i.e., within family) the duration of the pelagic larval phase is not the primary factor affecting patterns of genetic differentiation.

Using mtDNA (control region) and nuclear (ISSR) markers, I investigated the population genetic structure of three congeneric species pairs of pomacentrid coral reef fishes (Pomacentridae) in the context of species' borders theory. This theory predicts

that population located on the periphery of the species' range should be smaller and more fragmented and hence, display stronger genetic structure and lower genetic diversities compared to more centrally located populations. Each species pair consisted of one species sampled at two central locations within its geographic range, and another species sampled at the same locations but which constituted one location toward the centre of its range and another close to its edge. Contrary to expectations from theory, I did not find the predicted border effects in the population genetic structure of the species examined. Gene flow estimates did not differ among central and peripheral species. Genetic diversities were not lower in peripheral populations compared to central populations or in species sampled towards the periphery compared to those sampled in the centre of their ranges. Indeed, genetic diversities were much greater in the peripheral species compared to their central counterparts. The distribution of genetic variation indicated that secondary contact among differentiated lineages may, in part, be responsible for the high genetic diversity in these peripheral species. Elevated mutation rates mediated by environmental stress on the species' margin may have contributed further genetic variability in these species.

Table of Contents

List of Tables:

Chapter 2:

Chapter 3:

Chapter 5:

Chapter 6:

List of Figures:

Chapter 2:

Chapter 3:

Chapter 4:

Chapter 5:

Chapter 3: